



**Theranostics of the Brain:
An Integrated Approach of Imaging Targeting Nanoemulsions for
Pharmacodynamic Analysis of Glioblastoma and Other Brain
Diseases**

A Major Qualifying Project Report submitted to the faculty of
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Abstract

Glioblastoma is a heterogeneous disease such that the receptors expressed vary based on tumor location. Working with Nemucore Medical Innovations, Inc., theranostic nanoemulsions were designed and manufactured to combat Glioblastoma and other brain diseases. Engineered targeting ligands incorporated in the nanoemulsions assisted in delivery to specific regions. Magnetic Resonance Imaging determined the bio-distribution in healthy rats across the Blood-Brain Barrier. Statistical analysis was completed with T1 MRI data for 174 defined regions. A 3-dimensional heat map program was created to integrate MRI imaging and statistical analysis. In conclusion, data demonstrates targeting ligands on the nanoemulsions alter pharmacodynamics in rat brains, shown by a fully integrated imaging system.

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Executive Summary

I. Introduction

A. Glioblastoma

Glioblastoma Multiforme (GBM) is the most aggressive malignant brain tumor found in adults (Angihotri *et al.*, 2013). Annually, there are 18,000 newly diagnosed cases of GBM in the United States; of these new cases, less than 10% of the patients survive longer than five years (Tutt, 2011). Glioblastoma characteristics vary, in part due to the region of the tumor, giving rise to a need for targeted therapy based on lobe location. A theranostic treatment, combining both therapeutics and diagnostics into one modality, has the potential to solve this need (Kealar and Reineke, 2011).

B. Current Gold Standard

The current gold standard for treatment involves obtaining images with gadolinium-enhanced MRI and using these images for radiation therapy (Hou *et. Al.*, 2006). Temozolomide, a chemotherapeutic agent, is administered to the patient along with radiation therapy after a debulking surgery. Treatment analysis is completed on MRI machine software, which does not contain the capability to visually connect the statistical analysis with a visual interface.

C. Applications to Other Neurological Diseases

Other diseases of the brain have had receptors identified based on the location or function of the affected cells. Alzheimer's has been investigated with rivastigmine as a treatment, but this molecule is unable to pass through the BBB (Wilson *et. al.*, 2008); however, when combined with a targeted drug delivery system, the amount of drug able to reach the correct location would be much higher and may result in an improved therapeutic system. Other pathologies that this

method shows promise for include Parkinson's and Post Traumatic Stress Disorder (PTSD) (Olanow *et. al.*, 2006; Bremner *et. al.*, 2000).

II. Methods

A. Nanoemulsions

This project was built upon past research Nemucore Medical Innovations had completed on the NE drug delivery system (Ganta *et al.*, 2014a; Ganta *et. al.* 2014b; Ganta *et. al.*, 2015). NEs were targeted towards penetrating vasculature and glioblastoma cells by conjugating dermorphin, candoxin, or cereport to the NE surfaces. Receptors targeted were μ -opioid, α -7 nicotinic acetylcholine (nACh), and B2-Bradykinin receptors, respectively. NEs incorporated chelated gadolinium to allow for visualization with MRI. Upon manufacturing, characterization of NE stability was performed over a time period of 21 days. Size, polydispersity index, and zeta-potential were measured using a Malvern SV90. NEs manufactured were stored at 4°C and used for *in vivo* testing.

B. In Vivo Testing

MRI scans were performed using healthy rats anesthetized with isoflurane administered continuously by a nose cone. NE's were delivered systemically through a catheter in the tail vein, and cohorts (n=7) were run for non-targeted NE, as well as the three targets as identified above. Additional testing (n=5) was completed with a pretreatment of β -fulantrexamine, a μ -opioid receptor antagonist (Martin *et. al.*, 2008; Honore *et. al.*, 1996), and dermorphin NEs to confirm μ -opioid receptor targeting. Scans collected for each rat included a pre-scan, and scans at the 20, 40, and 60 minute time points.

C. 3D Statistical Heat Map

Currently, no software programs allow for drug distribution visualization with the 174 defined regions of a rat brain. By using Northeastern University's Rat Brain Atlas, an imaging analysis program was created. MRI data was analyzed with statistical means and displayed in 3D for visual analysis.

Statistical analysis was completed using a custom Matlab program. Initial T1 signal values were assigned to each of the 174 ROIs, with each region having a varying voxel size based on the rat scanned. Normalization of scans with the pre-scan of each rat for T1 weighted means followed. Specificity Index (SPI) values were calculated to determine targeted NE accumulation per ROI based on gadolinium concentration as compared to non-targeted NEs.

Visualization for the level of expression was completed through the development of a custom Matlab program. The visualization program takes in the SPI values for each of the 174 ROIs and determines the 75th, 80th, 85th, 90th and 95th percentile cutoffs for the dataset. It then uses these cutoffs to assign color to the defined space(s) representing each region in the imaged 3D brain or brain slice heat map. The 174 regions were defined as areas on 63 slices, each representing a slice of the rat brain with a thickness of 400 μm . The visualization program was produced so that users have the ability to produce imaged slices individually, or all at once, for the visualization of the determined uptake across the entire brain.

III. Results and Discussion

A. Nanoemulsions

Stability of the NEs was defined as: no significant change in the properties of the NEs occurred over the period of time measured. While small fluctuations did occur, these values are within ranges of similar NEs and do not affect the quality of the NEs or the tests completed with them [8-10]. Table 1 shows a representative 21-day stability testing table for a batch of dermorphin NEs.

Table 1: Dermorphin Stability Testing Results

Dermorphin NE	Day 0	Day 7	Day 14	Day 21
Size (nm)	150	153	153	149
Polydispersity Index	0.061	0.108	0.073	0.095
Zeta Potential (mV)	-41±11	-44±13	-43±10	-43±9

B. 3D Statistical Heat Map

Processing of *in vivo* data using custom data processing and visualization programs resulted in a collection of heat-mapped slices of the rat brain. Using these heat maps the accumulation of NE in specific areas of the brain can be seen for different targeting ligands and compared to areas expressing the respective receptors. Figure 1 shows a sample of maps for different brain slices with various receptors and their corresponding heat maps at different time points. The dermorphin NE shows accumulation in the basal ganglia and hypothalamus, the candoxin NE shows accumulation in the cerebrum, and the cereport NE shows accumulation in the entorhinal cortex.

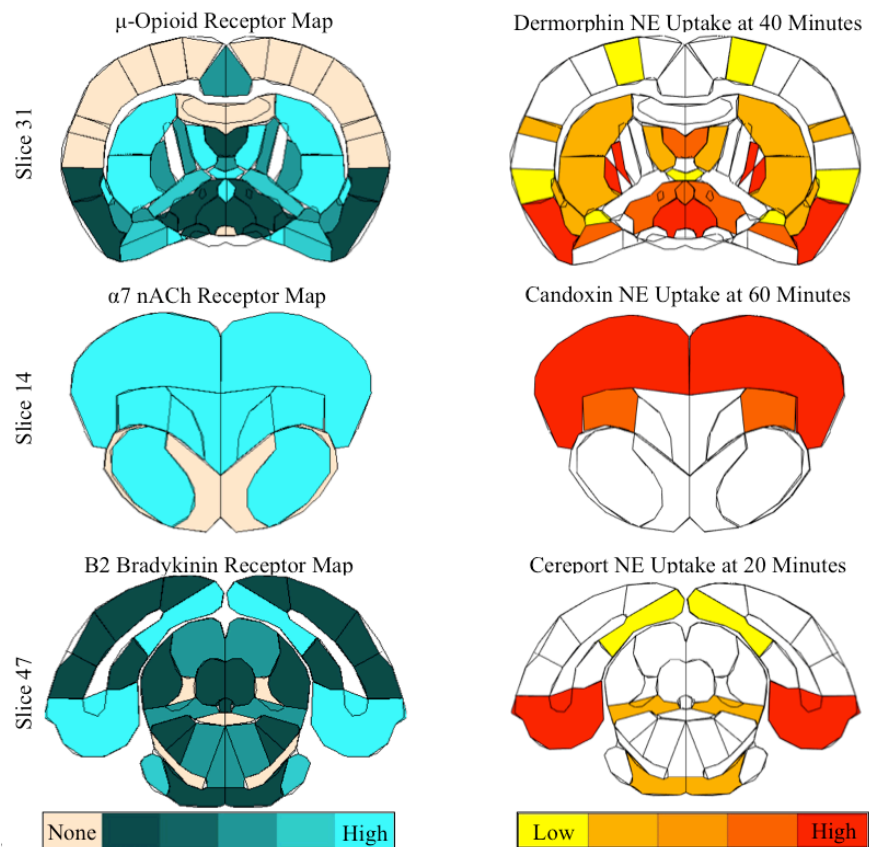


Figure 1: Sample brain slices demonstrating targeted nanoemulsion uptake for different receptors at varying time points

When all the slices are put together, a full 3D heat map is created. An example of this can be seen in Figure 2.

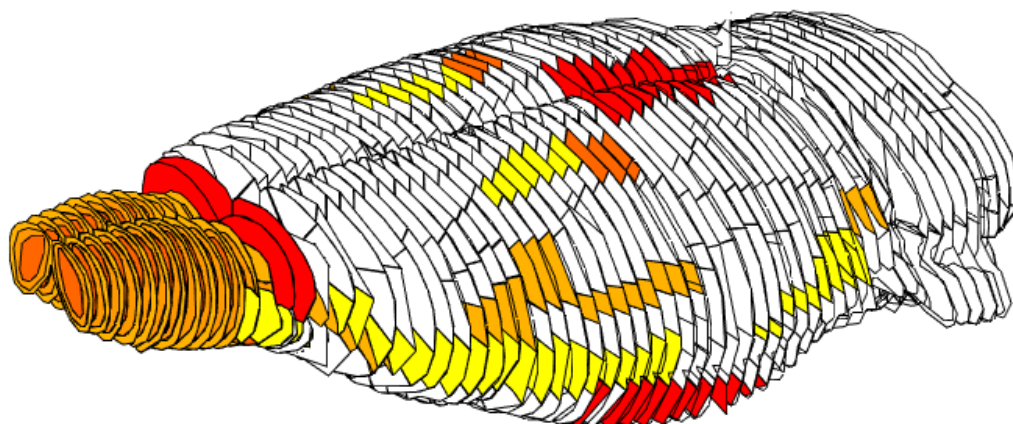


Figure 2: Full brain view of Dermorphin NE uptake at 40 minutes

IV. Conclusion

In conclusion, this technology has the potential to revolutionize drug delivery to the brain. Instead of being satisfied with getting the drug across the BBB and into the brain, researchers will be able to go one step further in targeting medicines to the specific lobes of the brain where the drug is needed. With applications in Glioblastomas and other brain diseases, these theranostic nanoemulsions have great potential. The visualization program that was designed and created with this project brings health care professionals the ability to visualize uptake to investigate the effectiveness of different targeting ligands used to deliver drugs to highly specific ROIs.

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1: Introduction

18,000 patients are diagnosed with Glioblastoma Multiforme (GBM) in the United States each year (Tutt, 2011). Of these, less than 10% of the patients survive longer than five years (Tutt, 2011). GBM is a level IV cancer as classified by the World Health Organization, making it the most aggressive form of malignant brain tumor cancer in adult patients (Louis et al., 2007; Agnihotri et. al, 2013). GBM is composed of glial cells developing from a mutation in astrocytes in the central nervous system (CNS). These glial cells create tumors that can become a significant amount of total brain tissue that thrives off of the large network of vasculature that provides nutrients, enhancing growth (Behzadian et. al, 1998).

Every case of Glioblastoma is different, and each patient is unique. A “one-size-fits all” approach will not be the future of cancer therapy; however, a theranostic approach shows great potential. Theranostics is the combination of therapeutics and diagnostics into a single modality (Kelkar, 2008). Ideally, a theranostic system will be able to provide feedback almost immediately, enhancing the quality and efficiency of clinical treatment. With this overall goal in mind, the objectives of this project are: to design a program to display a 3-dimensional (3D) heat map of Magnetic Resonance Imaging (MRI) T1 relaxation times in the brain, to design and synthesize targeting moieties, and to test for pharmacodynamics effects of the nanomedicines *in vivo*. Together, these objectives will lead to a nanoemulsion (NE) for the targeting and imaging of GBM *in vivo*, and a program to visualize these NEs.

1.1: Current Gold Standard

The current gold standard for the treatment of GBM is imaging the brain using an MRI, and using these images in resection surgery to better remove the tumor. Before going into

surgery, the GBM patient goes through a gadolinium-enhanced MRI to image the tumor, providing the surgeon knowledge on the location of the cancer (Hou et al, 2006). The MRI is able to show the differences in tissue types with gadolinium as an image-enhancing compound. The patient is then given an oral chemotherapy drug, Temozolomide (TMZ), which acts as a methylation agent. Due to the methylation of the DNA, cell death is triggered (Newlands et. al, 1997). TMZ has been shown to be effective, but a large margin for improvement remains. The drug is mainly effective with patients under the age of 45, and of those positively affected by the treatment, survival was increased by about 18 months (Yaneva et. al, 2010)

The main problems that arise while treating GBM is the lack of clear imaging, and the delivery of the therapeutic drugs across the Blood Brain Barrier (BBB) of the brain while minimizing the damage to the rest of the brain. Although MRI, the imaging method that has been used since 1985 for differentiation of tumors from healthy tissue (Grossman et.al, 2004), can show a high-resolution picture of the different tissues present, a high amount of “guess and check” is still done for the exact tumor location. Additionally, during chemotherapy and radiation treatments, highly accurate methods of quantifying the therapeutic extent of the drugs and exactly where the drugs are accumulating are not available. The second main problem is trying to get drugs past the BBB. The BBB is made up of endothelial cells that form tight junctions, which are permeable only to hydrophilic drugs or liquids. For a drug to be beneficial in treating GBM, it needs to be able to pass through the BBB easily while not affecting the surrounding healthy tissue.

1.2: Goals

This project consists of two main goals: to design and test a nanoemulsion drug delivery system and to design an interface to visualize *in vivo* data of the drug delivery system. The team began with designing a nanoemulsion that is capable of holding common chemotherapeutic drugs stable, that is able to contain a peptide used to target specific cells, and that contains an imaging agent. Once a functional nanoemulsion was made, it was tested *in vivo*, utilizing resources at Northeastern University to run MRI scans on healthy rat brains.

Upon collection of this *in vivo* MRI data, the raw data needed to be analyzed to visualize uptake of the nanoemulsions in different areas of the brain. A 3D heat map that can show the accumulation of the nanoemulsions across sixty-three cross-sectional slices of the brain was designed. With the heat map showing nanoemulsion accumulation in specific areas of the brain, selective targeting of cells can be seen.

1.3: Approach: Nanoemulsions

One of NemuCore Medical Innovations' (NMI) main areas of interest is the design of NEs for drug delivery. NEs used by the company are comprised of oil-in-water droplets with stabilizers, drugs, targeting peptides, and imaging agents (Mason, et al., 2006; Ledet et al., 2013). A major goal of this project is to design and enhance qualities of the NEs to achieve greater targeting specificity against GBM. Three cell receptors were identified previously for this project: the Alpha-7 nicotinic Acetylcholine Receptor (Alpha-7 nAChR), the B2 Bradykinin Receptor (B2BR), and the Mu-Opioid Receptor (MOR) (Day, Lacarra, Sacks, & Sadraei, 2015, unpublished). Continued research was completed for these receptors, focusing on various ligands for better targeting. Once chosen, the targeting ligands were chemically synthesized and

implemented onto the surface of the NMI-800 NEs. Once created, the NEs were tested *in vitro* for stability, and *in vivo* for targeting effectiveness.

NEs provide a novel way to combat the drug resistance found in GBM due to their designability and high level of customization (Ledet et al., 2013). NMI has previously identified drugs they wish to use against GBM, which can be incorporated into the final design once proof-of-concept experiments have been completed to confirm correct targeting of intended receptors. With the proper knowledge of ligand shape and specificity, manufacturing, chemotherapeutics, stability measurements, and *in vivo* testing, an optimal line of NEs will be designed and synthesized by NMI.

1.4: Approach: 3D Statistical Heat Map

Verifying the effectiveness of the designed drug delivery system required analysis of the location of the imaging medium, which is attached to the drug delivery vehicle, *in vivo*. There are currently no programs available which can accomplish this, therefore a custom one was created, addressing both NMI's specific need and a functional gap in the industry. The program's function is similar to that of a Positron Emission Tomography (PET) scan's initial output, at least insofar as tracking an imaging marker's position. Where this program's functionality differs is in the data it outputs. The focus of this program is in producing sound statistical data; the similarity to PET functionality is merely a positive reapplication of the technology in use.

In the creation of this visualization program, the outputs from a custom statistical analysis program and the rat brain wireframe code, a product created by the preceding work on this project, were used. As such, this project is dependent on the established rat brain atlas program as well.

The program's function is to produce accurate specificity index and t-test heat map images. These can be made for all time points at which rats are tested in each of the 174 regions of interest across all 63 brain slices. One method of allowing for the clear visualization of this data, even in the 3D variant, is shown in Figure 3. The program allows for the selection and display of individual slices of the 3D image for closer analysis, an example of such a slice can be seen below. This should be achievable in the same user-friendly manner as the data analysis and 3D image production. A similar program, which can map the densities of different receptors that are studied, was also created, allowing for the comparison of where the NEs are found versus where the targeted receptor is expressed.

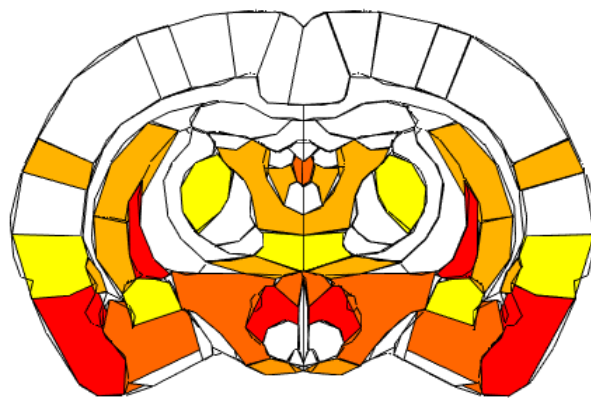


Figure 3: Example of a heat map slice:

1.5: Summary

Throughout the following chapters of this report, the biology of Glioblastoma Multiforme, current diagnostics and treatment of brain cancers, the function and properties of NEs and other small molecule drug delivery systems, and techniques for visualization of data through heat mapping are explored. A detailed discussion of the approach of this and the theory behind this design is then be presented, followed by preliminary designs tested throughout this iterative design process. An in-depth look at the final designs will be explained next, followed by a discussion, some general conclusions, and ideas on possible directions of future research.

2: Literature Review

2.1: Glioblastoma Multiforme

Glioblastoma Multiforme (GBM) is a form of malignant brain cancer present in adult patients. GBM is the most aggressive form of brain cancer with a classification of grade IV, the highest by the World Health Organization (WHO), due to its rapid proliferation, development in oligodendrocytes, and abnormal appearance under a microscope (Louis, 2007). There are 12,000-18,000 patients per year diagnosed with GBM in the United States alone (Tutt, 2011). Due to the rapid attack on the body and the difficulty to treat, less than 10% of those patients diagnosed each year will survive 5 years (Tutt, 2011). There are two types of Glioblastomas: primary and secondary. Primary glioblastoma expands quickly, making it the more aggressively invasive of the two types. Secondary glioblastomas are slower in their growth, starting off at a much lower grade tumor level, but as time passes this secondary type changes into an even more aggressive form (Ohgaki & Kleihues, 2007).

To understand and characterize the morphology of Glioblastoma, the types of cells that make up the tumor are examined. Gliomas can form from a variety of different cell types, and therefore come from different parts of the brain. The three most common types of cell-derived gliomas are oligodendrogliomas, astrocytomas, and oligoastrocytomas (Behin et. al, 2003). Oligodendrogliomas are primary glial brain tumor cells that are categorized by the WHO as grade II and grade III tumors. They are a lower grade because they are far less aggressive and respond well to chemotherapy (Uddin, 2015). The WHO classifies astrocytomas, tumors that are derived from immortalized astrocytes, the supportive tissue in the brain, as grade IV tumor cells (Kennedy, 2015). Oligoastrocytomas have very distinct regions of differentiation being both oligodendroglial and astrocytic in nature (Gupta 2005). The type of cell the glioblastoma is

comprised of affects the differing symptoms observed. Common symptoms include headache, drowsiness, or vomiting. All of these symptoms arise from the tumor pressure exerted onto the brain, often in areas that control motor function. This leads to patients experiencing weakness focused on one side of the body, visual changes, difficulty speaking, and encountering challenges when recalling both short and long term memory. Other symptoms include focal neurologic deficits, seizures, and headaches (Grossman et. al, 2004).

Another quality of glioblastoma is angiogenesis, the formation of new blood vessels. Glioblastoma tumors contain greater vascularization than normal brain tissue. This allows the tumor to receive a very high amount of nutrition and oxygen to enable rapid growth. When hypoxia is experienced in the tumor, the secretion of vascular endothelial growth factors (VEGFs) is induced. These growth factors have been found to be present at a significantly greater concentration in stem cell-like glioma cells (SCLGC) compared to non-SCLGC cells, and lead to increased vascularization within the tumor (Bao et. al, 2006).

The alignment of cells in a tumor allows for gaps for both oxygen and nutrition to enter the tumor area. This enhanced permeability and retention (EPR) effect is seen in many types of tumors. The permeability has been recognized as an exploitable characteristic for targeted drug delivery using diffusion. (Miura et. al, 2013).

Tumors grow rapidly, in part due to the increased expression of various receptors. Epidermal growth factor receptor (EGFR), one of the receptors overexpressed that contributes to unregulated tumor growth, was been observed in 62.5% of the 40 tumors that were examined. EGFR is found on the extracellular protein ligands. Additionally, it was seen that of these, 40% of the tumors expressed EGFR amplification (Haas-Kogan et.al, 2005). The growth factors on the gliomas are tumor-specific in order to optimize the tumor's success in the localized

environment and growth conditions (Nishikawa et. al, 1994). In normal brain tissue, the Fn14 gene is expressed, but only slightly. It has been found that Fn14 is overexpressed in traveling glioma cells (Tran et. al, 2003). Three of the many known receptors of the brain include the Alpha-7 nicotinic Acetylcholine Receptor (Alpha-7 nAChR), the B2 Bradykinin Receptor (B2BR), and the Mu-Opioid Receptor (MOR). Exploitation of the overexpression of these receptors on tumor cells opens up the possibility of targeted drug delivery (Ganta et. al., 2014a).

2.2: Current Gold Standard of Treatment

The current gold standard of treatment for Glioblastoma is to locate and excise the cancerous tissue. An MRI is taken of the patient's brain to locate the tumor's location in the brain prior to removal. Surgeons excise as much of the tumor as possible from the peripheral of the brain (Agnihotri et. al, 2013). Once the surgery has been successfully completed, the patient is treated with series of radiation and chemotherapy treatments. Temozolomide (TMZ) is the common oral chemotherapy that is given. TMZ acts by adding a methyl group to cell DNA, damaging DNA and triggering cell death. Even with these treatments being enacted in conjunction with one another there is only a 16.1% increase in the patient survival rate (Stupp et. al, 2005).

A GLIADEL® wafer is placed at the site of resection upon the removal of the tumor's mass. GLIADEL® is a biopolymer made of polycarboxyphenoxy-propane/sebacic acid anhydride containing 3.85% carmustine [BCNU]. This biopolymer wafer is designed to incrementally release the carmustine (a chemotherapeutic) into the site of resection for 2 to 3 weeks (Domb et. al, 1999). Carmustine's mechanism of action is not completely understood, but it is known that Carmustine is an alkylating agent that induces depolarization of mitochondrial

inner transmembrane potential, up-regulates Bax, down-regulates Bcl-2, activates caspase-3, and notably reduces collagen and thrombin-induced platelet aggregation (Zhang et. al., 2015).

Despite the multiple treatment methods available, there has been little improvement in patient mortality rates since the “war on cancer” began in 1972. This is partially because chemotherapeutic drugs being developed are hydrophobic and cannot pass through the Blood Brain Barrier (BBB) to enter the brain. The BBB is a highly selective membrane with tight junctions formed by capillary endothelial cells (Hawkins et. al, 2005). When EGFR kinase inhibitors are given to patients only about 10-20% of patients demonstrate a positive response due to the inability of the drug to cross the BBB and reach the cancerous tissue it is intended for (Mellinghoff et. al, 2005). Clearly there is a need for a new type of treatment that can pass through the BBB and effectively attack the GBM tumors, a common discussion topic in drug delivery research.

Many proposed treatment delivery methods involve circumventing the BBB. In order to bypass the BBB nanocarriers that can identify brain capillary endothelial cells and tumor cells have been proposed (Beduneau et. al, 2007). The primary areas in which there have been advances in the field of tumor drug delivery have been in targeting, increasing permeability, and improving retention effect (Maeda et. al, 2000). Nanocarriers have been specifically made to shield the drug from the body’s defense mechanisms, while still keeping the size appropriately small, typically in the 30-180 nanometer range.

2.3: Biology of the Brain

Approaching the problem of creating a drug delivery system that can overcome the unique challenge of getting the drug through the circulatory system and into the brain tissue

starts with an understanding of the BBB. The BBB is made up of densely packed endothelial cells that surround the vasculature of the brain. This includes the astrocytes and extracellular matrix that actively interacts with the barrier on the luminal surface of the endothelial cells. The BBB maintains homeostasis in the brain environment. To accomplish this, the barrier has tight regulations on the transport of solutes and cells in and out of the central nervous system tissue (Bhaskar et al., 2010).

The endothelial cells aid in the restricted permeability of the BBB through tight junctions between neighboring endothelial cells. There are different routes that materials can take in order to pass through the BBB as presented in Figure 4. The tight junctions allow small aqueous molecules such as oxygen and carbon dioxide to diffuse. In GBM tumors, these tight junctions are not as tight as in the normal lining, making the BBB more permeable, and therefore a higher amount of diffusion occurs. (Hawkins & Davis, 2005)

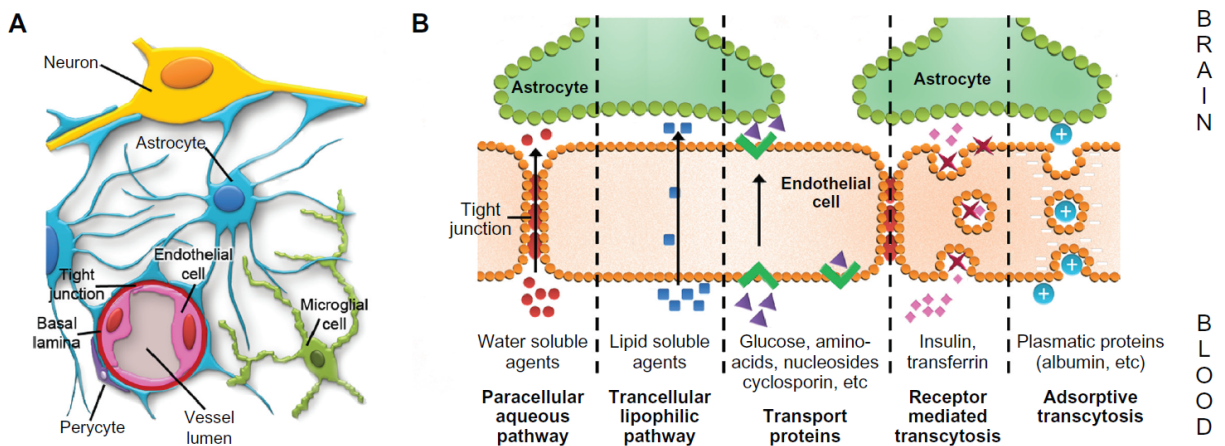


Figure 4: Different mechanisms of nutrition and molecular transport through the Blood Brain Barrier.¹

The BBB allows necessary molecules such as glucose, amino acids, and nucleosides to pass through the barriers with the associated carrier proteins. Materials can also pass through the BBB by receptor-mediated transcytosis. This process is used when a larger molecule needs to be

transported into the brain tissue, and is dependent on the receptors on the epithelial cells (Ramos & Campos, 2012).

The ultimate goal when working with drug delivery to the brain is using the natural processes already there to deliver the drug where it is needed, i.e. bio-mimicry. This reduces the amount of invasive procedures such as intraparenchymal injections. Other procedures include disrupting the BBB with high-intensity focused ultrasound or inserting a long-term drug delivery device (Bhaskar et. al., 2010).

A second barrier that needs to be considered is the blood cerebrospinal fluid (CSF) barrier. This is a primary barrier present in choroid plexus tissue (present in all ventricles in the brain) and is a thin layer of blood capillary and choroid plexus epithelial cells. The major difference between the BBB and the blood-CSF barrier is the exchange of specific compounds as demonstrated in Figure 5. Looking at calcium influx from the blood into the CSF, an example of the difference between these two barriers can be seen. Calcium influx is 10 times greater across the CSF barrier as compared to the BBB (Laterra et. al, 1999). This disparity in movement across the different barriers comes from the choroid plexus tissue, which is responsible for producing cerebrospinal fluid. This fluid is then circulated throughout the ventricles in the brain and surrounding subarachnoid layers that cover the entire brain (Johansson et. al, 1997).

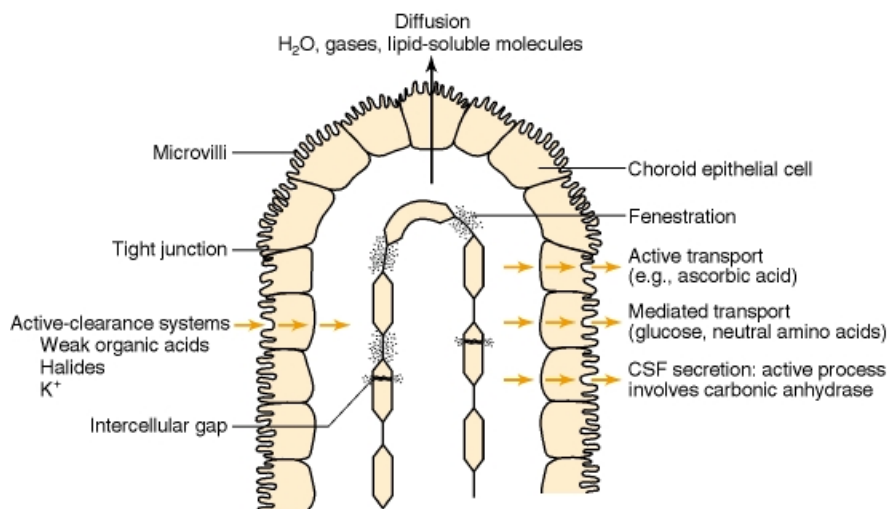


Figure 5: Visualization of the Blood- CSF Barrier and Molecular Transport.²

Studies have been carried out to examine the mechanisms of penetration used in the blood-CSF barrier. It has been found that both facilitated diffusion and active transport occur from blood into CSF. In regards to the diffusion from CSF into blood, active transport occurs at the blood-CSF barrier (Bhaskar et. al, 2010). This is an area that is continuously being researched by drug development teams.

2.4: Theranostics

The field of theranostics is relatively new in the medical community, and there has been a surge of activity in research and application of theranostics due to the rising concept of personalized medicine. Personalized medicine is the tailoring and application of medicine based on the pathological features and the differing physical responses of each patient. Theranostics is the concept of combining modalities of therapy and diagnostics together, with the goal of increasing medical effectiveness (Kelkar & Reineke, 2011). Theranostics covers a wide range of imaging tools and methods to help detect the pharmaceutical delivery during administration. One

² Laterra J, Keep R, Betz LA, et al. Blood—Cerebrospinal Fluid Barrier. In: Siegel GJ, Agranoff BW, Albers RW, et al., editors. *Basic Neurochemistry: Molecular, Cellular and Medical Aspects*. 6th edition. Philadelphia: Lippincott-Raven; 1999. Available from: <http://www.ncbi.nlm.nih.gov/books/NBK27998/>

such method of administration uses NEs, where the surface can be functionalized for imaging purposes and the interior payload can contain drugs.

2.4.1: Diagnostics

One of the main halves of theranostics is the diagnostic aspect, allowing for visualization of theranostic particle accumulation after administration to the patient. The field of diagnostics encompasses methods used to recognize and pinpoint the location of a morphological tissue or disease. Various imaging methods can be used based on the tissue to be imaged and studied. When imaging the brain for glioma location, Magnetic Resonance Imaging (MRI) is the common choice. One study examined the accuracy of the MRI technique and if the MRI accuracy could be increased by using Positron Emission Tomography (PET) with O-(2-[F]fluoroethyl)-L-tyrosine (FET), an amino acid. 31 different patients were examined, and it was determined that when only using MRI, 96% sensitivity and 53% specificity were found. However, MRI with FET-PET exhibited 93% sensitivity and 94% specificity, displaying a significant increase in specificity (Pauleit et. al, 2005).

Beyond MRI, fluorescence imaging techniques are another method in the application of theranostics on patients (Andersson-Engels et. al, 1997). Quantum dots comprise a fluorescence imaging method, and here the quantum dots are utilized for their optical properties, one of which is brightness (Zhang et. al, 2012). Computer-aided diagnosis (CAD) is being researched and improved with the intent of better medical imaging and radiology diagnostics. CAD is a tool used by radiology technicians as a second opinion to aid in making their final decision. This method is able to obtain lateral images, which may lead to an early diagnosis of disease (Doi, 2007).

2.4.2: Therapeutics

With the involvement of therapeutics, the diagnostic tools used take on an ability of duality, leading to theranostics. Past problems encountered when designing drugs and their delivery method are still issues when creating novel treatments, including systemic biodistribution, drug specificity towards target cells, first-pass clearance and metabolism of the drug and delivery method, bioavailability, systemic toxicity, and unfavorable side-effects from increased doses accounting for clearance rates (Torchilin, 2000). Using diagnostics in combination with therapy has eliminated or decreased many of these problems. Targeting theranostic particles often incorporate some form of targeting moiety on the surface that can selectively interact with biomolecules and receptors, such as an overexpressed receptor on tumor cells that is not seen on non-cancerous cells (*Biotechnology*, 2011). The specificity of the targeting aims to bring down the dosage administered because of a greater accumulation at the target location, allowing for less systemic toxicity. This brings the opportunity to lower the therapeutic threshold of a treatment for a patient while still achieving the effects desired.

The basics of drug delivery have challenges associated, but additional challenges are encountered when theranostic methods are applied to the brain. A tightly-packed barrier of endothelial cells with narrow junctions (the BBB) acts as a protective wrapping of the brain. The BBB filters what is taken up from the blood to the brain and modulates molecule uptake. The selective permeability of the BBB has led to two main approaches of drug delivery to the brain, invasive and non-invasive (Pehlivan, 2013). Invasive methods of delivery often involve surgery where a portion of the skull is removed, allowing for direct delivery to the brain. This can be achieved by an injection of the therapeutic or by using a delivery device mechanism. Delivery of

the payload in an invasive manner takes time and results in a long healing process for the patient after surgery is completed. Non-invasive delivery methods are being developed and researched in the nanomedical field. Products, such as NEs, are showing promise as their advantages to both the health care provider and patient.

2.5: Nanoemulsions

Nanoemulsions (NEs) are emulsions where the suspension droplet dispersion is at the nano-scale. This size is made possible due to the properties of surfactants, which work to decrease the surface tension interaction of the two liquids. Since NEs often consist of a hydrophilic and hydrophobic component, surfactants are commonly amphiphilic particles, allowing for organization at the liquid interface. The sizes of NEs commonly range from 100nm to 500nm, however particles with sizes above and below this range do exist (Shah et. al, 2010). Oil and aqueous phases are prepared separately and then mixed together, after which they are run through a microfluidizer, exposing the solution to a high pressure, high stress environment. Inside the microfluidizer, the high-pressure forces the mixed phases to go through a small porous mesh, allowing for mechanical extrusion and size control by the mesh pore sizes. Other factors affecting the size of the droplets include the maximum pressure experienced, length of extrusion time, and number of extrusion repetitions.

The current standard operation procedure for synthesizing NEs at NMI is a high shear microfluidization process where the two phases are thoroughly mixed before being introduced to the machine. The standard process includes a pressure of 25KPSI with 10 cycles experienced by the NE. The size range obtained by this process is 100nm to 150nm, which has been shown to

be an optimal size in the treatment of cancer (Ganta et. al, 2014). A range of NE research is currently being conducted at NMI.

2.5.1: The Aqueous Phase

The basic components of NEs synthesized at NMI are egg lecithin and PEG₂₀₀₀DSPE, which together will self-assemble by surrounding hydrophobic components in water and leading to the formation of NE (Ganta et. al, 2014). Surfaces of NMI's NEs consist primarily of surfactant, in this case the egg lecithin. Molecules found in egg lecithin include phosphatidylethanolamine (PE) and phosphatidylcholine (PC), both of which are amphiphilic surfactants. The next component is polyethylene glycol (PEG), which is conjugated to 1, 2-distearoyl-*sn*-glycero-3-phosphoethanolamine. The combined conjugate is labeled as PEG₂₀₀₀DSPE, and the PE in the conjugate behaves the same as the PE found in the egg lecithin. This allows the PEG₂₀₀₀DSPE to also integrate itself as part of the surfactant layer during self-assembly, and the PEG portion faces outwards. This PEG molecule helps to avert biomolecule and immune system adhesion, allowing for a longer circulation time of the NE (unpublished data, McCall, et. al, 2014).

2.5.2: The Oil Phase

Internal components of the NEs are dissolved in either safflower or flaxseed oil at NMI, both of which are obtained from commercial suppliers. The most prevalent fatty acid found in safflower oil is the linoleic acid, an omega-6 poly-unsaturated fatty acid (PUFA) (Babayan, 1987). Linoleic acid itself is not observed at significant levels in the brain, but linoleic acid is a precursor for the creation of arachidonic acid that is seen at significant levels in astrocytes. This

was proven with rats on a diet of high amounts of linoleic acid. Correspondingly rats were observed to have highly significant levels of arachidonic acid in brain tissue (Dopeshwarkar et al., 1971).

The main triglyceride material in flaxseed oil is α -linolenic acid, an Omega-3 PUFA (Vereshchagin & Novitskaya, 1965). Just as with the linolenic acid from safflower oil, α -linolenic acid is a precursor, in this case for eicosapentaenoic acid (EPA) and for docosahexaenoic acid (DHA). α -linolenic acid is not found in large amounts in the brain, but both EPA and DHA are seen with significant amounts in brain tissue (Burdge & Calder, 2005).

Drugs that are lipophilic can be added to the oil phase without modification, although some drugs do require modification to achieve effective loading in the NEs, such as the fatty acid derivative of TMZ (Cacaccio & Wrabel, 2014, unpublished). Use of either safflower or flaxseed oil has been observed to increase NE uptake to the brain; presumably the oil is used to assist in PUFA production in brain cells. NMI has expanded the functional potential of produced NEs through enhancing the oil for aid in causing more favorable distribution *in vivo*.

2.5.3: Glioblastoma Research and Efforts at Nemucore

NMI has assembled a strong foundational knowledge on the NEs with targeted delivery of chemotherapeutic drugs using NEs for breast and ovarian cancer (Ganta et al., 2014a; Ganta et al., 2014b). When research at NMI began on GBM, initial research showed that loading the NEs with safflower oil could enhance penetration of the BBB. Joseph Cacaccio and Eileen Wrabel, a previous team from the Biochemistry Department at Worcester Polytechnic Institute (WPI), worked with NMI over the 2013-2014 academic year on their Major Qualifying Project (MQP). This team was able to synthesize stable NEs. When loaded with chemotherapeutics, the NEs

exhibited a greater toxicity to cells than the free chemotherapeutics. Cacaccio and Wrabel also established that the NEs are taken up through *in vitro* studies. Another important accomplishment by Cacaccio and Wrabel was the modification of TMZ. This allowed loading of the drug into the NEs, and a higher toxicity was seen using the NEs than with the free TMZ. They also began research on possible targeting ligands, isolating the Alpha-7 nicotinic Acetylcholine Receptor (Alpha-7 nAChR) and the Mu-Opioid Receptor (MOR) as candidates from literature research (Cacaccio & Wrabel, 2014, unpublished; McCall et al., 2014).

2.5.4: Targeting and Imaging

To aid in the imaging capability of the NE, lanthanide gadolinium is chelated to diethylnetriamine penta-acetic acid (DTPA). This chelated compound is utilized as an imaging contrast enhancing agent and goes by the commercial name Magnevist (Oudkerk et. al 1995). This happens due to the adjacent protons' T1 relaxation times shortening, making this compound useful in imaging GBM as the particle will gather in locations having new vasculature and free protons. Both of these qualities are found nearby and in GBM. At NMI, the chelated gadolinium is further conjugated to phosphatidylethanolamine (PE), allowing the PE-Gd-DTPA to be inserted into the NE membrane, with the PE in the membrane and the Gd-DTPA portion on the surface (Ganta et. al, 2014).

Targeting: B2 Bradykinin, Alpha-7 nicotinic Acetylcholine, and Mu-Opioid Receptors

Continued research at NMI has led to identifying the three main receptors for focus: the B2 Bradykinin receptor (B2BR), the α -7 homo-pentamer nicotinic acetylcholine receptor (α 7nAChR), and the mu-opioid receptor (MOR). Previous research has been completed on

possible targeting ligands, as designing NEs, and testing NEs by a past MQP from the Biomedical Engineering Department of WPI (Day, Lacarra, Sacks, & Sadraei, 2015, unpublished). The chosen targeting ligands were conjugated to DSPE-PEG molecules to ensure incorporation of the targeting ligands with the NEs. To show that the targeting ligands are interacting with predicted and shown regions, a receptor-inhibiting drug can be used which should show statistically similar results when a non-targeted NE is used.

When used for the purpose of targeting B2BR, Cereport has been reported as increasing the BBB permeability due to the activation of B2BR and further transient opening of the BBB (Bartus et. al, 2000). For inhibition of the B2BR receptor, Icatibant presents itself as a suitable drug. This pharmaceutical is a peptidomimetic drug comprised of 10 amino acids and is an effective inhibitor of B2BR (Cockcroft et. al, 1994). Bradyzide, a pharmaceutical that has shown blockage of B2BR, could also be used (Burgess et. al 2000).

In vivo, the main location of $\alpha 7$ nAChR is in brain tissue, giving cause to this receptor as a viable NE target (Pohanka, 2012). Previous ligands used for the targeting of $\alpha 7$ nAChR involve derivations and modifications to toxins from cobras and cone snails (Zhan et. al 2010). For the $\alpha 7$ nAChR, nicotine, a parasymphomimetic alkaloid, has proven itself to be a strong agonist (Albuquerque et. al, 2009).

The MOR, is typically seen in both the brain and gastrointestinal tracts in mammals. A well-established agonist of MOR is dermorphin, a natural peptide opioid (Amiche et. al, 1988; Mizoguchi et. al, 2011; Broccardo et. al, 2003). An Opioid antagonist, Naloxone, is used to treat heroin overdose because it is such a strong competitive inhibitor of MOR. Additionally, naloxone has the added benefit of being the only known purely antagonist of opioid receptors to date, indicating that this pharmaceutical does not cause agonist effects (Evans et. al, 1974).

However, it has also been shown that naloxone has a relatively quick clearance time in rats (unpublished data). For this reason, β -funaltrexamine (β -FNA) is another option for MOR blocking, as this compound is able to completely block the receptors for at least week, and in some rats has been shown to block the receptors for up to 18 days (Martin, et. al, 1998).

2.6: Clinical Imaging of the Brain

The diagnosis and treatment of conditions like Glioblastoma have long been reliant on the ability to communicate the contents of the brain to medical experts without the need for invasive techniques. Regarding imaging of the brain, two techniques stand out in particular, Positron Emission Tomography (PET) and MRI.

PET scanning works by tracking of an ingested marker's movement through the brain. This particle emits positrons as it travels through the body and can be used to track the activity of specific regions of the brain as they interact with the particle (Bailey, 2005). MRI presents a more detailed view of the structure of the imaged tissue but cannot track functional activity to the same extent without additional tracking methods utilized.

2.7: Data Analysis

MRI imaging may be the current gold standard in clinical imaging of Glioblastoma, however processing the data from the machine remains a challenge. Upon running a single MRI scan, one receives several raw data files. These can easily be translated into an image, but need a significant amount of processing to be translated into numerical values related to each of the 174 regions of the brain. Highly trained clinicians are able to look at MRI images on a macroscopic level and understand what is happening in the soft tissues by looking at the variation of

brightness seen among different tissues (Scherfler, 2006). Researchers, however, often need the data in an analyzed manner, typically numerical.

Currently, moving data from raw MRI data to numerical form is a significant process that requires lots of time and resources while leaving a large margin for human error. A program that can quickly and accurately translate raw data into numerical values would enhance the quality and efficiency of translating raw MRI data into interpretable data for researchers.

2.8: Rat Brain Atlas

Dr. Craig Ferris and Dr. Praveen Kulkarni created the Atlas program to allow for effective visualization of sample brains. The program took 2-dimensional images of slices of rat brains and then utilized decimation and smoothing algorithms to produce a usable 3D map, or atlas, of the brain (Ferris et al., 2013). This brain atlas can be used to assist the analysis of MRI T1 response times in the brain by being applied in the definition of specific areas of the brain. The T1 response time data for each discrete region can then be analyzed separately (Day, Lacarra, Sacks, Sadraei, 2015).

2.9: Matlab

Matlab is a programming language commonly used across the engineering and scientific communities due to its ability to process and analyze large quantities of data effectively. As such it is an ideal candidate to analyze and manipulate the data procured from interaction with the Rat Brain Atlas program produced by Ferris and Kulkarni to obtain T1 relaxation data. Additionally, Matlab provides a robust visualization capacity which enables the visualization of results to be performed in the same virtual environment as they are produced, increasing simplicity and

reducing the risk of cross platform complications. Further, Matlab makes it easier to ensure that visualization code meets medical standards. Specifically IEC 61508 and ISO 26262 are met due to the existence of for sale certification kits that allow programs to be tested for standard compliance prior to release (“Matlab: The Language of Technical Computing”, *MathWorks*)

2.10: Statistical Analysis

2.10.1: Specificity Index

With raw T1 relaxation values in hand, data can be compiled from across a cohort, normalized, and analyzed by calculating the specificity index (SPI). Calculating the SPI can be done using the following equation:

$$\frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (Ax_{pre\ 1} - Ax_{t\ 1}) + \dots + \left(\frac{\text{Voxels Section}_n}{\text{Voxels Total}_n} \right) (Ax_{pre\ n} - Ax_{t\ n}) \right]}{n} \Bigg/ \frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (A_{pre\ 1} - A_{t\ 1}) + \dots + \left(\frac{\text{Voxels Section}_m}{\text{Voxels Total}_m} \right) (A_{pre\ m} - A_{t\ m}) \right]}{m}$$

In this equation, “Ax” is the targeted NE and “A” is the non-targeted NE. “Pre” represents the pre-scan that is done before NEs are injection, while “t” is the time point scan done 20, 40, or 60 minutes after injection of the NE. “Voxels Section” refers to the number of voxels for that specific region of the brain, while “Voxels Total” refers to the total number of voxels in the animal. This part of the equation allows for the normalization of animals with differently sized brains and for sections of different sizes, where “n” is the number of animals in the targeted cohort, while “m” is the number of animals in the non-targeted cohort. When calculating the SPI of the non-targeted NEs, this equation becomes:

$$\frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (A_{pre\ 1}) + \dots + \left(\frac{\text{Voxels Section}_n}{\text{Voxels Total}_n} \right) (A_{pre\ n}) \right]}{n}$$

$$\frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (A_{t\ 1}) + \dots + \left(\frac{\text{Voxels Section}_n}{\text{Voxels Total}_n} \right) (A_{t\ n}) \right]}{n}$$

The SPI is a relevant calculation because it allows for comparison of a targeted NE to the non-targeted NE on a cohort level.

2.10.2: Statistical Significance

As with any life sciences project, the ability to determine the statistical significance of data gathered is crucial. In the scope of this project, statistical analysis is required to determine the significance of NE interactions *in vivo*. A paired t-test can be used to determine the statistical significance of data within a set, as well as between sets. Specifically, a t-test can compare the targeted NE data to the non-targeted NE data to determine the level of statistical significance between the cohorts. A high level of statistical significance will improve confidence that the NEs are accumulating differently when targeting is involved, and the data is not just overcrowded with noise. T-tests can be conducted using Matlab, Microsoft Excel, or most statistical analysis programs.

3: Project Strategy

NMI has been researching and developing targeted NEs as therapies for cancer since founded in 2008. With a stable, size-controlled NE, the company has had preclinical animal trials for the targeted NEs for both breast and ovarian cancer, with plans to continue into Phase 1 clinical trials in the near future.

NMI has assembled a strong foundational knowledge on the NEs with targeted delivery of chemotherapeutic drugs using NEs for breast and ovarian cancer (Ganta et al., 2014a; Ganta et al., 2014b). A previous team from the Biochemistry Department at WPI worked with NMI during the 2013-2014 academic year on their MQP and created stable NEs. When loaded with chemotherapeutics, the NEs exhibited a greater toxicity to cells than the free chemotherapeutics. Additionally, the team was able to show the modification of TMZ to allow for loading into the NEs, and a higher toxicity was seen using the NEs than with the free TMZ. Research was started on potential receptors to target, identifying $\alpha 7nAChR$ and MOR as possibilities from literature (Cacaccio & Wrabel, 2014, unpublished; McCall et al., 2014).

Continued research identified the B2BR as another potential target (unpublished data) because of the transient opening of the BBB when the receptor is activated (Chen et al., 2000). Using these receptors, NEs with targeting ligands were synthesized for animal trials for the summer of 2014. Results from this study were the basis of another MQP team working with NMI. This group, from the Biomedical Engineering Department at WPI, worked on analyzing the data and creating a Matlab statistical heat map program during the 2014-2015 academic year. A correlative database of the receptor expression was made using data from literature research, and a wire frame atlas of the brain was created. The targeting capability of NEs created was tested *in vitro* using flow cytometry and florescent imaging; however, the proposed statistical

heat map was not completed, and this is still desired by NMI (Day, Lacarra, Sacks, & Sadraei, 2015, unpublished).

3.1: Initial Client Statement

Further research during the summer of 2015 at NMI led to the identification of other possible targeting molecules, based on inspiration from venomous animals and the mechanisms of attack the toxins use to penetrate the body. Supplementary examination of the mu-opioid receptor was completed, finding a targeted inhibitor drug to confirm that the NE was successfully targeting the chosen receptor. Further use of targeting ligands is now desired for increased confidence on the targeting capability of the NEs. Additionally, the Matlab statistical heat map program still needs to be created. As such, the initial client statement was given as:

Nemucore Medical Innovations, Inc., as part of its NCI U54-funded Center for Cancer Nanotechnology Excellence (CCNE) research, has developed a series of nanomedicines which penetrate the Blood-Brain Barrier and enter the brain. Magnetic Resonance Imaging (MRI) can be used to track these nanomedicines in vivo. The focal points of this project are the following:

- Designing and manufacturing experimental nanomedicines, as well as testing novel nanomedicines in vitro for uptake and potential cytotoxicity.*
- Creating a Matlab program capable of exhibiting gathered MRI drug delivery data in order to visualize drug distribution and intensity in vivo.*

3.2: Objectives

The overall objectives of this project are to work with NMI's technology of targeted NEs to target highly specific regions of the brain, and to create a 3D heat map of the brain to track the locations of the NEs in vivo.

3.2.1: Nanoemulsion Objectives

NMI's advanced NE technology has many aspects for this multi-functional NE to work as designed. As research is done to continue to improve this technology, there are a few areas this project will focus on. The overall objective will be to have functional NEs. To achieve this, smaller objectives have been determined and ranked.

The primary objectives, listed in order of importance, are as follows: the ability to cross the blood brain barrier, the ability to be imaged, and the ability to target specific regions of interest in the brain. These objectives will be measured through MRI scanning and a 3D heat map coloration scale.

The secondary objective of the NE design is to be able to target highly specific receptors throughout the brain. This will involve the use of different peptides to target different receptors. Comparison to non-targeted NEs will show if the targeting is effective. The ability to target specific receptors in the brain allows the dosage of the drug to be decreased, and in turn for the overall toxicity of the drug to decrease.

The tertiary objective of this project is to load the NEs with a chemotherapeutic drug to kill the Glioblastoma cells. The overarching goal is to be able to eliminate Glioblastoma in a patient, so therefore the NEs need to be toxic towards cancerous cells.

3.2.2: Heat Map Objectives

The primary objective of the produced 3D heat map is to display the regions of comparatively high drug uptake among all of the tested rats. This will be accomplished by plotting the regions in a 3D model of the subject brains and noting areas of high signal increase through the use of a heat map color gradient. By displaying the regions of high NE uptake, it is identifiable if the NEs are targeting the intended regions. It is essential to portray locations of drug accumulation in order to verify the objectives of the NEs, ensuring project progress. The non-primary objectives for the heat map are intended to improve the ability of the user to access and understand the information it portrays. This ensures any user with a basic understanding of MRI technology and imaging could use the program and be able to understand the images created.

The secondary objective is the addition of functionality to the visualization program, in such that individual slices of the heat mapped wireframe are selectable for individual viewing, allowing greater in depth analysis. In order to increase the ability for a doctor to watch the drug take effect on the tumor, there must be a simplified but informational image available. The tertiary objective is the optimization of the software's usability. This can be achieved through limiting the required input from an untrained user to non-technical tasks such as the selection of slices (by index number, not by location in the wireframe x, y, z coordinate system).

3.3: Constraints

As with any project, there are some constraints this project will have to work around in order to be successful. Both the NE and heat map aspects of this project have some constraints.

There are some general project constraints as well, including time and money. Animal work takes time, is expensive, and involves many different collaborators to be successful. Since NMI is funding this project, the money is less of a constraint than time, since only one academic year is given to complete the above objectives while NMI will be providing any needed supplies.

3.3.1: Nanoemulsion Constraints

As research is done to improve the NE technology, there are a few constraints to consider during the design process. First, it is important that the NEs stay within an identified size range, such as 120 nm to 160 nm, in order to retain storage stability. Second, the NE must be able to cross the BBB, for if it cannot reach the targeted region of the brain tissue, the design will be considered ineffective. A third constraint is the feasibility of manufacturing. Even though a peptide is designed, not all configurations are relatively easy to make, much less feasible. Some chemical reactions in producing selective peptides require more time and delicate, exact procedures. Additionally, all peptides designed will need to be PEGylated in order to be successfully incorporated into the NE surface.

3.3.2: Heat Map Constraints

The main constraints limiting the heat map program are as follows. Outliers in the MRI signal response data can result in the false reporting of NE accumulation in a region as being lower or higher than is true over the cohort tested. Due to the safety protocols in place at Northeastern University, the team members do not handle or carry out the experimentation with the rats, and it is therefore out of the team's control how the data is recorded. Errors in the manual alignment of the established rat brain structure and the actual MRI image of the rat brain could result in false reporting of the location of signal intensities, and therefore drug

concentration location. The program that allows for MRI scan and rat brain atlas alignment, Atlas, is not capable of correctly aligning the two automatically. This makes manual alignment mandatory. Finally, the heat map must be made using the previously defined Rat Brain Atlas Wireframe in Matlab, eliminating the possibility for use of other programming languages,

3.4: Design Standards

NMI is a private pharmaceutical development company; therefore, the company's goal is to get their medicines on the market for patients to use. With this end goal in mind, it is important that everything they do is completed and recorded correctly so they will eventually be able to gain approval from the United States Food and Drug Administration (FDA). It is also pertinent that all current standards are followed, as outlined in the following sections.

3.4.1: Nanoemulsion Standards

As of 2014, there have been no official regulations regarding nanomedicines, as they are being assessed case-by-case (Tinkle, 2014). However, guidance was issued in 2014 regarding the application of nanotechnology and confirming whether or not a product is considered nanotechnology. A main consideration of that is the size, ranging from 1 nm - 100 nm. While the intended size of the produced NE will be greater than 100 nm, they will still be under 1 μm in size, categorizing them as nanotechnology ("Guidance," 2014). Recommendations have been put forth for the regulation of nanomedicines due to their potential (Tinkle, 2014). The authors mention controls needed and evaluations to be done in order to establish that the product is therapeutic, reproducible, and safe. Manufacturing should be controlled since the NE synthesis involves a variety of complex processes. The product should be evaluated in terms of

pharmacokinetics and pharmacodynamics to ensure that properties of the NE are true to what the producers state, are therapeutic within safety ranges, and that the NE are characterized completely (Tinkle, 2014). The quality and stability of the NE are also important aspects (Tinkle, 2014). Manufacturing of the NEs will need to be done following Title 21, Section 820 of the United States Code of Federal Regulations, which outlines current Good Manufacturing Processes (cGMP) for medical devices, and Title 21, Section 211 of the United States Code of Federal Regulations, which outlines cGMPs for drugs. Further cGMP standards can be found in section 7.1.

3.4.2: Programing Standards

The primary engineering standard applying to the Matlab Code is IEC 61508 (International Electrotechnical Commission standard 61508). IEC 61508 defines standards of hazard exposure and risk of physical harm to human patients involved in the use and data collection of medical imaging software. Our program is in compliance with this standard due to the separation acquired data from any identifying features of each patient. NMI will need to store and data that applies to the patient population in a separate xml file in the format outlined by the Dublin Core Metadata Initiative xml schema. The Initiative xml schema guidelines are open to the public intended to allow the more effective storage and sharing of metadata.

3.5: Revised Client Statement

Since the initial client statement, NMI has kept a clear and focused image of the *in vivo* experimental portion. The MRI T1 visualization, by brain location and region, has a primary success / fail objective, and decisions for continued improvements of the program have been left

to the group with input from NMI. Therefore, the revised client statement is similar to the first, although clarifications are made connecting the targeting experiments and image analysis in order to expose the necessary connection between the two. With both, targeting specificity can be proven for continued research in the future. The final client statement is as follows:

Nemucore Medical Innovations, Inc., as part of its NCI U54-funded Center for Cancer Nanotechnology Excellence (CCNE) research, has developed a series of nanomedicines which penetrate the Blood-Brain Barrier and enter the brain. With the Nanoemulsion technology so far developed by Nemucore Medical Innovations, Inc., the aim is to create an inclusive imaging and analysis program to prove the targeting specificity of Glioblastoma Multiforme treatment and improve therapeutic diagnosis. A Matlab program able of visualizing MRI drug delivery data to show the distribution by intensity and location will be created. Upon designing and manufacturing novel Nanomedicines, in vivo MRI studies will be completed to improve the statistical power of the MRI data in showing specific targeting in the rat brain.

3.6: Project Management

Timely completion of this project will require careful planning and the guidance of many different mentors. A Gantt Chart of the tasks to be completed and the timeline of deadlines can be seen in Appendix A. Dr. Timothy Coleman, Dr. Niravkumar Patel, and Dr. Aleksandr Piroyan of NMI will provide insight and guidance with the biochemistry aspect of this project. Laurie Cote of NMI will provide guidance with the computer science aspect of this project. Dr. Craig Ferris and Dr. Praveen Kulkarni of Northeastern University will provide insight into the biology and function of the brain, as well as aiding with the completion of the MRI scans. Dr. Kwonmoo

Lee of WPI will advise the team on the design aspect of this project, as well as the use of medical imaging.

4: Design Considerations

Following the establishment of a project strategy, analysis was conducted in order to create preliminary designs for both the nanoemulsions and the visualization program for *in vivo* studies. These designs take into account and meet specifications, needs, and wants of recipients and prospective users.

4.1: Nanoemulsions Needs Assessment

4.1.1: Nanoemulsion Objectives

As the nanoemulsions will be used for imaging as well as drug delivery later on, it is important to consider objectives relating to the delivery, biocompatibility, manufacturing, and stability of them. In order to understand which of these objectives are the main focuses of the project, each objective was ranked on a 1-5 scale (5 being the most important) based on NMI's desired product. Table 1 displays the ranking for the objectives.

Table 2: Nanoemulsion Objectives

Objective	Score
High uptake by cells	4
Non-Toxic	4
Ease of Manufacturing	3
Stability over Time	5
Low Cost	2

As can be seen above, the highest-ranking objectives are a consistent stability, high cellular uptake, and non-toxicity to the animals. The lower objectives are ease of manufacturing

and low cost. By following these objectives, nanoemulsions can be manufactured consistently with optimal properties that can be used for both initial research and future pre-clinical studies.

4.1.2: Nanoemulsion Functions

After defining the core objectives in designing and synthesizing the nanoemulsions, it is important to also define the desired functions of the nanoemulsions. Below in Table 2 it can be seen the exact functions and specification that should be met by the designed nanoemulsions.

Table 3: Nanoemulsion Functions and Specifications

Function	Specification
Consistent Size	150 nm with Polydispersity Index (PDI) <0.1
Negatively Charged NE surface	-20 to -50 mV +/- <10mV
Stability over a long time	<10 nm size change over 3-4 weeks
Fluorescence capability for uptake studies	Rhodamine loading onto NEs
Targeting Capability	Target ligands based on chosen receptors
MRI compatibility	Attachment of imaging agents to the surface

In order to justify the specifications of the defined functions, it is important to look at research previously accomplished at NMI as well as at other institutions. It has been established by NMI that a size of ~150nm is ideal with a polydispersity index (PDI) <0.1 (Ganta et al., 2014). This allows for a feasible combination of components, a stable particle, and passage through loose junctions and fenestrations. The particles should have a negative surface charge of -20 to -50 mV ± 10mV to avoid aggregation and cell detection. As nanoemulsions may need to be stored between manufacturing and use, they need to be stable for periods of time. For this project, “stable” will be defined as <10 nm size change over 3 weeks (Cacaccio & Wrabel, 2014, unpublished; Day, Lacarra, Sacks, & Sadraei, 2015, unpublished). When testing uptake of the nanoemulsions in the brain, some form of tracking is needed. Therefore, the ability to connect different imaging agents (Gadolinium for MRI imaging, Rhodamine for flow cytometry uptake

studies) to the outside of the nanoemulsion for uptake in the brain is needed. Lastly, the ability to manufacture and attach different targeting agents, allows for a selective receptor mediated endocytosis uptake of the nanoemulsions in specific areas of the brain making the direction of the nanoemulsions controlled which is essential to the design.

4.1.3: Nanoemulsion Design Standards

Currently there are no design standards or regulations set in place by the Federal Food and Drug Administration (FDA) regarding nanomedicines. Instead, the FDA has turned to evaluating each nanomedicine on a case-by-case basis, with the main consideration being the active principle ingredient (API) (Lai et al., 2013, Sainz et al., 2015). Biologics with peptides fall into the category of biological medicinal product regulations, but when used at the nanoscale level of medicine, other parameters need to be examined (Bowman, 2010, Sainz, 2015). The FDA has joined with the Alliance for NanoHealth (ANH) in creating seven priorities in nanomedicine analysis challenges: biodistribution, mass transport, imaging methods, math models, computational models, and standardized analytical methods for manufacturing (Sanhai et al., 2008). Scientists in the field hope for a database comprised of nanoemulsion characteristics depending on the materials used, as a knowledge source such as this would contribute greatly to the standardization of nanoemulsions (Chan, 2006). With the small size of nanomedicines and their potential for targeting ligands, therapeutic loading, and imaging agents it is important to ensure the distribution and cytotoxicity of the nanoemulsions to be used are within safe ranges.

The Nanotechnology Characterization Laboratory has created guidelines for assays of nanoemulsions in regards to safety assessment (U.S. Institutes of Health, 2015). Of these safety

assessments, they are categorized by characteristics. These include size, surface characteristics, stability, zeta potential, efficacy of therapeutics and imaging, distribution, and targeting among others (www.ncl.cancer.gov). The functions listed previously can be quantified by using experimental procedures detailed in the Materials & Methods section.

4.1.4: Conceptual Nanoemulsion Designs

NMI has been working on the development of their theranostic nanoemulsions since it was founded in 2010. While this project focuses specifically on development of the NMI-800 series nanoemulsions, the general concept and some of the specifications have already been established by NMI. Figure 6 shows the nanoemulsions concept as established by NMI. The nanoemulsions are composed of a flaxseed oil core containing chemotherapeutic agents, a lipid layer, targeting ligands, and imaging agents. The oil core allows for the stabilization of the therapeutic and uptake by the brain. PEG-ylated binding ligands allow for uptake by selective cells. PEG-ylated $Gd^{+}DTPA$ allows for imaging in vivo.

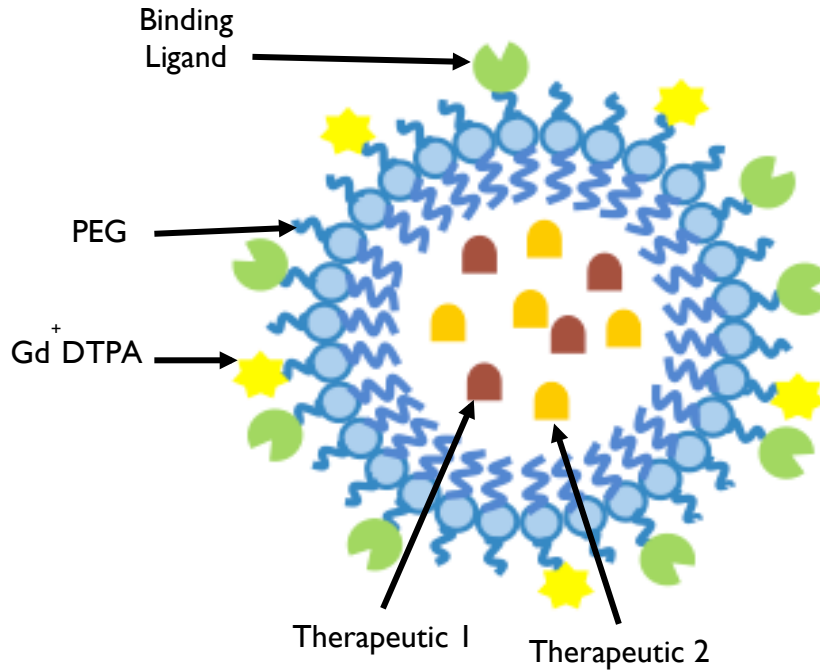


Figure 6: A Representative Schematic of a Nanoemulsion.

Targeting with Receptors: Bradykinin, Alpha-7, and Mu-Opioid Receptors

This project focuses specifically on the development and testing of different binding ligands. NMI has requested that the team focuses on the use of the Mu-Opioid Receptor (MOR), the Alpha-7 nicotinic Acetylcholine Receptor ($\alpha 7nAChR$), and the B2 Bradykinin Receptor (B2BR). NMI has chosen these receptors due to completed research showing expression in the brain, and because of previous work done on this project (Cacaccio & Wrabel, 2014, unpublished; Day, Lacarra, Sacks, & Sadraei, 2015, unpublished). The chosen targeting ligands were conjugated to DSPE-PEG molecules to ensure incorporation of the targeting ligands with the NEs.

The MOR is typically seen in both the brain and gastrointestinal tracts in mammals. A well-established agonist of MOR is dermorphin, a natural peptide opioid (Amiche et. al, 1988; Mizoguchi et. al, 2011; Broccardo et. al, 2003). *In vivo*, the main location of $\alpha 7nAChR$ is in

brain tissue, giving cause to this receptor as a viable NE target (Pohanka, 2012). Previous ligands used for the targeting of $\alpha 7$ nAChR involve derivations and modifications to toxins from cobras and cone snails (Zhan et. al 2010). When used for the purpose of targeting B2BR, Cereport has been reported as increasing the BBB permeability due to the activation of B2BR and further transient opening of the BBB (Bartus et. al, 2000).

Targeting Ligands: Dermorphin, Candoxin, and Cereport

Previous work at NMI has explored the efficacy of the peptides Dermorphin, Candoxin, and Cereport (Cacaccio & Wrabel, 2014, unpublished; Day, Lacarra, Sacks, & Sadraei, 2015, unpublished). Targeting of the MOR can be done with the Dermorphin peptide, seen in figure 7.

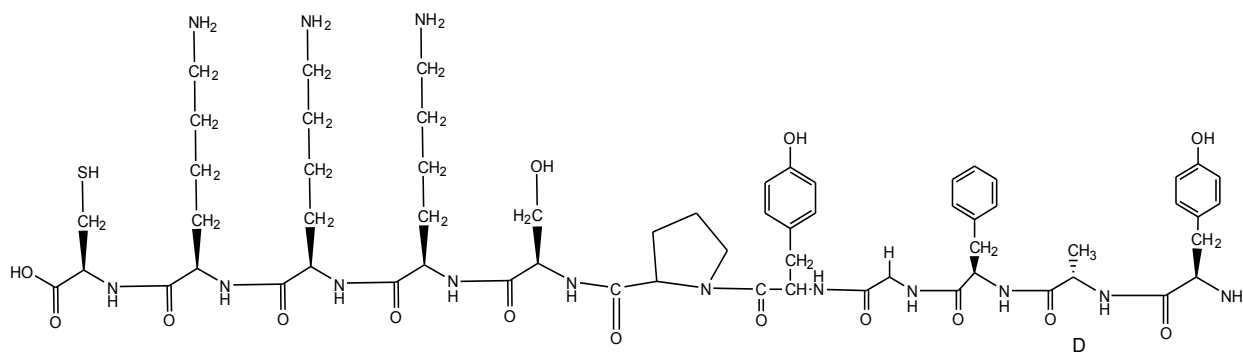


Figure 7: Dermorphin

The $\alpha 7$ nAChR can be targeted with Candoxin, seen in figure 8.

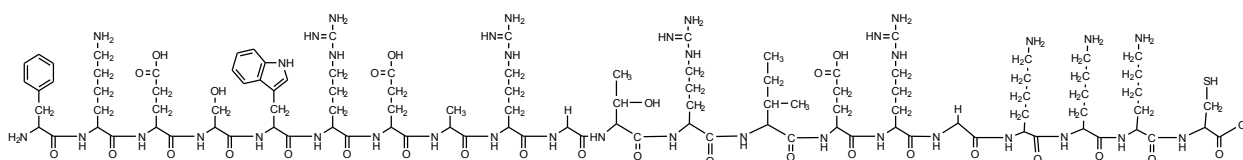


Figure 8: Candoxin

The B2BR antagonist Cereport can be used for targeting of this receptor. The structure of Cereport can be seen in figure 3.1

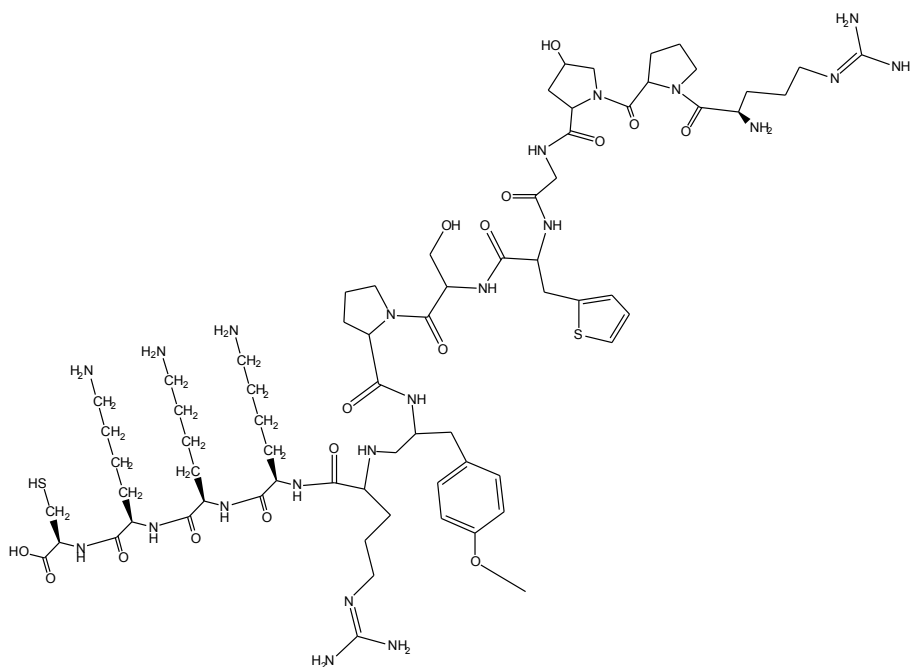


Figure 9: Cereport

Imaging with Gadolinium

To aid in the imaging capability of the NE, the lanthanide gadolinium is chelated to diethylnetriamine penta-acetic acid (DTPA). This chelated compound is utilized as an imaging contrast enhancing agent and goes by the name Magnevist (Oudkerk et. al 1995). This happens due to the adjacent protons' T1 relaxation times shortening, making this compound useful in imaging GBM as the particle will gather in locations having new vasculature and free protons. Both of these qualities are found nearby and in GBM. At NMI, the chelated gadolinium is further conjugated to phosphatidylethanolamine (PE), allowing the PE-Gd-DTPA to be inserted into the NE membrane, with the PE in the membrane and the Gd-DTPA portion on the surface (Ganta et. al, 2014). While gadolinium is known to be a toxic heavy metal, it has been established that in

such small doses in chelated form, it is harmless (Cacaccio & Wrabel, 2014, unpublished; Day, Lacarra, Sacks, & Sadraei, 2015, unpublished; Ganta et. al., 2014a, Ganta et. al., 2014b).

Levels of Imaging Particles and Targeting Peptides

NMI has a standard of 300 binding peptides and 300 particles of imaging agent per nanoemulsion (Ganta et. al. 2014a; Ganta et. al., 2014b.) The T1 relaxation time measured will directly correlate to the Gadolinium concentration that is present, and therefore indicate how many nanoemulsions are present. Knowing how much chemotherapeutic is in each nanoemulsion (measured by a high performance liquid chromatography (HPLC) assay), it then becomes possible to know how much drug is being delivered. Figure 10 represents this relationship visually.

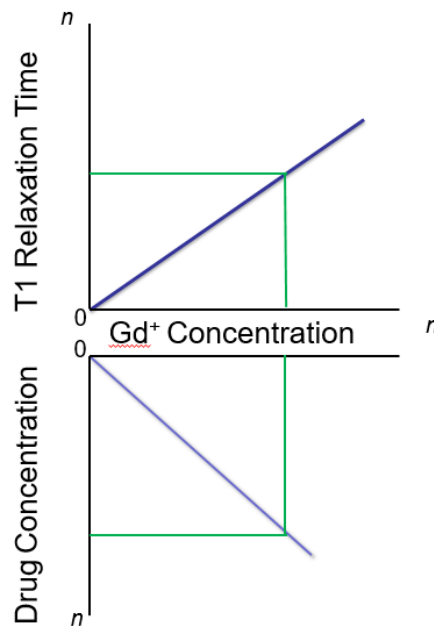


Figure 10: Relationship of T1 Relaxation Time to Drug Concentration

4.1.5: Alternative Nanoemulsion Design Features

As NMI has been developing the NE technology for several years, many engineering decisions were pre-defined for the team. However, as part of this project, the team did consider a few alternative design features to enhance the properties of the NE. In the creation of the targeting ligands, a short spacer sequence was added onto the end. This short sequence is intended to aid in keeping the peptide oriented out from the NE surface, and has been shown to enhance cell uptake (Stefanick *et al.*, 2013a, Stefanick *et al.*, 2013b). This design feature was accepted by NMI and incorporated into the NEs used in this project.

Another alternative design feature that the team considered was the use of different targeting ligands. Four alternative ligands were developed and accepted by NMI. They were not able to be tested during this project due to time limitations and a focus on the original targeting peptides, but these four have been designed and manufactured, and are currently in stock at NMI awaiting lipidation. These peptides are: ARIB (figure 11), ^DCandoxin (figure 12), and two others. The latter two peptides and sequences are proprietary materials.

Toxins from snakes and cone snails have been used in previous research for identifying various receptors of the nervous system to target. Of these, there are toxins that target nicotinic acetylcholine receptors (nAChR), known as alpha-Conotoxins (alpha-Ctxs) (Whiteaker, 2007). In a study completed by Whiteaker, an alpha-Ctx was derived from *C. arenatus*, and various alpha-Ctxs and analogues were analyzed (Whiteaker, 2007). Of those studied, ARIB [V11L, V16A] was shown to be highly selective for alpha-7 receptors, with an IC₅₀ of 0.356nM when tested for blocking of *Xenopus* oocyte-expressed nAChRs. The next most highly selective modified ligand was ARIB [V11L, V16D]. It was decided to select ARIB [V11L, V16A] to attach to DSPE-PEG-MAL for use in the NEs. A tail of CKKK amino acids was added to the N-

terminus, and it is important to note the di-sulfide bridge between the third and ninth residue, as well as between the fourth and seventeenth residue.

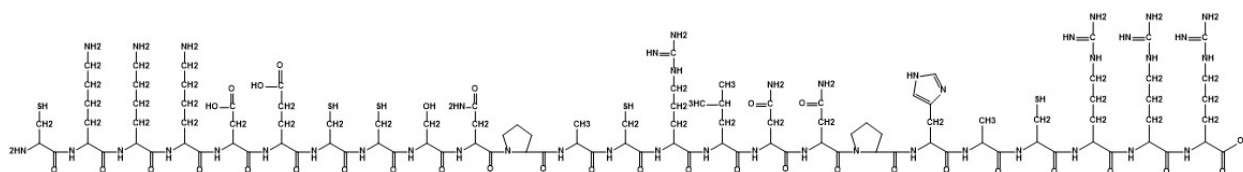


Figure 11: ARIB

The next ligand chosen was D-CDX, or the D-amino acid version of Candoxin, a known nACh toxin from the malayan krait, a highly venomous snake (Nirthanan, 2003). Nemucore has previously used candoxin as a targeting ligand to study the alpha-7 receptor with their NEs (Cacaccio & Wrabel, 2014, unpublished; Day, Lacarra, Sacks, & Sadraei, 2015, unpublished). One group of researchers synthesized the retro-inverse form of CDX, and performed competition-binding studies. The percentage of D-CDX to cross the BBB was twice as great as the amount of CDX to cross the BBB (Wei, 2015). In vivo imaging studies demonstrated the capability of D-CDX to cross the BBB was much greater than that of CDX when conjugated to liposomes. (Wei, 2015). For these reasons, the retro-inverse form of CDX was chosen as a targeting ligand.

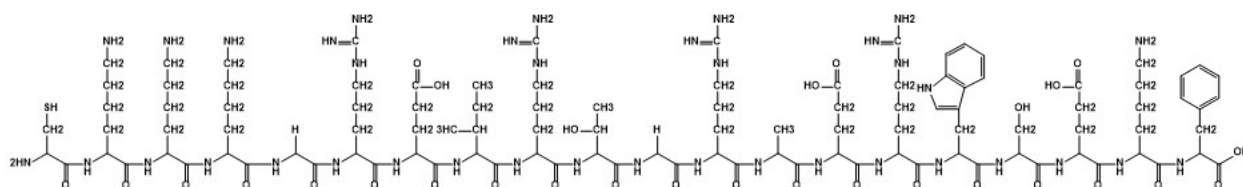


Figure 12: ^DCandoxin

Additionally, two more ligands were chosen as targeting ligands for liposomal use. These ligands target lipoprotein receptors, which appear in high density in the brain, and cross the BBB. The second of the two ligands is the retro-inverse form of the first ligand. The D-isomer

has been shown to survive significantly longer in serum than the first ligand and accumulates to a greater degree in the brain. Due to these ligands' ability to cross the BBB with high efficacy, they were chosen as ligands to be conjugated for experimentation. Due to confidentiality the names of the ligands, sources, and diagrams of the ligands have been omitted.

4.2: Programming Needs Assessment

In order to be effective, the finished program must meet specific criteria. The user interface must be simple and well explained with a user guide and through in-program prompts such that any user with no previous Matlab or programming experience could operate it easily and efficiently. The final visual must be clear and easy to understand, with differences between the specificity indexes being clearly communicated in the gradation of coloration across the display.

4.2.1: Objectives

The visualization program is intended for use by individuals with a focus on biology, as opposed to those who are necessarily well versed in programming. As such, the program needed to be optimized for user friendliness by limiting the required interaction with the user through simple and critical steps. The program additionally needed to be able to import, read, and interpret large quantities of data without crashing and within a reasonable time frame. Finally the program required imaging functionality from its base language, Matlab, in order to be able to effectively produce the 3D brain model.

4.2.2: Functions

The program's ability to process data and the ability to produce images are ranked above optimizing it for user friendliness, as they are important for the actual functionality of the program, as opposed to reducing time consumption during its use.

Table 4: Programming Functions and Specifications

Function	Specification
Take in and manipulate data	Written in a language capable of accepting and manipulating excel files
Produce an image based on acquired data	Written in a programming language with image creation capability
Automate program	Program only requires data and conditions to effectively produce the 3D brain map

4.2.3: Decisions

In order for the program to be capable of carrying out its critical functions (data analysis and image creation), it was decided to create the program in the Matlab programming language. Matlab is a standard data analysis program in the engineering field due to its ability to process large data sets that other data analysis tools, such as Microsoft excel, cannot. Matlab additionally has an inbuilt suite of image creation and manipulation tools. These advantages were determined to more than reconcile Matlab's perceived lack of user friendliness. This characteristic was addressed through the implementation of a user manual and text based prompts in the usage of the program.

4.2.4 Alternative Designs

Following the identification of the selected programming language the team produced and presented to the sponsor two conceptual approaches to the creation of a three dimensional Heatmap of the rat brain. The first conceptual method was the production of a program that

would produce a 3D model of the rat brain by producing colored surface objects (3-dimensional, rotatable images) to represent each region of the brain. These regions would then be assembled together to form the whole rat brain for comparison of uptake across the areas of the brain, with the functionality of Matlab's "slice" command giving the ability to view the internal segments of the rat brain model from any angle. The second conceptual method was the application of coloration to each of the wireframe slices. This would be accomplished by defining each of the regions as they appear in the wireframe so that they could be reproduced as flat colored images by Matlab's fill3 () function. The primary difference between these two approaches is the form taken by the produced 3-dimensional heatmap, as the required data analysis and definition of regions (the processes for which are described in sections and respectively) remain the same. The surface production approach would create a volumetric heat mapped model of the brain which could then be analyzed through the use of Matlab's "slice" command to view its internal components. In contrast the wireframe coloration would produce a representative model of the brain, with stacked 2-dimensional heat mapped slices of the brain forming a 3-dimensional structure with empty space between the slices to allow the visualization of the brain's shape. The surface approach would provide a more understandable visualization of the brain, as it would depict a full rat brain instead of a series of slices. The wireframe approach however depicts the same data with the same degree of efficiency as the surface approach, with the additional advantage of requiring less memory to produce due to the computational disadvantages of the surface objects used in the alternate approach. Despite the less visually pleasing nature of the wireframe approach, it was ultimately selected due to its parity with the surface approach in terms of communicating the data coupled with its lower system requirements.

5: Materials and Methods

With the previously outlined needs, objectives, and goals in mind, the following procedures were developed and enacted. All work was done following NMI's standard operating procedures (SOPs), and is disclosed appropriately according to NMI's confidentiality agreement.

5.1: Materials

L- α -phosphatidylethanolamine transphosphatidylated (Egg, Chicken) (ePE) were purchased from Avanti Polar Lipids (Alabaster, AL). Egg phosphatidylcholine (Lipoid[®] E80) was received from Lipoid GmbH (Ludwigshaffen, Germany). 1,2-distearoyl-sn-glycero-3-phosphoethanolamine-N-[methoxy-(polyethyleneglycol)-2000] (mPEG₂₀₀₀-DSPE) and 1,2-distearoyl-sn-glycero-3-phosphoethanolamine-N-[maleimide(polyethylene glycol)-2000] (ammonium salt) (DSPE-PEG₂₀₀₀-MAL) were purchased from Laysan Bio Inc., (Arab, AL). Dermorphin, Candoxin, Cereport were purchased from A1 BioTech, (Richmond, VA). All other chemicals and solvents used were of the highest available grade.

5.2: Nanoemulsions

5.2.1: Manufacturing

Synthesis of lipidated gadolinium chelate (Gd-DTPA-ePE)

The lipidated gadolinium (III) chelate was synthesized by a revised method used by NMI. A solution of 1 g (1.377 mmol) of L- α -phosphatidylethanolamine transphosphatidylated (egg PE) and 300 μ L of triethylamine in 10 mL of chloroform was added dropwise to a solution of diethylenetriaminepentaacetic dianhydride (DTPA) (4.0 g, 11.197 mmol) dissolved in 200.0 mL of dimethylsulfoxide (DMSO). The mixture was stirred for 3 hours under nitrogen atmosphere at

25°C after which the chloroform was removed by gas nitrogen stream, and the reaction mixture was stirred overnight at 25°C. The mixture was dialyzed (3.5 kDa MWCO) for 2 hours against 15% DMSO, then for 2 hours against 7.5% DMSO, and for 2 hours against 3.75% DMSO in water. For the remaining 66 hours of dialysis, the mixture was dialyzed against DI-water. The mixture was lyophilized for 72 hours to obtain 1.35 g (1.226 mmol) of intermediate DTPA-PE. The crude intermediate so obtained was dissolved in 75 mL of DMSO. The solution of 0.485 g (1.839 mmol) of gadolinium (III) chloride in 3.0 mL of DI-water was added dropwise to the DTPA-PE solution. The solution was stirred overnight at 25°C. Then the reaction mixture was purified by dialysis against 5% DMSO for 2 hours and then a pure DI-water for 70 hours. The solution was lyophilized and 1.41 g (1.124 mmol) of Gd-DTPA-ePE was obtained.

Synthesis of Lapidating Targeting Ligands

Synthesis of DSPE-PEG₂₀₀₀-Demorphin

55.3 mg (0.0188 mmol) of DSPE-PEG₂₀₀₀-MAL was dissolved in 40ml of 50 mM HEPES buffer. 29.1 mg (0.0226 mmol) of free peptide was added to the solution above. Reaction mixture was stirred for 4 hours at room temperature and then 20 hours at 4°C. The next day the mixture was dialyzed at 25°C against DI water using MWCO 6-8K dialysis membrane for 72 hours with frequent water change. Dialyzed solution was frozen and freeze-dried for 72 hours. The yield of the product was 56.7 mg (71.3%) of white powder.

Synthesis of DSPE-PEG₂₀₀₀-Candoxin

13.3 mg (0.0045 mmol) of DSPE-PEG₂₀₀₀-MAL was dissolved in 10ml of 50 mM HEPES buffer. 13.4 mg (0.0054 mmol) of free peptide was added to the solution above. Reaction

mixture was stirred for 4 hours at room temperature and then 20 hours at 4°C. The next day the mixture was dialyzed at 25°C against DI water using MWCO 6-8K dialysis membrane for 72 hours with frequent water change. Dialyzed solution was frozen and freeze-dried for 72 hours. The yield of the product was 20.1 mg (82.2%) of white powder.

Synthesis of DSPE-PEG₂₀₀₀-Cereport

29.1 mg (0.0099 mmol) of DSPE-PEG₂₀₀₀-MAL was dissolved in 20ml of 50 mM HEPES buffer. 19.7 mg (0.0119 mmol) of free peptide was added to the solution above. Reaction mixture was stirred for 4 hours at room temperature and then 20 hours at 4°C. The next day the mixture was dialyzed at 25°C against DI water using MWCO 6-8K dialysis membrane for 72 hours with frequent water change. Dialyzed solution was frozen and freeze-dried for 72 hours. The yield of the product was 31.9 mg (70.1%) of white powder.

Preparation of Theranostic Nanoemulsion

Nanoemulsion formulation with gadolinium and targeting ligand on the surface was prepared by high shear homogenization method using lab scale LV1 Microfluidizer (Microfluidics Corporation, Newton, MA). Aqueous phase of the nanoemulsion formulation was prepared by dissolving egg lecithin (2.4% w/v), and PEG₂₀₀₀DSPE (0.3% w/v) in 4 ml of glycerol-water, to which the appropriate amount of targeting ligand such that 300 molecules were on the surface of each droplet was added. The sample was vortexed for one minute and stirred for 2 h to achieve complete dissolution of all components. Oil phase consisted solely of flaxseed oil for initial testing. Aqueous and oil phases were heated (60°C, 2 min), mixed and then homogenized at 25,000 psi for 10 cycles to obtain the nanoemulsion formulations.

Corresponding non-targeting nanoemulsions were prepared in the same manner without any targeting ligand added.

Nanoemulsion Characterization by Particle size and zeta potential analysis

Particle size distribution of nanoemulsions were determined with dynamic light scattering method using a Zetasizer ZS (Malvern, UK). The samples were diluted in deionized water and the droplet size was determined at 90° angle and at 25°C temperature using refractive index of 1.45. PDI was used as a measure for calculating particle size distribution. The zeta potential value of nanoemulsion was determined with Zetasizer ZS based on the electrophoretic mobility of the nanoemulsion droplets.

5.2.2: Use of Nanoemulsions

In vivo Imaging of Healthy Rat Brains

Variable TR images were acquired using RARE pulse sequence (TE=12.5 and TR: 450, 800, 1400, 2200, 6000, msec.) Images were acquired with a field of view [FOV] 3cm², data matrix = 128×128×20 slices, thickness = 1 mm. T1 measurements were computed using Paravision 5.1 software (Bruker, Billerica, Massachusetts) by fitting absolute signal at particular TR. Isoflurane was constantly supplied throughout the imaging session using a nose cone to maintain a respiratory rate between 40 and 60 breaths per minute. During image acquisition, the respiratory rate was monitored continuously using a small animal heating and monitoring system (SA Instruments, Stony Brook, NY). After the first baseline scan (pre-dose scan) of whole brain, rats were administered a total dose by tail vein injection of targeted nanoemulsion enriched in Gd⁺ (n=7). An additional cohort of animals was also injected with a non-specific Gd⁺-enriched

nanoemulsion (n = 7) as a control. The injection volume was determined using the following equation, which is derived during the manufacturing of the nanoemulsions:

$$\left(\frac{1ml}{0.0159mmol \frac{Gd}{kg}} \right) \times \left(\frac{0.072mmol \frac{Gd}{ml}}{1kg} \right) \times R kg = V ml$$

where R represents the mass of the rat in kilograms, and V represents the volume of injection in milliliters.

In a subsequent study rats (n = 5) were pretreated via an intracerebroventricular (ICV) injection with 40 nano-moles (1.227mg B-FNA in 1ml of 0.9% saline; 16µl of solution) of the selective MOR antagonist B-funaltrexamine hydrochloride (B-FNA) (Tocris Bioscience, Bristol, England) (Martin et al., 1998). Three to four days later they were tested with the targeted nanoemulsion. After dosing, MR scans were commenced to capture post dosing time points of 20min, 40min and 60min.

MRI Alignment and Data Analysis

Each healthy rat brain scan at 0min, 20min, 40min and 60min was registered to a 3D segmented and annotated Rat Brain Atlas (Ekam Solutions LLC, Boston MA.). The alignment process was facilitated by an interactive graphic user interface EVA. The affine registration involved translation, rotation, and scaling in all 3 dimensions independently. The matrices that transformed the subject's anatomy to the atlas space were used to embed each slice within the atlas. All transformed pixel locations of the anatomy images were tagged with the segmented atlas regions, creating a fully segmented representation of each subject. T1 parameter values for each ROI were computed based on each segmented map.

Percent Change

% Change decrease in T1 values at each time point and in each major regions and specific regions was calculated at 20min, 40min and 60min time point as described:

% Change in T1 value

$$= \frac{(T1 \text{ in region 1 prescan} - T1 \text{ in region 1 at post time point})}{(T1 \text{ in region 1 prescan})} \times 100$$

Statistical student's t tests were performed on % change of T1 value for the 174 brain regions of each subject. T-test statistics using a 95% confidence level, 2-tailed distributions, and heteroscedastic variance assumptions were performed.

Specificity Index

With raw T1 relaxation values in hand, data can be compiled from across a cohort and normalized by calculating the specificity index (SPI). Calculating the SPI can be done using the following equation:

$$\frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (Ax_{pre\ 1} - Ax_{t\ 1}) + \dots + \left(\frac{\text{Voxels Section}_n}{\text{Voxels Total}_n} \right) (Ax_{pre\ n} - Ax_{t\ n}) \right]}{n} \Bigg/ \frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (A_{pre\ 1} - A_{t\ 1}) + \dots + \left(\frac{\text{Voxels Section}_m}{\text{Voxels Total}_m} \right) (A_{pre\ m} - A_{t\ m}) \right]}{m}$$

In this equation, “Ax” is the targeted NE and “A” is the non-targeted NE. “Pre” represents the pre-scan that is done before NEs are injection, while “t” is the time point scan done 20, 40, or 60 minutes after injection of the NE. “Voxels Section” refers to the number of voxels for that

specific region of the brain, while “Voxels Total” refers to the total number of voxels in the animal. This part of the equation allows for the normalization of animals with differently sized brains and for sections of different sizes, where “n” is the number of animals in the targeted cohort, while “m” is the number of animals in the non-targeted cohort. When calculating the specificity of the non-targeted NEs, this equation becomes:

$$\frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (A_{pre\ 1}) + \dots + \left(\frac{\text{Voxels Section}_n}{\text{Voxels Total}_n} \right) (A_{pre\ n}) \right]}{n} \div \frac{\left[\left(\frac{\text{Voxels Section}_1}{\text{Voxels Total}_1} \right) (A_{t\ 1}) + \dots + \left(\frac{\text{Voxels Section}_n}{\text{Voxels Total}_n} \right) (A_{t\ n}) \right]}{n}$$

Statistical Significance

A paired t-test was completed using Microsoft Excel software to determine the statistical significance of results between cohorts

5.3: Programming

To accurately convey results to the parties whom they would concern, a visual aid in the form of a heat mapped brain was produced to make SPI and T-test data more understandable and accessible. This was achieved by plotting out the locations in the 3D brain model that corresponded to each of the 174 regions of interest. Regions are then assigned coloration based on the SPI value or the level of statistical significance. This coloration assignment tool was also used to display the theoretical locations of receptors throughout the brain, to allow for

comparison between the hypothesized targeting behavior and the behavior that was observed experimentally.

5.3.1: Quality Control

To ensure that the visualization code worked as intended, the coloration and mathematic analysis code needed to be run through quality control procedures. This ensured that the individual components of the visualization process worked as intended, and were therefore capable of producing an accurate end image. The coloration code was tested by feeding in a series of data sets in which only single regions met the criteria for coloration. The resulting images were then analyzed to confirm the region intended to meet the criteria was colored, and was the sole region assigned color. This procedure was undertaken for all 174 regions of interest across all 63 imaged brain slices.

6: Design Verification

Previous results from NMI and raw results from experiments completed show promise towards the success of this project. This section is a presentation of the raw results for the project, leading to a positive go-ahead for the remainder of the project.

6.1: Nanoemulsions

Each batch of nanoemulsion is tested to ensure that the batch was manufactured within the required limits. The batch is then monitored for up to three weeks to ensure the stability of the nanoemulsions. Stability testing of nanoemulsions includes testing the size, polydispersity index (PDI), and zeta potential of a small aliquot from each batch. Results can be seen in tables 4-7. At the time of testing with the non-targeted nanoemulsion, the nanoemulsion was mostly frozen during transportation to the testing site. A check-up stability test was done with a sample retrieved after MRI scans were completed to ensure no significant damage was done to the NEs.

Table 5: Stability Measurements for Non-targeted Nanoemulsion

Non-targeted Nanoemulsion	Day 0	Day 6
Size (nm)	140.2	155.2
PDI	0.078	0.121
Zeta Potential (mV)	-60.8	-52.0
Zeta Potential Standard Deviation	9.65	13.4

Table 6: Stability Measurements for Dermorphin Nanoemulsion

Dermorphin Nanoemulsion	Day 0	Day 7	Day 14	Day 21
Size (nm)	150.1	143.0	143.0	149.2
PDI	0.061	0.108	0.073	0.095
Zeta Potential (mV)	-40.5	-44.4	-43.1	-42.8
Zeta Potential Standard Deviation	10.5	12.5	9.52	9.41

Table 7: Stability Measurements for Candoxin Nanoemulsion

Candoxin Nanoemulsion	Day 0	Day 7	Day 14	Day 21
Size (nm)	142.2	149.7	147.9	153.9
PDI	0.061	0.129	0.093	0.087
Zeta Potential (mV)	-49.2	-38.1	-39.6	-39.5
Zeta Potential Standard Deviation	12.4	10.5	10.0	9.48

Table 8: Stability Measurements for Cereport Nanoemulsion

Cereport Nanoemulsion	Day 0	Day 7	Day 14	Day 21
Size (nm)	137.1	139.9	146.3	144.0
PDI	0.065	0.108	0.099	0.126
Zeta Potential (mV)	-52.2	-48.3	-34.7	-44.0
Zeta Potential Standard Deviation	13.0	14.1	9.66	11.6

6.2: MRI Raw Results

Upon running MRI scans, the output is a large number of data files that need to be processed to obtain T1 relaxation times (in milliseconds). Reaching the T1 values involves both the manual alignment of the scans to the rat brain atlas, and the use of a custom Matlab code (Day, Lacarra, Sacks, & Sadraei, 2015, unpublished). Dr. Praveen Kulkarni of Northeastern University developed this code and alignment method. A guide for the completion of this alignment process can be found in Appendix B. Completion of this process outputs a Comma Separated Values (CSV) file for each time point scan for the animal with data for each of the 174 regions of the brain. This data includes the number of voxels for the region, the mean T1 relaxation time, and the standard deviation. This data then needs to be further processed to look at the difference in relaxation times for the time points as compared to the pre-scans, and to combine with other animals of the same treatment to take advantage of the power of having a full cohort of animals. This analysis can be done using Microsoft Excel (Appendix C) or with the statistical analysis code the team developed, described in section 6.3.

6.3: Statistical Analysis Program

A statistical analysis program, seen in Appendix E, was developed to automate the data processing, shorten the time needed to process data, and minimize the possibility of human error. This process was previously done in Microsoft Excel many times, giving the team data that could be used to cross-check the output of the program. A guide for the processing of this data in Microsoft Excel can be seen in Appendix C. The program was tested, and found to output the same values as when the data was processed in Microsoft Excel, leaving the team confident in the validity of this program. This output can then be fed into the 3D heat mapping program. A guide for use of this statistical analysis program can be found in Appendix D.

6.4: Heat Map Quality Control

In order to verify that the data processing and image production component of the Heat Map generating program was correct, a quality control procedure was developed and implemented. The data processing component was run with Microsoft Excel files containing primarily zero values in the regions accessed by the program. A value of 1 was placed in the index location of the region the excel file was intended to be used to test. Files with data entered in this manner were produced for all 174 ROIs. The heat mapping function was run testing each individual region on each individual slice and results were compared against the original labeled Rat Brain Atlas slices. A test was considered successful when the area lighting up red on the heat mapped slice matched the index of the “1” on the excel sheet. The marking locations and file indices of slices that demonstrated errors in either area were corrected and retested. Examples of the plotting methodology can be found in Appendix F. Completion of this process gave the team confidence in the integrity of the mapping program.

7: Final Design Validation

As the medical technology developed and researched in this project is expected to have far reaching effects, there are many different areas that are expected to be impacted. These factors will affect different areas such as economic, environmental, ethical, political, safety and health, societal, and sustainability concerns. These areas are explored below.

7.1: Engineering, Industry, and Manufacturing Standards Met

7.1.1: Nanoemulsion Standards

NMI is developing NEs with the ultimate goal of being used to treat humans. To get to that point, FDA approval will be needed. Currently, there are no design standards or regulations from the FDA regarding nanomedicines. Instead, the FDA evaluates each nanomedicine on a case-by-case basis. As described in section 4.3.1, the individual components of the NE will be examined. Another area the FDA will assess is compliance to the regulations outlined in the United States Code of Federal Regulations. Specifically, compliance to Title 21, Section 211: current good manufacturing processes (cGMP) for finished pharmaceuticals (21 CFR 211) will be assessed.

21 CFR 211.22 explains the responsibilities of quality control unit. This regulation states that a quality control unit that has the ability to approve or reject finished product must be established, that this unit must have adequate lab space, that this unit is responsible for approving or rejecting procedures, and that everything this unit does must be in writing. Nemucore is continually testing each batch of NE to ensure all specifications are met.

21 CFR 211.25 and 21 CFR 211.28 describe the qualifications and responsibilities of the personnel engaged in the process. With these regulations, anyone involved in the manufacturing

process must have adequate training, must be dressed with the appropriate personal protective equipment, and must follow appropriate hygiene habits. At NMI, everyone is trained and then observed to ensure they are competent in their abilities. Proper hygiene and adherence to safety protocols are enforced and monitored by an outside supervisor.

21 CFR 211.63 states that equipment used in the manufacturing process must be of the proper design, size, and location. 21 CFR 211.65 states that equipment should be constructed so that it can be used properly, and 21 CFR 211.67 describes that equipment must be cleaned and maintained properly. Section 21 CFR 211.68 states that all electronic equipment should be routinely calibrated and inspected. At NMI, all equipment in the lab is placed to maximize efficiency. All equipment is routinely inspected, tested, calibrated, and maintained as necessary.

21 CFR 211.100 says that all procedures should be written out and followed exactly, and that any deviations from them need to be recorded and justified. NMI maintains a strict set of standard operation procedures (SOPs). These SOPs are followed at all times, and new ones are designed as necessary. The SOPs include the exact equipment that is to be used, meeting 21 CFR 211.105. The SOPs in place also provide guidelines for maintaining sterility and disposing of contaminated components, meeting 21 CFR 211.113.

21 CFR 211.160 provides some general requirements for laboratories. This includes the establishment of specifications for the product(s). NMI has a set of specifications the NEs must fit to be considered acceptable, and each batch is tested to ensure these specifications are met. These tests are typically carried out weekly for three weeks upon the NEs being manufactured, confirming the stability of the NEs and meeting 21 CFR 211.166.

All of the animals used for the MRI studies were purchased through Charles River laboratories and maintained following protocols set in place by Northeastern University. The

housing at Northeastern University meets all required standards, ensuring the 21 CFR 211.173 is met.

NMI has a custom program, Pharma-Designs, that is used to track all information on each batch of NE. This includes lot numbers, and supplier information for every component that is incorporated along the way. Printed reports can then easily be produced as needed, and all information is backed-up onto a server indefinitely. This system meets 21 CFR 211.180, 21 CFR 211.184, 21 CFR 211.186, 21 CFR 211.188, and 21 CFR 211.194.

7.1.2: Programming Standards

The primary engineering standard applying to the Matlab Code is IEC 61508 (International Electrotechnical Commission standard 61508). It is important to note that this is only in regard to the intended future use of the program and heat map. IEC 61508 defines standards of hazard exposure and risk of physical harm to human patients involved in the use and data collection of medical imaging software. The imaging method (MRI) and cohort based data analysis used in this project ensure that patients are safe from both physical harm and the exposure of personal medical information.

In an effort to ensure all patients are properly protected, the team has recommended to NMI that any data which applies to the patient population be stored in a separate xml file in the format outlined by the Dublin Core Metadata Initiative xml schema. The Initiative xml schema guidelines are open to the public intended to allow the more effective storage and sharing of metadata.

7.2: Economic Impact

With the development of the custom program created in Matlab, the economical factor is relatively low. Matlab can be obtained through a license, a cost that customers would have to plan for. Currently the 3D statistical heat map is open source, but if NMI continues to develop the software there is potential for the program to be patented. Once the patent is obtained, NMI would be able to sell the software to obtain a profit.

Regarding the nanoemulsions, the cost of manufacturing involves differing factors. One of these factors is the maintenance of microfluidizer machine, which includes machine parts replacements and personnel maintenance. Additionally there is the cost of obtaining the components as well as the processing. Customized proteins can be costly, and after they arrive at NMI further modification of the tail end of the protein is needed to allow for proper integration with the nanoemulsions.

The specific targeting capabilities of the NEs will enable them to be strong chemotherapeutic agents. The customizable targeting can enable a lower cost of chemotherapeutics to patients, as a lower amount of drug will need to be delivered to the tumor to cause significant results. The chemotherapeutic nanoemulsions are also projected to be less destructive to the body because of their targeting capabilities, which would decrease medical costs for both the patient care facilities and the patients.

7.3: Environmental Impact

The environment can be affected through manufacturing, distribution, and use of a product. With the NEs, strict care is taken in the chemical synthesis of the components and of the final NEs to ensure proper disposal of all waste. Waste removal follows standard laboratory care,

and little waste is created during the manufacturing of the NEs. Shipping costs of the final products will include standard boxes, insulating styrofoam containers, and refrigerating agents such as cold packs. These materials together will ensure the NEs remain cool, as they should be refrigerated at all times. Patient care facilities are expected to dispose of any additional materials as they would biohazardous materials.

With the 3D statistical heat map, one does not have to worry about shipping the software as it can be downloaded. The use of the Matlab code should not greatly affect the amount of energy used by a computer. The general use of a computer on a daily basis will require more power than the use of the created software, and so the impact of the software should not be great on the environment.

7.4: Ethical Impact

For the current status of the project, there were some ethical considerations. Animals were used for the testing of NEs. The rats were cared for properly with humane treatment standards. When this endeavor reaches clinical trials, further considerations will have to be made before it can be approved by a Board of Review. There would be greater regulations and a larger emphasis on all cytotoxic effects. For example, if a component of the NEs causes an adverse effect on the patient, there is the ethical trade-off of treatment versus detrimental health risks. This sort of trade-off can be seen in current cancer treatments, such as chemotherapy and radiotherapy. The safety of the NEs will be a prime area of interest in all future clinical studies.

7.5: Political Impact

Currently this theranostic treatment is a novel guided therapy, with no concrete predecessor in the United States Patent and Trademark Office. As such, the path to patenting this viable technology will be a landmark in medicine if it is registered as the first. Collaborators from Northeastern University will be included due to their contribution of the Rat Brain Atlas and completion of rat MRI cohorts.

In the future, as it is projected for this treatment to be refined and accepted by society, healthcare providers will impact the way policies are handled as patients are treated. Insurance companies, healthcare practitioners and pharmaceutical companies are likely to be involved in the use and regulation of this product. At this time the product is still in the beginning stages, but as more research is completed federal funding may enter the picture as well as larger corporations as their interest increases. The government will assist in the regulation of manufacturing, distribution, and use of all theranostic devices used.

7.6: Safety and Health Impact

In this continuation of a previous project, no additional testing was completed on human cells lines or with human subjects. The visual statistical analysis the coded program outputs creates no health concerns for the user. In the future, as the theranostic treatment will be used for real analysis of NE performance in humans, there will be more thought needed. The NEs targeting capability will need to be confirmed through monitoring, as well as potential systemic cytotoxic effects through inappropriate payload delivery. The therapy will follow FDA standards and regulations, ensuring that the biocompatibility and efficacy of the NEs are not only

acceptable, but exceed all current expectations. Patient safety will be, as always, the primary concern with the application of this therapeutic system.

7.7: Societal Impact

The overarching goal of this project is to create a theranostic drug delivery system with visualization capabilities for glioblastoma multiforme, one of the most aggressive forms of cancer. However, this method of combining the therapy with the real-time imaging of an MRI to confirm targeting opens the door for other potential uses. By attaching Gd^{+} to the nanoemulsions, the visualization accuracy rivals that of PET scans, and the cost of an MRI is typically less. With the application of the imaging technology used here, theranostic treatments could be developed for other brain pathologies, aggressive diseases, or cancers found in the body.

With theranostic NEs as a viable treatment option in the future, patients will reap the benefits from this enhanced form of chemotherapy and recover at a quicker rate. Not as much time will be spent in the hospital trying to regain strength and the lessening of physical strain will lead to a lower emotional and mental strain. In this way both the mental and physical health of cancer patients undergoing this treatment will be improved.

7.8: Sustainability

The 3D statistical heat map allows for an interface that is sustainable, workable, and improvable for years to come. Matlab is a relatively common and simple programming language, and the Matlab platform is compatible across different operating systems. Additionally, if the program was desired to be in a different programming language, the logic and theory behind the

script could be translated into another language. The capabilities of the program allow for better end results as it evolves based on user preference.

With the nanoemulsions, there is not much recyclability as there is with other materials. During the process of synthesizing components of the NEs, it may be necessary to revisit and examine steps and materials to see if there are alternative materials that may lead to a better result.

7.9: Manufacturability

Currently, nanoemulsions are made in-house at NMI. This is a day-long process, and requires extensive preparation in gathering all of the components. Once prepared, batches are known to be stable for at least three weeks. The NMI lab is fully equipped to handle the current manufacturing needs; however, in the future when the project is scaled up and larger batches are needed, a scaled-up manufacturing space and procedure that meets all GMP standards will become necessary.

8: Discussion

8.1: Nanoemulsions

Nanoemulsions were characterized by examining the sizes and Zeta potentials of the particles. While the sizes were in the range of 130-160 nm, publications NMI has been a part of in the past have shown nanoemulsions to be used for cancer therapy in the range of 130 – 150 nm with a PDI of 0.1 or lower. Additionally, previous Zeta potentials were in the range of -40mV to -50mV with standard deviations up to ± 13 mV (Ganta et al., 2014A; Ganta et al., 2014B; Ganta et al., 2015), and the Zeta potentials of these NEs were in the range of -30mV to -50mV, with standard deviations up to ± 13 mV. While the results are not exactly the same at every measurement, the ranges are similar to that of values previously published by NMI for different purposes, and therefore considered a success.

8.1.1: Dermorphin Nanoemulsions

Mapping of the MOR shows high levels of receptor to be present in the Basal Forebrain and the Thalamus. A full map of the MOR can be found in Appendix G. With the Dermorphin NE, it was expected that accumulation of nanoemulsion would be seen in these MOR rich areas. While not every ROI matched up perfectly, there was some significant NE accumulation in these areas. Appendix K shows the complete voxel-weighted SPI results for all three time points of the cohort (n=7) tested with the Dermorphin NE, as compared to the cohort (n=7) of animals treated with the non-targeted NE.

8.1.2: Dermorphin Nanoemulsions upon Blocking of the Mu-Opioid Receptor

The proof-of-concept experiment that was done was to treat the animals with a component that would block the receptor, therefore out-competing the nanoemulsions. It was decided that if the nanoemulsions were indeed being targeted to the receptor they were designed for, which was now blocked, the nanoemulsions would have the same effect as the non-targeted nanoemulsions. Originally, naloxone was identified as a MOR antagonist (Wand et. al., 2011; Usenko et. al., 2002). Upon further research and analysis of the results of an experiment where animals were dosed via the tail vein catheter with Naloxone (2mg/kg in 0.9% saline) 10 minutes before the nanoemulsion injection, it was discovered that naloxone was cleared from the brain in about 40 minutes (Glass et. al., 1994), and therefore was washing out before the completion of the MRI scans. These results can be found in Appendix M.

Further research identified β -funaltrexamine hydrochloride (B-FNA) as an irreversible MOR antagonist, with slight Kappa-opioid receptor (KOR) agonistic properties (Martin *et. al.*, 1998). This proof-of-concept experiment was then repeated with B-FNA as the MOR blocker, as described in section 5.1.2.

The results from testing dermorphin NE on a cohort (n=5) that had been pretreated ICV with 40 nano-moles of B-FNA in 0.9% saline did not match the non-targeted NE results as predicted, but did show a difference in where the NE was accumulating in the brain. NEs appear to be accumulating in the Diencephalon, an area with some MORs, but not an area where the unblocked dermorphin NEs or the non-targeted NEs accumulate. The Olfactory Bulb, an area with some MORs present, shows NE accumulation without B-FNA blocking, but shows no NE accumulation when B-FNA is present. A full map of these voxel-weighted SPI results at 20, 40, and 60 minutes can be seen in Appendix L.

After ICV treatment of B-FNA, the animals were given 3 to 4 days to recover before use in this experiment. As B-FNA is a MOR antagonist, it is possible that there was a slight up-regulation of MOR receptors over this time period. These new MORs would be unblocked, and therefore provide a location for the dermorphin NEs to bind. As a KOR agonist, it is likely that the KOR was affected by the B-FNA. Further research will be required to understand KOR expression in the brain, investigate dermorphin's avidity for the KOR, and to determine if KORs or Delta-opioid receptors (DORs) may be providing alternate binding sites for the dermorphin NEs.

8.1.3: Candoxin Nanoemulsions

A receptor map of the Alpha-7 receptor, which can be found in Appendix H, shows high levels of the Alpha-7 receptor to be expressed in the Frontal Lobe, Hippocampal Formation, Amygdaloidal Nuclear Complex, and the Tectum. Analysis of the Candoxin NE SPI values over the 20, 40, and 60 minute time points (seen in Appendix N) show accumulation in the Frontal Lobe, Limbic Lobe, Insular Cortex, Thalamus, and Epithalmus. It seems as though many NEs are limited in where they are able to reach. While these results are not exactly as hypothesized, further analysis of how the NEs are being transported through the brain may explain these results more clearly.

8.1.4: Cereport Nanoemulsions

Analysis of the B2BR location throughout the brain shows this to be a very prevalent receptor. Particularly high areas of receptor include the Diencephalon (Hypothalamus, Pituitary, and Thalamus), the Hippocampal Formation, the Amygdaloidal Nuclear Complex, the Limbic Lobe, and the Basal Ganglia. The cohort (n=7) that was tested with the Cereport NEs, showed

NE accumulation in the Diencephalon, Hippocampal Formation, Amygdaloidal Nuclear Complex, and Cerebral Peduncle. While not perfect, these results are very promising toward the future of these Cereport NEs. Full results of the SPI values for this cohort as compared to the non-targeted NE cohort (n=7) across the 20, 40, and 60 minute time points can be found in Appendix O.

8.2: Entry into the Brain

An original hypothesis of this project was that the NEs were entering the brain by adsorptive transcytosis through the BBB. It was thought that the lipid core of the NE was recognized as a natural fat by the brain, allowing it to pass through. Further analysis of results, particularly those of the non-targeted NE (found in Appendix J), have challenged this theory. Research of the flow of CSF through the brain has shown to be similar to the locations of the non-targeted NEs. Specifically, the CSF enters through the brain stem in the center, flows around the front, up over the top, and then flows out through the Metencephalon, Mesencephalon, and the Medulla Oblongata. An increased amount of non-targeted NE can be seen in the Metencephalon, Mesencephalon, and the Medulla Oblongata, right where the CSF would accumulate. Since it is known that the blood-CSF barrier is easier to cross than the BBB, it is possible that the NEs are entering the CNS through the blood-CSF barrier and then entering the brain. An easy location for this entry could be the Choroid Plexus, the region of the brain that produces CSF. Permeability is enhanced at this region to allow for easier passage of necessary nutrients and large molecules. Given the research that was completed in this study, a final conclusion on how the NEs are entering the brain cannot be drawn; however, future research should take this possibility into account and explore it further.

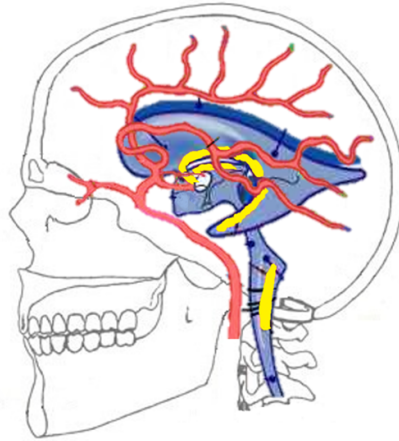


Figure 13: Brain Vasculature and CSF. Image depicts the major brain vasculature, in red, and CSF, in blue. Location of the Choroid Plexus is indicated by the yellow.

8.3: Statistical Calculations Program

The statistical code is a program to efficiently calculate and process the T1-relaxation times into usable SPI and t-test values for the heat map program. This program was written using Matlab and provides a user friendly interface with which users can provide input files for processing. The code removes the need to perform the calculations by hand and is more efficient, accurate, and reliable than the previous method using Microsoft Excel, as it does not allow for user error in copying, pasting, and equation actions.

8.3.1: Motivation for Development

After the images from the MRI are processed by the atlas and the T1-relaxation times are received, the SPI value needs to be calculated. For each rat, there are about 5,000 data points to evaluate and calculate. Once these data points are analyzed and the SPI values and respective t-test are calculated, they must be organized into the 174 regions of the rat brain. This formatted data sheet is then sent to be processed through the Heat Map program. Originally all of these

calculations were completed in multiple Excel sheets. This process not only took 4 hours per rat, but also lent itself to human error in data calculations. The statistical code was developed in order to create a system to be able to process the MRI data and go from MRI scan to heat map quickly and efficiently. Utilizing this program, a cohort can be processed in about two minutes, with no errors. The added benefits of having this code made are the reduction of needed training to carry out the statistical calculations, the reduction of time needed, and the increased accuracy. In addition, if there are changes that are needed in the equations in the future the changes can be easily reflected in the code.

8.3.2: General Code Structure

The code is written in an object-oriented style. Many different aspects of the data files are represented as “objects” within the code. Each object contains properties which define its characteristics, as well as methods that define which part of the analysis the object is responsible for. When combined, these objects produce spreadsheets containing SPI values for each cohort.

The program is designed in a hierarchical structure. At the top of the hierarchy are the objects responsible for rendering the user interface. The user provides a “manifest” file which provides details about each data file. For each file, the manifest specifies the location of the file on disk, the treatment the file belongs to, and the time point of the file. The program reads in the manifest file and passes the collection of data files to the “SPI analysis” object. The SPI analysis object organizes each data file into its own “treatment file” object. The treatment file objects each contain a unique list of “rat” objects, each of which represent a rat within the cohort. The SPI analysis object uses each of these objects in the hierarchy to perform calculations on the data and produce the resulting output file.

8.3.3: Accuracy Against Excel Calculations

Once the code was written, the data points were compared with the Microsoft Excel calculated values to ensure that the calculations were being carried out correctly. The numbers matched between the user done and code completed calculations. It is also important to note that Matlab's "format long" parameter keeps values to the 15th significant digit after the decimal point, unlike Microsoft Excel which only keeps the 15th significant digit overall. Therefore, the values from the statistical code are equivalent to those calculated using Microsoft Excel.

8.3.4: Troubleshooting

Upon completion of the code, there was an issue that came up with compatibility between the computer that the code was written and originally run on and the computers at Nemucore. The difference was in the versions of Matlab on the computers which affected the User Interface. The User Interface was written using a 2015 version of Matlab, but the computers at Nemucore have the student's 2014 version of Matlab. This problem led to the code having to be changed in order to accommodate for the older version so that the company can use the program after this project is completed.

The final issue faced was ensuring the output was compatible with the next step in the project pathway. The regional data input for the heat map program had to be structured in a specific way in order to make sure that the correct coloring was placed in the correct regions of the brain. Since the program's output was the input for the heat map program, code had to be added to include the necessary formatting function.

8.3.5: Final Product

With these issues fixed and the code now downloaded and functional on Nemucore's computers, the company has the ability to process the T1 relaxation times into SPI and t-test data in about two minutes. The steps and exact guide on how to use this program are outline in a user guide, which can be found in Appendix D. A print-out of the code with all necessary comments can be seen in Appendix E.

8.4: 3D Heat Map

In order to allow the visualization of the data produced by the data analysis program, the task of producing of a 3D heat mapping program was set. The criteria for this program included taking in data previously outputted from the statistical analysis code, analyzing data to determine cut-off values for categorizing NE uptake for each region, and imaging the uptake for each discrete region of the brain using a white to red gradient, all with minimal input from the user.

8.4.1: Development Process

Upon the start of the project, Nemucore gave a client statement of utilizing the wireframe Rat Brain Atlas developed previously (Day, Lacarra, Sacks, & Sadraei, 2015, unpublished) to develop a 3D heat map to demonstrate NE uptake across the brat brain. To begin, a simple example program demonstrating the function of the intended code was produced, which placed colored circles into each region to denote NE uptake. This result was approved by Nemucore, and a program that applied color to each brain region instead of labeling them with colored circles was put into production. This program was also designed to produce a user friendly interface to allow for continued use with individuals not fully versed in Matlab code.

8.4.2: Program Components and Functional Process

The main feeder program, “UseableMapFeedSPI,” calls the data storage file “plotable.mat,” which contains the wireframe rat brain atlas produced previously (Day, Lacarra, Sacks, & Sadraei, 2015, unpublished), as well as the region coloring function “slicemap” that comprises the majority of the program’s functionality. The feeder program, “UseableMapFeedSPI” loads the storage file and consults the user for input. The input prompt asks for the file to pull SPI data from, slice identifier number, and which time point the user wants to image. The “UseableMapFeedSPI” program then calculates the cutoff points for heat map coloration and sends the SPI values, the cutoff values, and region defining points for the specified slice number to the “slicemap” function to overlay the relevant slice of the wireframe on the colored regions and produce a heat mapped slice image. The “UsableMapFeedSPI” program can be found in Appendix Q. The “slicemap” function can be found in Appendix R.

The variant of this program, which is used to produce a heat mapped model of the entire brain, also contains a call to the “plotable.mat” file and the “slicemap” function. This feeder program, “UseableMapFeedSPIALLATONCE,” loads the storage file and asks the user for the input file and the time point. The “UseableMapFeedSPIALLATONCE” then calculates the SPI cutoff values, and sends the SPI values, cutoff values, and region defining points for the regions of each of the 63 slices to the ”slicemap” function. The “slicemap” function then overlays all 63 slices of the wire frame over the colored regions and procures a full 3D heat map of the data.

The “slicemap” Function

The “slicemap” coloration function contains a call to the fill3 () function in the Matlab imaging library. It takes in the region defining points, the SPI value for the region, and the cutoff values. The function then determines if the SPI value is above, below, or equal to each of the cutoff values and assigns coloration to the region accordingly. Output from the program is seen in a slice with regions colored based on a scale, representing no significant signal to high significant signal.

8.4.3: Issues faced

The most significant challenge in the process of producing the 3D heat map was in defining each of the regions based on the locations of points in the wireframe. This was carried out through the use of the analysis tools provided in Matlab’s figure viewing window, primarily the line following tool. This tool was used to highlight individual points that occupied important positions for the definition of each of the regions and display the x, z, and y coordinates of said points. These coordinates were then recorded for each defining point for each region. This process was at high risk for error, as mistakes in the entry of a point location could throw off the shape and location of a displayed slice in the final program. Additionally, this process had a limited accuracy due to distortion present in the original wireframe, causing some of the produced images to appear to be deformed.

The next large issue in the construction of the program involved converting the code into a user friendly state. Matlab is sensitive to changes in capitalization, which can lead to difficulty in recognizing and calling the correct variables. Various variables had originally been defined similarly to previous code received from NMI’s partners at NEU, but were found to be

inconsistent. This resulted in a debugging process which involved addressing each line of code that returned an error message. By capitalization of some called variables, and initializing common capitalization variants of other variables, the issue was resolved.

8.4.4: Final Product Use

The use of the final product was streamlined to minimize the required input from the user. This expansion of use demonstrates the capability of this program to be used without intensive training. Someday, this may be applied so that other researchers and clinical practitioners will be able to effectively use this technology. To run, ensure all required files are in the same folder as the program. The files required include the source file for the data, the coloring function “slicemap”, the “plotable.mat” storage object, and the feeder program itself, either “UseableMapFeedSPI” or “UseableMapFeedSPIALLATONCE.”. With these, the user simply needs to run the feeder program and enter the desired data source, slice number, and time point to produce an image when prompted. A user guide, found in Appendix P, contains specific details for successful use of the program. The raw code for these programs can be found in Appendix Q.

8.4.5: Interpretation of the Heat Maps

The produced images indicate which areas of the brain have an accumulation of NEs as compared to that of the non-targeted NEs through the calculation of the SPI. The colored regions are those in the top quartile of SPI values, or those that had the most increase of accumulation from the non-targeted NE to the targeted NE. A yellow to red scale which increases every 5th percentile from 75% up is used to demonstrate different SPI values. A white area indicates that

the SPI value for that region was not in the top quartile. The heat map images indicate in a visual manner where the targeted NE is accumulating as opposed to the non-targeted NE on a cohort basis, leading to easy interpretation by those less familiar with the 174 ROIs, but knowledgeable about the geography of the brain.

8.5: The Receptor Mapping Program

To analyze the effectiveness of different targeting ligands in reaching the desired receptors, the 3D heat mapping program was expanded to create 3D maps of the Mu-Opioid, Alpha-7, and B2 Bradykinin, receptors. These maps, which can be produced as single slices as well as the entire brain, function the same way as the SPI heat mapping program. Receptors were mapped on a teal scale, with dark teal being low levels of receptors and bright teal being high levels of receptors. Tan was used to represent a region with no receptor. The receptor values that are represented in these heat maps come from autoradiography studies that were found in literature. The receptors were classified numerically as outlined in Table 9 to allow them to be read by the feeder program “receptorMap” and mapped onto the rat brain atlas using the “slicemap” program.

Table 9: Receptor Expression Conversion

Receptor Expression	Alphabetical Value	Numerical Value
None	N/A	0
Patchy	P	1
Low	L	1
Medium to Low	M-L	2
Medium	M	3
Medium to High	M-H	4
High	H	5

The Mu-Opioid Receptor map can be found in Appendix G, the Alpha-7 Receptor map can be found in Appendix H, and the B2 Bradykinin Receptor map can be found in Appendix I. The “receptorMap” feeder program can be found in Appendix S.

9: Conclusions and Recommendations

In conclusion, this technology has the potential to revolutionize drug delivery to the brain. Instead of being satisfied with just getting the drug across the BBB and into the brain, researchers will be able to go one step further in targeting medicines to the specific lobes of the brain where the drug is needed. With applications in Glioblastomas and other brain diseases, these theranostic nanoemulsions have great potential to revolutionize neuro-medicine. The ability to cross the BBB and reach specific lobes of the brain via systemic delivery will allow many current therapeutics to be used without the need for an invasive brain surgery.

The visualization program that was designed and created with this project brings health care professionals the ability to visualize uptake to investigate the effectiveness of different targeting ligands used to deliver drugs to highly specific ROIs. Many current heat maps only allow for visualization of the surface of the brain. The ability to examine 400 μ m thick cross-sectional slices of the frontal plane from anywhere along the length of the brain provides increased accessibility to areas not on the surface of the brain. This program also allows for quantitative analysis of the 174 ROIs, opening up the ability to perform statistical analysis on the results.

9.1: Limitations

As this technology continues to be explored, there are a few limitations to be aware of. The nanoemulsions have been tested to be stable for up to 21 days. Beyond that, there are no guarantees. This short “shelf-life” would make clinical use a challenge, for new nanoemulsions would have to be made just before use. The possibility of freezing for storage may be an option, but extensive studies would be needed to make this an option. A batch of non-targeted

nanoemulsions was accidentally frozen, and when thawed the stability testing was still in an acceptable range, showing promise for this. When freezing, it would be important to ensure that ice crystals did not form and burst the nanoemulsions, but use of a cryo-protectant such as Dimethyl Sulfoxide (DMSO) would introduce toxic side effects to the drug. Freezing to increase shelf-life may be a possibility, but shelf-life would currently remain as a limitation to this technology.

Economics are another major limitation of this technology. Nanoemulsions can be customized with the drugs and targets that the patient needs most, but the customization of the drugs can become very expensive very fast. Additionally, MRI scanning is expensive and time consuming, and requires a highly trained technician and access to a machine. While money should never limit a patient receiving the care they need, this technology will need to become more economic to reach its full potential.

9.2: Other Applications of this Technology

While this project set out with GBM as the primary target for the theranostic system developed, there are additional applications of this technology. Various brain diseases, such as Alzheimer's, Parkinson's, and PTSD could one day benefit from this application of medical technology. Alzheimer's has been investigated using rivastigmine, which inhibits acetylcholinesterase and butyrylcholinesterase, as a therapeutic treatment. This molecule is unable to pass through the BBB (Wilson, et al., 2008), however, when combined with a targeted drug delivery system, the amount of drug able to reach the intended location would be much higher and therefore result in an improved therapeutic system. One of the receptors targeted in this project, the $\alpha 7nAChR$, has also been identified as a target for slowing the progression of

Parkinson's disease (Quik, et al., 2015). Parkinson's is often treated with levodopa, which helps to continuously produce dopaminergic stimulation, but this can cause dyskinesia, or impairment of intended movement (Olanow, et al., 2006; Quik, et al., 2015). By targeting the $\alpha7nACh$ receptors, the dyskinesia effects can be reduced (Quik, et al., 2015). Additionally, levodopa could be loaded into a theranostic delivery modality to allow for increased systemic delivery time and for a greater amount of total levodopa to reach the target site. A longer-term release of the levodopa would also aid in reducing the dyskinesia experienced (Olanow, et al., 2006).

There have been two receptors identified as having abnormal function in patients with PTSD, serotonin and GABA_A (Liu, et al, 2013; Randall, et al., 1995). One of the serotonin receptors, 5-HT1A, has been shown through research to be involved in anxiety and in regulating mood (Luo, et al., 2011). As 5-HT1A is effected over a variety of areas in the brain by PTSD (Liu, et al., 2011; Liu, et al., 2013; Luo, et al., 2011; Wang, et al., 2009), this receptor, if targeted with a theranostic, could lead to an opening of improved treatment, therapy, and research of serotonin-PTSD effects. Benzodiazepines (BZDs) work with the GABA_A receptors to increase the inhibitory effect of the GABA neurotransmitter. This in turn leads to an inhibition of anxiety, an increase in sedation and relaxation of muscle, and cognitive effects (Ravindran & Stein, 2009). Various BZDs are used as a supplemental treatment of PTSD, usually to treat irritability, hyper-awareness, and sleep disturbance, but there is still a need to further research this class of molecules with the GABA_A receptor (Mohamed & Rosenheck, 2008; Ravindran & Stein, 2009). Using theranostic agents with a BZD conjugated to the surface could be used to expand the research of the GABA_A receptor and the role of BZDs in treating PTSD.

9.3: Future work

As the project continues and NMI grows as a company, there are many actions to continue this project and move it closer to reaching the ultimate goal of curing patients. While some items can be done in the immediate future, others will occur further along in the pharmaceutical development process. Immediately, the team suggests the testing of the four new targeting peptides that have been designed and made. These peptides were designed with the goal of being tested in the project, however various delays and the use of the original peptides prevented the team from testing the new peptides. With the peptides already in stock at NMI, this would be a good place for a future team to pick-up. Section 4.1.5 provides an outline of these peptides.

The NMI-800 nanoemulsion is not currently loaded with any chemotherapeutic agent. NMI has shown the possibility of loading nanoemulsions with a variety of different chemotherapeutic agents; however, the challenge of finding the optimal drug(s) for the NMI-800 series nanoemulsions remains open. Future teams may want to look at the creation of the nanoemulsions with different drugs for both stability and effectiveness. These nanoemulsions can then be taken into pre-clinical and clinical trials by NMI as promising data is acquired.

As outlined in section 9.2, there is great potential for this technology to have many applications in other brain diseases. While section 9.2 provides a brief outline of some of these possibilities, a great deal of research will be needed to bring this project to these different applications. Teams will be able to look at different receptors to target, targeting ligands, and drugs to deliver to the specific areas of the brain.

10: Glossary

Alpha-7 nicotinic Acetylcholine Receptor ($\alpha 7$ nAChR) – a type of nAChR that is a homo-pentamer composed of five α -7 subunits. It is located in the brain, spleen, and lymph nodes and its activation increases Ca^{2+} permeability. It is located on the endothelial cells of the blood-brain barrier, and has been shown to be involved in angiogenesis and cancer mediation/proliferation.

β -funaltrexamine (B-FNA) - an alkylating antagonist of the opioid receptor that is selective for Mu Opioid Receptors, so much so that by binding to the Mu Opioid Receptors it is a valid indicator of the receptor locations.

Blood Brain Barrier (BBB) - the mechanism that controls the passage of molecules from the blood into the cerebrospinal fluid and the tissue spaces surrounding the cells of the brain and thus protects the brain from the effects of substances harmful to it. The endothelial cells lining the walls of the brain capillaries are more tightly joined together at their edges than those lining capillaries supplying other parts of the body, which allows the passage of solutions and fat-soluble compounds but excludes particles and large molecules.

B2 Bradykinin Receptor (B2BR) – a G-protein coupled receptor for Bradykinin. Activation of this receptor induces vasodilation, as well as increasing vascular permeability. It is expressed throughout most tissues in the brain to varying degrees.

Central Nervous System (CNS) - The part of the nervous system consisting of the brain and the spinal cord. This are is highly protected from the rest of the body.

Cerebral Spinal Fluid (CSF) - A clear, colorless bodily fluid found in the brain and spine that provides mechanical and immunological protection to the brain.

Computer-Aided Diagnostics (CAD) - The use of computer software to improve diagnostics through obtaining lateral images which allow for early diagnostics of a disease.

Current Good manufacturing Processes (cGMP) - A set of regulations set in place by the United States Food and Drug Administration outlining standards that must be met during a given manufacturing process.

Delta-Opioid Receptor (DOR)- a class of opioid receptors found in the olfactory bulb, cerebral cortex, nucleus accumbens and the caudate putamen. DOR receptors are located presynaptically on primary afferents where they inhibit the release of neurotransmitters. Through both spinal and supraspinal sites, the receptor is involved in the antinociceptive/analgesic actions of some opioids. (McDonald & Lambert, 2005)

Diethylenetriaminepentaacetic acid (DTPA) - A linker used to attach Gd^{+} to the PEG-ylated surface of the nanoemulsion.

Enhanced Permeability and Retention (EPR) Effect- The property by which molecules of certain sizes tend to accumulate in tumor tissue much more than in normal tissue.

Epidermal Growth Factor Receptor (EGFR) - A cell surface receptor that binds to epidermal growth factor.

Food and Drug Administration (FDA) - A branch of the United States government that regulates the manufacturing quality and safety of food, drugs, and medical devices with the goal of protecting public health.

Flow Cytometry- a laser-based technology in which cells are passed single-file through a light beam that is set to excite fluorescent markers, while a detector analyzes fluorescent signals emitted from the cells. This system allows high throughput quantitative analysis of cells through the use of fluorescent markers.

Gadolinium (Gd⁺DTPA) – An imaging agent that can be attached to the surface of the nanoemulsions which will alter the T1 relaxation time of the MRI and therefore enable imaging of the nanoemulsions *in vivo*.

Glioblastoma Multiforme (GBM) - A glioma consisting chiefly of undifferentiated anaplastic cells frequently arranged radially about an irregular focus of necrosis, usually occurring in the cerebrum of adults. Also called grade IV astrocytoma.

Good Manufacturing Practices (GMP) - An industry recognized standard for manufacturing of drugs that ensures the drugs are made in an acceptable sterile manner.

Intracerebroventricular (ICV) - A type of injection that involves opening up the skull and delivering the drug directly to the brain.

Kappa-Opioid Receptor (KOR) - a class of opioid receptors that does not cause respiratory depression. KOR agonists display an anti-opioid action attenuating analgesia elicited by endogenously released or exogenously administered MOR agonists. This action is caused by a distinct distribution of KOR receptors on primary cells located within the nucleus raphe magnus, a group of cell bodies situated in the midbrain. (McDonald & Lambert, 2005)

Magnetic Resonance Imaging (MRI) - diagnostic medical imaging technologies that uses strong magnets and pulses of radio waves to manipulate the natural magnetic properties in the body to generate a visible image.

Mu-Opioid Receptor (MOR) – a class of opioid receptors that distinguish themselves from other classes by their high affinity for enkephalins and low affinity for dynorphins. They are primarily found in the tissue of the CNS, with their secondary location in the intestines. They are G protein-coupled receptors with opioids as their primary antagonist.

Nanoemulsion (NE) - A nano-sized droplet of oil contained in water, with a surfactant phospholipid monolayer creating a barrier between the immiscible liquids, creating a micelle-like structure. They are created through a high stress, mechanical-extrusion process that creates droplets of uniform size.

Nemucore Medical Innovations, Inc. (NMI) - clinical development company dedicated to the development and commercialization of life-saving molecularly targeted therapeutics for the treatment of multi-drug resistant cancers.

Nontargeted (NT, A) - Having no receptor ligands on the surface, but still incorporating all other aspects of the drug delivery system, see Targeted for definition.

Normalization- The normal distribution is one of the key distributions providing the basis for probability statistics, so that when a particular distribution is not normal, some transformation of the data may be attempted so as to achieve a normal distribution—for example charting the logarithms of values instead of the values themselves. This is known as normalizing the distribution.

Polydispersity index (PDI) - A measure for calculating particle size distribution.

Positron Emission Tomography (PET) - An imaging system that detects gamma ray emission from radioactive tracers.

Rat Brain Atlas (RBA) - a 3D, segmented, annotated atlas was developed from high resolution anatomical MRI images obtained from male adult rats. The output file delineates each region uniquely. They are suitable for further numerical analyses such as constructing pixel image data set (of any size) or surface mesh.

Region of Interest (ROI) - A specific geometrically defined area of the brain that serves a specific function based off of its location

Stem Cell-Like Glioma Cells (SCLGCs) - Cells within a glioma population that share characteristics with neural stem cells. These cells promote tumor angiogenesis through vascular angiogenesis growth factor.

Subsystem of Brain - A grouping of region of interests that comprise a larger area of the brain that has a multitude of functions.

Specificity Index (SPI) - the condition of being peculiar to a particular individual, region, or group of organisms.

T1-weighted image - A basic pulse sequences in MRI and demonstrates differences in the T1 relaxation times of tissues, used with softer tissue types.

Temozolomide (TMZ) – An alkylating agent used as a first-line chemotherapeutic for Glioblastoma Multiforme.

Theranostic – development of more specific individualized therapies for various diseases, and to combine diagnostic and therapeutic capabilities into a single agent.

Three-Dimensional (3D) - The quality of having defined dimensions along the x-axis, y-axis, and z axis.

Transcytosis- A mechanism for transcellular transport in which a cell encloses extracellular material in an invagination of the cell membrane to form a vesicle, then moves the vesicle across

the cell to eject the material through the opposite cell membrane by the reverse process. Transcytosis is also known as vesicular transport.

Targeted- The process whereby a newly synthesized molecule is directed to its correct location within the cell. Receptor targeting is determined by short sequences of ligands on the surface, which direct it to the correct destination

T-test - A test to calculate the probability that mean values for a particular measurement are significantly different in two sets of data.

Vascular Endothelial Growth Factor (VEGF) - A signal protein produced by cells that stimulates vasculogenesis and angiogenesis.

Voxel - short for 'volume element', the volume of tissue in a body that is represented by a pixel in a cross-sectional image.

World Health Organization (WHO) - a specialized agency of the United Nations that focuses on international public health.

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Appendix A: Project Timeline

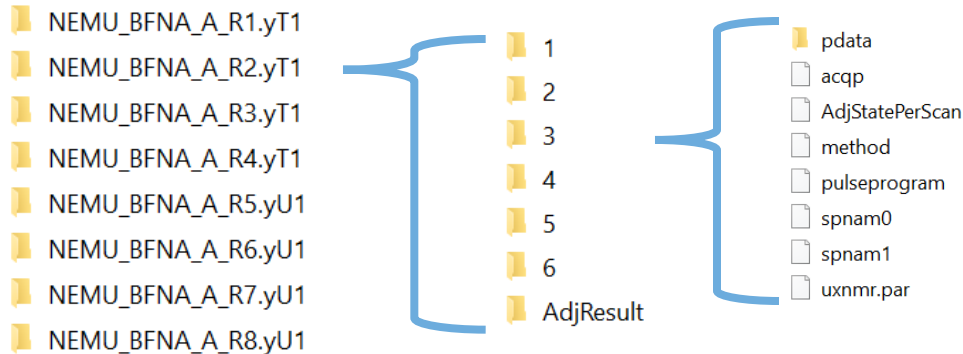
Task Name	Duration	Start	Finish
Overall MQP Project	176 days	Thu 8/27/15	Thu 4/28/16
Weekly meetings with TPC	161 days	Wed 9/9/15	Wed 4/20/16
Bi-weekly Call with Dr. Ferris/Praveen	161 days	Wed 9/9/15	Wed 4/20/16
Bi-Weekly Meeting with Prof. Lee	151 days	Mon 9/21/15	Mon 4/18/16
A-term 1: Introduction	17 days	Thu 8/27/15	Fri 9/18/15
Background Reading	123 days	Thu 8/27/15	Sat 2/13/16
NMI's Technology and research that has already been done	7 days	Thu 8/27/15	Fri 9/4/15
2014 BME MQP and 2013 Biochem MQP	7 days	Thu 8/27/15	Fri 9/4/15
BBB structure, function, and penetraton	5 days	Mon 9/7/15	Fri 9/11/15
Brain Diseases	5 days	Mon 9/14/15	Fri 9/18/15
Brain anatomy and physiology	5 days	Mon 9/14/15	Fri 9/18/15
What is MRI and how we can use it	5 days	Mon 9/14/15	Fri 9/18/15
Current Matlab heat map programs	12 days	Thu 8/27/15	Fri 9/11/15
Discussion of Overall Problem	3 days	Wed 9/16/15	Fri 9/18/15
Formal Hypothesis and Outline of Experiments	1 day	Fri 9/18/15	Fri 9/18/15
A-term 2: Specific Literature Search	21 days	Fri 9/18/15	Fri 10/16/15
Specific Literature Review	21 days	Fri 9/18/15	Fri 10/16/15
Glioblastoma receptors expressed	5 days	Mon 9/21/15	Fri 9/25/15
Irreversible blocking of receptors	5 days	Mon 9/21/15	Fri 9/25/15
Drugs used for glioblastomas and other brain diseases	5 days	Mon 9/21/15	Fri 9/25/15
Matlab functions to go from MRI to visual data	10 days	Mon 9/21/15	Fri 10/2/15
Using the rat brain atlas	6 days	Fri 9/18/15	Fri 9/25/15
Write Literature Review and Introduction	20 days	Mon 9/14/15	Fri 10/9/15
A-term 3: Phase 1a Experimentation for MQP	15 days	Mon 9/28/15	Fri 10/16/15
Lab Training	3 days	Mon 9/28/15	Wed 9/30/15
Make new A2 nanoemulsions	2 days	Mon 9/28/15	Tue 9/29/15

MRI with A2 and B-FNA	3 days	Wed 9/30/15	Fri 10/2/15
Alignment of Scans in Atlas	1 day	Mon 9/28/15	Mon 9/28/15
Statistical Analysis of Data	1 day	Mon 9/28/15	Mon 9/28/15
Intro, lit review, project strategy chapters due	0 days	Thu 10/15/15	Thu 10/15/15
Review Data and Alter Plan	7 days	Fri 10/16/15	Mon 10/26/15
B-Term: Phase 2a Experimentation for MQP	38 days	Tue 10/27/15	Thu 12/17/15
Data Collection Phase 1	38 days	Tue 10/27/15	Thu 12/17/15
Make new nanoemulsions: A2, A3, and A4	19 days	Tue 10/27/15	Fri 11/20/15
Run MRIs	25 days	Mon 11/2/15	Fri 12/4/15
Alignment of Scans with Atlas	1 day	Tue 10/27/15	Tue 10/27/15
Statistical Analysis of MRI results	1 day	Tue 10/27/15	Tue 10/27/15
Mapping of 63 brain slices	1 day	Tue 10/27/15	Tue 10/27/15
Break down of Statistical Analysis Code	1 day	Tue 10/27/15	Tue 10/27/15
Review Literature Review and Add or Remove Sections	25 days	Tue 10/27/15	Mon 11/30/15
Meet with Susan to Discuss Intellectual Property	0 days	Thu 12/10/15	Thu 12/10/15
Review and finalize first 4 chapters of paper	9 days	Mon 12/7/15	Thu 12/17/15
Intro, lit review, project strategy, alternative design, design verification chapters due	1 day	Thu 12/17/15	Thu 12/17/15
Review Data and Establish Future Experimental Plan	1 day	Mon 12/21/15	Mon 12/21/15
C-Term1: Phase 2b Experimentation for MQP	23 days	Thu 1/14/16	Sat 2/13/16
Data Collection Phase II	23 days	Thu 1/14/16	Sat 2/13/16
Comparison of and Scientific analysis of all MRI data up-to-date	16 days	Thu 1/14/16	Thu 2/4/16
Begin work on new statistical analysis code	22 days	Thu 1/14/16	Fri 2/12/16
Quality Control of 63 mapped out slices	17 days	Thu 1/14/16	Fri 2/5/16
C-Term 2: Phase III Experiments	20 days	Mon 2/8/16	Fri 3/4/16
Creation of receptor maps	12 days	Mon 2/8/16	Tue 2/23/16
Prepare fresh batches of Nanoemulsions (A2, A3, and A4)	5 days	Mon	Fri 2/26/16

		2/22/16	
Finish up MRI experiments (clean, complete cohorts)	5 days	Mon 2/29/16	Fri 3/4/16
Use new Statistical code and 3D heat map to analyze data	5 days	Mon 2/29/16	Fri 3/4/16
Fine tune Matlab code for optimization and user friendliness	9 days	Tue 2/23/16	Fri 3/4/16
Write Final Methodology	20 days	Mon 2/8/16	Fri 3/4/16
Meet with Susan to Discuss Intellectual Property	1 day	Wed 3/2/16	Wed 3/2/16
Draw Conclusions	5 days	Mon 2/29/16	Fri 3/4/16
Review Methods, Results, Conclusions	5 days	Mon 2/29/16	Fri 3/4/16
D-Term: Complete Writing and Presentation	34 days	Mon 3/14/16	Thu 4/28/16
Write Results Section	6 days	Mon 3/14/16	Mon 3/21/16
Write Discussion and Conclusions	6 days	Mon 3/21/16	Mon 3/28/16
Review Intellectual Property with Susan	0 days	Tue 3/29/16	Tue 3/29/16
Review and Edit Entire Paper	14 days	Mon 3/14/16	Thu 3/31/16
Create Presentation	11 days	Fri 4/1/16	Fri 4/15/16
Edit and Practice Presentation	6 days	Wed 4/13/16	Wed 4/20/16
PROJECT PRESENTATION DAY	1 day	Thu 4/21/16	Thu 4/21/16
Final Paper Edits with Tim and Susan	4 days	Fri 4/22/16	Wed 4/27/16
FINAL PAPER DUE TO WPI	1 day	Thu 4/28/16	Thu 4/28/16
Review Entire Project and Discuss Future Projects	0 days	Fri 4/29/16	Fri 4/29/16
Create poster for Nemucore	11 days	Fri 4/29/16	Fri 5/13/16
Write up publication(s)	176 days	Thu 8/27/15	Thu 4/28/16

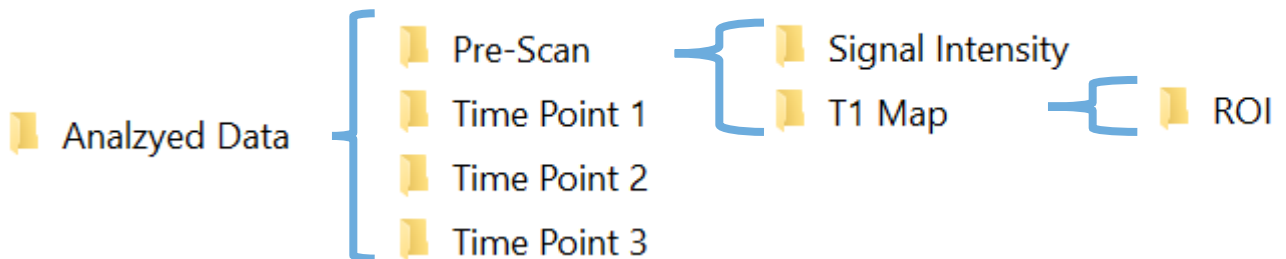
Appendix B: MRI Alignment in Atlas Step-through

- 1) Extract all files from the Zip Folder given. There will be one main folder from the Zip Folder, with as many folders as there were animals in the cohort inside. Each of these folders will contain numbered folders for as many scans were done. Identify which ones are the: Pre-Scan and important time markers, such as 20, 40, & 60 minutes. When the numbered folders are opened, there you will see the “method” file, to be used in step 3.



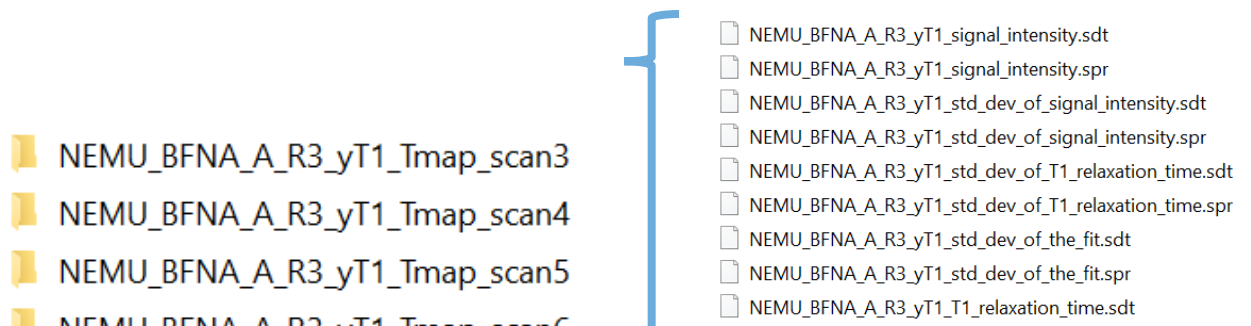
In this case, Scan 3 was the Pre-Scan, and Scans 4, 5, & 6 were 20, 40, & 60 minutes respectively. Not all Scans extracted will be needed. In this case, Scans 1 & 2 were not part of the protocol and so not analyzed.

- 2) Before extracting data from the files, set up an organized system of files. Create one master folder, such as “Analyzed Data”. In this folder, create a folder for the Pre-Scan, and all important time points. Inside each of those folders create two more folders, “Signal Intensity” & “T1 Map”, and inside each “T1 Map” folder create a “ROI” folder.



Note: Time Points 1, 2, 3 are arbitrary. Often they will mean 20, 40, 60 minutes. It is completely acceptable to label folders as “20 Minutes”, “40 Minutes”, and “60 Minutes” if preferred. Be consistent with labeling as you go.

- 3) Open Matlab R2014a by going to the Start Menu and navigating to the program or by using the Search Bar. In the program, open the ‘ExtractT1’ folder. Run the

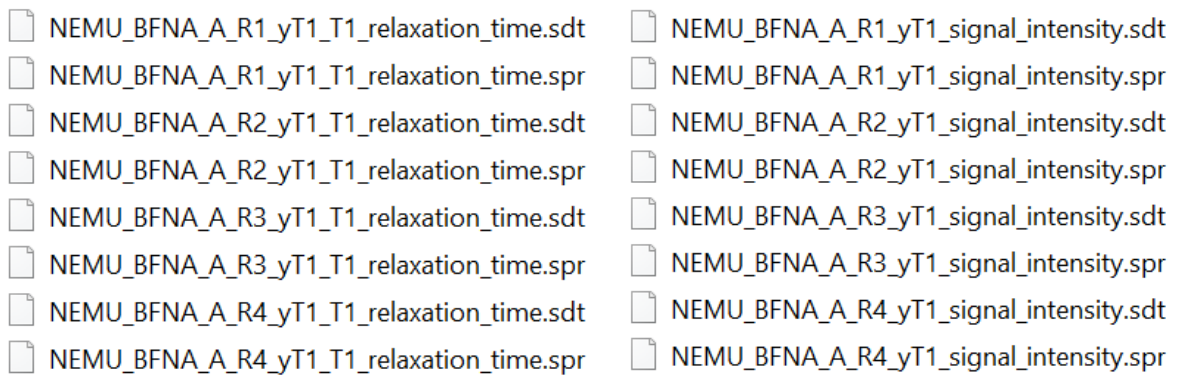


extractTvalNC.m program for all rats involved in order to obtain information from the Pre-Scan and important time points. For each, choose the appropriate Rat folder, then Scan Folder, then choose the “method” file. Each run of the program will create an additional folder within each rat folder, with 10 files. 5 files will be “.spr”, and 5 files will be “.sdt.” Files should be Signal Intensity, Std dev of signal intensity, std dev of T1 relaxation time, std dev of the fit, and T1 relaxation time.

In each _Tmap_scan# folder created, 10 files will be created. Files that will be used from each scan include signal_intensity.sdt, signal_intensity.spr, T1_relaxation_time.sdt, and T1_relaxation_time.spr.

- Return to the “Analyzed Data” folder. Now it is time to sort the “.sdt” and “.spr” files extracted. For each Time Point Folder (or 20 Minutes, 40 Minutes, 60 Minutes), copy & paste the corresponding Signal Intensity and T1 Relaxation Time files. Sort the Signal Intensity files into the Signal Intensity folder, and the T1 Relaxation Time files into the T1 Map folder. Be sure that the files are being sent to the correct Time Point folder, as the files “.sdt” and “.spr” are not labeled by time in their names.

ROI



Left: View of the inside of the T1 Map folder. Right: View of the inside of the Signal Intensity folder.

- Open up Atlas Software by navigating through the Start Menu or using the Search Bar. Once open, click on ‘File’ menu, choose ‘Load Atlas’ option, and select Rat_Atlas.nii. Choose Orientation of Axial: S-I for both image and headers. If the atlas loads with solid-colors for the sections of the brain, go to the ‘View’ menu, and choose the option ‘Show Atlas Contours.’ If the outlines are dim, go to the ‘Image’ tab, ‘Brightness controls’ section, and then using the ‘Scan’ slider bar to make the Atlas outline more visible.

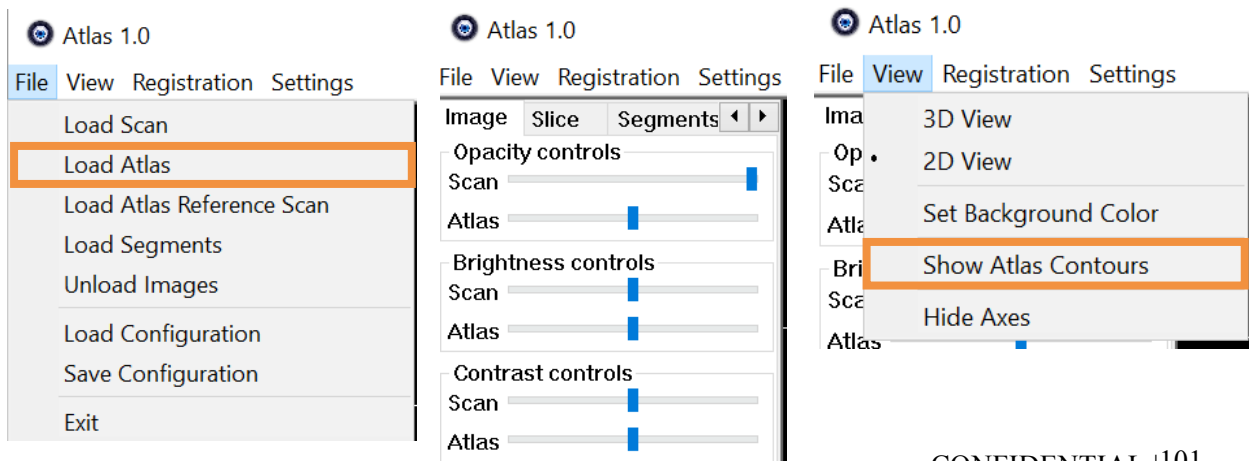


Image of the 'File' drop-down menu, with the 'Load Atlas' option in an orange box; Image of the Atlas sidebar displaying Image controls; Image of the 'View' menu in Atlas, with the 'Show Atlas Contours' option in an orange box.

Image of the Atlas window after loading the Rat Atlas, with the atlas contours shown.

- 6) Click on the 'File' menu, choose 'Load Scan' option, and navigate to the "Analyzed Data", "Pre-Scan", "Signal Intensity" folder. Select the file for the first rat. (Signal Intensity is done before the T1 Relaxation Time because Signal Intensity provides a clearer image for alignment). Choose Orientation of Axial: I-S for the image. You may need to adjust the brightness of the scan. This can be done by going to the 'Image' tab, 'Brightness controls' section, and then using the 'Scan' slider bar. Contrast can be adjusted in the same way.
- 7) Load all the remaining Pre-Scan, Signal Intensity files for all rats in the cohort as described in the previous step.

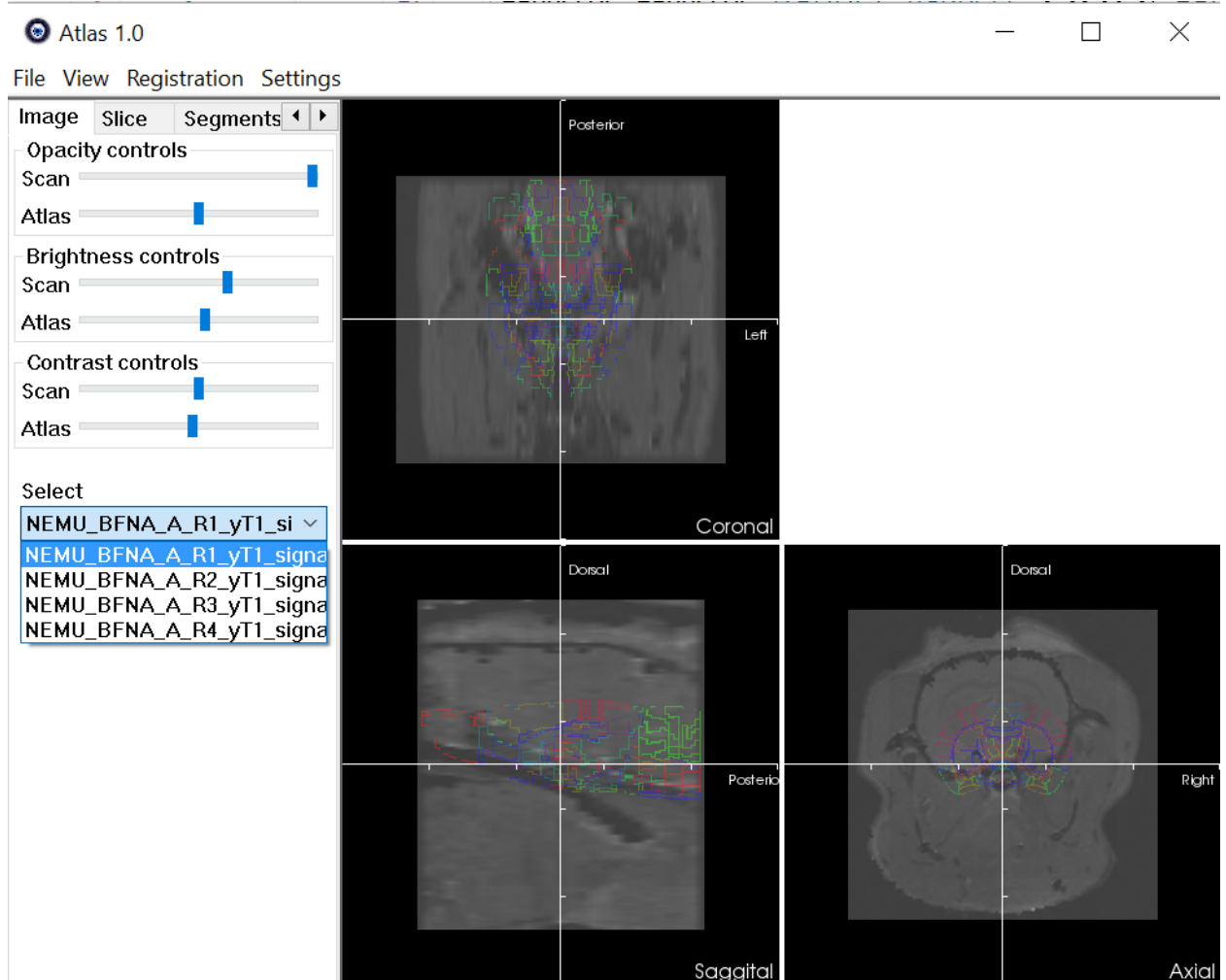
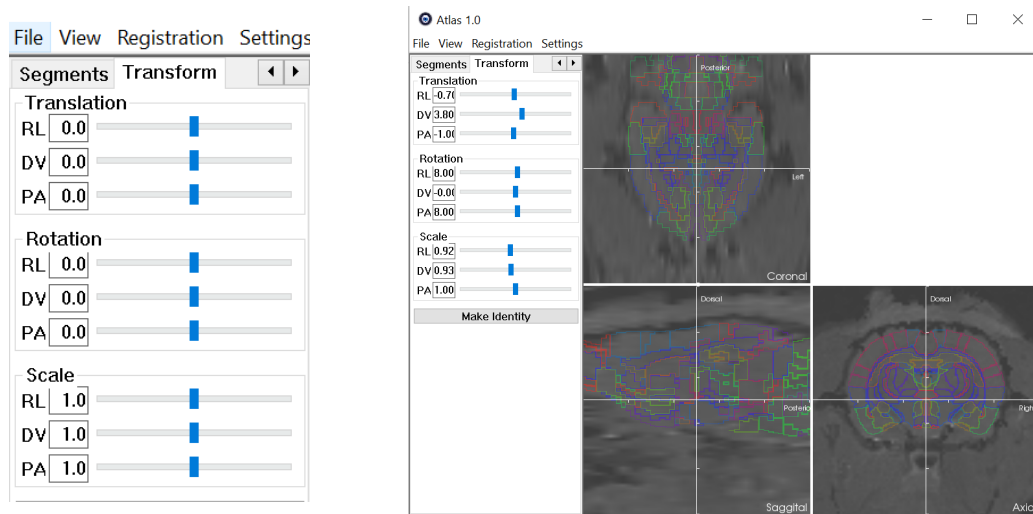


Image of scans & Rat Atlas loaded correctly. All four rats were loaded together. Note that this image is before the alignment was completed.

- 8) Beginning with one scan, adjust the position for optimal alignment with the atlas. DO NOT MOVE THE ATLAS. Begin to move the scan so it aligns well with the atlas. Go to the 'Transform' tab and use the following commands' slider bars as indicated.
- Rotation – 'PA', 'RL,' slider bar
 - Translation – 'DV', 'RL' slider bar.
 - Scale as needed (typical appropriate range is 0.91 to 1.03). It is best if all the scale slider bars ('RL', 'DV', & 'PA') are at the same value/

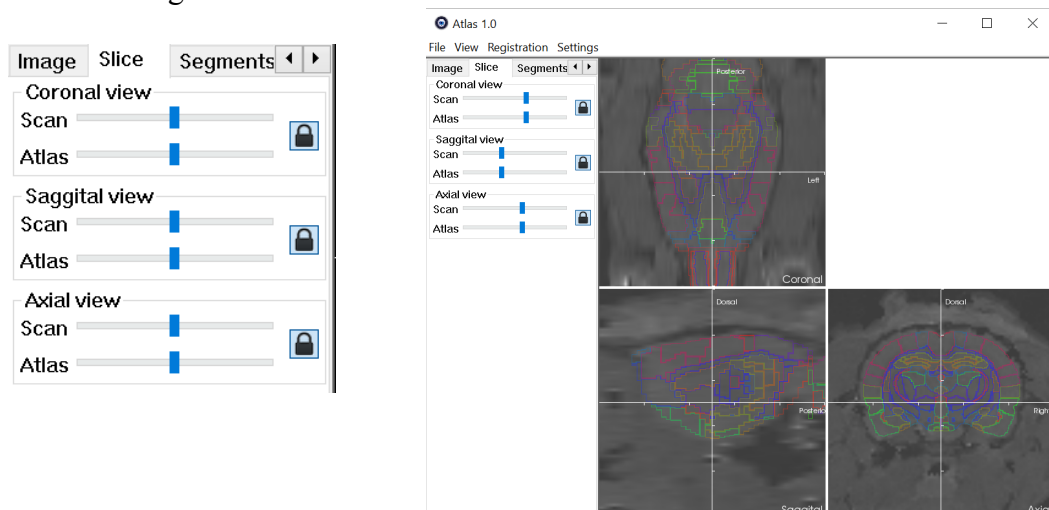
Note - you can zoom in on the pictures by holding the Right button and moving the mouse. This can help with aligning the scan to the atlas. It is desirable for the white portion of the brain to end at the outline of the rat atlas. The black area indicates the



CSF surrounding the brain, and the next area of white is the rat skull.

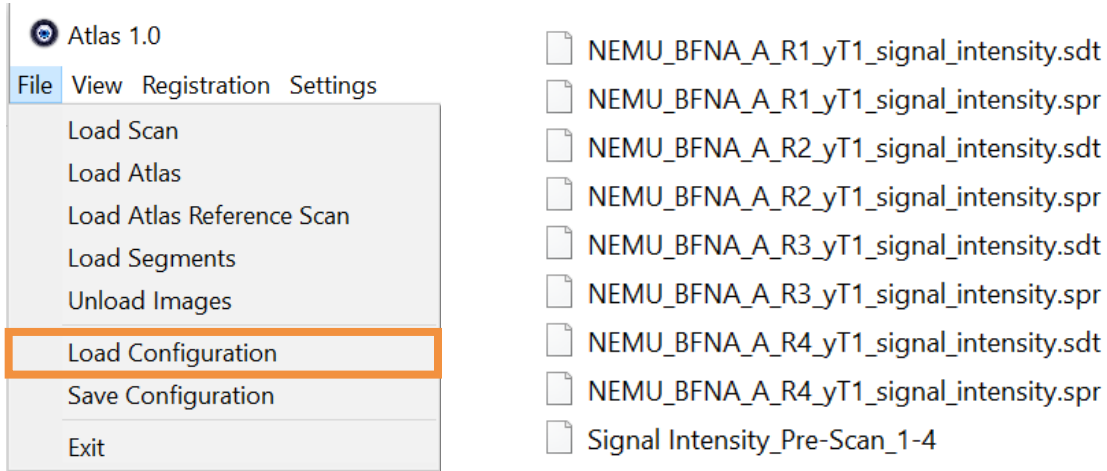
Left: Image of the 'Transform' side bar with the slider options. Note that PA = Posterior / Anterior, DV = Dorsal / Ventral, and RL = Right / Left. Right: an aligned rat brain with the 'Transform' side bar, show the changes of the scan alignment.

- 9) Confirm that the location of the scan to the atlas is well aligned by going to the 'Slice' tab and moving the Coronal and Axial sliders. This will allow the entire brain alignment to be checked against the atlas. Adjust the location under the 'Transform' tab as necessary for better alignment.



Left: Image of the 'Slice' side bar, showing the slider options for the different views. DO NOT click the 'Lock' button to the 'Unlocked' position, as this will cause the view of the scan and atlas to not show the same slice. Right: an aligned rat brain with the 'Slice' side bar, displaying some of the different views available to check the alignment.

- 10) Repeat steps 8 & 9 for all remaining Pre-Scans loaded. They can be accessed by the 'Image' tab, and choosing scans from the 'Select' drop-down menu. The drop-down menu can be seen in the figure after step 7.
- 11) Once everything is set, click on the 'File' menu, chose the option 'Save Configuration', and save the configuration with an appropriate name in the Signal Intensity folder of the



Pre-Scan.

Left: Image of the 'Save Configuration' option in the 'File' drop-down menu. Right: Image of what files should be in the "Signal Intensity" folder after saving the configuration. Note that the configuration should be an '.xml' file.

- 12) Click on the 'File' menu and choose the option 'Unload Images.' This will unload both the scans and the Rat Atlas.

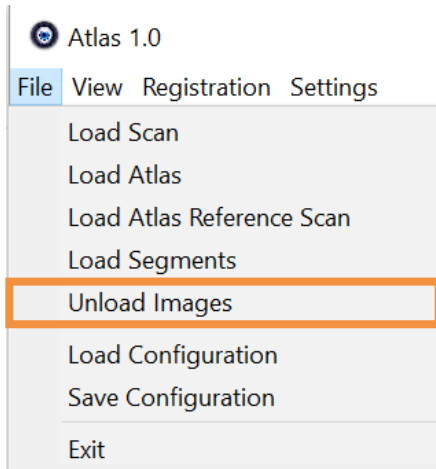


Image of the 'Unload Images' option in the 'File drop-down menu.

- 13) Repeat steps 6-12 with the Signal Intensity files for the other time points. When the last configuration has been saved, unload the images.
- 14) Load the Rat Atlas as done previously. Load all T1 Relaxation Time files for the Pre-Scan by navigating to the correct folder and loading as done in step 6. However, **do not**

align these files! Save the configuration in the T1 Map folder in the Pre-Scan folder. Unload the configuration, and do the same for all relevant time points. Unload the last configuration.

15) Find the Configuration files (.xml) recently created in their respective folders. Right click on the configuration file, and choose the option “Edit with Notepad++”. Open both the Signal Intensity and T1 Relaxation Time configurations for the Pre-Scan in this way.

16) For each rat, copy the matrix numbers in between <Matrix> to <Matrix> in the Signal Intensity file.

Top: Image of the T1 Relaxation Scans Configuration with no alignment performed. Middle: Image of the

```

C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\T1_Relaxation_Pre-Scan_1-4.xml - Notepad++
File Edit Search View Encoding Language Settings Macro Run Plugins Window ?
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2 <scan>
3 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R1_yt1_T1_relaxation_time.spc</path>
4 <matrix>1 0 0 0 1 0 0 0 0 1 -1 0 0 0 1 </matrix>
5 <orientation>OrientationIS</orientation>
6 </scan>
7 <scan>
8 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R2_yt1_T1_relaxation_time.spc</path>
9 <matrix>1 0 0 0 1 0 0 0 0 1 -1 0 0 0 1 </matrix>
10 <orientation>OrientationIS</orientation>
11 </scan>
12 <scan>
13 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R3_yt1_T1_relaxation_time.spc</path>
14 <matrix>1 0 0 0 1 0 0 0 0 1 -1 0 0 0 1 </matrix>
15 <orientation>OrientationIS</orientation>
16 </scan>
17 <scan>
18 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R4_yt1_T1_relaxation_time.spc</path>
19 <matrix>1 0 0 0 1 0 0 0 0 1 -1 0 0 0 1 </matrix>
20 <orientation>OrientationIS</orientation>
21 </scan>
22 <atlas>
23 <path>C:\AtlasProgram\EVA\LEBRatBrainAtlasV1_1\Rat_Atlas.nii</path>
24 <matrix>1 0 0 0 1 0 0 0 0 1 0 0 0 0 1 </matrix>
25 <orientation>OrientationSI</orientation>
26 </atlas>
27 </imagesConfiguration>

```

```

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File Edit Search View Encoding Language Settings Macro Run Plugins Window ?
Signal Intensity_Pre-Scan_1-4.xml T1_Relaxation_Pre-Scan_1-4.xml
1 <imagesConfiguration>
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3 <path>C:\Users\NemucoreITAdmin\Desktop\RAI MRI DATA\Treatment_A\NEMU_BFNA_A_R1_yt1\NEMU_BFNA_A_R1_yt1_Tmap_scan3\NEMU_BFNA_A_R1_yt1
4 <matrix>1.0521 -0.129182 0 -0.8 0.128474 1.04634 -0.104528 3.6 0.0135031 0.109974 0.994522 -1.1 0 0 0 1 </matrix>
5 <orientation>OrientationIS</orientation>
6 </scan>
7 <scan>
8 <path>C:\Users\NemucoreITAdmin\Desktop\RAI MRI DATA\Treatment_A\NEMU_BFNA_A_R2_yt1\NEMU_BFNA_A_R2_yt1_Tmap_scan3\NEMU_BFNA_A_R2_yt1
9 <matrix>1.06853 -0.055995 0 -0.4 0.0555821 1.06057 -0.121869 3.6 0.00682462 0.130221 0.992546 -1.2 0 0 0 1 </matrix>
10 <orientation>OrientationIS</orientation>
11 </scan>
12 <scan>
13 <path>C:\Users\NemucoreITAdmin\Desktop\RAI MRI DATA\Treatment_A\NEMU_BFNA_A_R3_yt1\NEMU_BFNA_A_R3_yt1_Tmap_scan3\NEMU_BFNA_A_R3_yt1
14 <matrix>1.07934 -0.0373425 0 -0.6 0.0371188 1.0531 -0.173648 3.8 0.00654505 0.18569 0.984808 -1.4 0 0 0 1 </matrix>
15 <orientation>OrientationIS</orientation>
16 </scan>
17 <scan>
18 <path>C:\Users\NemucoreITAdmin\Desktop\RAI MRI DATA\Treatment_A\NEMU_BFNA_A_R4_yt1\NEMU_BFNA_A_R4_yt1_Tmap_scan3\NEMU_BFNA_A_R4_yt1
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20 <orientation>OrientationIS</orientation>
21 </scan>
22 <atlas>
23 <path>C:\AtlasProgram\EVA\LEBRatBrainAtlasV1_1\Rat_Atlas.nii</path>
24 <matrix>1 0 0 0 1 0 0 0 0 1 0 0 0 0 1 </matrix>
25 <orientation>OrientationSI</orientation>
26 </atlas>
27 </imagesConfiguration>

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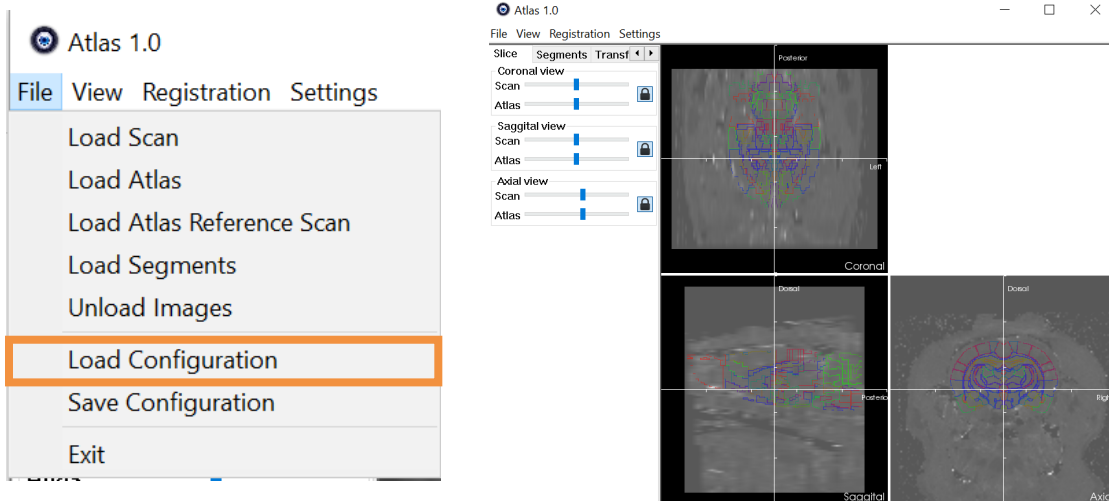
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File Edit Search View Encoding Language Settings Macro Run Plugins Window ?
Signal Intensity_Pre-Scan_1-4.xml T1_Relaxation_Pre-Scan_1-4.xml
1 <imagesConfiguration>
2 <scan>
3 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R1_yt1_T1_relaxation_time.spc</path>
4 <matrix>1.0521 -0.129182 0 -0.8 0.128474 1.04634 -0.104528 3.6 0.0135031 0.109974 0.994522 -1.1 0 0 0 1 </matrix>
5 <orientation>OrientationIS</orientation>
6 </scan>
7 <scan>
8 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R2_yt1_T1_relaxation_time.spc</path>
9 <matrix>1.06853 -0.055995 0 -0.4 0.0555821 1.06057 -0.121869 3.6 0.00682462 0.130221 0.992546 -1.2 0 0 0 1 </matrix>
10 <orientation>OrientationIS</orientation>
11 </scan>
12 <scan>
13 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R3_yt1_T1_relaxation_time.spc</path>
14 <matrix>1.07934 -0.0373425 0 -0.6 0.0371188 1.0531 -0.173648 3.8 0.00654505 0.18569 0.984808 -1.4 0 0 0 1 </matrix>
15 <orientation>OrientationIS</orientation>
16 </scan>
17 <scan>
18 <path>C:\Users\NemucoreITAdmin\Desktop\for the user guide\T1 Map\NEMU_BFNA_A_R4_yt1_T1_relaxation_time.spc</path>
19 <matrix>1.06984 0.0190231 0 -0.4 -0.0185349 1.08171 -0.121869 4.6 -0.0022758 0.132817 0.992546 -1.5 0 0 0 1 </matrix>
20 <orientation>OrientationIS</orientation>
21 </scan>
22 <atlas>
23 <path>C:\AtlasProgram\EVA\LEBRatBrainAtlasV1_1\Rat_Atlas.nii</path>
24 <matrix>1 0 0 0 1 0 0 0 0 1 0 0 0 0 1 </matrix>
25 <orientation>OrientationSI</orientation>
26 </atlas>
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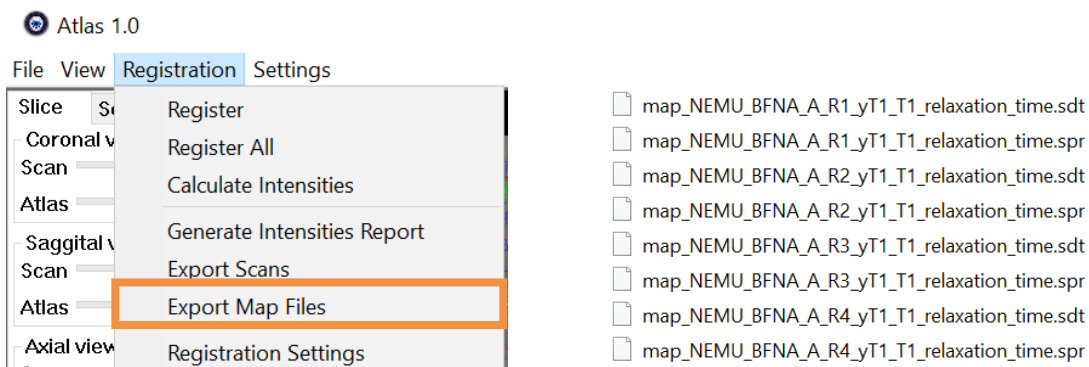
Signal Intensity Pre-Scan Alignment with co-ordinates. Co-ordinates to be copied are highlighted in gray for the first rat. Bottom: Image of the T1 Relaxation Scan Configuration with all correct values from the Signal Intensity Pre-Scan Alignment for each rat.

- 17) Replace the numbers between <matrix> to <matrix> with the copied numbers for the correct rat in the T1 Relaxation Times configuration. See previous image.
- 18) Repeat steps 18 & 19 for all rats in the Signal Intensity and T1 Relaxation Time files. Save the changes after ensuring correct copy & pasting.
- 19) Repeat steps 17-20 for all relevant time point scans.
- 20) Go to the Atlas program, click on the 'File' menu, and choose the 'Load Configuration' option. Select T1 Relaxation Time Configuration for the Pre-Scan time point. Confirm that the Atlas is lined up well with the Scans by going to the 'Slice' tab and moving sliders. Adjust if necessary.



Left: Image of the 'Load Configuration' option on the 'File' drop-down menu. Right: Image of the T1 Relaxation scan with the Rat Atlas. View is of the 'Slice' side bar. Note how the difficulty in determining the brain edges with T1 Relaxation scans versus Signal Intensity scans. This is why Signal Intensity scans are used for alignment, and those co-ordinates are then used with the T1 Relaxation scans.

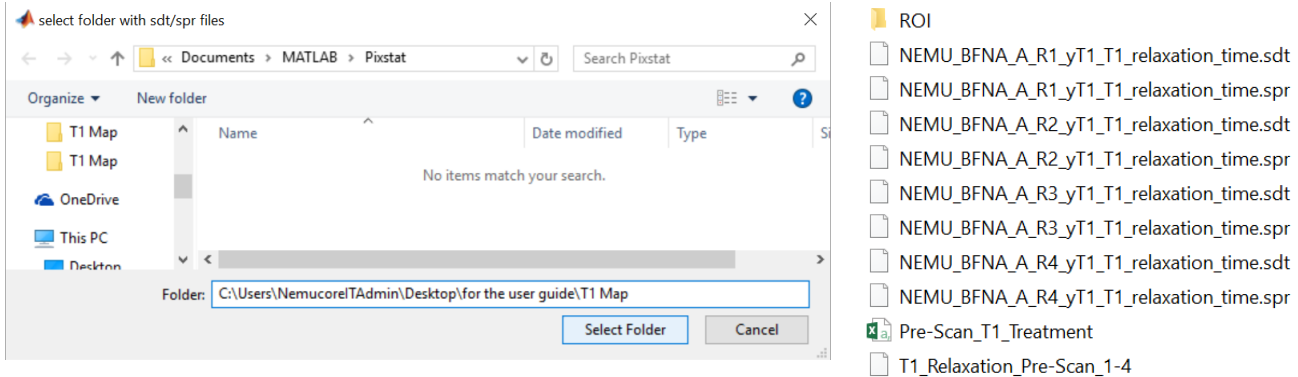
- 21) Under the "Registration" Menu, choose "Export Map Files." When asked for a folder to



save the files in, navigate to the ROI folder in the T1 Map folder of the scan.

Left: Image of the 'Registration' drop-down menu with the option 'Export Map Files' highlighted. Right: Image of files in the ROI folder after exporting Map Files.

- 22) Unload Images when completed by going to the 'File' drop-down menu and selecting 'Unload Images.'
- 23) Complete steps 22-24 for all Time Point Configurations.
- 24) Open Matlab, and run pixstat.m (found in folder Pixstat). Copy the folder T1Map location to the bar when prompted by the program. Save the output file appropriately (Pre_T1) in the T1 Map folder. The output file should be a '.csv' file, and will be openable by Excel.



Left: Image depicting how to input the T1 Map location into the prompt bar of the pixstat.m program.
 Right: Image showing an updated view of the T1 Map folder. Note the Excel file.

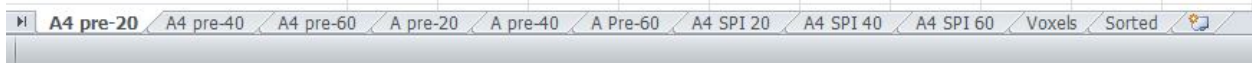
- 25) Repeat for all time points.
- 26) Voxels, Mean, and STDEV will be listed for each rat at that time point. Values for Mean and STDEV are in milliseconds.

	A	B	C	D	E	F	G	H
1	Region of	10th cereb	1st cerebe	2nd cereb	3rd cerebe	4th cerebe	5th cerebe	motor trig
2	ROI-ID	1	2	3	4	5	6	7
3	NEMU_BFNA_A_R1_yT1_T1_relaxation_time							
4	Num of Vc	70	39	280	325	247	588	48
5	Mean	1919.69	1884.31	1790.91	1861.34	1953.47	2042.56	1774.83
6	Std Dev	189.8	362.43	321.31	328.18	437.61	475.07	253.38
7	NEMU_BFNA_A_R2_yT1_T1_relaxation_time							
8	Num of Vc	79	39	279	292	305	566	72
9	Mean	2477.84	1834.23	1919.66	1984.72	2104.77	2455.51	2000.99
10	Std Dev	883.45	424.33	339.88	474.2	453.93	936.96	343.05
11	NEMU_BFNA_A_R3_yT1_T1_relaxation_time							
12	Num of Vc	72	41	264	322	320	514	61
13	Mean	3000.26	2197.44	2274.91	2418.37	2489.1	2571.08	2000.79
14	Std Dev	1352.86	435.74	468.89	543.94	570.77	1052.28	301.35
15	NEMU_BFNA_A_R4_yT1_T1_relaxation_time							
16	Num of Vc	73	35	270	343	317	500	69
17	Mean	2546.96	2293.49	2097.04	2343.6	2405.57	2685.56	2021.75
18	Std Dev	478.95	287.88	390.17	383.25	439.89	575.84	324.96

- 27) Continue with further analysis in Excel or through a statistical Matlab code.

Appendix C: Voxel Weighted Specificity Index on Microsoft Excel Step-Through

Step 1: Open Microsoft Excel and create 11 sheets in the workbook. Label accordingly based on the nanomedicine being tested.



Step 2: Insert T1 relaxation time data for each animal in the cohort for the specified nanomedicine for the pre-scan.

A4 Targeted													
pre scan													
Region of Interest(ROI)	10th cereb	1st cereb	2nd cereb	3rd cereb	4th cereb	5th cereb	motor trig	root of tri	6th cereb	7th cereb	facial nucl	8th cereb	9th
ROI-ID	1	2	3	4	5	6	7	8	9	10	11	12	
NM1800A4_1_r21_T1_relaxation_time	2353.75	2093.17	2033.77	2154.07	2170.32	2250.74	2018.84	2345.71	2414.32	2241.11	2699.33	2322.31	
NM1800A4_2_r21_T1_relaxation_time	2967.48	2106.93	2167	2205.45	2152.37	2479.42	1971.57	2259.62	2691.76	2420.39	2313	2614.91	
NM1800A4_3a_r91_T1_relaxation_time	2553.44	2387.88	2245.1	2224.97	2115.19	2290.49	1863	2283.38	2287.11	2161.45	2052.32	2162.52	
NEMU_A4_R13_yW1_T1_relaxation_time	2615	1867	2266	2147	1999	2293	1839	2019	2357	2594	1894	2263	
NEMU_A4_R14_yW1_T1_relaxation_time	2449	2171	2064	2056	2284	2351	1752	2736	2270	2449	1921	2399	
NEMU_A4_R15_yW1_T1_relaxation_time	2341	2290	2100	2056	2092	2267	1758	2225	2392	2193	1906	2240	
NEMU_A4_R16_yW1_T1_relaxation_time	2269	1826	1940	2019	2116	2311	1822	2096	2337	2382	1943	2357	

20 minutes													
Region of Interest(ROI)	10th cereb	1st cereb	2nd cereb	3rd cereb	4th cereb	5th cereb	motor trig	root of tri	6th cereb	7th cereb	facial nucl	8th cereb	9th
ROI-ID	1	2	3	4	5	6	7	8	9	10	11	12	
NM1800A4_1_r21_T1_relaxation_time	2115.11	2068.9	2155.89	2066.92	2011.8	2005.92	2031.28	2065.23	1979.1	2079.92	1941.8	2047.66	
NM1800A4_2_r21_T1_relaxation_time	2331.68	2037.84	2087.88	2093.14	2174.59	2185.16	1876.93	2296.96	2260.06	2135.03	2029.29	2191.41	
NM1800A4_3a_r91_T1_relaxation_time	2329.2	2075.65	2010.31	2030.38	1868.56	2044.12	1781.03	2032.25	2251.95	2307.68	1990.26	2240.16	
NEMU_A4_R13_yW1_T1_relaxation_time	2286	1960	2114	2081	2027	2205	1913	1985	2317	2374	1744	2038	
NEMU_A4_R14_yW1_T1_relaxation_time	2502	1569	2133	2006	2125	2319	1802	2430	2350	2587	1846	2397	
NEMU_A4_R15_yW1_T1_relaxation_time	2083	1863	2024	2039	2091	2270	1673	2158	2213	2245	1791	2241	
NEMU_A4_R16_yW1_T1_relaxation_time	2245	1936	1965	2017	2027	2180	1830	2227	2382	2141	1866	2195	

Step 3: Insert T1 relaxation time data for each animal in the cohort for the specified nanomedicine for the time point. Be sure the tab matches the time point and nanoemulsion.

A4 Targeted													
pre scan													
Region of Interest(ROI)	10th cereb	1st cereb	2nd cereb	3rd cereb	4th cereb	5th cereb	motor trig	root of tri	6th cereb	7th cereb	facial nucl	8th cereb	9th
ROI-ID	1	2	3	4	5	6	7	8	9	10	11	12	
NM1800A4_1_r21_T1_relaxation_time	2353.75	2093.17	2033.77	2154.07	2170.32	2250.74	2018.84	2345.71	2414.32	2241.11	2699.33	2322.31	
NM1800A4_2_r21_T1_relaxation_time	2967.48	2106.93	2167	2205.45	2152.37	2479.42	1971.57	2259.62	2691.76	2420.39	2313	2614.91	
NM1800A4_3a_r91_T1_relaxation_time	2553.44	2387.88	2245.1	2224.97	2115.19	2290.49	1863	2283.38	2287.11	2161.45	2052.32	2162.52	
NEMU_A4_R13_yW1_T1_relaxation_time	2615	1867	2266	2147	1999	2293	1839	2019	2357	2594	1894	2263	
NEMU_A4_R14_yW1_T1_relaxation_time	2449	2171	2064	2056	2284	2351	1752	2736	2270	2449	1921	2399	
NEMU_A4_R15_yW1_T1_relaxation_time	2341	2290	2100	2056	2092	2267	1758	2225	2392	2193	1906	2240	
NEMU_A4_R16_yW1_T1_relaxation_time	2269	1826	1940	2019	2116	2311	1822	2096	2337	2382	1943	2357	

20 minutes													
Region of Interest(ROI)	10th cereb	1st cereb	2nd cereb	3rd cereb	4th cereb	5th cereb	motor trig	root of tri	6th cereb	7th cereb	facial nucl	8th cereb	9th
ROI-ID	1	2	3	4	5	6	7	8	9	10	11	12	
NM1800A4_1_r21_T1_relaxation_time	2115.11	2068.9	2155.89	2066.92	2011.8	2005.92	2031.28	2065.23	1979.1	2079.92	1941.8	2047.66	
NM1800A4_2_r21_T1_relaxation_time	2331.68	2037.84	2087.88	2093.14	2174.59	2185.16	1876.93	2296.96	2260.06	2135.03	2029.29	2191.41	
NM1800A4_3a_r91_T1_relaxation_time	2329.2	2075.65	2010.31	2030.38	1868.56	2044.12	1781.03	2032.25	2251.95	2307.68	1990.26	2240.16	
NEMU_A4_R13_yW1_T1_relaxation_time	2286	1960	2114	2081	2027	2205	1913	1985	2317	2374	1744	2038	
NEMU_A4_R14_yW1_T1_relaxation_time	2502	1569	2133	2006	2125	2319	1802	2430	2350	2587	1846	2397	
NEMU_A4_R15_yW1_T1_relaxation_time	2083	1863	2024	2039	2091	2270	1673	2158	2213	2245	1791	2241	
NEMU_A4_R16_yW1_T1_relaxation_time	2245	1936	1965	2017	2027	2180	1830	2227	2382	2141	1866	2195	

A4 Targeted												
pre scan												
20 minutes												

Step 4: Subtract the time point T1 value from the pre-scan T1 value for each animal in the cohort.

A4 pre-20												
NMI800A4_1_r21_T1_relaxation_time	238.64	24.27	-122.12	87.15	158.52	244.82	-12.44	280.48	435.22	161.19	757.53	274.65
NMI800A4_2_r21_T1_relaxation_time	635.8	69.09	79.12	112.31	-22.22	294.26	94.64	-37.34	431.7	285.36	283.71	423.5
NMI800A4_3a_r91_T1_relaxation_time	224.24	312.23	234.79	194.59	246.63	246.37	81.97	251.13	35.16	-146.23	62.06	-77.64
NEMU_A4_R13_yW1_T1_relaxation_time	329	-93	152	66	-28	88	-74	34	40	220	150	225
NEMU_A4_R14_yW1_T1_relaxation_time	-53	602	-69	50	159	32	-50	306	-80	-138	75	2
NEMU_A4_R15_yW1_T1_relaxation_time	258	427	76	17	1	-3	85	67	179	-52	115	-1
NEMU_A4_R16_yW1_T1_relaxation_time	24	-110	-25	2	89	131	-8	-131	-45	241	77	162

Step 5: Insert voxel data for each animal in the cohort. This comes from the CSV files.

voxel data													
NMI800A4_1_r21_T1_relaxation_time	46	40	168	205	269	502	43	257	200	26	95	68	
	26276	0.001751	0.001522	0.006394	0.007802	0.010237	0.019105	0.001636	0.009781	0.007612	0.000989	0.003615	0.002588
NMI800A4_2_r21_T1_relaxation_time	50	37	182	250	294	567	45	263	215	36	93	64	
	28068	0.001781	0.001318	0.006484	0.008907	0.010475	0.020201	0.001603	0.00937	0.00766	0.001283	0.003313	0.00228
NMI800A4_3a_r91_T1_relaxation_time	79	26	215	239	195	350	32	208	244	57	69	100	
	26754	0.002953	0.000972	0.008036	0.008933	0.007289	0.013082	0.001196	0.007775	0.00912	0.002131	0.002579	0.003738
NEMU_A4_R13_yW1_T1_relaxation_time	58	36	250	326	303	545	36	303	329	54	98	52	
	32433	0.001788	0.00111	0.007708	0.010051	0.009342	0.016804	0.00111	0.009342	0.010144	0.001665	0.003022	0.001603
NEMU_A4_R14_yW1_T1_relaxation_time	83	26	278	307	293	552	70	304	383	32	88	108	
	33556	0.002473	0.000775	0.008285	0.009149	0.008732	0.01645	0.002086	0.009059	0.011414	0.000954	0.002622	0.003219
NEMU_A4_R15_yW1_T1_relaxation_time	54	35	283	370	264	438	63	269	246	36	91	69	
	33768	0.001599	0.001036	0.008381	0.010957	0.007818	0.012971	0.001866	0.007966	0.007285	0.001066	0.002695	0.002043
NEMU_A4_R16_yW1_T1_relaxation_time	66	50	277	378	278	492	62	299	295	28	105	87	
	36088	0.001829	0.001386	0.007676	0.010474	0.007703	0.013633	0.001718	0.008285	0.008174	0.000776	0.00291	0.002411

Step 6: Use the “SUM” function on Excel to find the total number of voxels for each animal.

voxel data													
NMI800A4_1_r21_T1_relaxation_time	46	40	168	205	269	502	43	257	200	26	95	68	
	26276	0.001751	0.001522	0.006394	0.007802	0.010237	0.019105	0.001636	0.009781	0.007612	0.000989	0.003615	0.002588
NMI800A4_2_r21_T1_relaxation_time	50	37	182	250	294	567	45	263	215	36	93	64	
	28068	0.001781	0.001318	0.006484	0.008907	0.010475	0.020201	0.001603	0.00937	0.00766	0.001283	0.003313	0.00228
NMI800A4_3a_r91_T1_relaxation_time	79	26	215	239	195	350	32	208	244	57	69	100	
	26754	0.002953	0.000972	0.008036	0.008933	0.007289	0.013082	0.001196	0.007775	0.00912	0.002131	0.002579	0.003738
NEMU_A4_R13_yW1_T1_relaxation_time	58	36	250	326	303	545	36	303	329	54	98	52	
	32433	0.001788	0.00111	0.007708	0.010051	0.009342	0.016804	0.00111	0.009342	0.010144	0.001665	0.003022	0.001603
NEMU_A4_R14_yW1_T1_relaxation_time	83	26	278	307	293	552	70	304	383	32	88	108	
	33556	0.002473	0.000775	0.008285	0.009149	0.008732	0.01645	0.002086	0.009059	0.011414	0.000954	0.002622	0.003219
NEMU_A4_R15_yW1_T1_relaxation_time	54	35	283	370	264	438	63	269	246	36	91	69	
	33768	0.001599	0.001036	0.008381	0.010957	0.007818	0.012971	0.001866	0.007966	0.007285	0.001066	0.002695	0.002043
NEMU_A4_R16_yW1_T1_relaxation_time	66	50	277	378	278	492	62	299	295	28	105	87	
	36088	0.001829	0.001386	0.007676	0.010474	0.007703	0.013633	0.001718	0.008285	0.008174	0.000776	0.00291	0.002411

Step 7: Find the voxel weight for each ROI of each animal by dividing the number of voxels for the ROI by the total number of voxels for the animal.

voxel data													
NMI800A4_1_r21_T1_relaxation_time	46	40	168	205	269	502	43	257	200	26	95	68	
	26276	0.001751	0.001522	0.006394	0.007802	0.010237	0.019105	0.001636	0.009781	0.007612	0.000989	0.003615	0.002588
NMI800A4_2_r21_T1_relaxation_time	50	37	182	250	294	567	45	263	215	36	93	64	
	28068	0.001781	0.001318	0.006484	0.008907	0.010475	0.020201	0.001603	0.00937	0.00766	0.001283	0.003313	0.00228
NMI800A4_3a_r91_T1_relaxation_time	79	26	215	239	195	350	32	208	244	57	69	100	
	26754	0.002953	0.000972	0.008036	0.008933	0.007289	0.013082	0.001196	0.007775	0.00912	0.002131	0.002579	0.003738
NEMU_A4_R13_yW1_T1_relaxation_time	58	36	250	326	303	545	36	303	329	54	98	52	
	32433	0.001788	0.00111	0.007708	0.010051	0.009342	0.016804	0.00111	0.009342	0.010144	0.001665	0.003022	0.001603
NEMU_A4_R14_yW1_T1_relaxation_time	83	26	278	307	293	552	70	304	383	32	88	108	
	33556	0.002473	0.000775	0.008285	0.009149	0.008732	0.01645	0.002086	0.009059	0.011414	0.000954	0.002622	0.003219
NEMU_A4_R15_yW1_T1_relaxation_time	54	35	283	370	264	438	63	269	246	36	91	69	
	33768	0.001599	0.001036	0.008381	0.010957	0.007818	0.012971	0.001866	0.007966	0.007285	0.001066	0.002695	0.002043
NEMU_A4_R16_yW1_T1_relaxation_time	66	50	277	378	278	492	62	299	295	28	105	87	
	36088	0.001829	0.001386	0.007676	0.010474	0.007703	0.013633	0.001718	0.008285	0.008174	0.000776	0.00291	0.002411

Step 8: Multiply the pre - time point T1 values from step 4 by the voxel weight values from step 7 for each ROI of each animal in the cohort.

ROI	NMI800A4_1_r21_T1_relaxation_time	NMI800A4_2_r21_T1_relaxation_time	NMI800A4_3a_r91_T1_relaxation_time	NEMU_A4_R13_yw1_T1_relaxation_time	NEMU_A4_R14_yw1_T1_relaxation_time	NEMU_A4_R15_yw1_T1_relaxation_time	NEMU_A4_R16_yw1_T1_relaxation_time					
1	0.417774	0.036946	-0.78079	0.679927	1.622845	4.677258	-0.02036	2.743316	3.312681	0.159497	2.738824	0.71077
2	1.132607	0.091076	0.513034	1.000338	-0.23274	5.944329	0.151732	-0.34988	3.306808	0.366003	0.94004	0.965655
3	0.662142	0.303431	1.886815	1.73832	1.797595	3.223051	0.098043	1.95242	0.320664	-0.31155	0.160056	-0.2902
4	0.588351	-0.10323	1.171646	0.663398	-0.26159	1.478741	-0.08214	0.317639	0.40576	0.366294	0.453242	0.360744
5	-0.13109	0.466444	-0.57164	0.457444	1.388336	2.562404	-0.1043	2.772202	-0.9131	-0.1316	0.196686	0.006437
6	0.41258	0.442579	0.636934	0.186271	0.007818	-0.03891	0.158582	0.53373	1.304016	-0.05544	0.309909	-0.00204
7	0.043893	-0.15241	-0.19189	0.020949	0.685602	1.785968	-0.01374	-1.08537	-0.36785	0.186987	0.224036	0.390545

Step 9: Calculate the average number of voxels for each ROI across the cohort.

ROI	voxels	62	36	236	296	271	492	50	272	273	38	91	78
1	46	40	168	205	269	502	43	257	200	26	95	68	
2	50	37	182	250	294	567	45	263	215	36	93	64	
3	79	26	215	239	195	350	32	208	244	57	69	100	
4	58	36	250	326	303	545	36	303	329	54	98	52	
5	83	26	278	307	293	552	70	304	383	32	88	108	
6	54	35	283	370	264	438	63	269	246	36	91	69	
7	66	50	277	378	278	492	62	299	295	28	105	87	
8	62	36	236	296	271	492	50	272	273	38	91	78	

Step 10: Repeat steps 2 through 9 for the rest of the time points, and for the non-targeted nanoemulsion.

Step 11: Use the "Paste Transpose" function in Microsoft Excel to move the results from step 8 to the "SPI" sheet for the time point.

The screenshot shows an Excel spreadsheet with multiple sheets. The 'Voxels' sheet contains a grid of data for 78 ROIs across 8 time points (A4 pre-20, A4 pre-40, A4 pre-60, A4 SPI 20, A4 SPI 40, A4 SPI 60, and two additional SPI sheets). Orange arrows point from the 'Voxels' sheet to the corresponding time point sheets, indicating that data is being pasted or transposed there. The 'Voxels' sheet also includes a 'Sorted' column and a 't-test' column.

Step 12: Calculate the SPI by dividing the average of the time point scans by the average of the pre-scans.

ROI (ROI)	2014_collette	SPI	t-test	A4 pre-20	MM100A	MM100B	MM100C	MM100D	MM100E	MM100F	MM100G	MM100H	MM100I	MM100J	MM100K	MM100L	MM100M	MM100N	MM100O	MM100P	MM100Q	MM100R	MM100S	MM100T	MM100U	MM100V	MM100W	MM100X	MM100Y	MM100Z	Average	SPI	t-test	
1 10th Cerebellar Lobule	N/A	N/A	0.6039	0.3274	0.4177	1.1261	0.6624	0.5885	-0.111	0.4125	0.0489	3.1265	0.5458	0.0526	0.4182	0.9897	1.7441	0.1188	1.2934	5.8116	0.6039	0.3274	57	Giomeru L	L	0.49728	0.05233	0.87373	0.15672	57	Giomeru L	L	0.7654	0.53525

Step 13: Run a t-test comparing the targeted array to the non-targeted array.

ROI (ROI)	2014_collette	SPI	t-test	A4 pre-20	MM100A	MM100B	MM100C	MM100D	MM100E	MM100F	MM100G	MM100H	MM100I	MM100J	MM100K	MM100L	MM100M	MM100N	MM100O	MM100P	MM100Q	MM100R	MM100S	MM100T	MM100U	MM100V	MM100W	MM100X	MM100Y	MM100Z	Average	SPI	t-test	
1 10th Cerebellar Lobule	N/A	N/A	0.6039	0.3274	0.4177	1.1261	0.6624	0.5885	-0.111	0.4125	0.0489	3.1265	0.5458	0.0526	0.4182	0.9897	1.7441	0.1188	1.2934	5.8116	0.6039	0.3274	57	Giomeru L	L	0.49728	0.05233	0.87373	0.15672	57	Giomeru L	L	0.7654	0.53525

Step 14: Copy and paste the VALUES calculated in steps 12 and 13 to the beginning of the sheet (by the ROI labels).

ROI (ROI)	2014_collette	SPI	t-test	A4 pre-20	MM100A	MM100B	MM100C	MM100D	MM100E	MM100F	MM100G	MM100H	MM100I	MM100J	MM100K	MM100L	MM100M	MM100N	MM100O	MM100P	MM100Q	MM100R	MM100S	MM100T	MM100U	MM100V	MM100W	MM100X	MM100Y	MM100Z	Average	SPI	t-test	
1 10th Cerebellar Lobule	N/A	N/A	0.6039	0.3274	0.4177	1.1261	0.6624	0.5885	-0.111	0.4125	0.0489	3.1265	0.5458	0.0526	0.4182	0.9897	1.7441	0.1188	1.2934	5.8116	0.6039	0.3274	57	Giomeru L	L	0.49728	0.05233	0.87373	0.15672	57	Giomeru L	L	0.7654	0.53525

Step 15: Use the “VLOOKUP” function in Microsoft Excel to sort the SPI and T-test data by the 22 larger ROIs.

ROI ID	ROI	2014	collette	SPI	T-test	A4 pre-20	NM1800A	NM1800B	NM1800C	NEMU_A	NEMU_B	NEMU_C	Average	A pre-20	NM1800	NM1800B	NM1800C	NEMU02	NEMU02	NEMU02	Average	SPI	T-test					
1	10th cerebellar lobule	N/A	N/A	0.60339	0.32774	0.43777	1.3261	0.60214	0.58055	-0.3111	0.42058	0.40189	1.30205	0.45458	0.03256	0.42842	0.98977	1.34421	0.13968	0.32934	1.81816	0.60339	0.32774	57	Glomerular L	L	0.49728	0.08223

Step 16: Repeat steps 11 through 15 for the other timepoints.

Step 17: On the “Voxels” tab, copy and paste (using both the “Values” and “Transpose” functions in Microsoft Excel) the information from step 9 in. Then, use Microsoft Excel’s “VLOOKUP” function to sort by the 22 larger ROIs.

Region of Interest	ROI-ID	voxels	ROI ID	ROI	approx # voxels
10th cerebellar lobule	1	62	57	Glomerular Layer	452
1st cerebellar lobule	2	36	53	External Plexiform Layer	400
2nd cerebellar lobule	3	236	59	Granular Cell Layer	521
3rd cerebellar lobule	4	296	152	Tenia Tecta	104
4th cerebellar lobule	5	271	20	Anterior Olfactory Nucleus	263
5th cerebellar lobule	6	492	102	Caudal Piriform Ctx	233
motor trigeminal nucleus	7	50	103	Rostral Piriform Ctx	747
root of trigeminal nerve	8	272	31	Anterior Cingulate Area	497
6th cerebellar lobule	9	273	125	Retrosplenial Caudal Ctx	185
7th cerebellar lobule	10	38	126	Retrosplenial Rostral Ctx	491
facial nucleus	11	91	64	Insular Ctx	953
8th cerebellar lobule	12	78	156	Visual 1 Ctx	449
9th cerebellar lobule	13	72	157	Visual 2 Ctx	455
anterior thalamic nucleus	14	111	150	Temporal Ctx	120
anterior accumbens	15	30	52	Entorhinal Ctx	711
accumbens	16	173	23	Auditory Ctx	550
accumbens	17	191	50	Ectorhinal Ctx	76
anterior hypothalamic nucleus	18	84	114	Perirhinal Ctx	246
anterior lateral olfactory nucleus	19	111	116	Parietal Ctx	199
anterior olfactory nucleus	20	263	120	Prietary Somatosensory Ctx	511

“VLOOKUP”

Step 18: Move the data from step 14 and step 17 into the “Sorted” tab.

A4	Section	ROI ID	ROI	B2 Bradykinin Receptor Expression	approx # voxels	SPI 20	SPI 40	SPI 60	Top quartile	t-test 20	t-test 40	t-test 60
Cerebral	Olfactory Bulb	57	Glomerular Layer	L	452	0.497	0.490	0.386	0.700	0.05223	0.035	0.012
		53	External Plexiform Layer	P	400	0.765	0.782	0.535		0.53525	0.512	0.084
		59	Granular Cell Layer	H	521	0.771	0.788	0.538		0.48525	0.313	0.009
	Olfactory Areas	152	Tenia Tecta	P	104	0.876	0.857	0.566		0.71152	0.613	0.100
		20	Anterior Olfactory Nucleus	P	263	1.037	0.736	0.375		0.95068	0.509	0.013
		102	Caudal Piriform Ctx	H	233	0.744	0.914	0.771		0.29618	0.685	0.128
	Limbic Lobe	103	Rostral Piriform Ctx	H	747	0.523	0.533	0.449		0.13742	0.059	0.022
		31	Anterior Cingulate Area	H	497	0.202	0.323	0.457		0.01457	0.009	0.008
		125	Retrosplenial Caudal Ctx	H	185	0.524	0.680	0.869		0.34747	0.319	0.669
	Insular Cortex	126	Retrosplenial Rostral Ctx	H	491	0.386	0.504	0.473		0.05111	0.067	0.065
		64	Insular Ctx	H	953	0.736	0.748	0.663		0.4157	0.281	0.076
		Occipital Lobe	156	Visual 1 Ctx	P	449	0.190	0.354	0.449		0.01213	0.046
	157		Visual 2 Ctx	P	455	0.253	0.440	0.522		0.04329	0.042	0.082
	Temporal Lobe	150	Temporal Ctx	P	120	0.741	0.578	0.756		0.48785	0.245	0.406
		52	Entorhinal Ctx	H	711	0.403	0.548	0.534		0.05037	0.109	0.094
		23	Auditory Ctx	P	550	0.636	0.673	0.692		0.15544	0.132	0.052
		50	Ectorhinal Ctx	P	76	2.666	1.552	1.387		0.34218	0.547	0.557
		114	Perirhinal Ctx	P	246	0.375	0.450	0.432		0.0215	0.013	0.006
Parietal Lobe	116	Parietal Ctx	P	199	0.480	0.391	0.616		0.08051	0.003	0.136	
	130	Primary Somatosensory Ctx Barrel Field	P	611	0.283	0.658	0.583		0.01069	0.108	0.042	
	131	Primary Somatosensory Ctx Forelimb	P	359	0.400	0.542	0.816		0.11063	0.063	0.332	
	132	Primary Somatosensory Ctx Hindlimb	P	199	0.314	0.421	0.571		0.07062	0.111	0.227	
	133	Primary Somatosensory Ctx Jaw	P	449	0.612	0.541	0.570		0.24276	0.096	0.024	

Step 19: Use Microsoft Excel’s “QUARTILE” function to calculate the top quartile for the SPI values (over all three time points).

A4	Section	ROI ID	ROI	B2 Bradykinin Receptor Expression	approx # voxels	SPI 20	SPI 40	SPI 60	Top quartile	t-test 20	t-test 40	t-test 60
Cerebral	Olfactory Bulb	57	Glomerular Layer	L	452	0.497	0.490	0.386	0.700	0.05223	0.035	0.012
		53	External Plexiform Layer	P	400	0.765	0.782	0.535		0.53525	0.512	0.084
		59	Granular Cell Layer	H	521	0.771	0.788	0.538		0.48525	0.313	0.009
	Olfactory Areas	152	Tenia Tecta	P	104	0.876	0.857	0.566		0.71152	0.613	0.100
		20	Anterior Olfactory Nucleus	P	263	1.037	0.736	0.375		0.95068	0.509	0.013
		102	Caudal Piriform Ctx	H	233	0.744	0.914	0.771		0.29618	0.685	0.128
	Limbic Lobe	103	Rostral Piriform Ctx	H	747	0.523	0.533	0.449		0.13742	0.059	0.022
		31	Anterior Cingulate Area	H	497	0.202	0.323	0.457		0.01457	0.009	0.008
		125	Retrosplenial Caudal Ctx	H	185	0.524	0.680	0.869		0.34747	0.319	0.669
	Insular Cortex	126	Retrosplenial Rostral Ctx	H	491	0.386	0.504	0.473		0.05111	0.067	0.065
		64	Insular Ctx	H	953	0.736	0.748	0.663		0.4157	0.281	0.076
		Occipital Lobe	156	Visual 1 Ctx	P	449	0.190	0.354	0.449		0.01213	0.046
	157		Visual 2 Ctx	P	455	0.253	0.440	0.522		0.04329	0.042	0.082
	Temporal Lobe	150	Temporal Ctx	P	120	0.741	0.578	0.756		0.48785	0.245	0.406
		52	Entorhinal Ctx	H	711	0.403	0.548	0.534		0.05037	0.109	0.094
		23	Auditory Ctx	P	550	0.636	0.673	0.692		0.15544	0.132	0.052
		50	Ectorhinal Ctx	P	76	2.666	1.552	1.387		0.34218	0.547	0.557
		114	Perirhinal Ctx	P	246	0.375	0.450	0.432		0.0215	0.013	0.006
Parietal Lobe	116	Parietal Ctx	P	199	0.480	0.391	0.616		0.08051	0.003	0.136	
	130	Primary Somatosensory Ctx Barrel Field	P	611	0.283	0.658	0.583		0.01069	0.108	0.042	
	131	Primary Somatosensory Ctx Forelimb	P	359	0.400	0.542	0.816		0.11063	0.063	0.332	
	132	Primary Somatosensory Ctx Hindlimb	P	199	0.314	0.421	0.571		0.07062	0.111	0.227	
	133	Primary Somatosensory Ctx Jaw	P	449	0.612	0.541	0.570		0.24276	0.096	0.024	

Step 20: Use Microsoft Excel's "Conditional formatting" to highlight the SPI and T-test data as desired.

The screenshot shows the Microsoft Excel ribbon with the 'Conditional Formatting' tab selected. The 'Conditional Formatting' button is circled in orange. Below the ribbon is a data table with the following structure and values:

E	F	G	H	I	J	K	L	M	N	O	P
aykinin tor ision	approx # voxels		SPI 20	SPI 40	SPI 60	Top quartile:	t-test 20	t-test 40	t-test 60		
	452		0.497	0.490	0.386	0.700	0.052	0.035	0.012		
	400		0.765	0.782	0.535		0.535	0.512	0.084		
	521		0.771	0.788	0.538		0.485	0.313	0.009		
	104		0.876	0.857	0.566		0.712	0.613	0.100		
	263		1.037	0.736	0.375		0.951	0.509	0.013		

Appendix D: Statistical Analysis Code Walk Through

Software Requirements

In order to run this program the following software is needed:

- A licensed version of Matlab
- The MATLAB Statistics and Machine Learning Toolbox

This software has been tested on both Windows and Linux operating systems, but should also be compatible with the Mac OSX operating system as well.

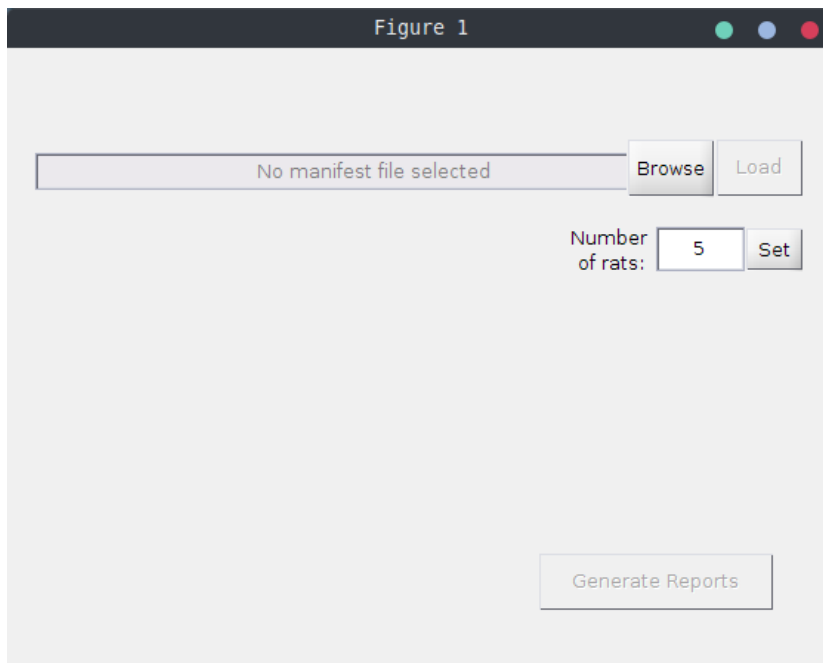
Running the Program

First, open the following files in MATLAB:

- SPIGenerator.m
- SelectionMenu.m
- ReportOption.m
- RatAnalysis.m
- TreatmentFile.m
- Rat.m

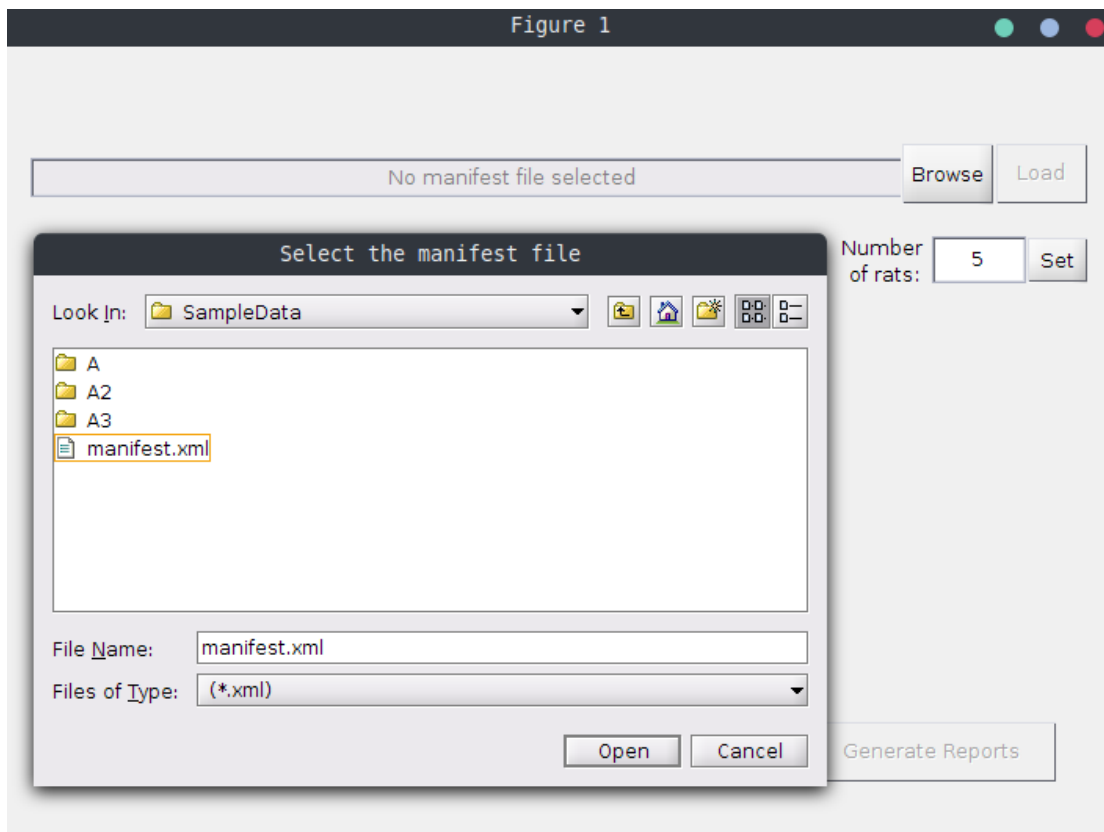
Then, simply run SPIGenerator.m

If the software dependencies above are properly installed, the user will be presented with the following interface:

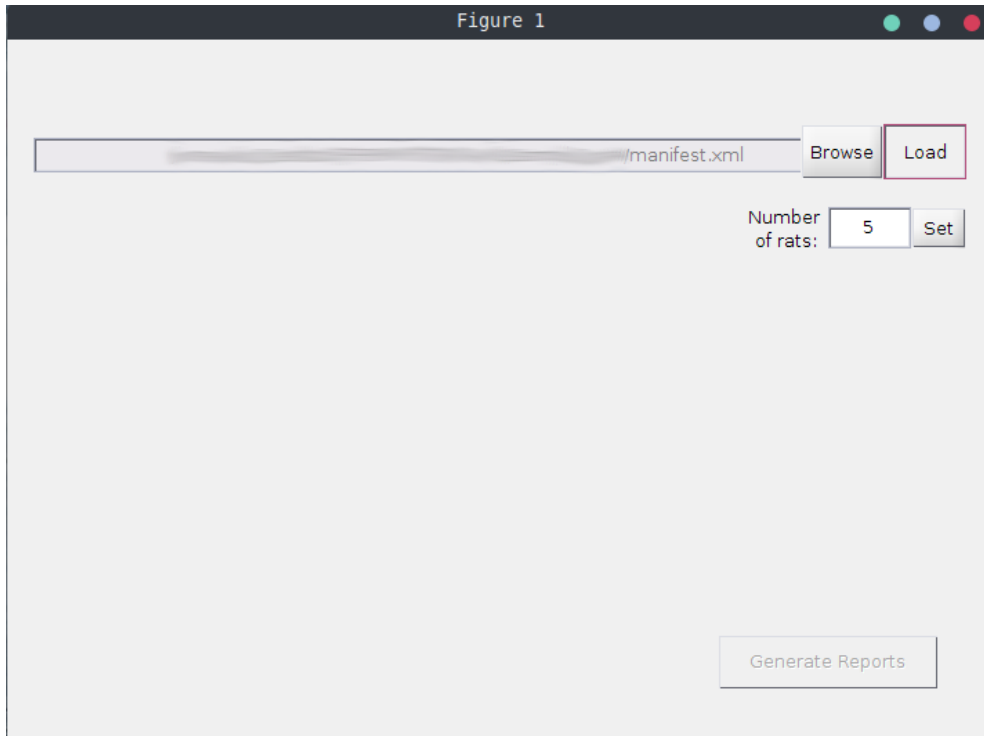


Loading the manifest file

A manifest file must then be loaded into the software. Press the 'Browse' button in the top right corner of the interface. A file browser window will appear. Navigate to the manifest XML file and press 'open'. **For more information regarding the manifest file, see the section on creating a manifest file.**



After opening the manifest file, click the load button:

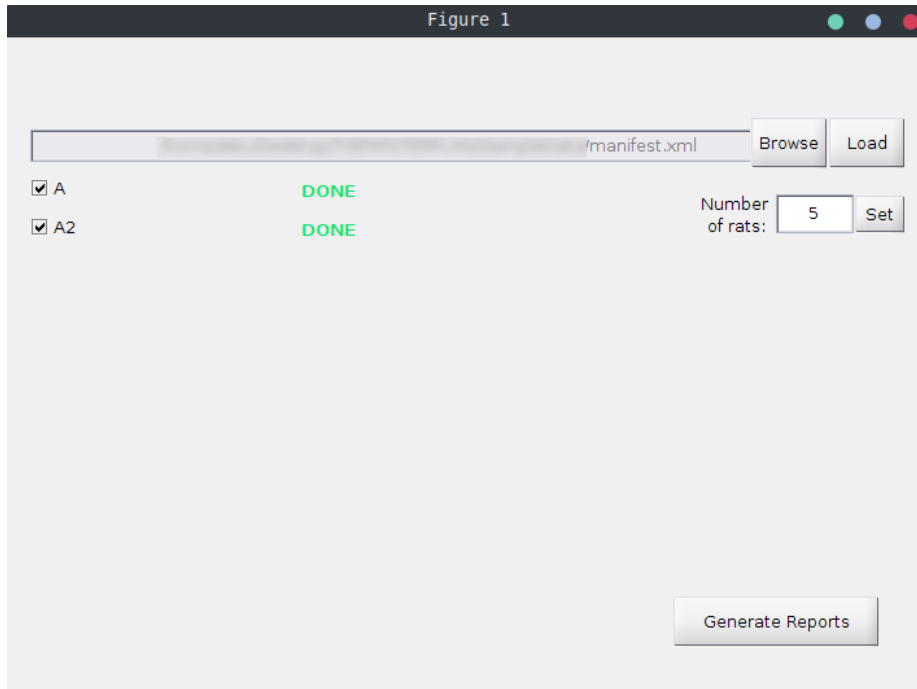


The manifest file will then be loaded into the program. This process typically takes a few seconds to complete.

Generating Reports

When the manifest file has finished loading, a list of report options will appear. A CSV report will be generated for all options that are checked. Uncheck any reports that do not need to be generated. Finally, click Generate Reports.

Wait as each report is generated. This process usually takes about a minute for each report, but performance will vary widely depending on the speed of the computer and scale of the data. As each report is finished generating, a message will appear next to each checkbox indicating that it has finished:



Generated reports are saved in the same directory as the MATLAB code files.

The Manifest File

The manifest file is an XML document that is provided to the Treatment Analyzer. It is a configuration file that tells the program the following information:

- The name of the untargeted treatment (e.g. A)
- The name of the targeted treatment (e.g. A2, A3, BFNA)
- The Rat MRI CSV files associated with each treatment
- The time that each treatment file was taken at (e.g. 15 minutes, 30 minutes, 45 minutes, etc)

The following is an example of a simple manifest file:

```
<files>
  <untargeted name="A">
    <path time="0">./SampleData/A/A_Pre_T1.csv</path>
    <path time="20">./SampleData/A/A_20Min_T1.csv</path>
    <path time="40">./SampleData/A/A_40Min_T1.csv</path>
    <path time="60">./SampleData/A/A_60Min_T1.csv</path>
  </untargeted>
  <targeted name="A2">
    <path time="0">./SampleData/A2/A2_Pre.csv</path>
    <path time="20">./SampleData/A2/A2_20.csv</path>
    <path time="40">./SampleData/A2/A2_40.csv</path>
    <path time="60">./SampleData/A2/A2_60.csv</path>
  </targeted>
</files>
```


Creating a manifest file

The content of the manifest file is formatted as XML.

Creating a manifest file is simple. Start with an empty XML file. The file may have any name as long as it uses the XML file extension.

All XML documents must have a root element. This example will use as the root:

```
<files>
</files>
```

Inside the root element, add tags for the targeted and untargeted sections. It does not matter if the targeted section is placed before the untargeted section or vice versa. Both arrangements are equally acceptable.

```
<files>
  <targeted>
</targeted>
  <untargeted>
</untargeted>
</files>
```

Next, add a name property to the targeted and untargeted sections. This is used to specify the name of the treatment and must be included.

```
<files>
  <targeted name="BFNA">
</targeted>
  <untargeted name="A">
</untargeted>
</files>
```

Inside each of the targeted and untargeted sections, add tags that point to the location on the computer that the input CSV data is saved at.

For instance, if there are three CSV files saved at the following locations on disk for the BFNA treatment:

- C:/Users/person/Desktop/file1.csv
- C:/Users/person/Documents/file2.csv
- C:/Users/person/Documents/Example/file3.csv

Then add three <path> entries under the targeted section:

```

<files>
  <targeted name="BFNA">
    <path>C:/Users/person/Desktop/file1.csv</path>
    <path>C:/Users/person/Documents/file2.csv</path>
    <path>C:/Users/person/Documents/Example/file3.csv</path>
  </targeted>
  <untargeted name="A">
  </untargeted>
</files>

```

Each <path> tag must also have a time attribute specifying the time slice for which the data was collected. It does not matter how the path elements are ordered in the manifest file.

```

<files>
  <targeted name="BFNA">
    <path time="40">C:/Users/person/Desktop/file1.csv</path>
    <path time="60">C:/Users/person/Documents/file2.csv</path>
    <path time="15">C:/Users/person/Documents/Example/file3.csv</path>
  </targeted>
  <untargeted name="A">
  </untargeted>
</files>

```

Finally, repeat the previous steps for the untargeted section.

```

<files>
  <targeted name="BFNA">
    <path time="40">C:/Users/person/Desktop/file1.csv</path>
    <path time="60">C:/Users/person/Documents/file2.csv</path>
    <path time="15">C:/Users/person/Documents/Example/file3.csv</path>
  </targeted>
  <untargeted name="A">
    <path time="15">C:/Users/person/file4.csv</path>
    <path time="40">C:/Users/person/Documents/atreatment.csv</path>
    <path time="60">C:/Users/person/Documents/Files/foo.csv</path>
  </untargeted>
</files>

```

Appendix E: Statistical Analysis Raw Code

SPI Generator

```
%Run to run the rest of the code.
import RatAnalysis
import TreatmentFile
import SelectionMenu
import ReportOption
import Brain

%This turns off the warning about modified variable names in a Matlab
%table.
warning('off','MATLAB:table:ModifiedVarnames');
%use high precision numbers with many significant digits
format long;

selectionMenu = SelectionMenu();
```

Rat

```
%Handle class define objects that references the data contained in the object.
% Copying the object creates another reference to the same data.
classdef Rat<handle
    %Represents a particular rat with many regions in it
    properties
        ratName;
        ratData;
    end
    methods
        %Constructor for the representation of a Rat. A constructor is a
        %template for the object. Where you specify how to create a new
        %object- what makes up your object.
        function obj = Rat(ratName, ratData)
            obj.ratName = ratName;
            obj.ratData = ratData;
        end

        %Sums all of the voxels in all regions of the specific rat that the
        %object represents
        function voxels = totalVoxels(obj)
            %obj.ratData(1,:) is the first row (Number of voxels) in the
            %table of data for a rat. We then convert this row into an
            %array(list) and sum all of the values. Voxels returns with
            %total number of voxel in a rat.
            voxelRow = obj.ratData(1,:);
            voxels = Rat.nansum(table2array(voxelRow));
        end

        %Returns a percentage representing the percentage of voxels in the
```

```

%specified region
function ratio = roiVoxelPct(obj, roi)
    %number of voxels in the ROI
    roiVoxels = obj.regionVoxels(roi);
    totalVoxels = obj.totalVoxels();
    ratio = roiVoxels/totalVoxels;
end

%Retrieves the number of voxels in a given region of the rat
function voxels = regionVoxels(obj, roi)
    try
        voxels = obj.ratData{1,roi};
    catch
        voxels = 0;
    end
end

%Retrieves the mean value in a given region of the rat
function mean = regionMean(obj, roi)
    try
        mean = obj.ratData{2,roi};
    catch
        mean = 0;
    end
end

%Retrieves the standard deviation value in a given region of the rat
function stdDev = regionStdDev(obj, roi)
    try
        stdDev = obj.ratData{3,roi};
    catch
        stdDev = 0;
    end
end
end

%Static method:
%
% An object is essentially a blueprint for something. For example, an
% object representing a vehicle is kind of like a schematic:
% We might create my car object by saying
% DeannasCar = Car('2010','Toyota','Camry',Gray') if we wanted to
% programatically create my gray 2010 Toyota Camry.
% The object (or blueprint) might also have some methods defined for it:
% leftBlinker, rightBlinker, accelerate, brake, repaint... etc.
%
% So hypothetically, if we wanted to repaint my car we could just call
% DeannasCar.repaint('Red'), and now the car is red. Hopefully in
% this example, it's also clear that when we call DeannasCar.repaint('Red'),
% It doesn't make every other car in the world red as well.
% Only Deanna's car will get repainted.
%
% Sometimes, though, we want to be able to define methods that don't
% really need the blueprint to be constructed in order to run. To continue

```

```

% With the example, sometimes we want to be able to make a method that belongs to
% the Car class even though we haven't actually created a specific
% instance of a car object to run it on (like DeannasCar).
% That's where static methods come in. We can make a static method like
% numberOfWheels. We do this because in this example, we can
% pretty safely make the generalization that all cars have 4 wheels.
% We can call this method by simply doing Car.numberOfWheels().
% Note that we don't do DeannasCar.numberOfWheels() -- we do
% Cars.numberOfWheels because the static numberOfWheels()
% isn't meant to be run on a specific car -- this is a method
% that is defined for ALL cars in general.
methods (Static)
    %Sometimes in the table of data, we get a stray entry at the end of
    %a row that is not actually a number (NaN = Not a Number). For
    %example, when we read in a CSV with the values, "1,2,3,4,5,"
    %Matlab actually interprets this as a table with the values
    % "1,2,3,4,5,NaN" because of the trailing comma at the end.
    %This causes problems when we try to sum the entire row because
    %Matlab doesn't know how to sum numbers with something that's not a
    %number. We circumvent this by creating a quick method that treats
    %all NaN values as 0 and sums the rest of the numbers.
    function y = nansum(x)
        nans = isnan(x);
        x(nans) = 0;
        y = sum(x);
    end
end
end
end

```

Rat Analysis

```

classdef RatAnalysis<handle
    %properties for the RatAnalysis objec. Containers.Map-a Map object is a data structure
    %that allows you to retrieve values using a corresponding key. Keys (sections (20,40,60))
    can
        %be real numbers or text strings and provide more flexibility for data
        %access than array indices, which must be positive integers. Values (TreatmentFile objects))
    can
        %be scalar or nonscalar arrays.
    properties
        manifestPath;
        targetedFiles = containers.Map('keyType','double','valueType','any');
        untargetedFiles = containers.Map('keyType','double','valueType','any');
        numRats = 5;
    end

    methods
        %Reads in the manifest file and parses each of the files into
        %separate TreatmentFile objects
        function obj = parseManifestFile(obj)
            %Try and catch are used to handle when things don't work as
            %expected in the code. Everything in the "try" section gets

```

```

%run, and if it fails, execution jumps to the catch section
%where we can specify what kind of error message to produce, or
%how we should recover from the error (if at all).
try
    %XMLread is a method that allows us to parse an XML file.
    %We use it since the manifest file is in XML format.
    xmlDoc = xmlread(obj.manifestPath);
    %Grab the set of targeted treatment files.Tagname in
    %manifest is anything in < >.
    tFiles = xmlDoc.getElementsByTagName('targeted');
    %Grab the set of untargeted treatment files.
    utFiles = xmlDoc.getElementsByTagName('untargeted');
    obj.parseFileSet(tFiles, true);
    obj.parseFileSet(utFiles, false);

catch ME
    switch ME.identifier
        case 'MATLAB:xml:FileNotFound'
            err = ['ERROR: The path you specified for the '...
                , 'manifest file: "%s" either does not exist or the ' ...
                , 'program does not have permission to read the file. ' ...
                , 'Please check to make sure that everything ' ...
                , 'is spelled properly.'];
            error(err,obj.manifestPath);
        otherwise
            error(getReport(ME));
    end
end
end

%The manifest file contains a section for both targeted and
%untargeted treatment files. This method takes in one of those sets
%and parses each file within the treatment set.
function obj = parseFileSet(obj, tagSet, targeted)
    try
        %getElementsByTagName- built in function. getting all
        %similar path tags in a set
        pathEls = tagSet.item(0).getElementsByTagName('path');
        treatmentName = char(tagSet.item(0).getAttribute('name'));
        %for all of the path tags in set
        for i=1:pathEls.getLength()
            %get the path items in order they appear. starts
            %counting at 0
            fileEl = pathEls.item(i - 1);
            %Gets the path to the file that this element in the
            %manifest is referencing
            filePath = char(fileEl.getTextContent());
            %Gets the time slice that this file represents
            timeString = char(fileEl.getAttribute('time'));
            time = str2double(timeString);
            if isnan(time)
                error(['ERROR: Non-number time provided in manifest ' ...
                    , 'file: "%s". Please use an integer when ' ...

```

```

        , 'specifying the "time" field in the ' ...
        , 'manifest file.'], timeString);
    end

    %parse the data from this file into a TreatmentFile object
    treatmentFile = TreatmentFile(filePath, targeted, treatmentName, time);
    %separate untargeted and targeted rat files into separate
    %arrays
    if(targeted)
        obj.targetedFiles(time) = treatmentFile;
    else
        obj.untargetedFiles(time) = treatmentFile;
    end
end

%Try and catch are used to handle when things don't work as
%expected in the code. Everything in the "try" section gets
%run, and if it fails, execution jumps to the catch section
%where we can specify what kind of error message to produce, or
%how we should recover from the error (if at all). Below, an
%error message gets generated if the "targeted" or "untargeted"
%sections of the manifest file fail to be read in correctly.
catch ME
    switch ME.identifier
        case 'MATLAB:nonStrucReference'
            err = ['ERROR: Could not find %s section in the '...
                , 'manifest file. Make sure that it exists '...
                , 'and that it is spelled correctly.'];
            if targeted
                error(err, 'targeted');
            else
                error(err, 'untargeted');
            end
        otherwise
            error(getReport(ME));
    end
end
end

%Generates either the numerator or the denominator value for the
%targeted equation
%prescan refers to the prescan file and compare scan refers to the
%other file that is being compared to the prescan file - same
%treatment
function [sum, ratValues] = weightedROIDiff(obj, targeted, roiID, compareTime)
    if targeted
        dataSet = obj.targetedFiles;
    else
        dataSet = obj.untargetedFiles;
    end

    sum = 0;
    %prescan data will be filled in here
    preScan = dataSet(0);

```

```

%time file data willl be filled in here
compareScan = dataSet(compareTime);

ratValues = zeros(1,obj.numRats);
for i=1:obj.numRats
    %start with the first rats in each file. loops through rest
    preScanRat = preScan.ratCollection(i);
    compareScanRat = compareScan.ratCollection(i);
    %calling voxel percentage
    roiPct = compareScanRat.roiVoxelPct(roiID);

    %retrieves values and solves one rat at a time, but as it
    %loops it will sum the values leaving you with the
    %numerator or denominator of the overall equation.
    compareScanMean = compareScanRat.regionMean(roiID);
    preScanMean = preScanRat.regionMean(roiID);

    preScanRatVal = roiPct * preScanMean;
    compareScanRatVal = roiPct * compareScanMean;
    ratValue = preScanRatVal - compareScanRatVal;
    ratValues(i) = ratValue;
    sum = sum + ratValue;
end
end

%Generates the targeted equation value for the roi. Compares the
%prescan treatment file against the treatment file corresponding to compareTime
function [spi, testVal] = targetedSPI(obj, roiID, compareTime)
    [targetedResult, targetedValues] = obj.weightedROIDiff(true, roiID, compareTime);
    [untargetedResult, untargetedValues] = obj.weightedROIDiff(false, roiID,
compareTime);
    [~,testVal] = ttest2(targetedValues, untargetedValues,'Tail','both');
    spi = targetedResult/untargetedResult;
end

%Generates the targeted equation value for the roi. Compares the
%prescan treatment file against the treatment file corresponding to compareTime
function [spi, testVal] = untargetedSPI(obj, roiID, compareTime)
    [preScanResult, preScanValues] = obj.weightedROIMean(roiID, 0);
    [compareScanResult, compareScanValues] = obj.weightedROIMean(roiID, compareTime);
    [~,testVal] = ttest2(preScanValues, compareScanValues,'Tail','both');
    spi = preScanResult/compareScanResult;
end

%Generates either the numerator or denominator for the untargeted
%SPI value
function [sum, ratValues] = weightedROIMean(obj, roiID, time)
    sum = 0;
    dataSet = obj.untargetedFiles(time);

    ratValues = zeros(1,obj.numRats);
    for i=1:obj.numRats
        treatmentRat = dataSet.ratCollection(i);

```



```

        roiPct = treatmentRat.roiVoxelPct(roiID);
        meanVal = treatmentRat.regionMean(roiID);
        ratValue = roiPct * meanVal;
        ratValues(i) = ratValue;
        sum = sum + ratValue;
    end
end

function tbl = outputSPITable(obj, treatmentFile)
    regionTable = treatmentFile.regionTable;
    numRegions = width(regionTable);
    tbl = cell(numRegions,3);

    for i=1:numRegions
        if(treatmentFile.targeted)
            [SPI, testVal] = obj.targetedSPI(i, treatmentFile.time);
        else
            [SPI, testVal] = obj.untargetedSPI(i, treatmentFile.time);
        end

        tbl{i,2} = SPI;
        tbl{i,3} = testVal;
        tbl{i,1} = regionTable{1,i};
    end

    tbl = cell2table(tbl);
    tbl.Properties.VariableNames = {'ROI_ID','SPI','T_Test'};
    tbl.Properties.RowNames = regionTable.Properties.VariableNames;
    fileName = treatmentFile.generateFileName();
    writetable(tbl, fileName, 'writeRowNames', true);
end
end
end

```

Report Option

```

classdef ReportOption < handle
    %REPORTOPTION Summary of this class goes here
    % Detailed explanation goes here

    properties
        checkbox;
        ratAnalysis;
        treatmentFileSet;
        statusText;
        index;
        panel;
        reportName;
    end

    methods
        function obj = ReportOption(ratAnalysis, treatmentFileSet, index)
            obj.ratAnalysis = ratAnalysis;
        end
    end
end

```

```

obj.treatmentFileSet = treatmentFileSet;
obj.index = index;
obj.reportName = treatmentFileSet(0).treatmentName;

obj.panel = uipanel('BorderStyle','none');
setpixelposition(obj.panel,[0.5,0.5,1,0.1]);
obj.checkbox = uicontrol('Style','checkbox','String',obj.reportName, ...
    'value',1);

obj.statusText = uicontrol('Style','text',...
    'String','DONE',...
    'ForegroundColor', [0,0.9,0.4], ...
    'FontWeight', 'bold', ...
    'Visible', 'off');
end

function value = getCheckboxValue(obj)
    value = get(obj.checkbox, 'value');
end

function obj = setBoxPosition(obj, panelHeight)
    offset = panelHeight - (100 + (obj.index * 30));
    setpixelposition(obj.checkbox, [20,offset,150,30]);
    setpixelposition(obj.statusText, [200, offset - 10, 100, 30]);
end

function obj = showStatusText(obj, bool)
    if(bool)
        set(obj.statusText, 'visible', 'on');
    else
        set(obj.statusText, 'visible', 'off');
    end
    drawnow;
end
end
end
end

```

```

Selection Menu classdef SelectionMenu<handle
    properties
        fig;
        ratAnalysis;

        browseButton;
        browsePathText;
        loadButton;
        ratCountBox;
        ratCountText;
        ratCountButton;
        generateButton;
        reportOptions;
    end
end

```

methods

```
function obj = SelectionMenu()
    obj.ratAnalysis = RatAnalysis();
    obj.fig = figure();
    obj.makeUIPanel();

    %Put buttons/components in the correct position to begin
    obj.resizeui();
end

%Creates the initial panel with UI controls
function obj = makeUIPanel(obj)
    %Make an empty window with no controls
    %Hide the toolbars at the top of the menu
    set(obj.fig, 'MenuBar', 'none');
    set(obj.fig, 'ToolBar', 'none');
    set(obj.fig, 'ResizeFcn', @obj.resizeui);

    %Add some text next to the browse button to show the selected
    %path
    obj.browsePathText = uicontrol(obj.fig,'Style','edit',...
        'String','No manifest file selected',...
        'Enable', 'off');

    %Add a button to browse for the manifest file
    obj.browseButton = uicontrol(obj.fig,'Style','pushbutton', ...
        'String','Browse', ...
        'Callback', @obj.browseManifest);

    %Add a button to load the manifest file
    obj.loadButton = uicontrol(obj.fig,'Style','pushbutton', ...
        'String','Load', ...
        'Enable', 'off', ...
        'Callback', @obj.loadManifest);

    %Add a button to generate the reports
    obj.generateButton = uicontrol(obj.fig,'Style','pushbutton', ...
        'String','Generate Reports', ...
        'Enable', 'off', ...
        'Callback', @obj.generateSelectedReports);

    %Add a button to generate the reports
    obj.ratCountBox = uicontrol(obj.fig,'Style','edit', ...
        'String','5');

    %Add a button to generate the reports
    obj.ratCountText = uicontrol(obj.fig,'Style','text', ...
        'String','Number of rats:');

    %Add a button to generate the reports
    obj.ratCountButton = uicontrol(obj.fig,'Style','pushbutton', ...
        'String','Set', ...
        'Callback', @obj.validateRatCountBox);
```

```

end

%When called, opens the file browser so the user can navigate to
%the manifest file
function obj = browseManifest(obj, ~, ~, varargin)
    [fileName,filePath] = uigetfile('*.xml','Select the manifest file');
    fullName = strcat(char(filePath), char(fileName));
    set(obj.browsePathText,'String',fullName);
    set(obj.loadButton,'Enable','on');
    obj.ratAnalysis.manifestPath = fullName;
end

function obj = loadManifest(obj, ~, ~, varargin)
    obj.ratAnalysis.parseManifestFile();
    obj.generateReportList();
    obj.resizeui();
end

function obj = validateRatCountBox(obj, ~, ~, varargin)
    input = get(obj.ratCountBox, 'String');
    value = str2double(input);
    %Value is invalid
    if isnan(value) || value < 0
        set(obj.ratCountBox, 'String', '5');
        value = 5;
    end
    obj.ratAnalysis.numRats = value;
end

function generateReportList(obj)
    %Initialize the list of report options
    obj.reportOptions = ReportOption.empty(0,2);
    obj.reportOptions(1) = ReportOption(obj.ratAnalysis, obj.ratAnalysis.untargetedFiles,
1);
    obj.reportOptions(2) = ReportOption(obj.ratAnalysis, obj.ratAnalysis.targetedFiles,
2);
    set(obj.generateButton,'Enable','on');
end

%This function is run whenever the panel is resized.
function resizeui(obj, ~, ~, varargin)
    % Get figure width and height
    figPos = get(obj.fig, 'Position');
    figwidth = figPos(3);
    figHeight = figPos(4);

    setpixelposition(obj.browseButton,[figwidth-140, figHeight-100, 60, 40]);
    setpixelposition(obj.browsePathText, [20,figHeight-95, figwidth-100, 25]);
    setpixelposition(obj.loadButton, getpixelposition(obj.browseButton) + [60 0 0 0]);
    setpixelposition(obj.generateButton, [figwidth-200, 40, 160, 40]);

    setpixelposition(obj.ratCountBox, [figwidth-120, figHeight - 150, 60, 30]);
    setpixelposition(obj.ratCountText, [figwidth-180, figHeight - 150, 60, 30]);

```

```

        setpixelposition(obj.ratCountButton, [figwidth-60, figHeight - 150, 40, 30]);

        for i=1:length(obj.reportOptions)
            opt = obj.reportOptions(i);
            opt.setBoxPosition(figHeight);
        end
    end

    function obj = generateSelectedReports(obj, ~, ~, varargin)
        brain = Brain(obj.ratAnalysis);
        for i=1:length(obj.reportOptions)
            opt = obj.reportOptions(i);
            opt.showStatusText(false);
        end

        for i=1:length(obj.reportOptions)
            opt = obj.reportOptions(i);
            checked = opt.getCheckboxValue();

            if(checked)
                brain.generateOutputTable(opt.treatmentFileSet);
                opt.showStatusText(true);
            else
                opt.showStatusText(false);
            end
        end
    end
end
end
end
end
end

```

Treatment File

```

classdef TreatmentFile<handle
    properties
        path;
        regionTable;
        ratCollection;
        time;
        targeted;
        treatmentName;
        rowsPerRat = 4;
    end

    methods
        %Constructor for TreatmentFile. Therefore you need path and time
        %to have a TreatmentFile.
        %ratCollection-creates an empty list that will later be filled in
        %with the rat data

        function obj = TreatmentFile(path, targeted, treatmentName, time)
            obj.path = path;
        end
    end
end

```

```

obj.ratCollection = [];
obj.time = time;
obj.targeted = targeted;
obj.treatmentName = treatmentName;

%Constructors can also call methods that help for setup (fill in ratCollection). This
% will parse all of the CSV data for the treatment file and populate
% the list of rats.
obj.parseCSV();
end

%make the csv file data usable and interpret that data for use in
%Matlab
function obj = parseCSV(obj)
    %Parse the CSV data as a MATLAB table. readtable is a built in
    %function. readtable(location, whether or not read Row Names,
    %yes or no)
    treatmentData = readtable(obj.path, 'ReadRowNames', true);

    %Separate and remove the ROI table from the rest of the table
    obj.regionTable = treatmentData(1:1,:);
    treatmentData(1,:)=[];

    %number of rows left in table. for loop starts at 1, goes up by
    %4 (rowsPerRat) each time, and then stops at numRows
    numRows = height(treatmentData);
    for i = 1:obj.rowsPerRat:numRows
        %Grab every four rows of the table so that we can put this
        %data into a rat object.
        ratSubTable = treatmentData(i:i+3,:);

        %Get the name of the rat, for example:
        %'NEMU_BFNA_A3_R9_yv1_T1_relaxation_time'
        ratName = ratSubTable.Properties.RowNames{1};

        %Make a new rat object. The first parameter represents the
        %name of the rat, and the second parameter is a table
        %containing the number of voxels, mean, and std dev values
        %as rows
        ratData = ratSubTable(2:end,:);
        newRat = Rat(ratName, ratData);

        %Add the newly parsed rat into the list of rats for this
        %treatment file
        obj.ratCollection = [obj.ratCollection; newRat];
    end
end

%Generates a name for the report to be generated
function filename = generateFileName(obj)
    filename = sprintf('%s pre-%d.csv', obj.treatmentName, obj.time);
end

```

```
end
end
```

Brain

```
classdef Brain<handle
    %Represents a brain of a rat and contains the different groupings and
    %sections

    properties
        groupings;
        ratAnalysis;
    end

    methods
        function obj = Brain(ratAnalysis)
            obj.ratAnalysis = ratAnalysis;

            %Define the sections of the brain
            olfactoryBulb = Section('Olfactory Bulb', {57,53,59});
            olfactoryAreas = Section('Olfactory Areas', {152,20,102,103});
            limbicLobe = Section('Limbic Lobe', {31,125,126});
            insularCortex = Section('Insular Coretex', {64});
            occipitalLobe = Section('Occipital Lobe', {156,157});
            temporalLobe = Section('Temporal Lobe', {150, 52, 23, 50, 114});
            parietalLobe = Section('Parietal Lobe', {116, 130, 131, 132, 133, 134, 135, 136,
137});
            frontalLobe = Section('Frontal Lobe', {166,88,75,63,115,55,79,80});
            hippocampalFormation = Section('Hippocampal Formation',
{25,26,27,28,29,48,170,40,41});
            amygdaloidNucComplex = Section('Amygdaloid Nuclear Complex',
{24,30,15,68,61,35,83,49});
            basalGanglia = Section('Basal Ganglia',
{42,44,162,165,153,16,17,58,167,146,174,111,51,139});
            basalForebrainSect = Section('Basal Forebrain', {33,145,78,151});
            septum = Section('Septum', {91,39});
            hypothalamus = Section('Hypothalamus',
{18,73,104,149,138,94,22,43,100,81,86,143,164,77,89,119});
            pituitary = Section('Pituitary', {19,92});
            thalamus = Section('Thalamus',
{14,34,71,76,82,98,120,158,161,163,168,169,118,109,85,72,127});
            epithalamus = Section('Epithalamus', {60, 101});
            cerebellum = Section('Cerebellum',
{2,3,4,5,6,9,10,12,13,1,65,140,36,99,37,38,54,69,84,105});
            pons = Section('Pons',
{106,7,112,45,154,74,129,93,110,107,108,56,96,8,11,70,148,87});
            tectum = Section('Tectum', {62,147});
            cerebralPeduncle = Section('Cerebral Peduncle', {21,90,141,142,124,171,67,95,32,128,
...
                117,47,121,66,144,159,160,122,123,97,46,113,155,172,173});
        end
    end
end
```

```

    %Define the groupings of the brain
    cerebralCortex = Grouping('Cerebral Cortex',
{olfactoryBulb,olfactoryAreas,limbicLobe, ...

insularCortex,occipitalLobe,temporalLobe,parietalLobe,frontalLobe,hippocampalFormation});
    basalForebrain = Grouping('Basal Forebrain',
{amygdaloidNucComplex,basalGanglia,basalForebrainSect,septum});
    diencephalon = Grouping('Diencephalon',
{hypothalamus,pituitary,thalamus,epithalamus});
    metencephalon = Grouping('Metencephalon',{cerebellum,pons});
    mesencephalon = Grouping('Mesencephalon',{tectum,cerebralPeduncle});
    medullaOblongata = Grouping('Medulla Oblongata',{});

    %Set the groupings of the brain
    obj.groupings = {cerebralCortex,basalForebrain,diencephalon, ...
        metencephalon,mesencephalon,medullaOblongata};
end

function obj = generateOutputTable(obj,treatmentFileSet)
    row = 0;
    regionTable = treatmentFileSet(0).regionTable.Properties.VariableNames;
    treatmentName = treatmentFileSet(0).treatmentName;
    outputTable = cell2table(cell(174,13));
    outputTable.Properties.VariableNames = {'A','Section','ROI_ID','ROI',...
        'Approx_Voxels','NA','SPI_20','SPI_40','SPI_60','Quartile', ...
        'T_test_20','T_test_40','Ttest_60'};
    for i = 1:length(obj.groupings)
        grouping = obj.groupings{i};
        for j = 1:length(grouping.sections)
            section = grouping.sections{j};
            for k = 1:length(section.regions)
                region = section.regions{k};
                %Fill in the grouping name
                outputTable{row + k,1} = {grouping.name};
                %Fill in the section name
                outputTable{row + k,2} = {section.name};
                %Fill in the region ID
                outputTable{row + k,3} = {region};
                %Fill in region name
                regionName = regionTable(region);
                outputTable{row + k,4} = {regionName};

                [twentySPI, twentyTest] = obj.getTreatmentSetSPI(treatmentFileSet,
region, 20);

                [fortySPI, fortyTest] = obj.getTreatmentSetSPI(treatmentFileSet, region,
40);

                [sixtySPI, sixtyTest] = obj.getTreatmentSetSPI(treatmentFileSet, region,
60);

                %Fill out SPI 20,40,60
                outputTable{row + k,7} = {twentySPI};
                outputTable{row + k,8} = {fortySPI};
            end
        end
    end
end

```



```

        outputTable{row + k,9} = {sixtySPI};

        %Fill out T-Test 20,40,60
        outputTable{row + k,11} = {twentyTest};
        outputTable{row + k,12} = {fortyTest};
        outputTable{row + k,13} = {sixtyTest};
    end
    row = row + length(section.regions);
end
fileName = sprintf('VoxelWeighted_SPI_%s.csv',treatmentName);
writetable(outputTable, fileName, 'WriteRowNames', true);
end
end

function [SPI, testVal] = getTreatmentSetSPI(obj, treatmentFileSet, roiID, time)
    treatmentFile = treatmentFileSet(time);
    if(treatmentFile.targeted)
        [SPI, testVal] = obj.ratAnalysis.targetedSPI(roiID, time);
    else
        [SPI, testVal] = obj.ratAnalysis.untargetedSPI(roiID, time);
    end
end
end
end
end
end

```

Grouping

```

classdef Grouping
    %Represents a grouping of sections within the brain%

    properties
        name;
        sections;
    end

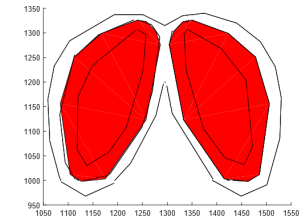
    methods
        function obj = Grouping(name, sections)
            obj.name = name;
            obj.sections = sections;
        end
    end
end
end

```

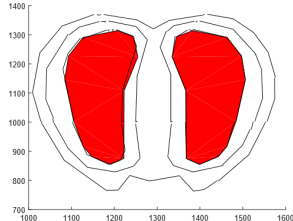
Appendix F: Quality Control Images

To ensure that the Matlab program was mapping correctly to the 3D rat brain atlas, a quality control process was completed. This process involved using an excel sheet of all “0”s and one “1” to map out a singular region. Each region of each slice was tested. A sample of one region from each slice can be found below.

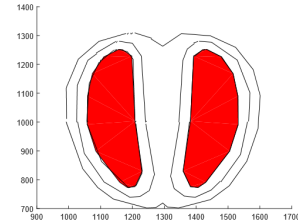
Slice 1:



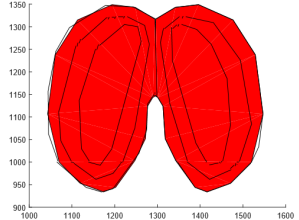
Slice 6:



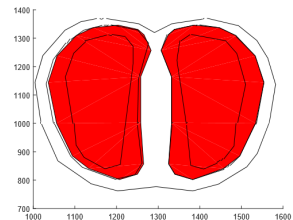
Slice 11:



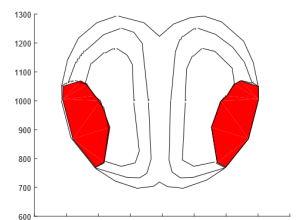
Slice 2:



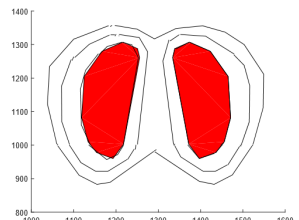
Slice 7:



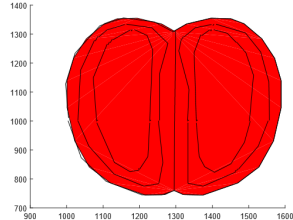
Slice 12:



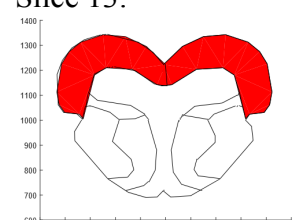
Slice 3:



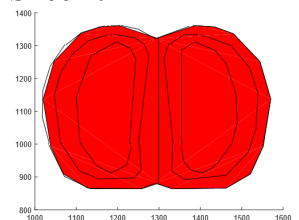
Slice 8:



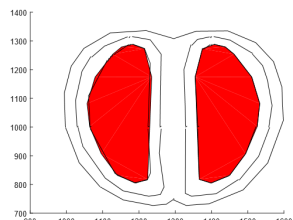
Slice 13:



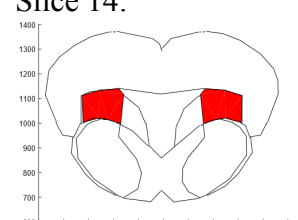
Slice 4:



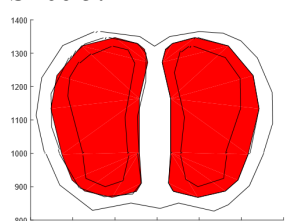
Slice 9:



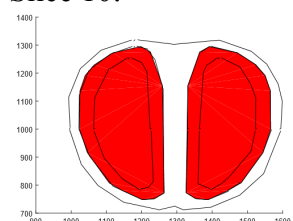
Slice 14:



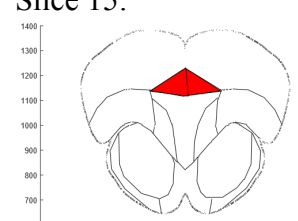
Slice 5:



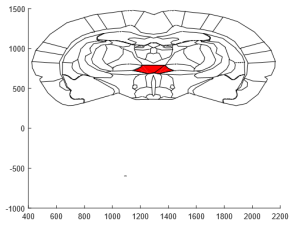
Slice 10:



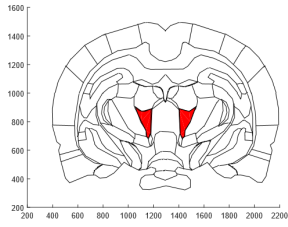
Slice 15:



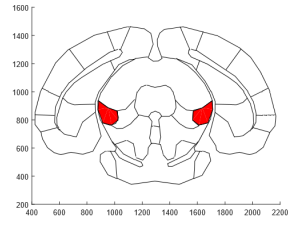
Slice 34:



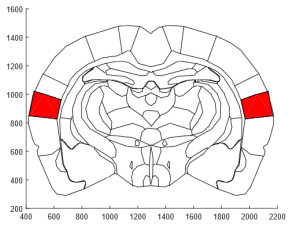
Slice 40:



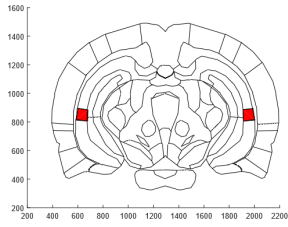
Slice 46:



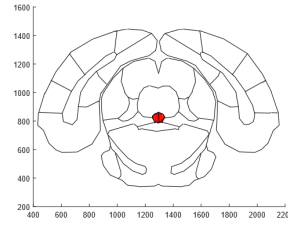
Slice 35:



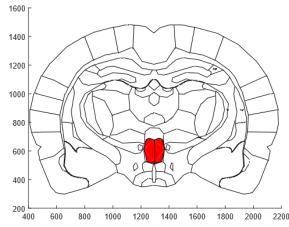
Slice 41:



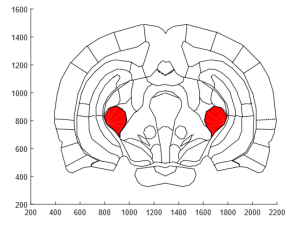
Slice 47:



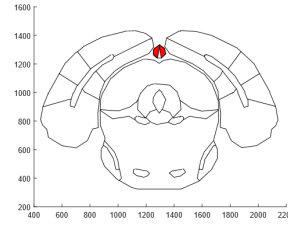
Slice 36:



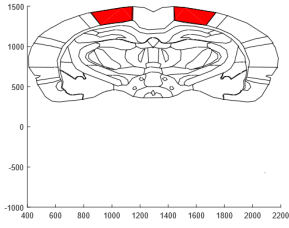
Slice 42:



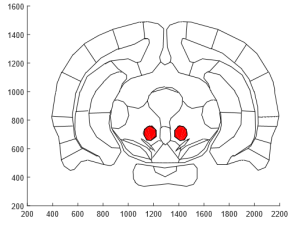
Slice 48:



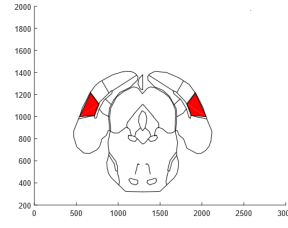
Slice 37:



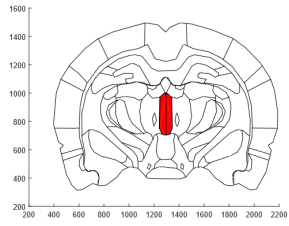
Slice 43:



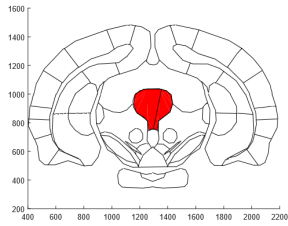
Slice 49:



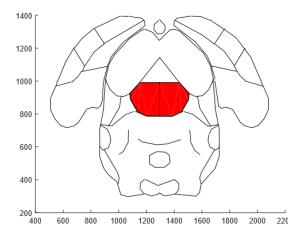
Slice 38:



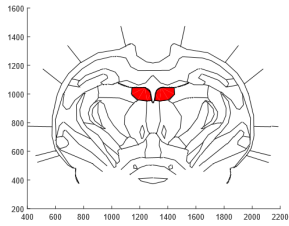
Slice 44:



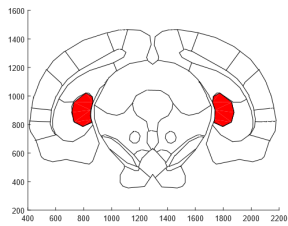
Slice 50:



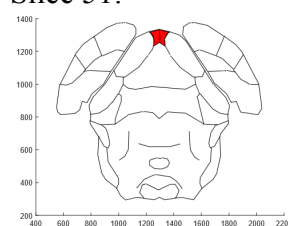
Slice 39:



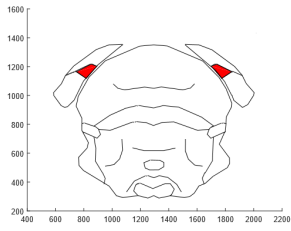
Slice 45:



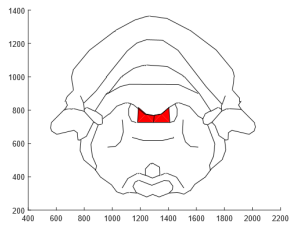
Slice 51:



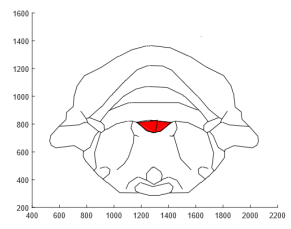
Slice 52:



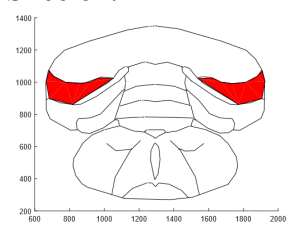
Slice 53:



Slice 54:

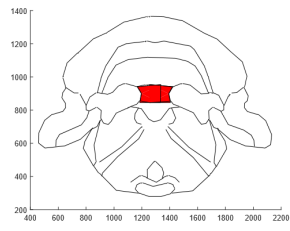


Slice 61:

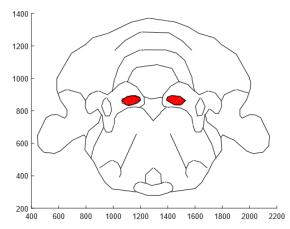


Slice 62:

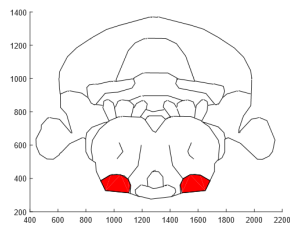
Slice 55:



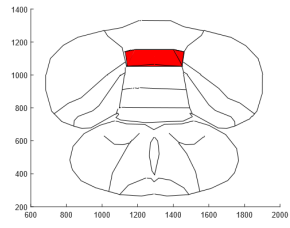
Slice 56:



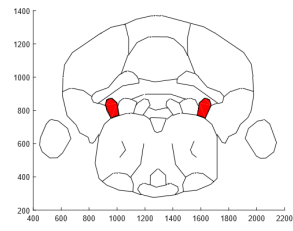
Slice 57:



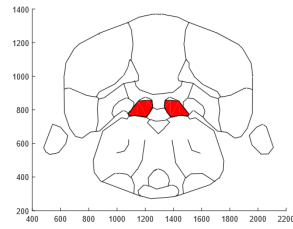
Slice 63:



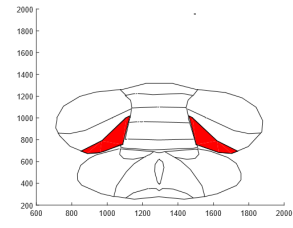
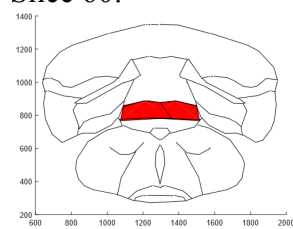
Slice 58:



Slice 59:



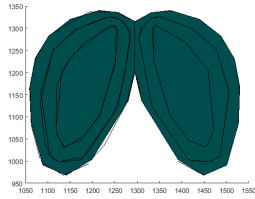
Slice 60:



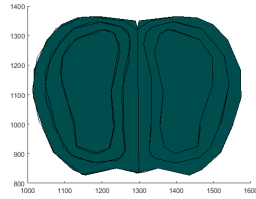
Appendix G: Mu-Opioid Receptor Map



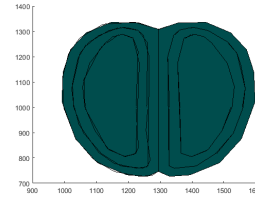
Slice 1:



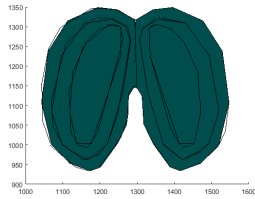
Slice 5:



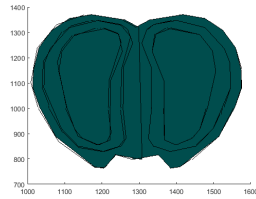
Slice 9:



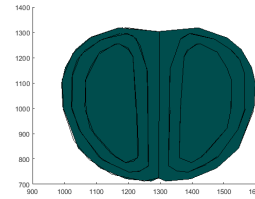
Slice 2:



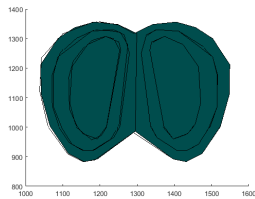
Slice 6:



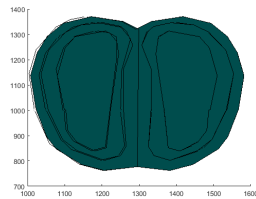
Slice 10:



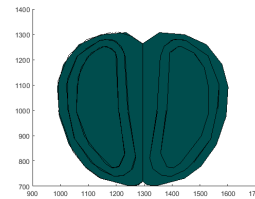
Slice 3:



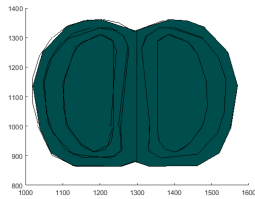
Slice 7:



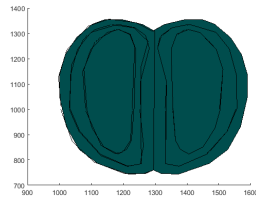
Slice 11:



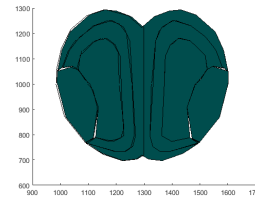
Slice 4:



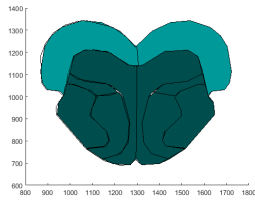
Slice 8:



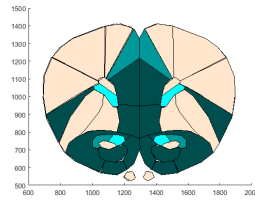
Slice 12:



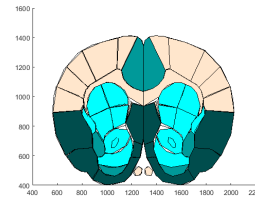
Slice 13:



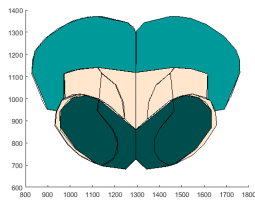
Slice 18:



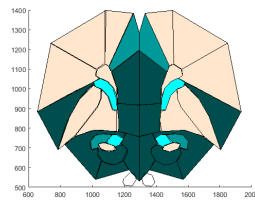
Slice 23:



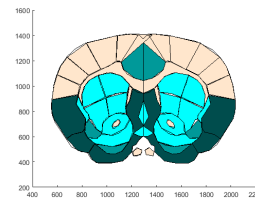
Slice 14:



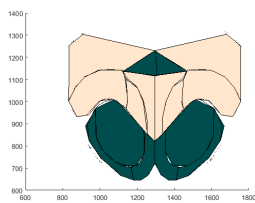
Slice 19:



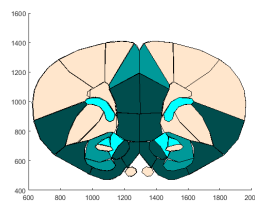
Slice 24:



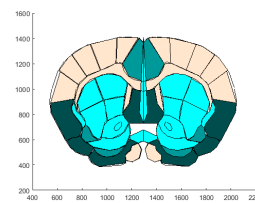
Slice 15:



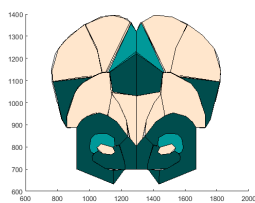
Slice 20:



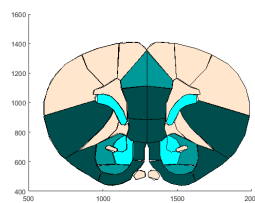
Slice 25:



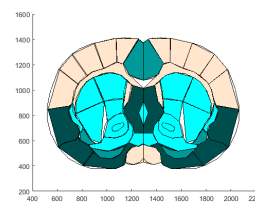
Slice 16:



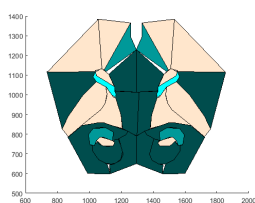
Slice 21:



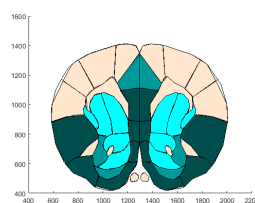
Slice 26:



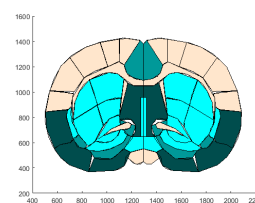
Slice 17:



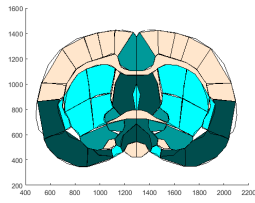
Slice 22:



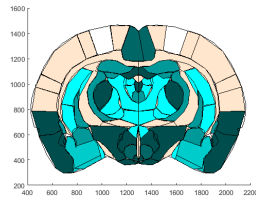
Slice 27:



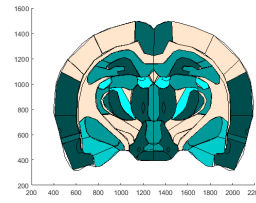
Slice 28:



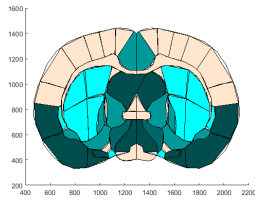
Slice 33:



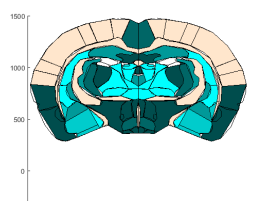
Slice 38:



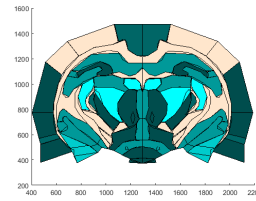
Slice 29:



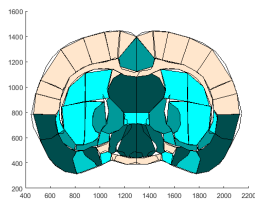
Slice 34:



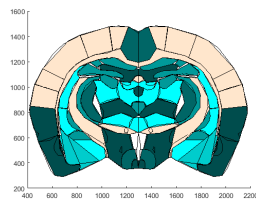
Slice 39:



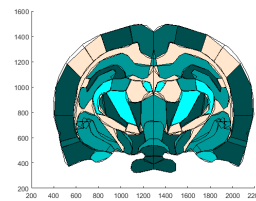
Slice 30:



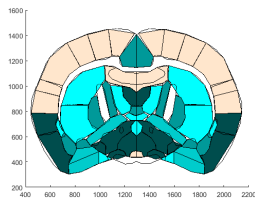
Slice 35:



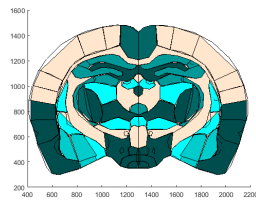
Slice 40:



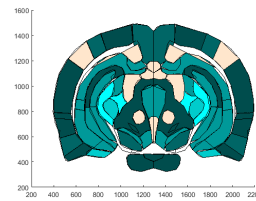
Slice 31:



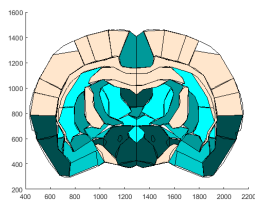
Slice 36:



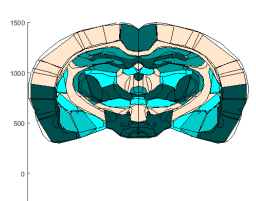
Slice 41:



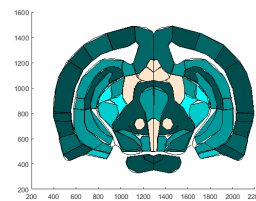
Slice 32:



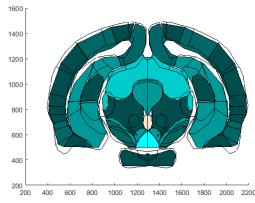
Slice 37:



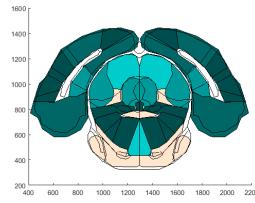
Slice 42:



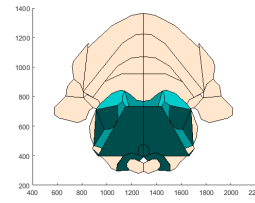
Slice 43:



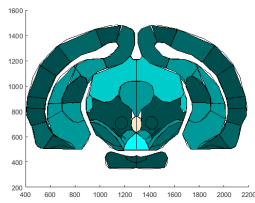
Slice 48:



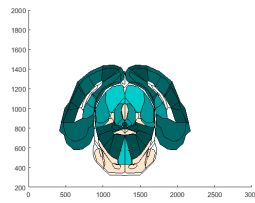
Slice 53:



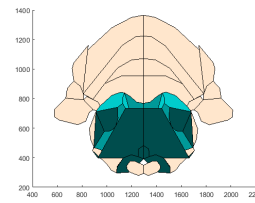
Slice 44:



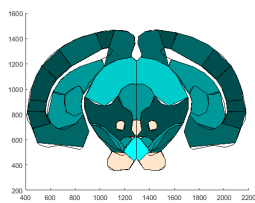
Slice 49:



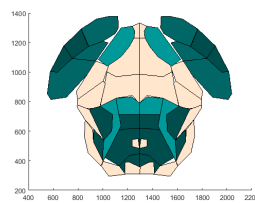
Slice 54:



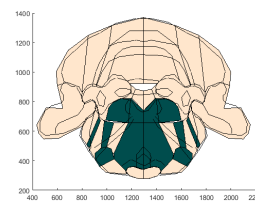
Slice 45:



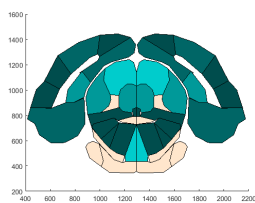
Slice 50:



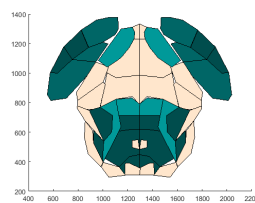
Slice 55:



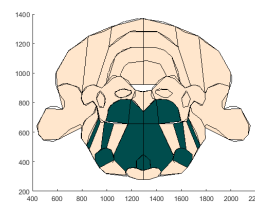
Slice 46:



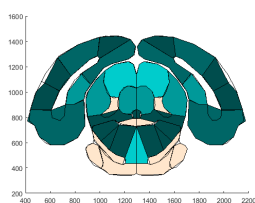
Slice 51:



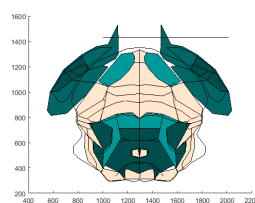
Slice 56:



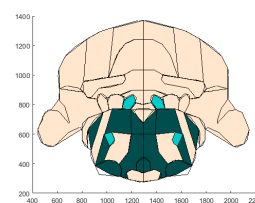
Slice 47:



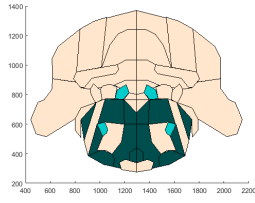
Slice 52:



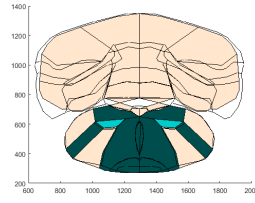
Slice 57:



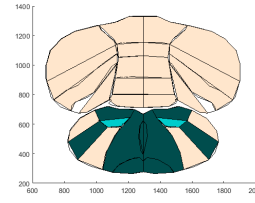
Slice 58:



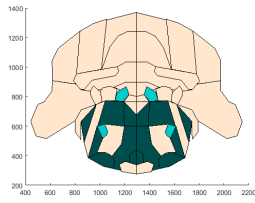
Slice 60:



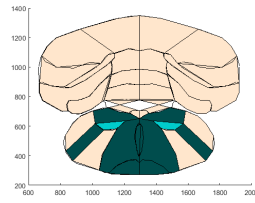
Slice 62:



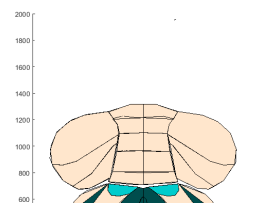
Slice 59:



Slice 61:



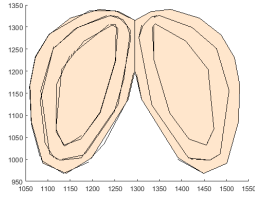
Slice 63:



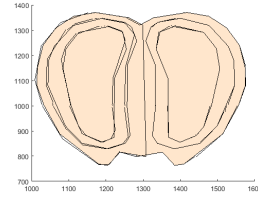
Appendix H: Alpha-7 Receptor Map



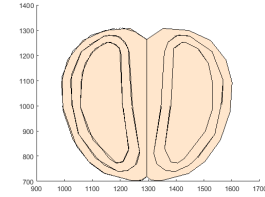
Slice 1:



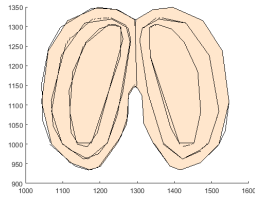
Slice 6:



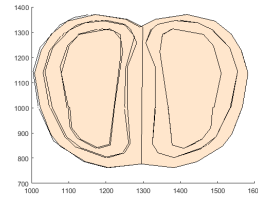
Slice 11:



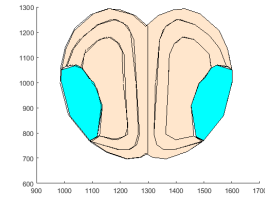
Slice 2:



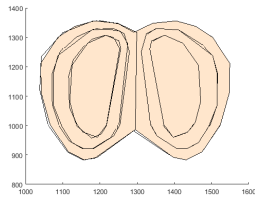
Slice 7:



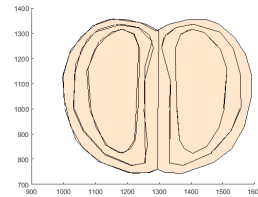
Slice 12:



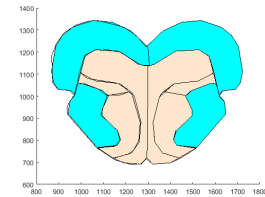
Slice 3:



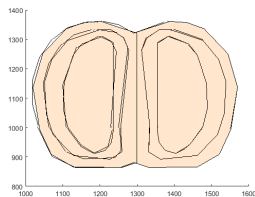
Slice 8:



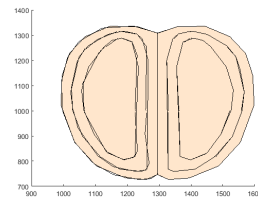
Slice 13:



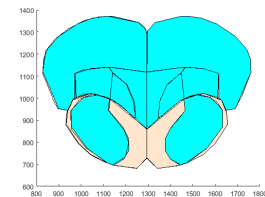
Slice 4:



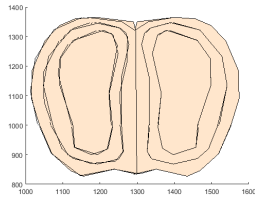
Slice 9:



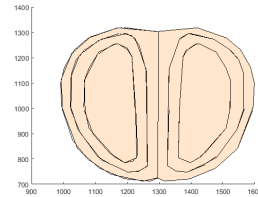
Slice 14:



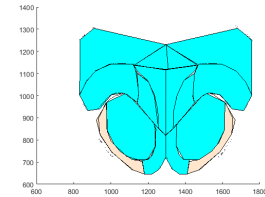
Slice 5:



Slice 10:



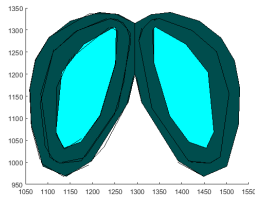
Slice 15:



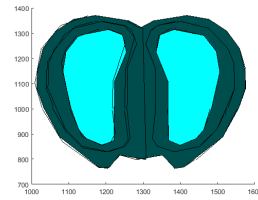
Appendix I: B2 Bradykinin Receptor Map



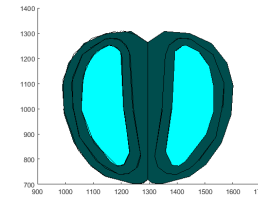
Slice 1:



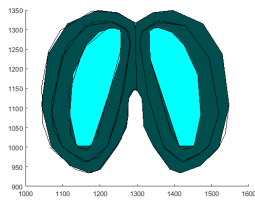
Slice 6:



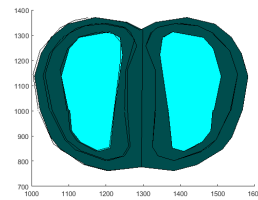
Slice 11:



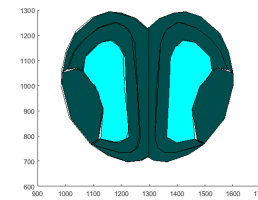
Slice 2:



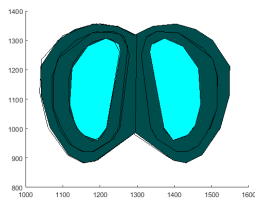
Slice 7:



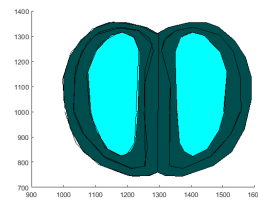
Slice 12:



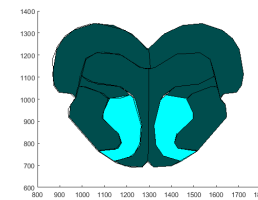
Slice 3:



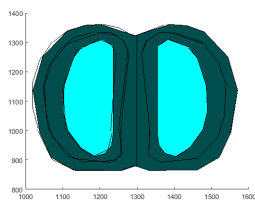
Slice 8:



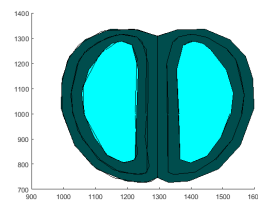
Slice 13:



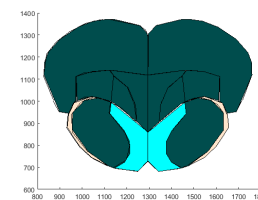
Slice 4:



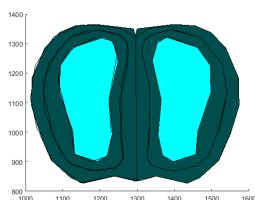
Slice 9:



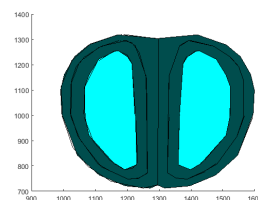
Slice 14:



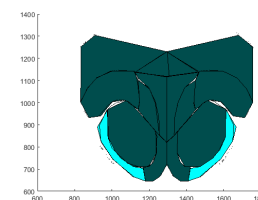
Slice 5:



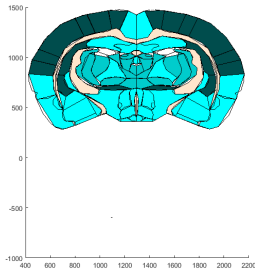
Slice 10:



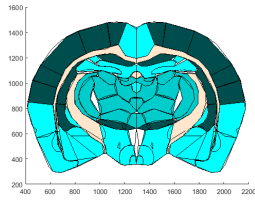
Slice 15:



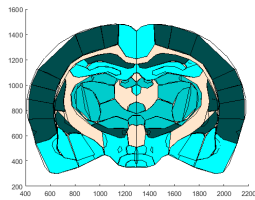
Slice 34:



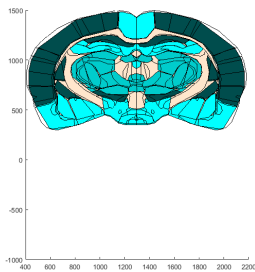
Slice 35:



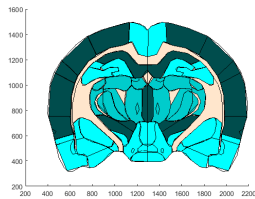
Slice 36:



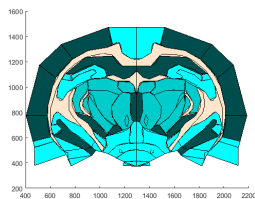
Slice 37:



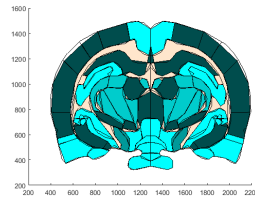
Slice 38:



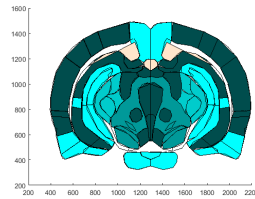
Slice 39:



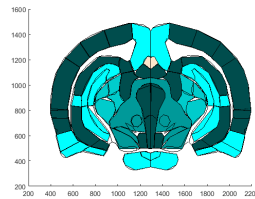
Slice 40:



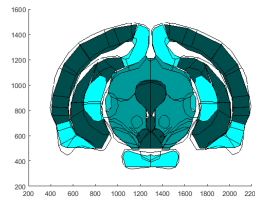
Slice 41:



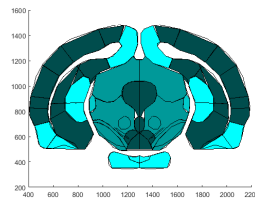
Slice 42:



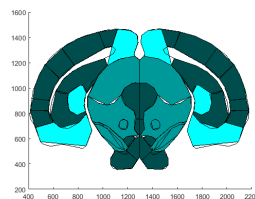
Slice 43:



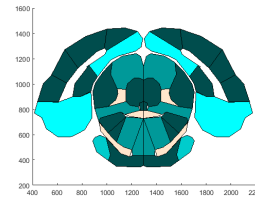
Slice 44:



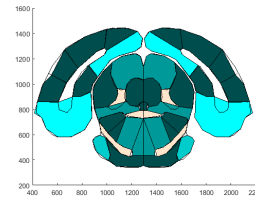
Slice 45:



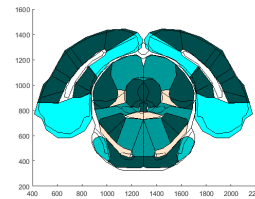
Slice 46:



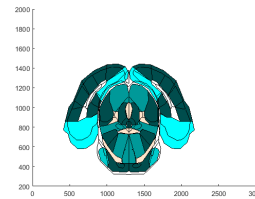
Slice 47:



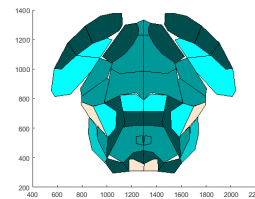
Slice 48:



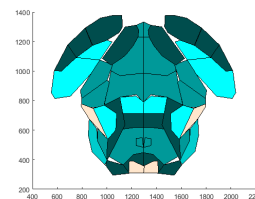
Slice 49:



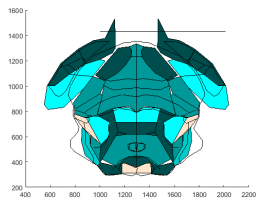
Slice 50:



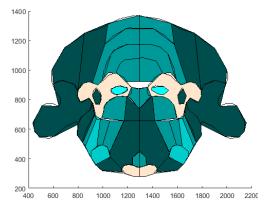
Slice 51:



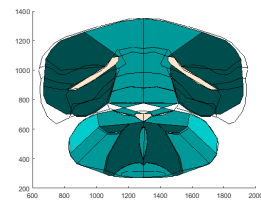
Slice 52:



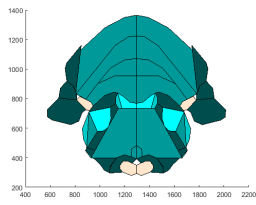
Slice 56:



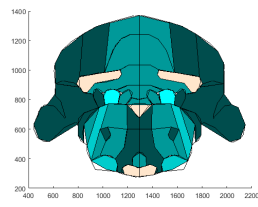
Slice 60:



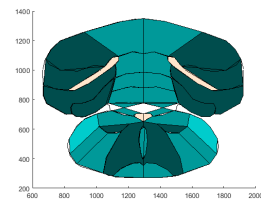
Slice 53:



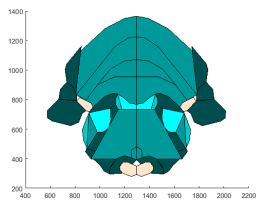
Slice 57:



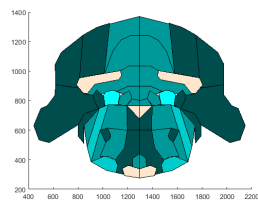
Slice 61:



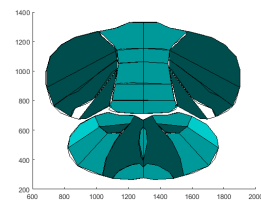
Slice 54:



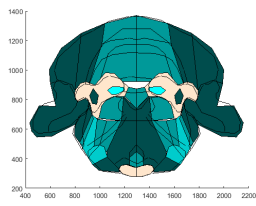
Slice 58:



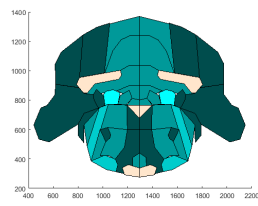
Slice 62:



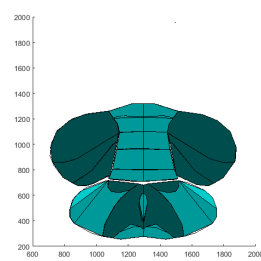
Slice 55:



Slice 59:



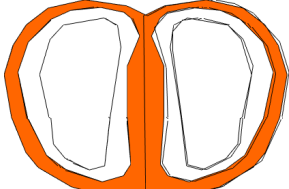
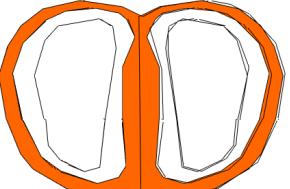
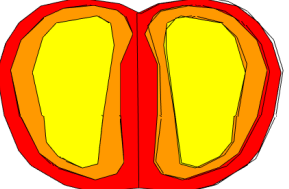
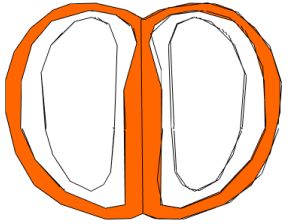
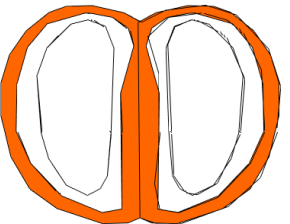
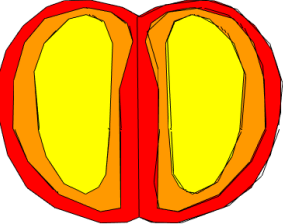
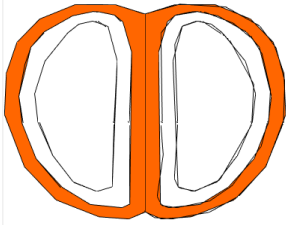
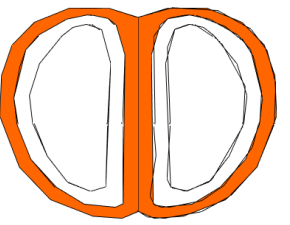
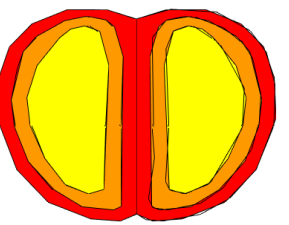
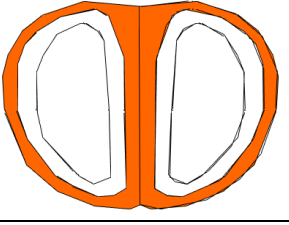
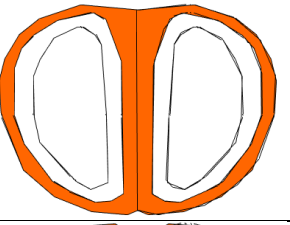
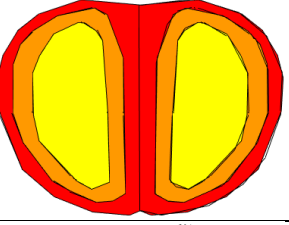
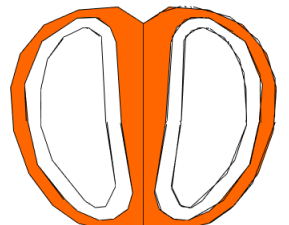
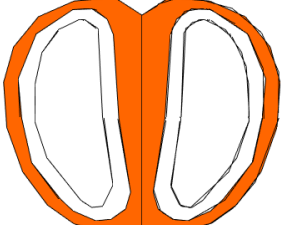
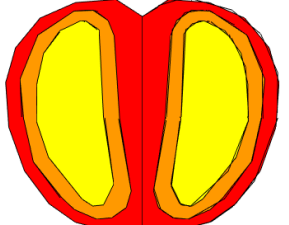
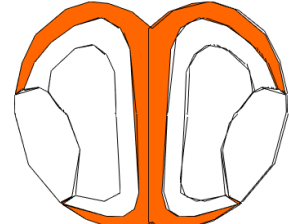
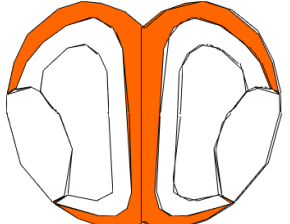
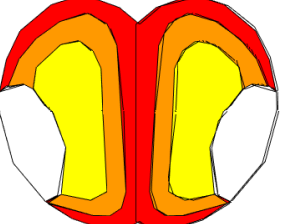
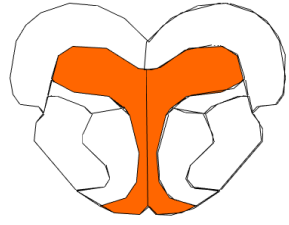
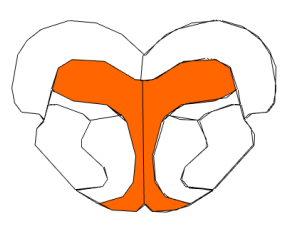
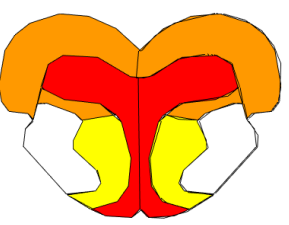
Slice 63:

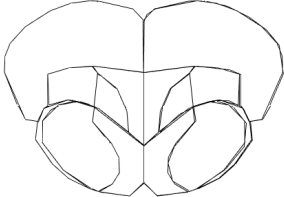
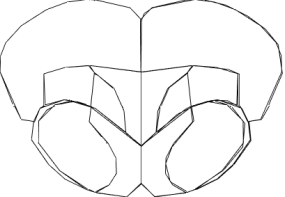
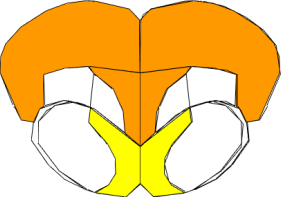
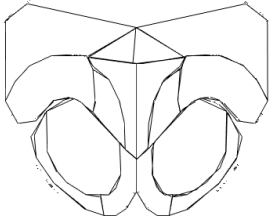
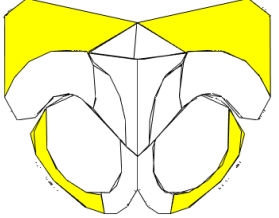
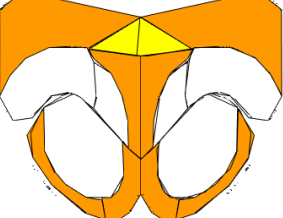
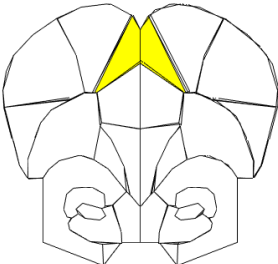
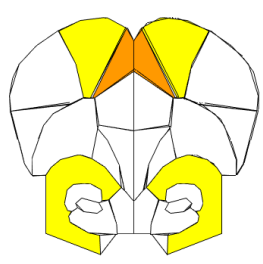
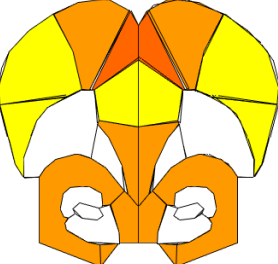
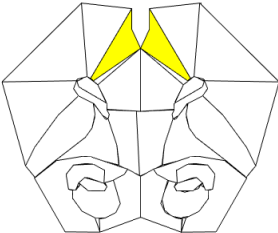
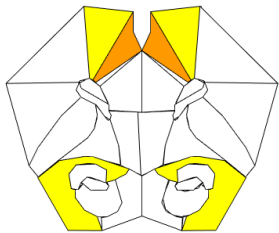
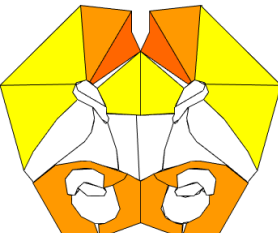
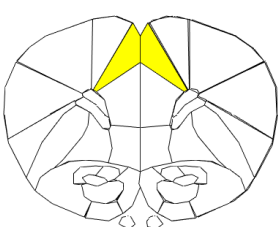
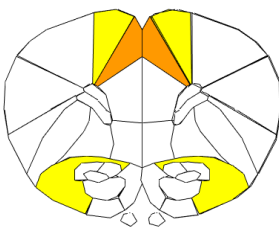
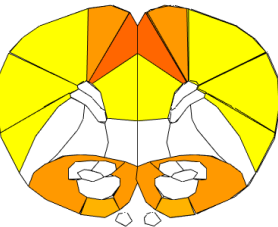
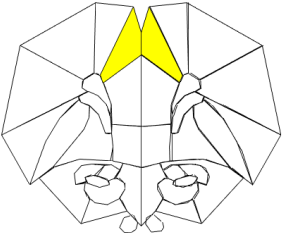
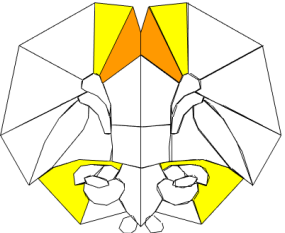
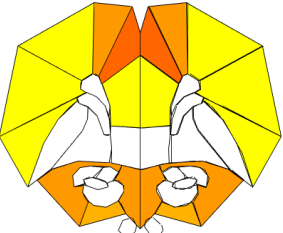
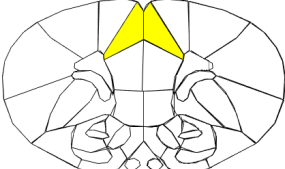
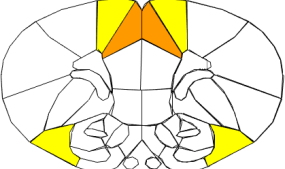
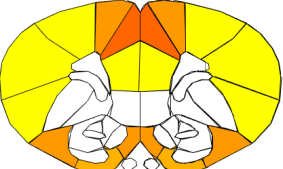


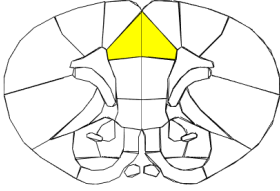
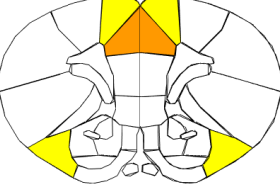
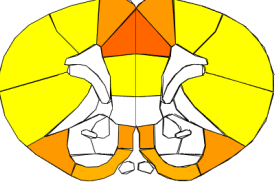
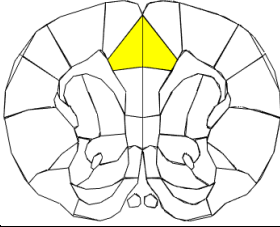
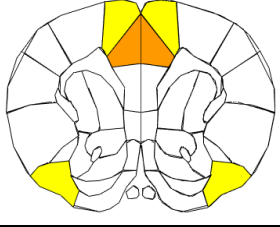
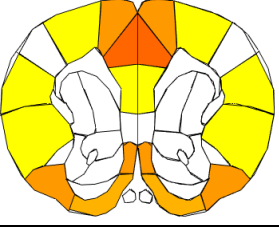
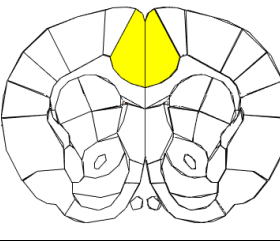
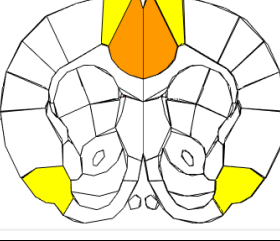
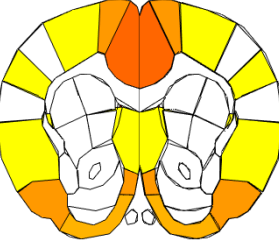
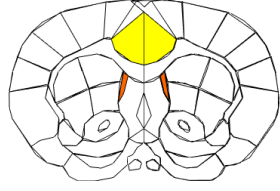
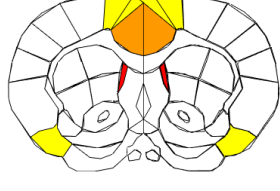
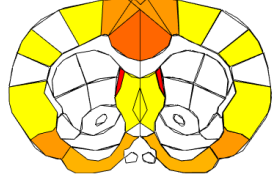
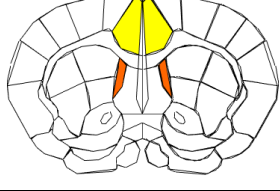
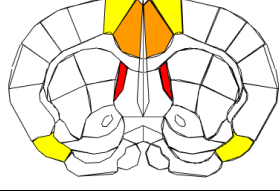
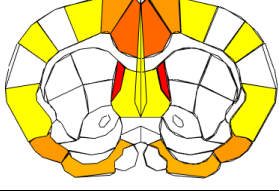
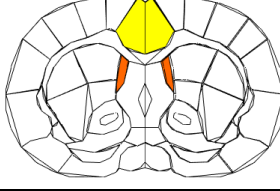
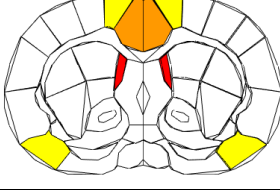
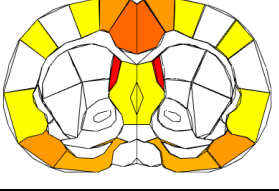
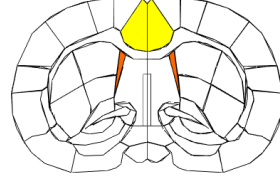
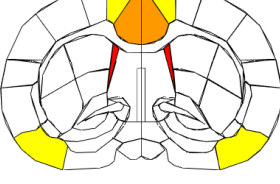
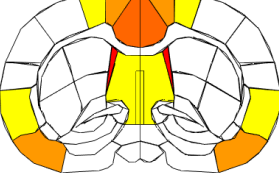
Appendix J: Non-Targeted Nanoemulsion Results



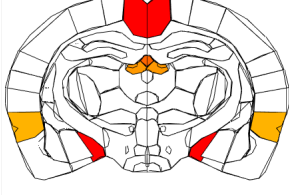
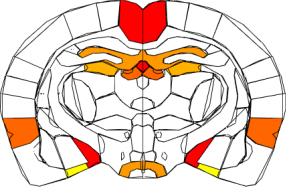
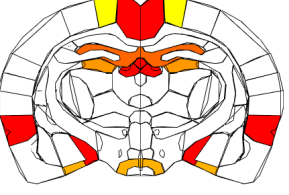
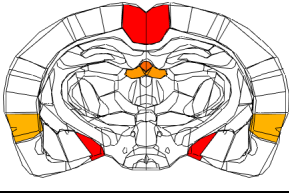
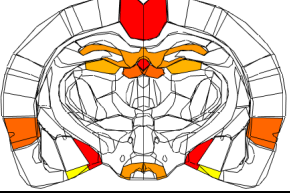
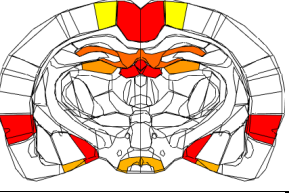
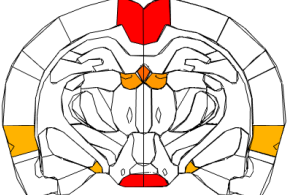
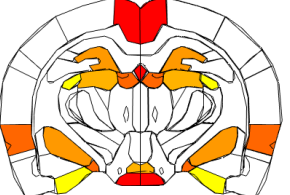
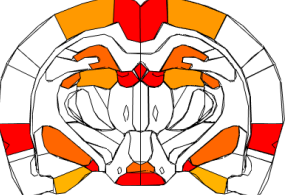
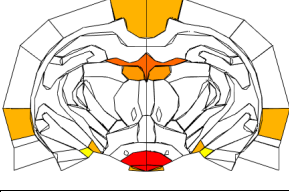
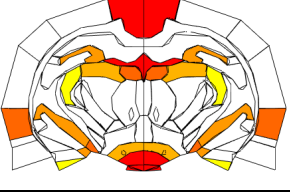
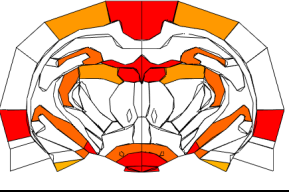
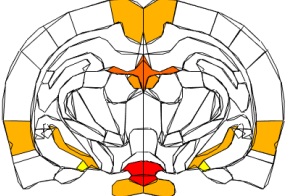
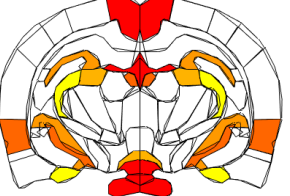
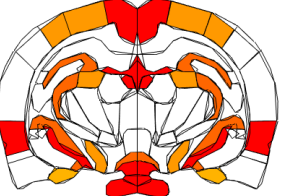
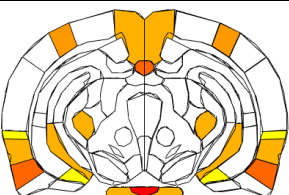
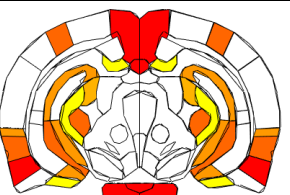
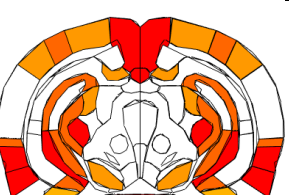
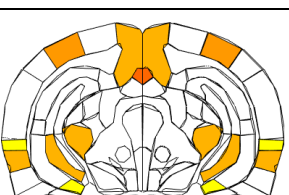
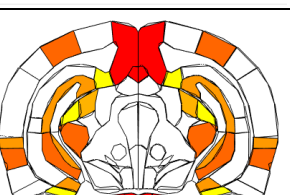
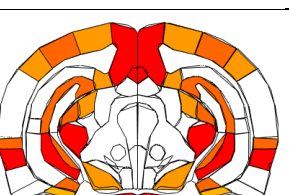
Slice Number	20 minutes	40 Minutes	60 Minutes
1			
2			
3			
4			
5			
6			

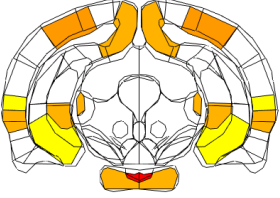
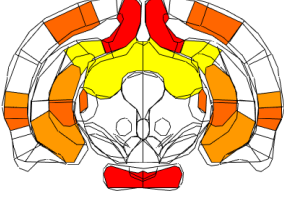
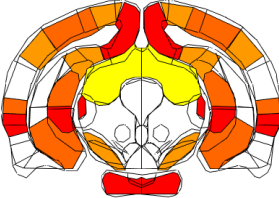
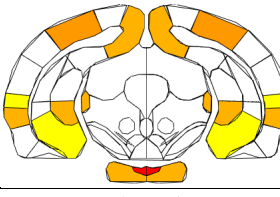
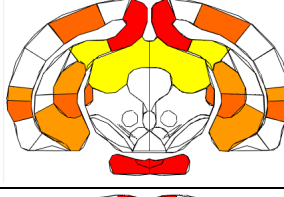
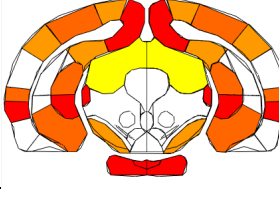
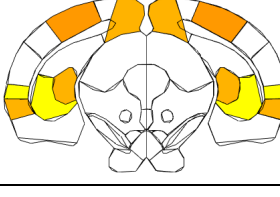
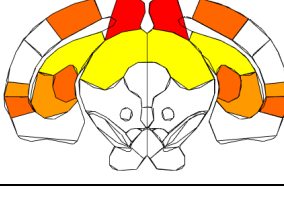
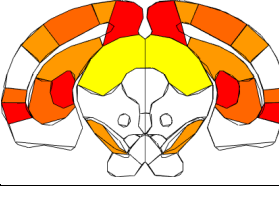
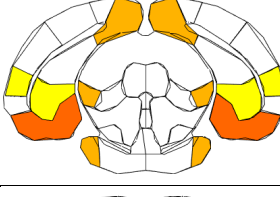
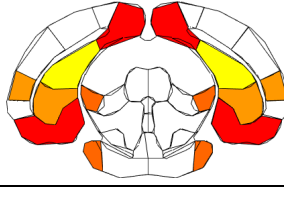
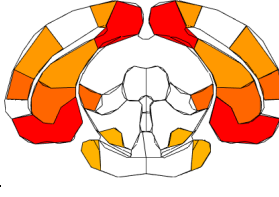
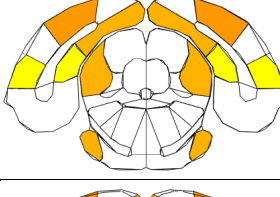
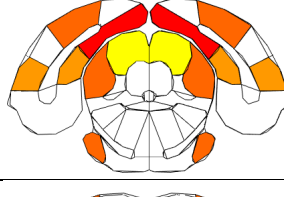
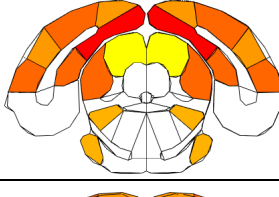
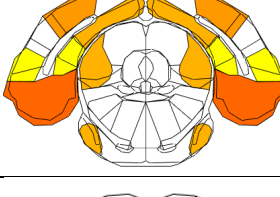
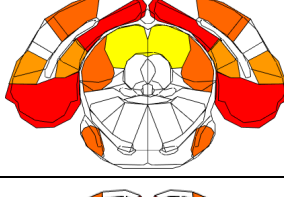
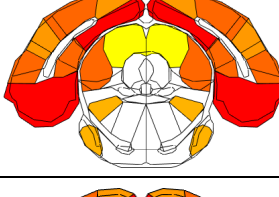
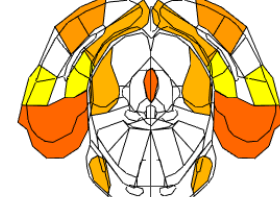
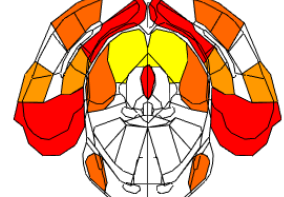
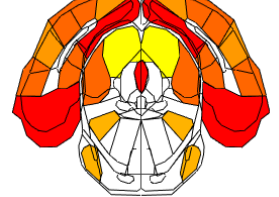
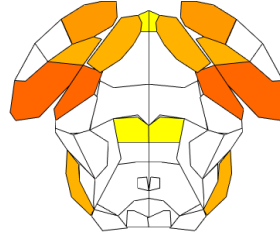
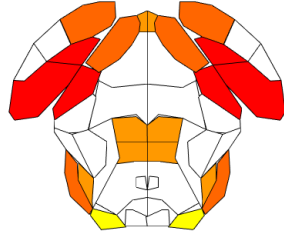
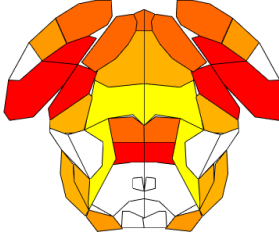
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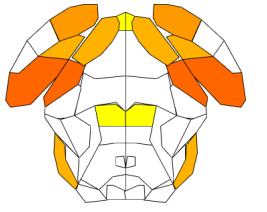
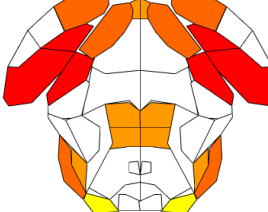
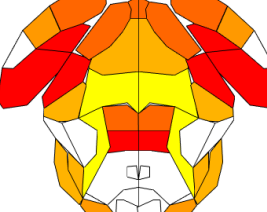
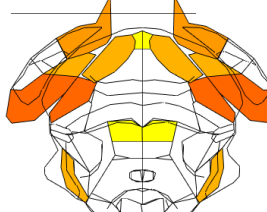
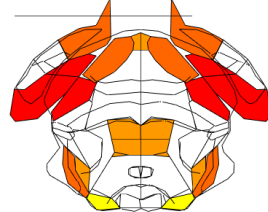
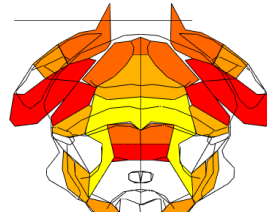
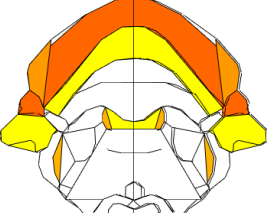
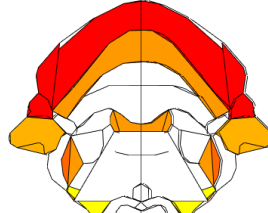
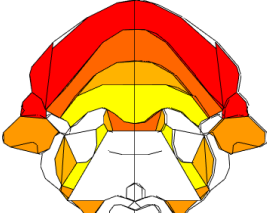
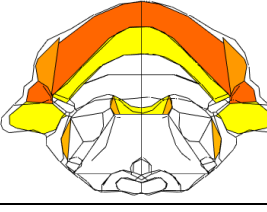
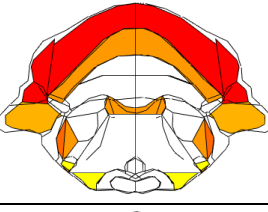
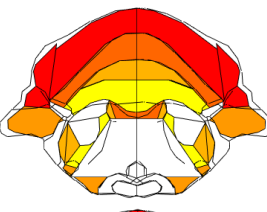
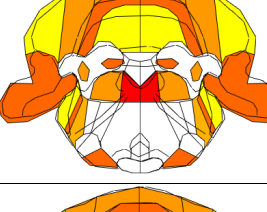
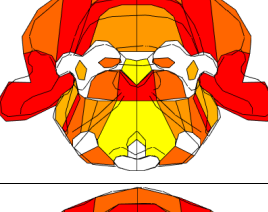
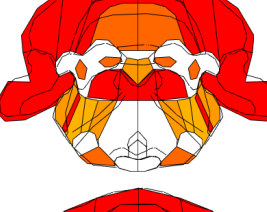
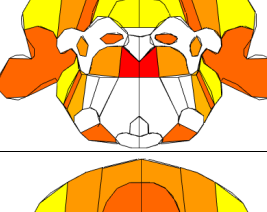
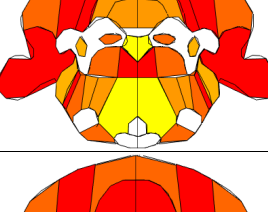
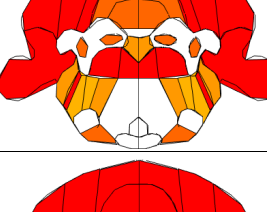
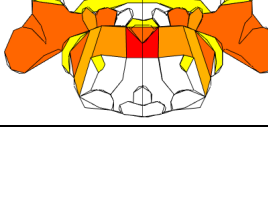
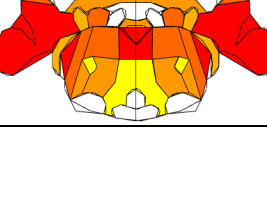
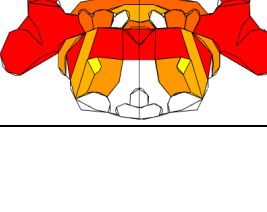
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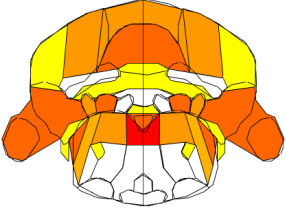
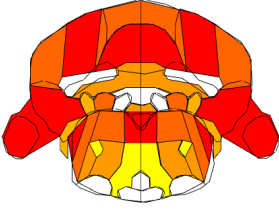
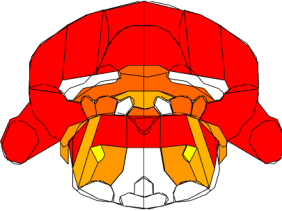
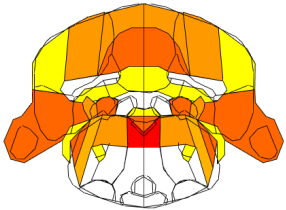
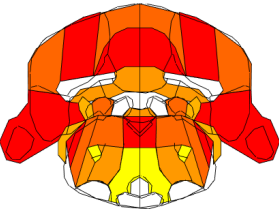
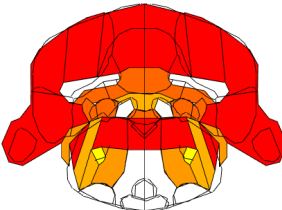
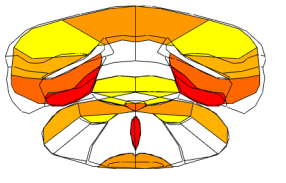
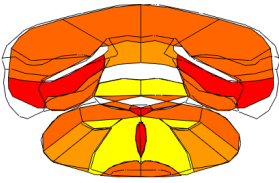
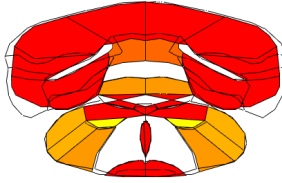
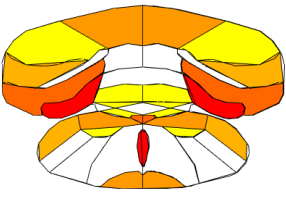
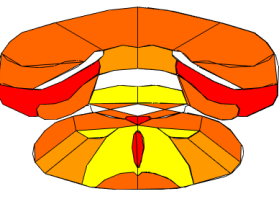
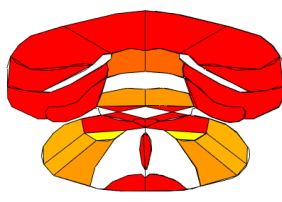
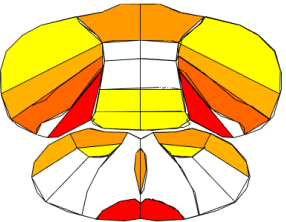
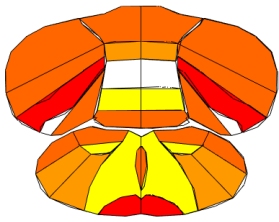
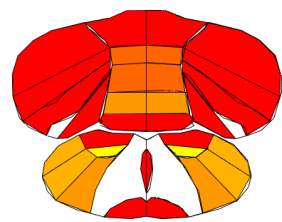
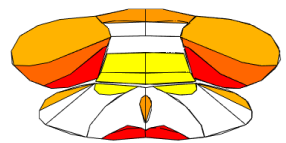
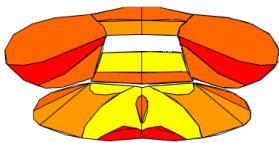
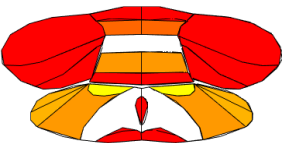
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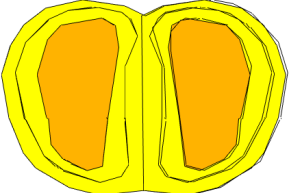
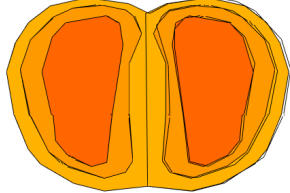
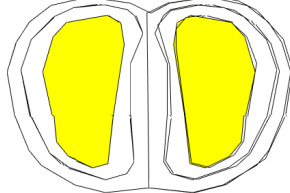
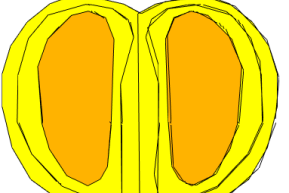
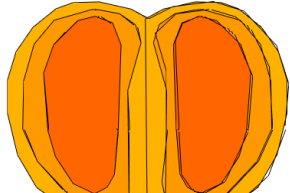
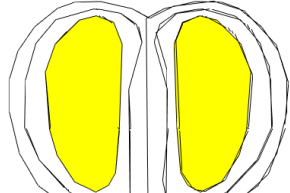
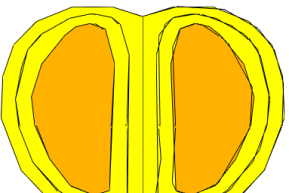
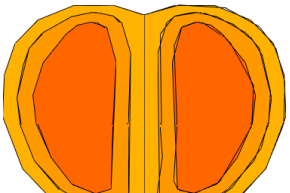
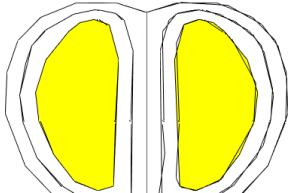
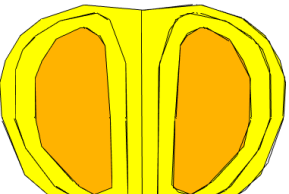
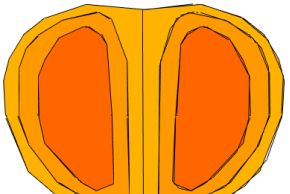
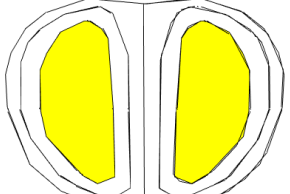
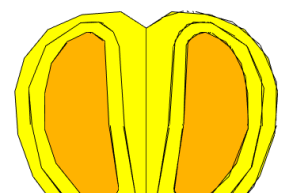
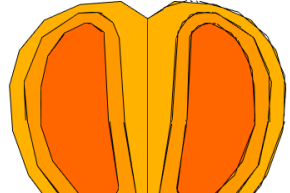
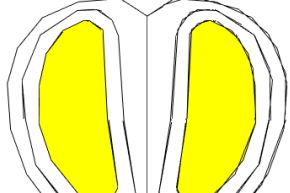
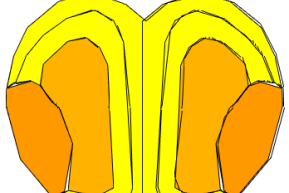
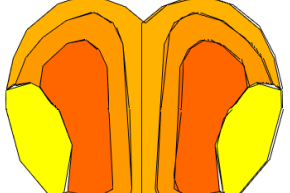
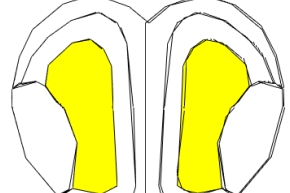
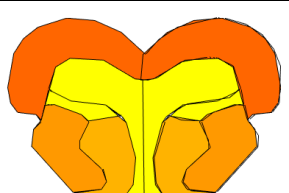
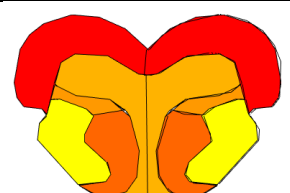
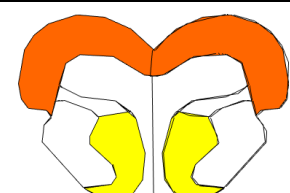
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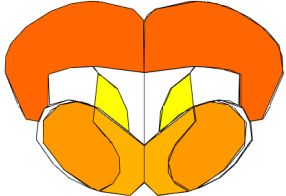
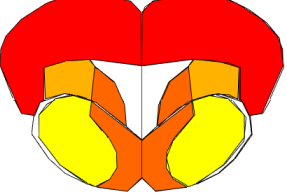
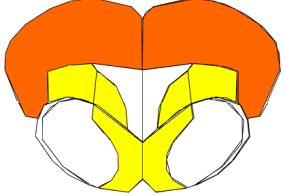
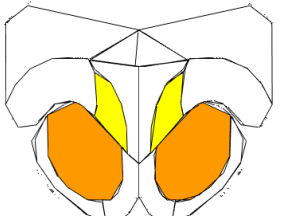
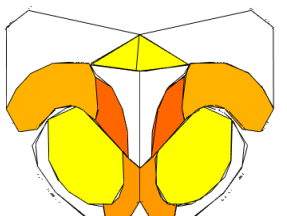
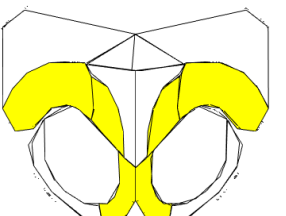
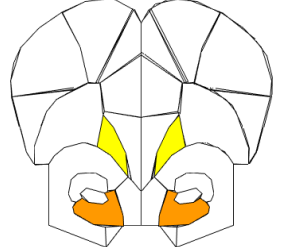
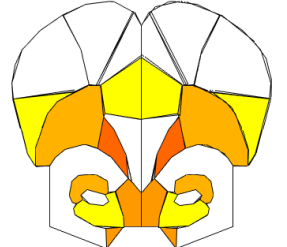
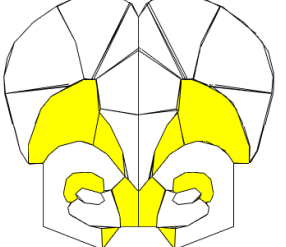
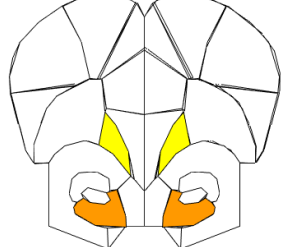
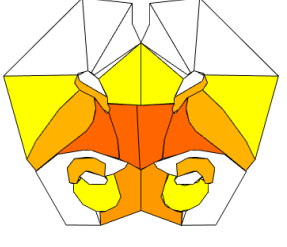
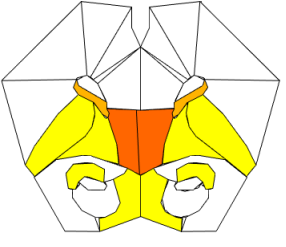
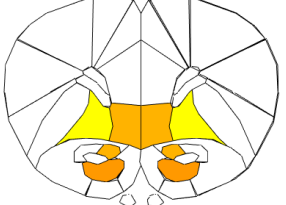
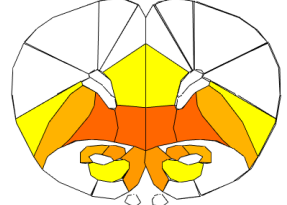
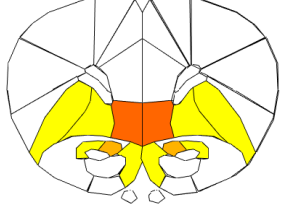
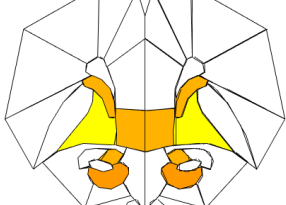
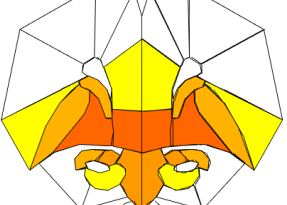
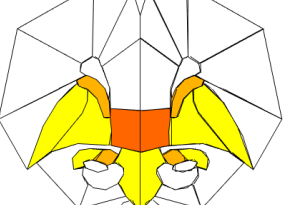
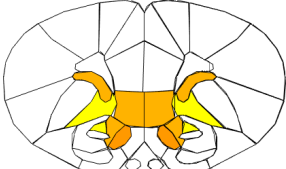
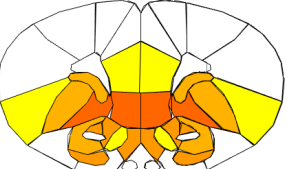
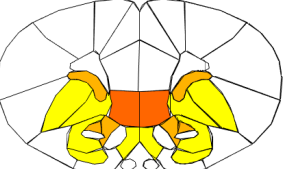
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Appendix K: Dermorphin Nanoemulsion Results

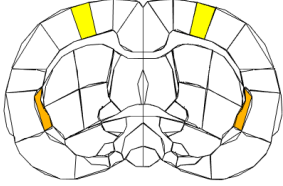
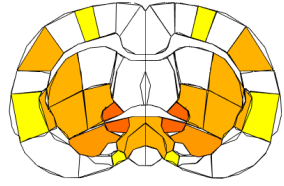
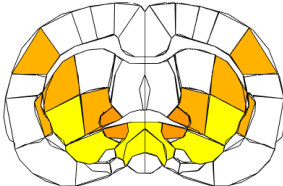
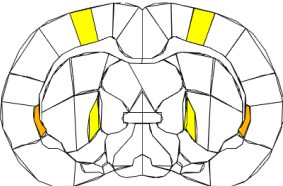
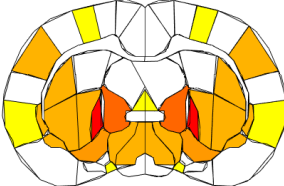
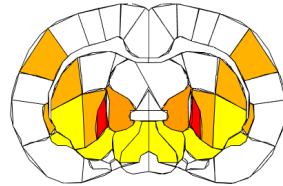
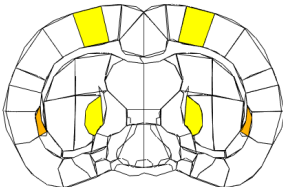
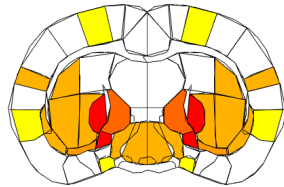
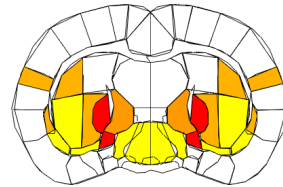
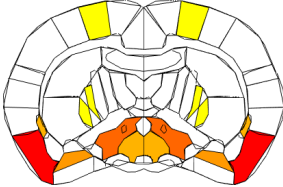
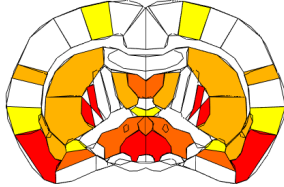
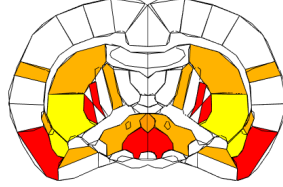
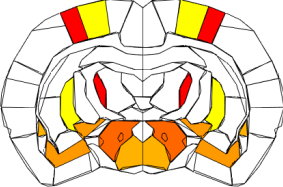
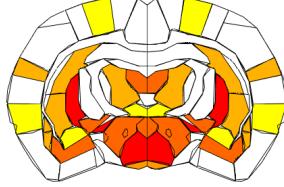
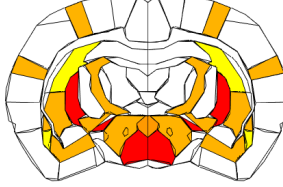

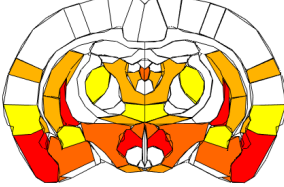
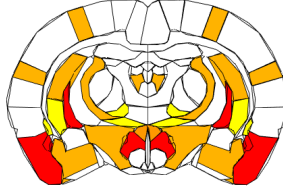
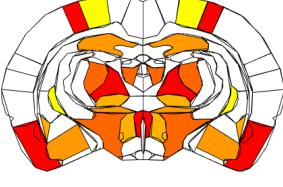
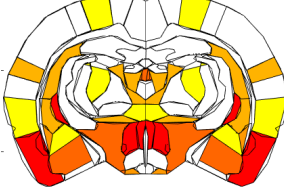
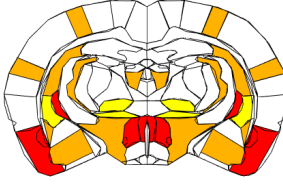
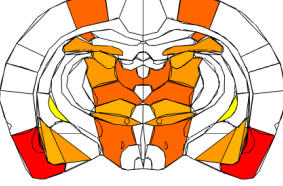
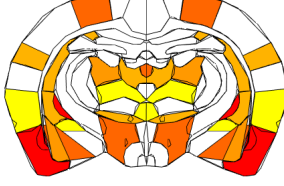
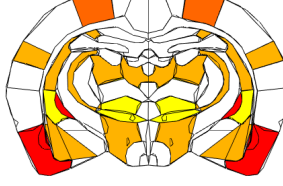


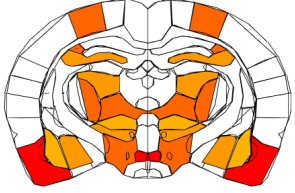
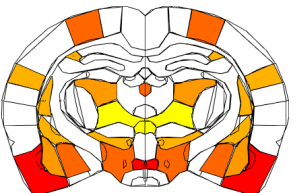
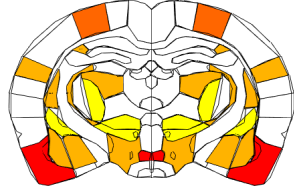
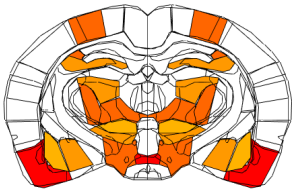
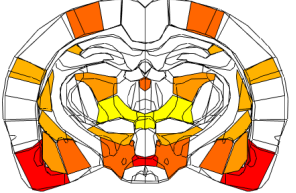
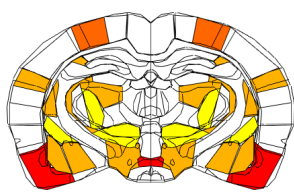
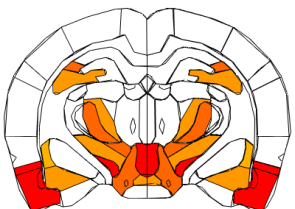
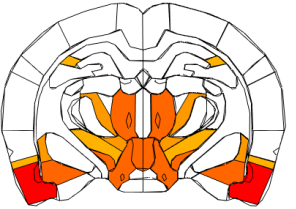
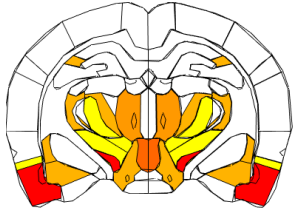
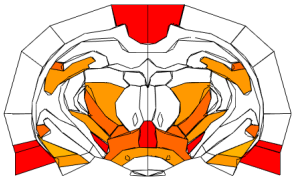
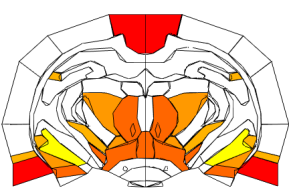
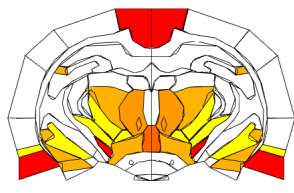
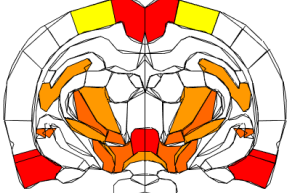
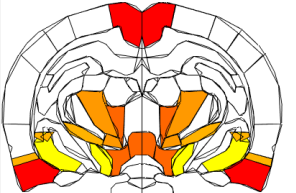
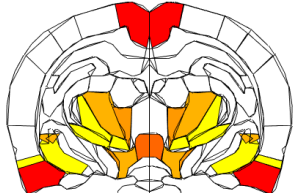
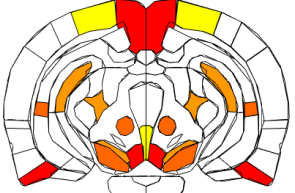
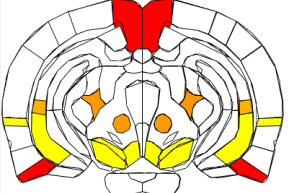
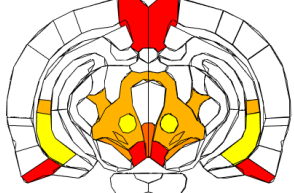
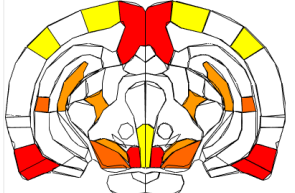
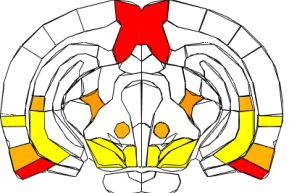
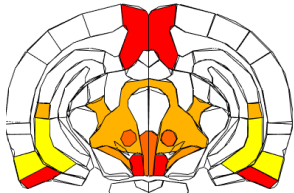
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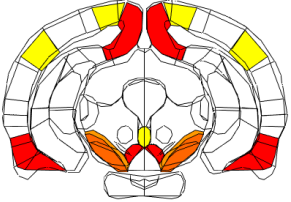
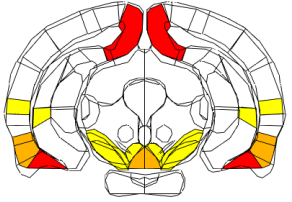
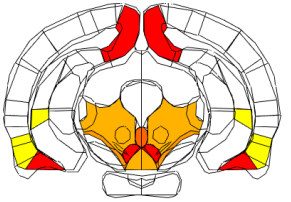
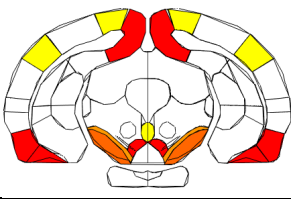
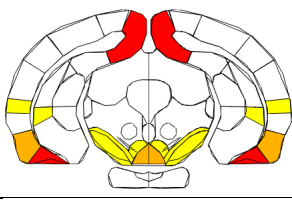
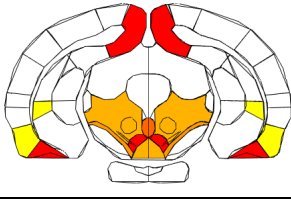
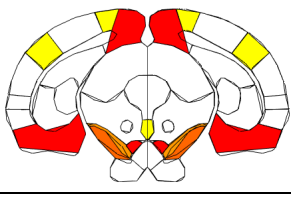
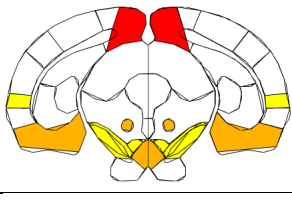
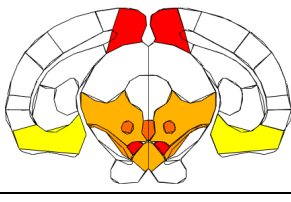
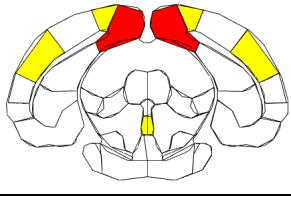
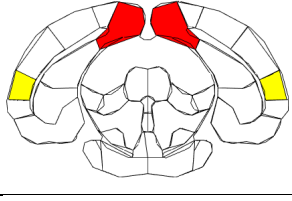
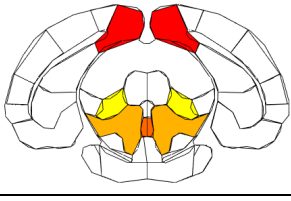
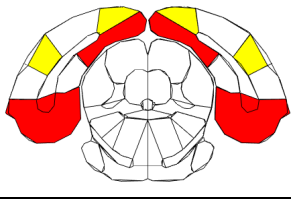
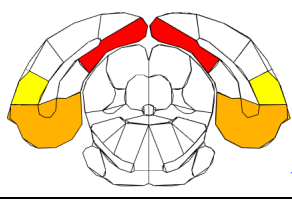
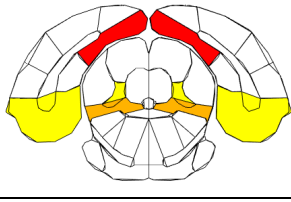
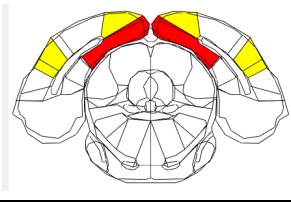
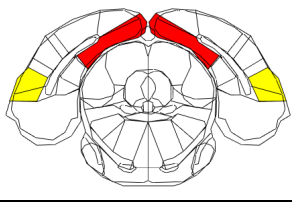
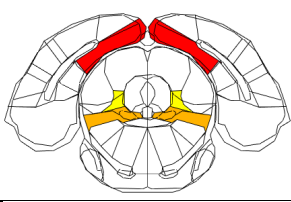
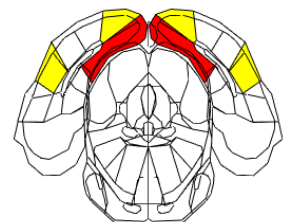
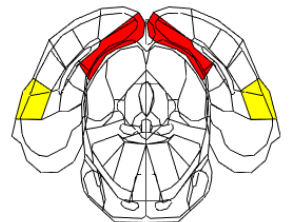
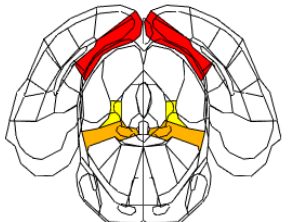
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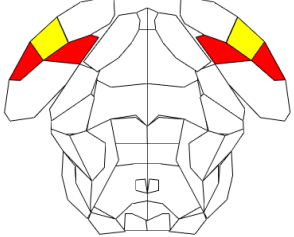
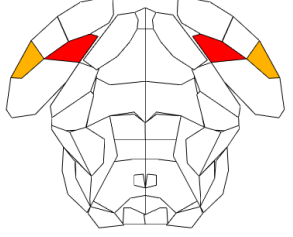
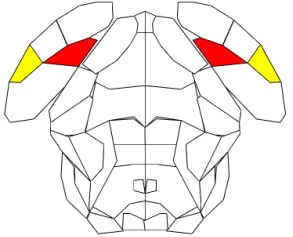
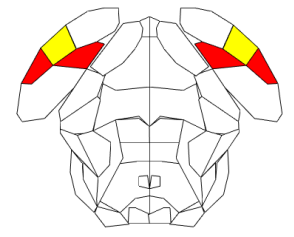
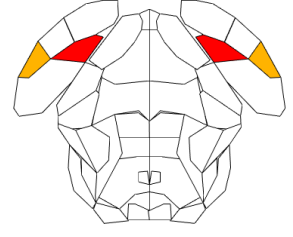
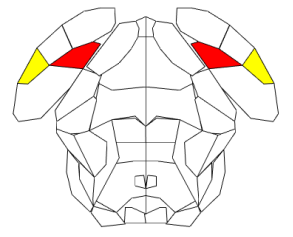
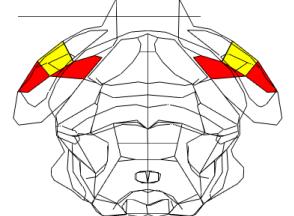
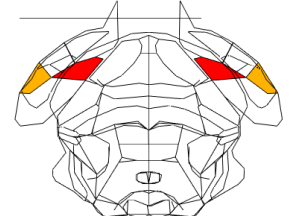
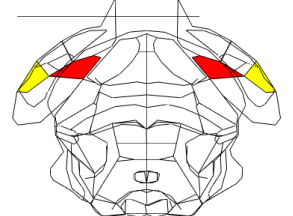
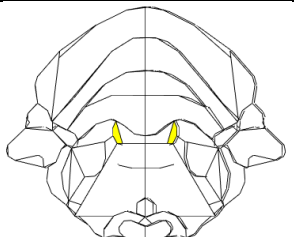
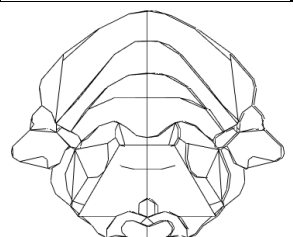
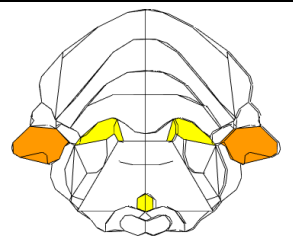
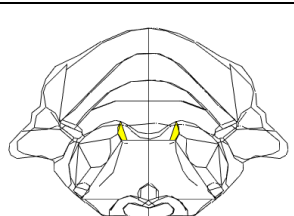
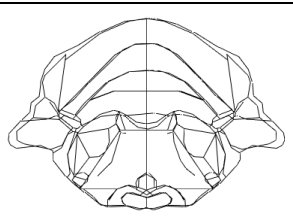
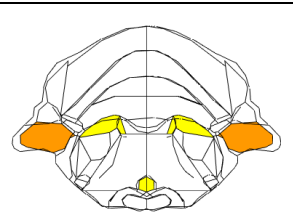
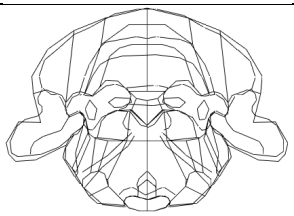
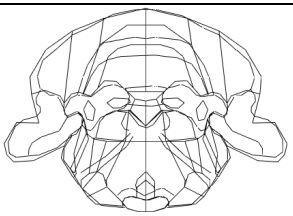
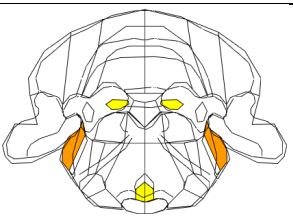
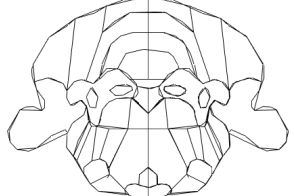
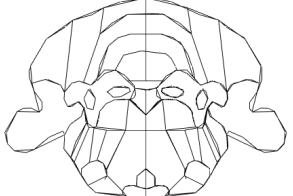
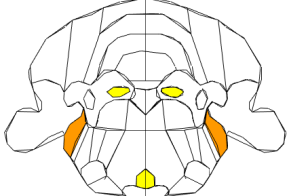
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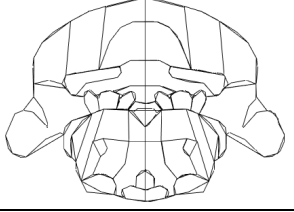
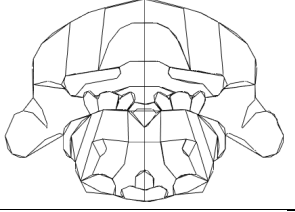
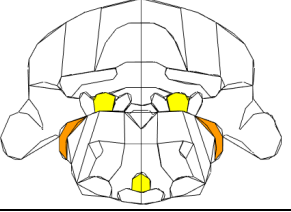
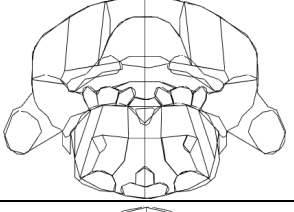
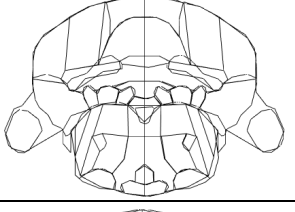
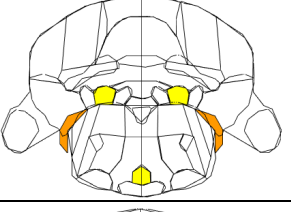
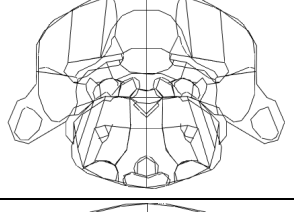
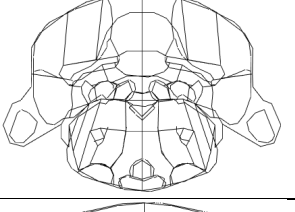
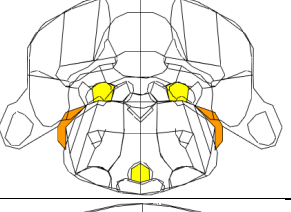
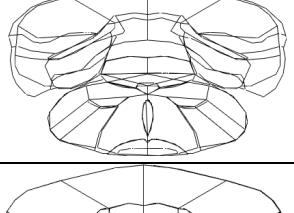
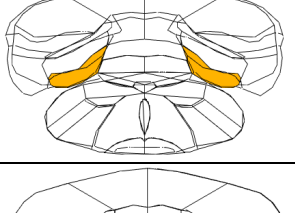
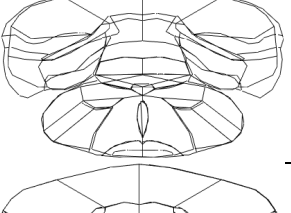
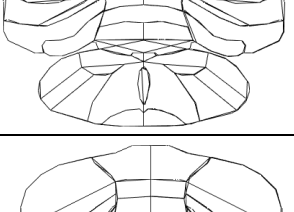
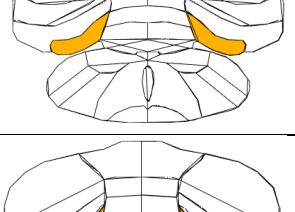
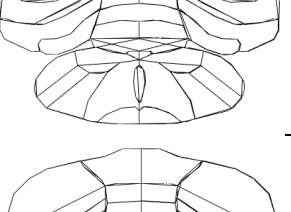
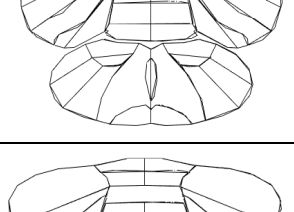
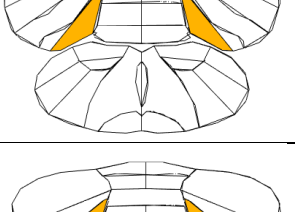
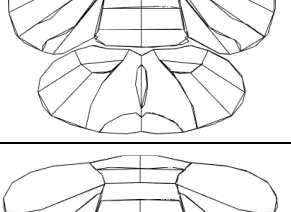
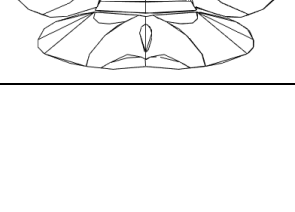
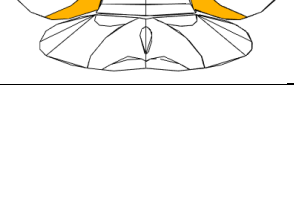
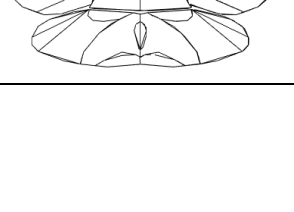
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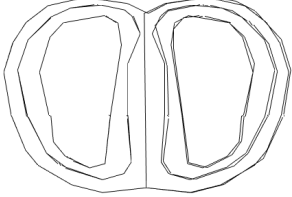
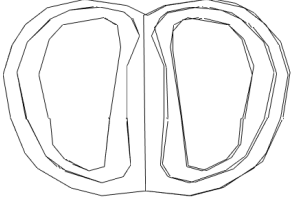
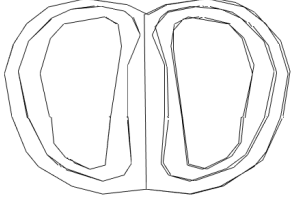
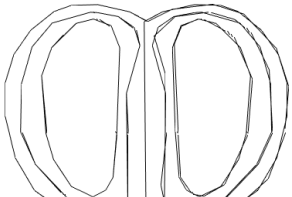
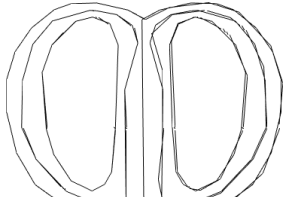
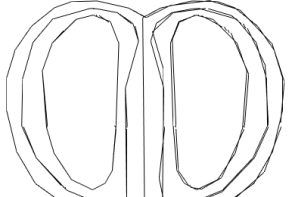
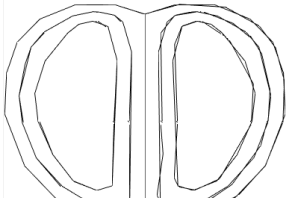
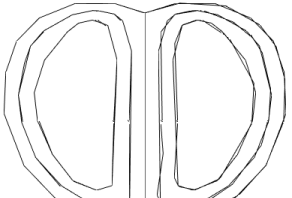
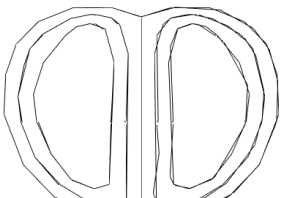
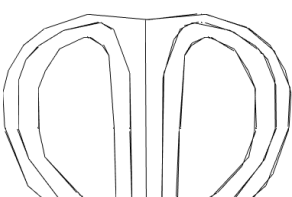
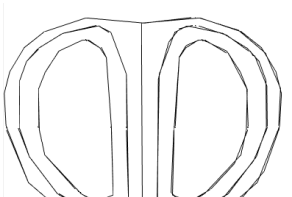
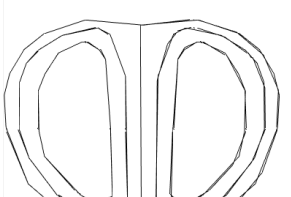
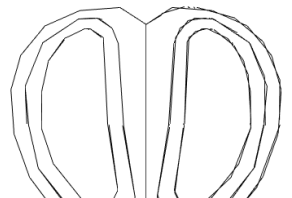
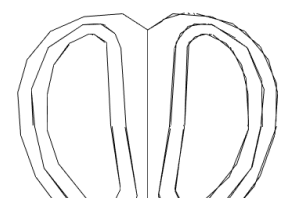
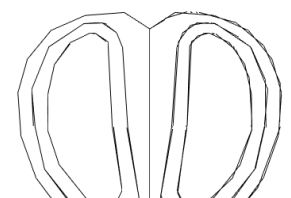
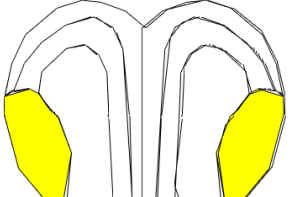
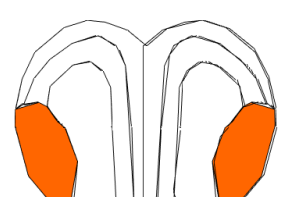
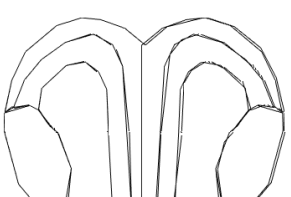
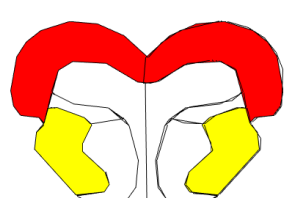
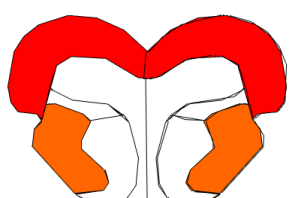
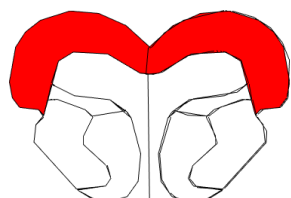
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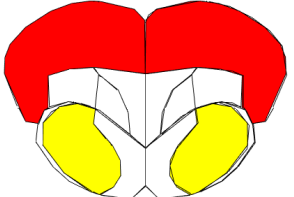
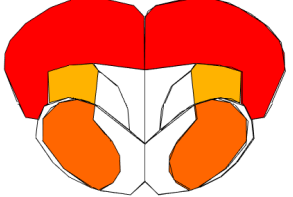
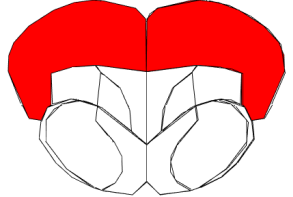
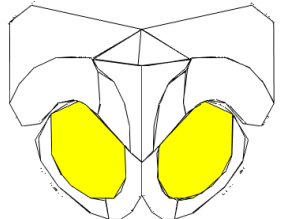
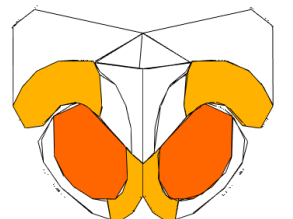
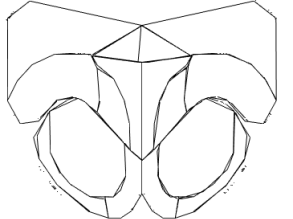
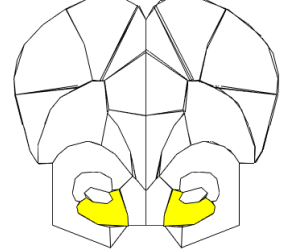
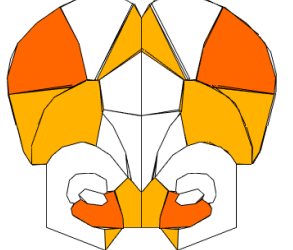
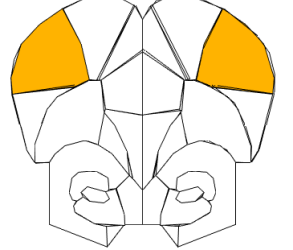
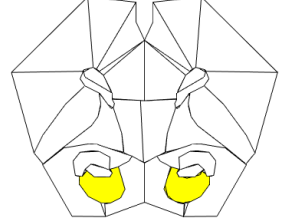
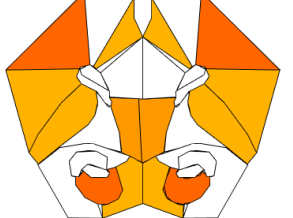
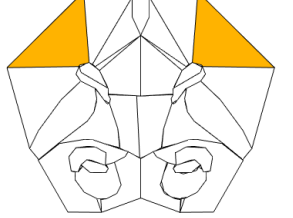
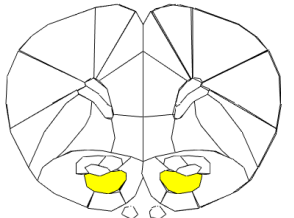
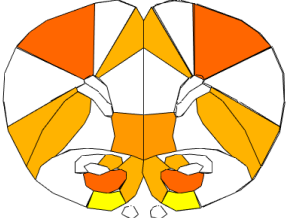
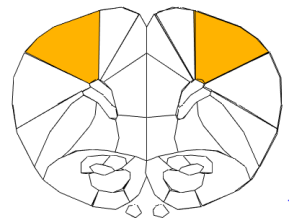
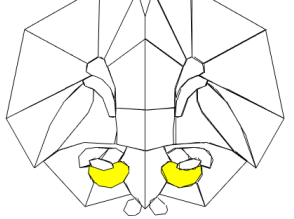
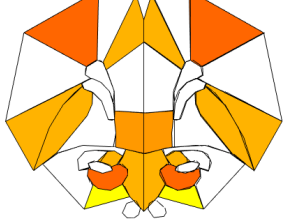
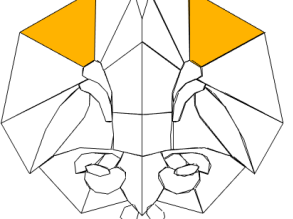
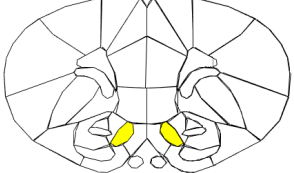
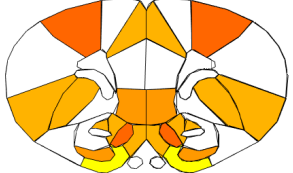
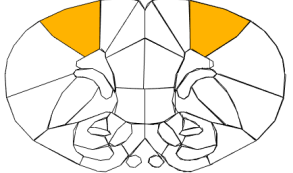
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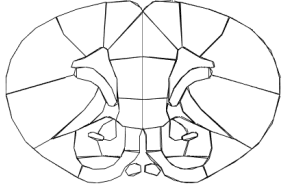
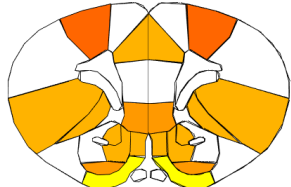
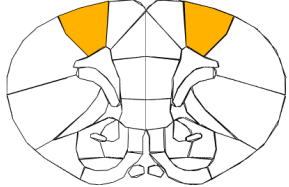
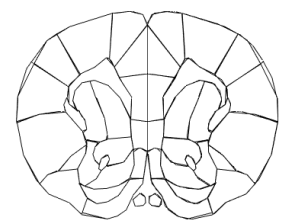
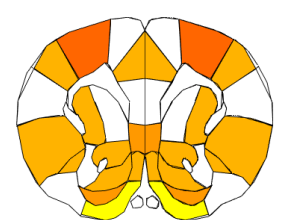
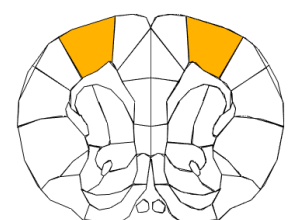
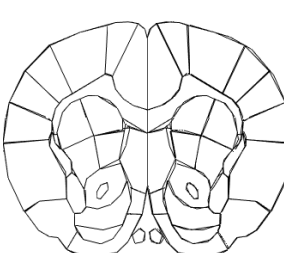
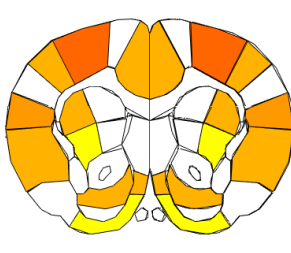
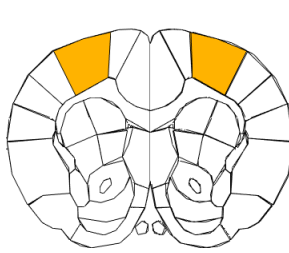
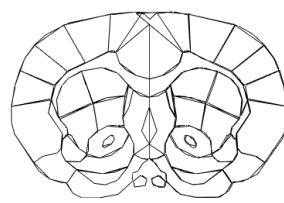
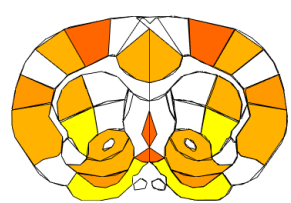
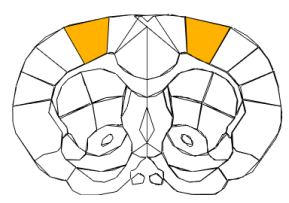
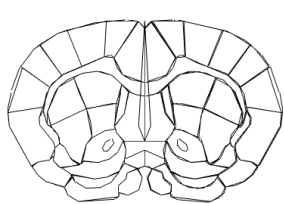
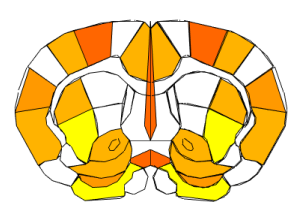
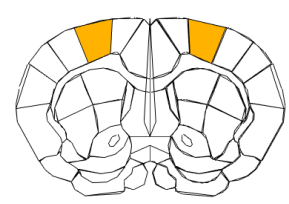
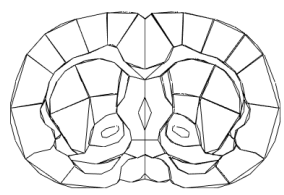
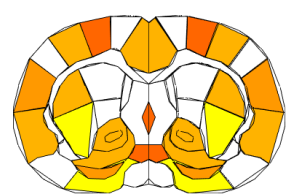
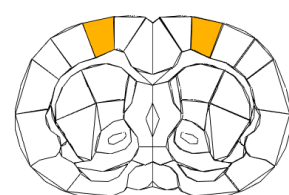
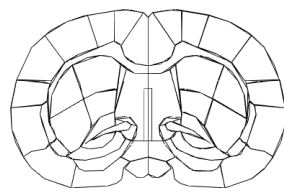
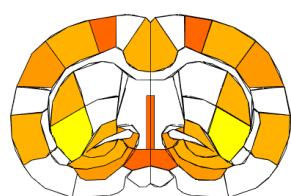
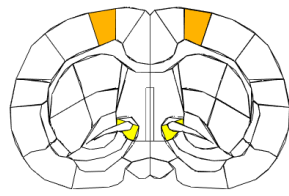
Appendix L: Dermorphin Nanoemulsion Blocked with β -Funaltrexamine Results

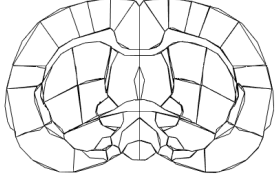
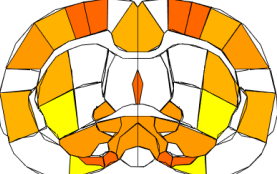
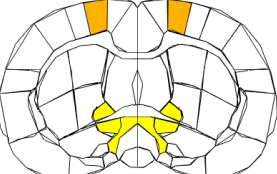
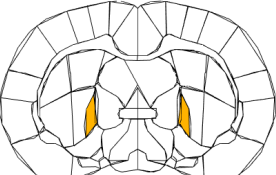
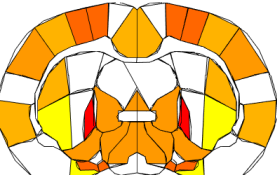
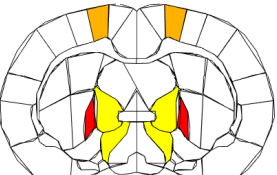
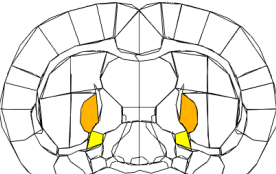
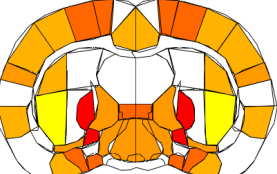
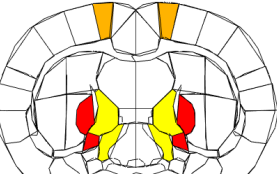
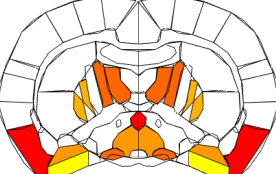
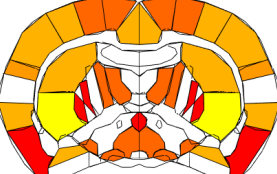
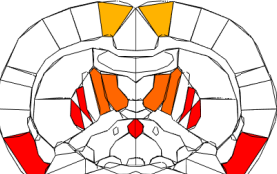
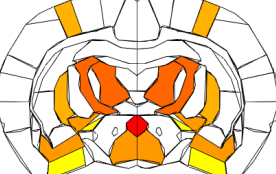
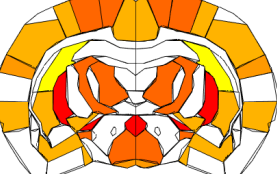
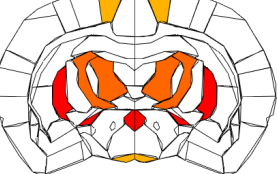
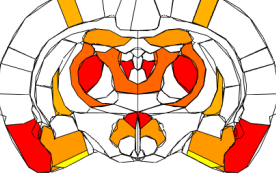
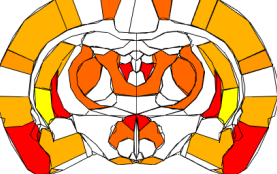
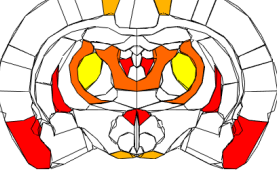
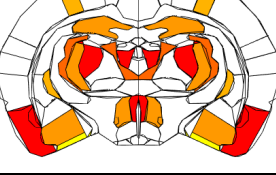
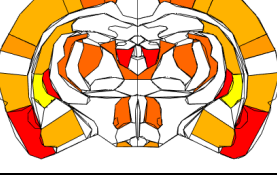
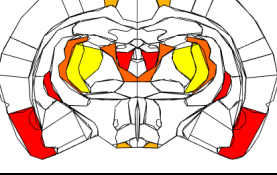
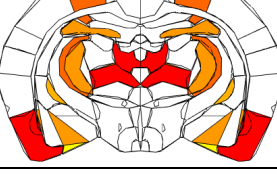
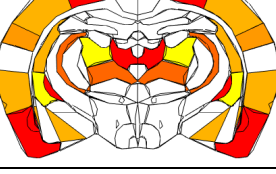
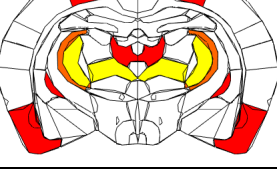


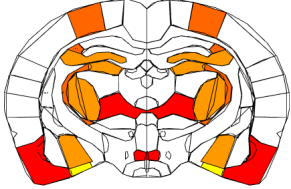
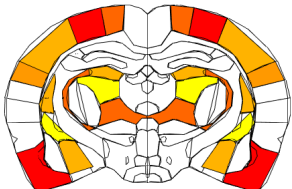
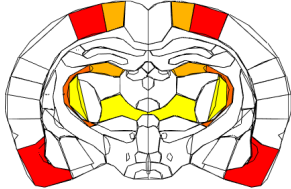
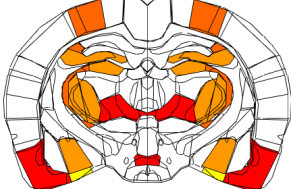
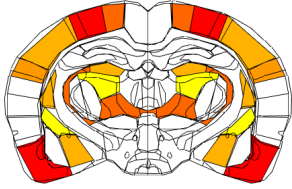
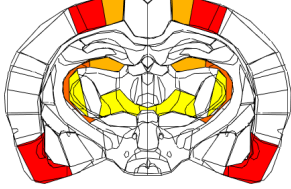
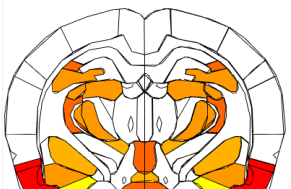
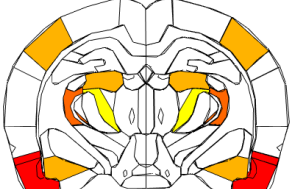

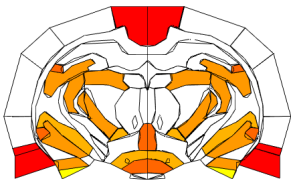
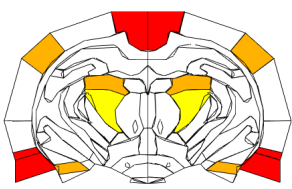
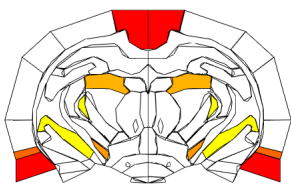
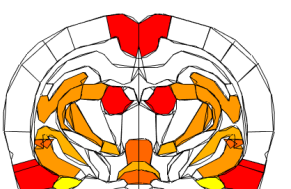
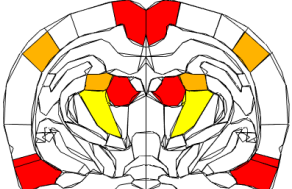
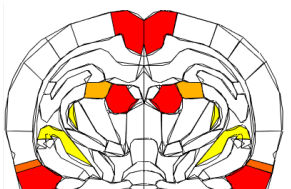

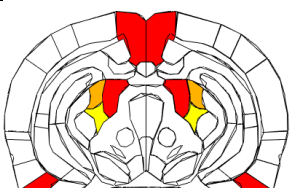
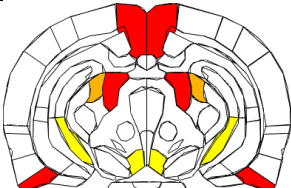
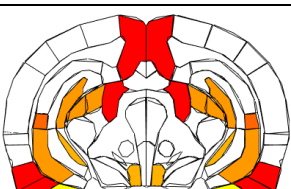
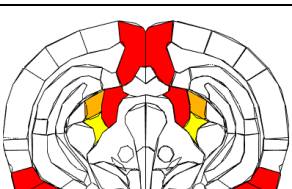
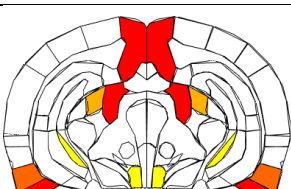
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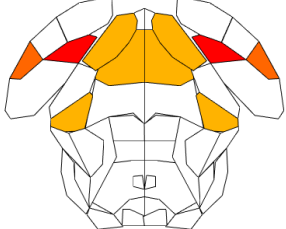
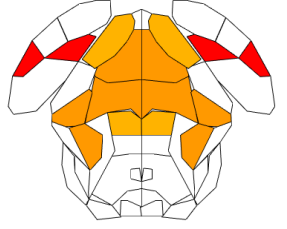
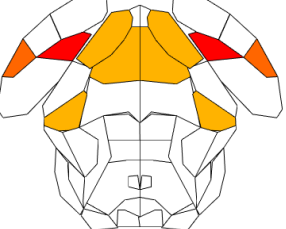
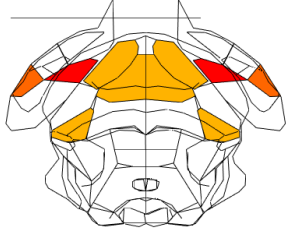
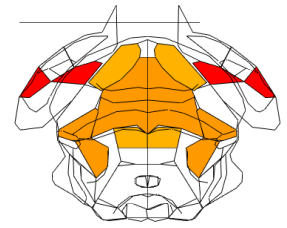
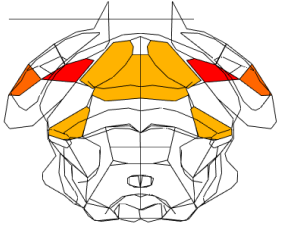
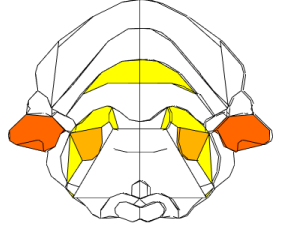
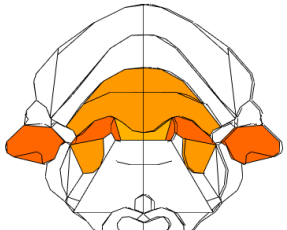
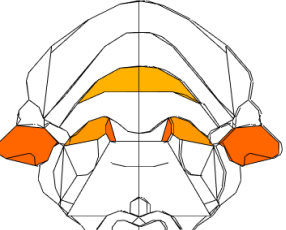
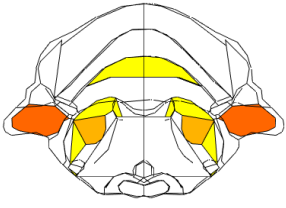
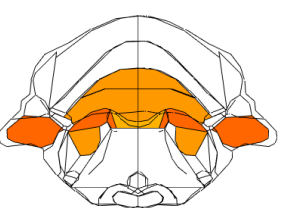
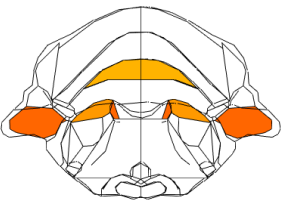
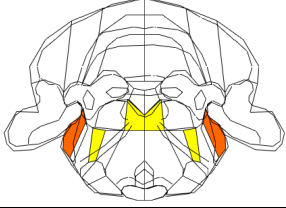
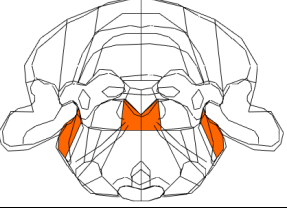
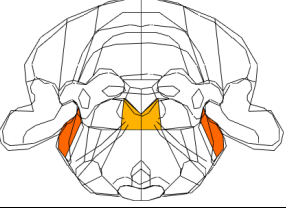
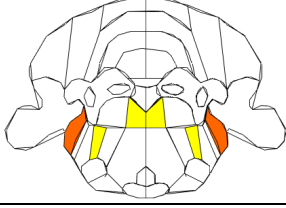
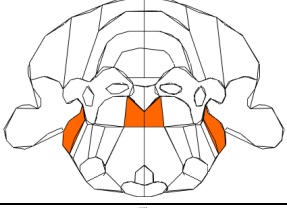
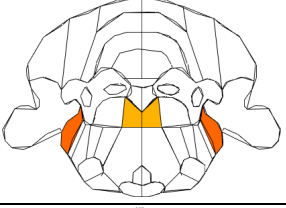
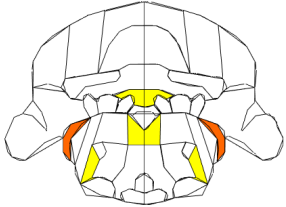
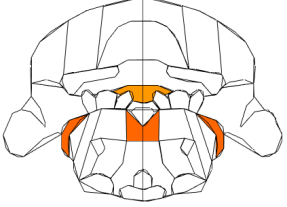
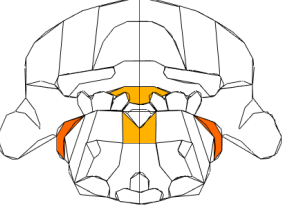
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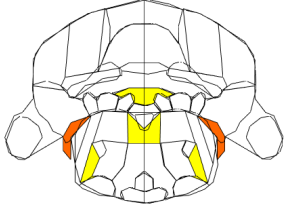
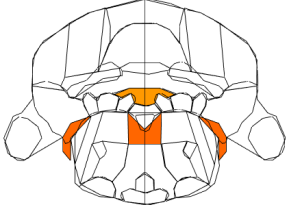
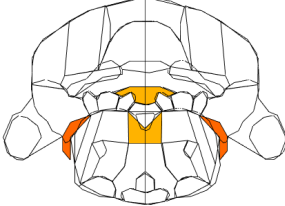
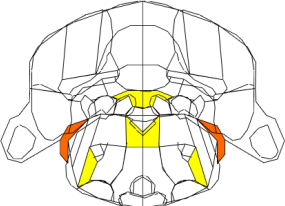
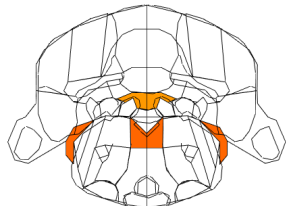
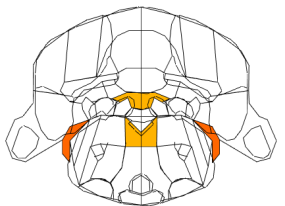
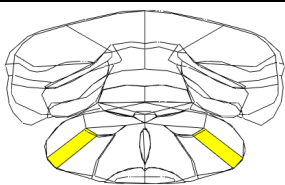
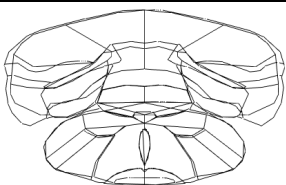
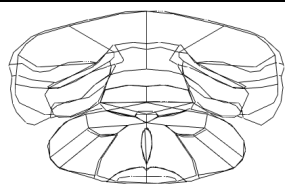
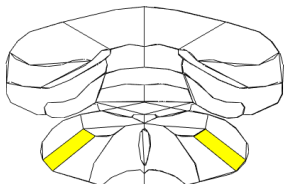
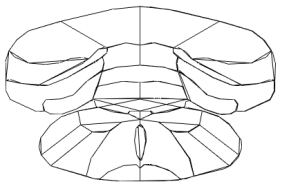
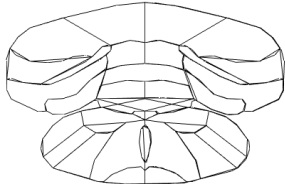
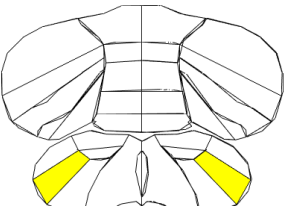
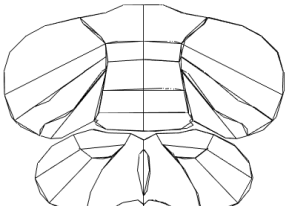
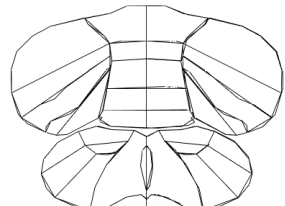
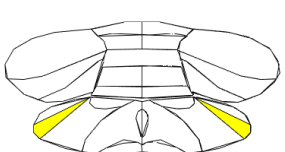
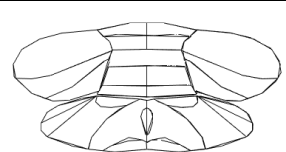
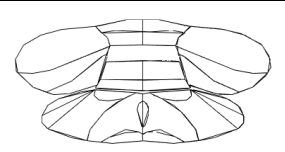
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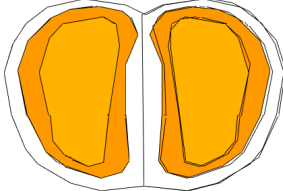
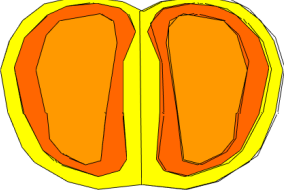
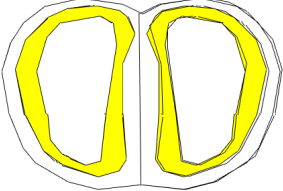
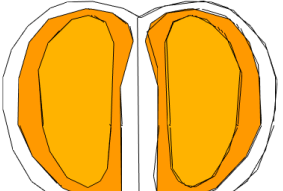

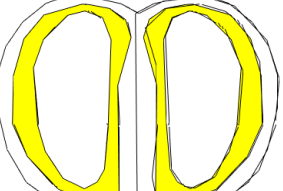
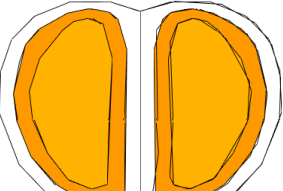
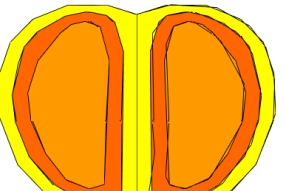
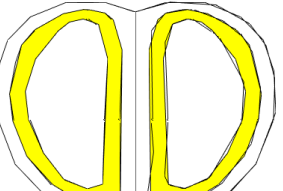
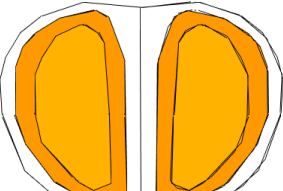
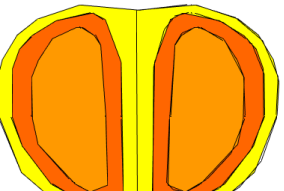
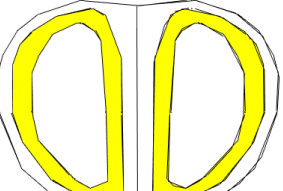
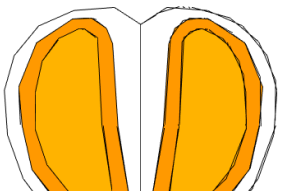
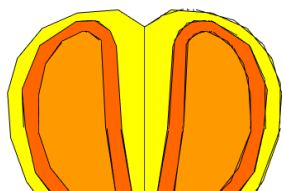
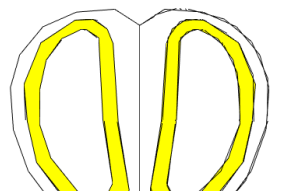
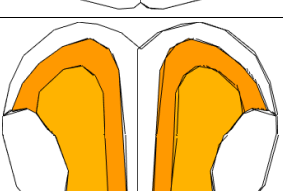
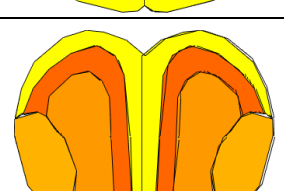
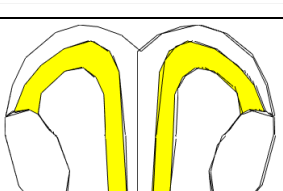
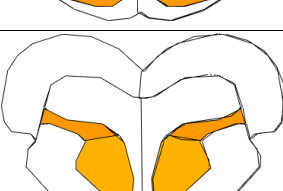
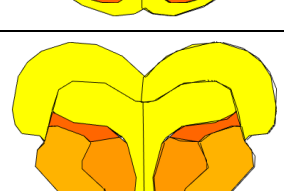
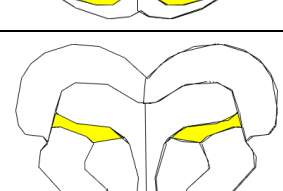
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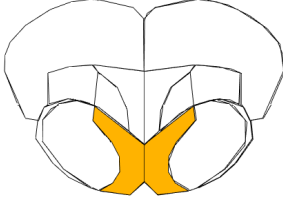
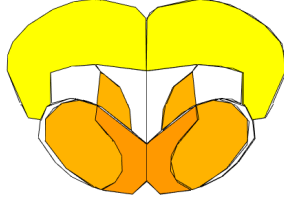
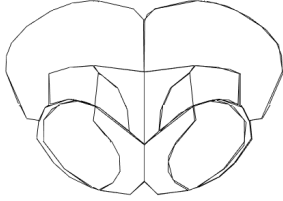
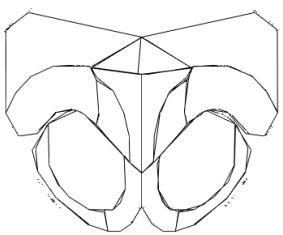
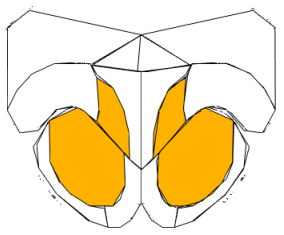
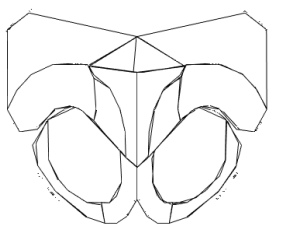
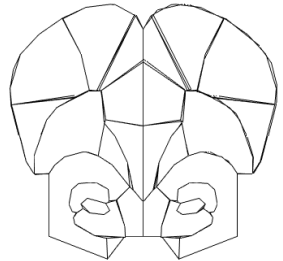
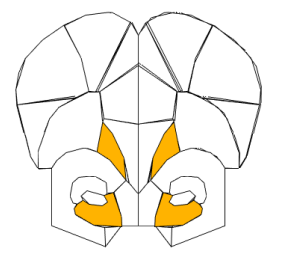
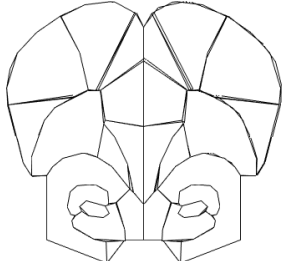
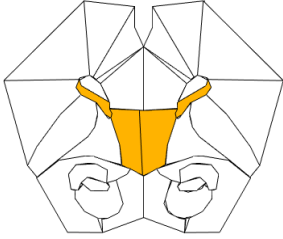
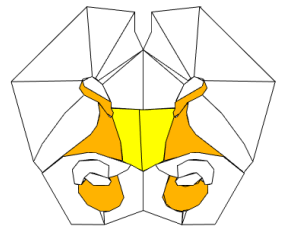
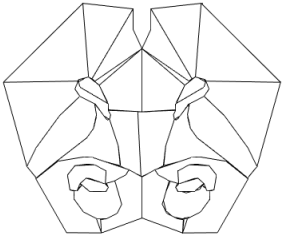
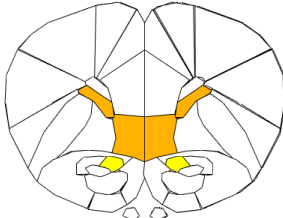
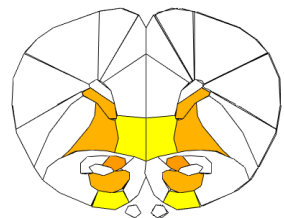
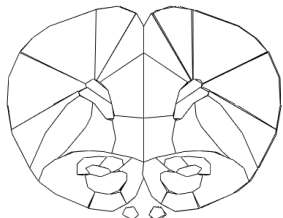
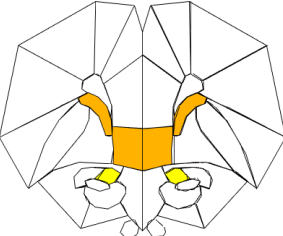
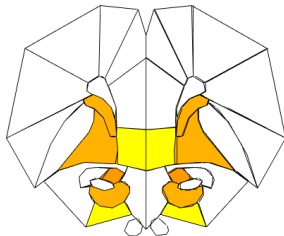
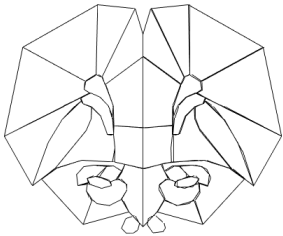
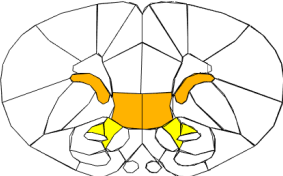
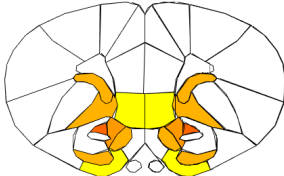
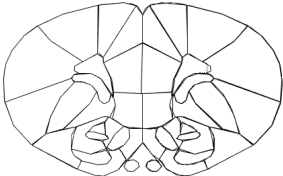
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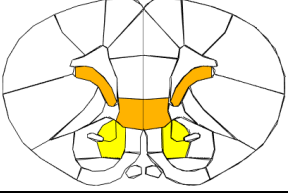
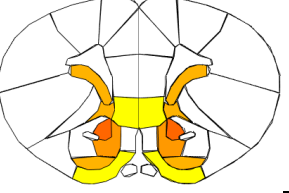
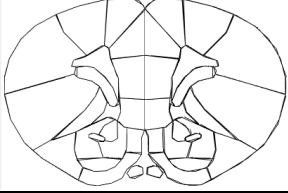
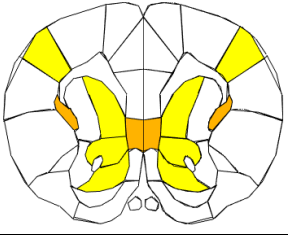
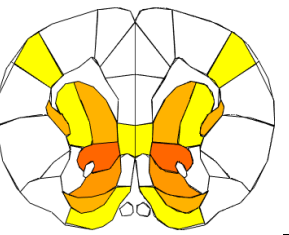
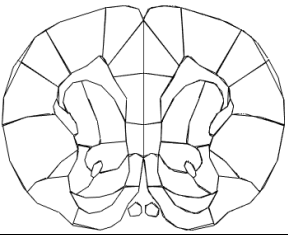
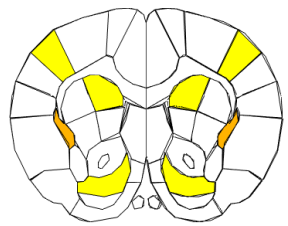
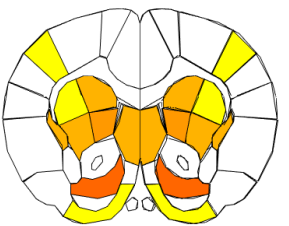
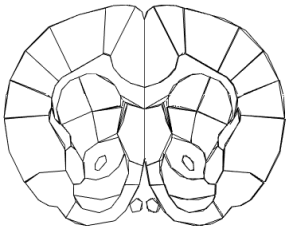
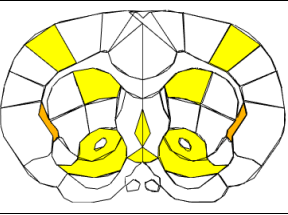
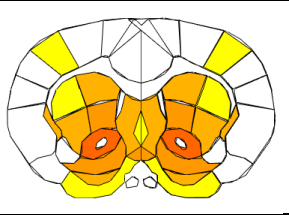
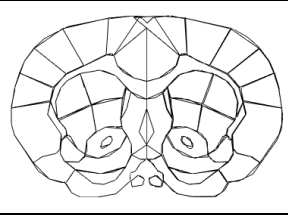
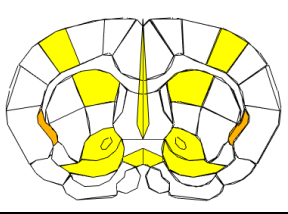
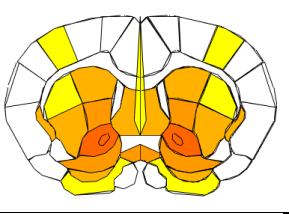
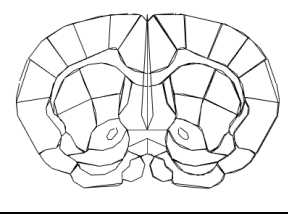
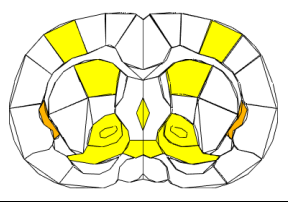
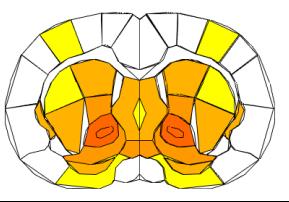
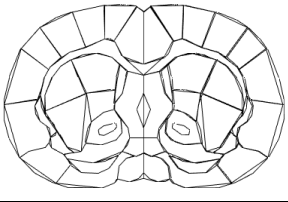
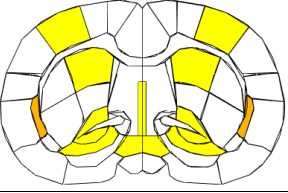
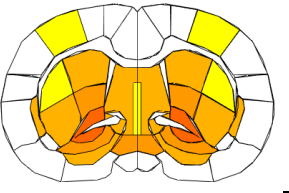
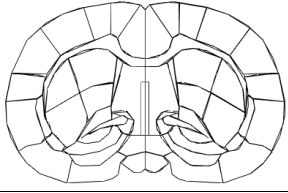
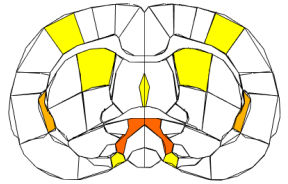
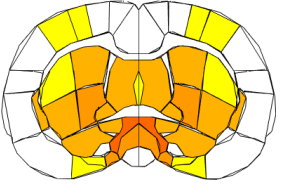
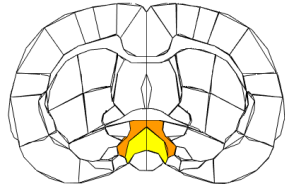
Appendix M: Dermorphin Nanoemulsions Blocked with Naloxone Results

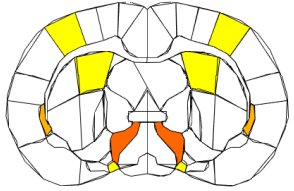
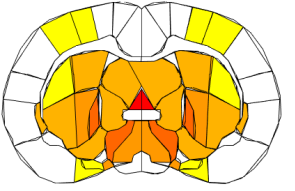
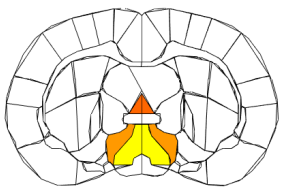
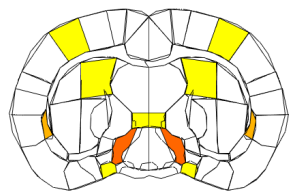
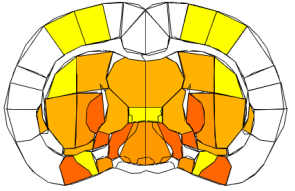
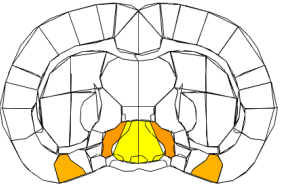
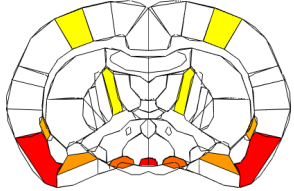
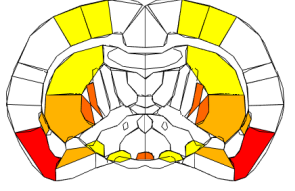
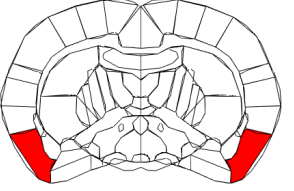
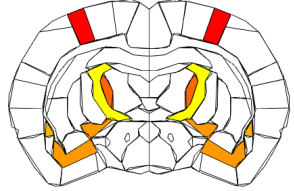
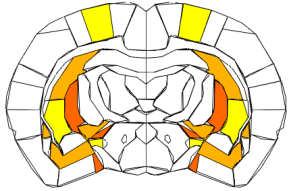
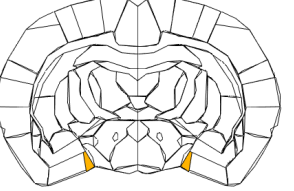
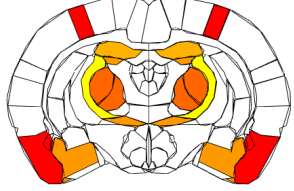
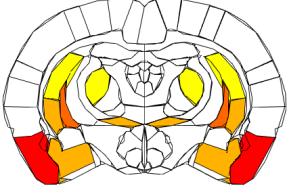
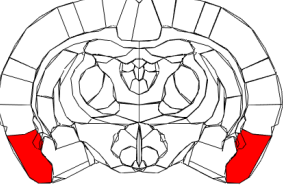
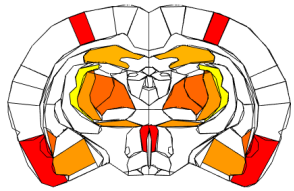
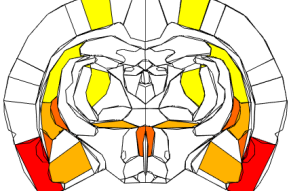
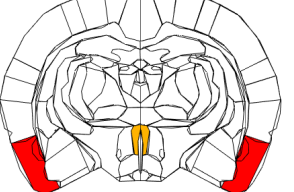
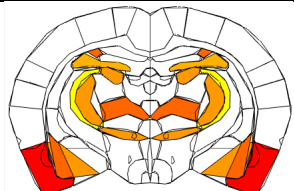
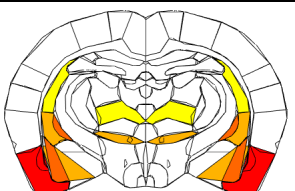
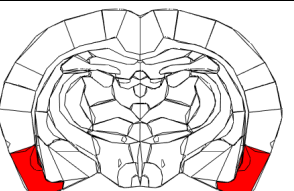
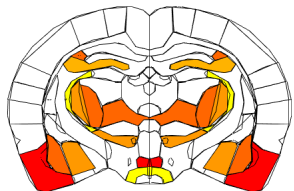
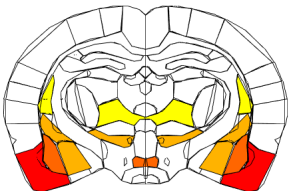
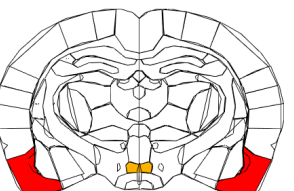


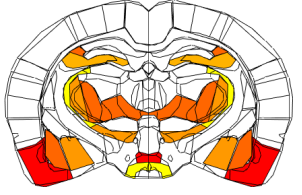
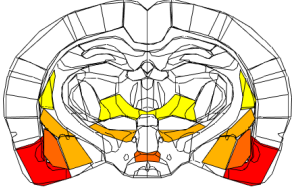
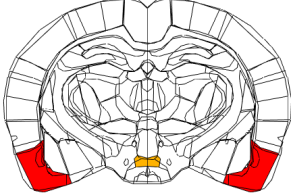
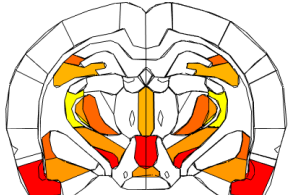

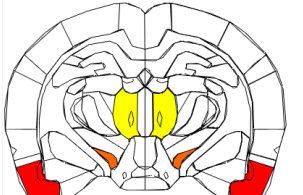
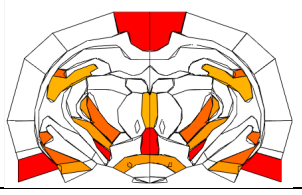
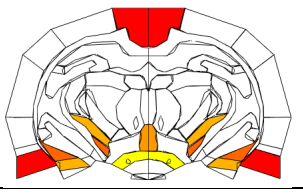
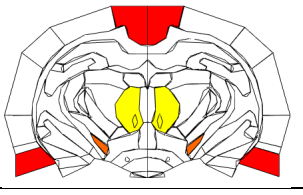
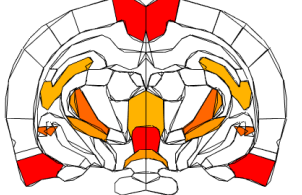
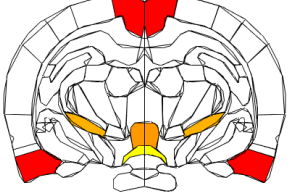
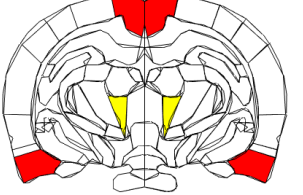
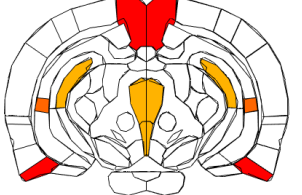
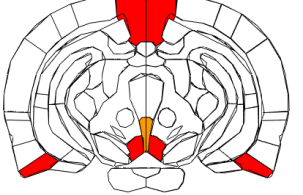
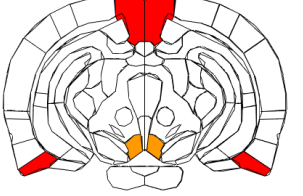
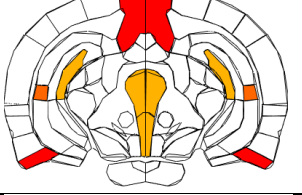
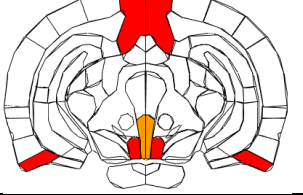
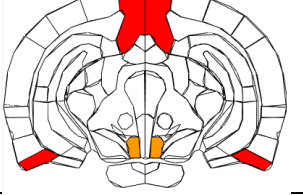
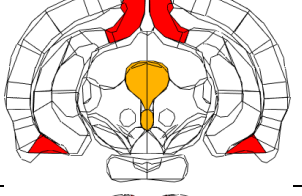
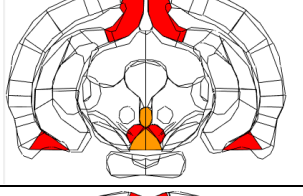
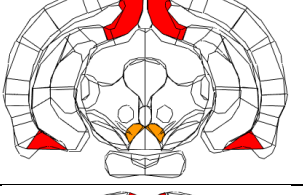
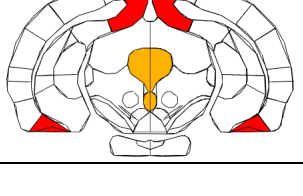
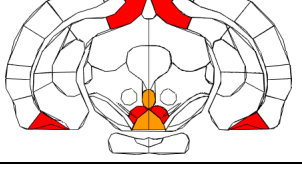
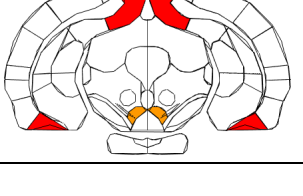
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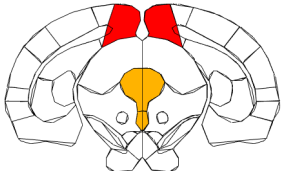
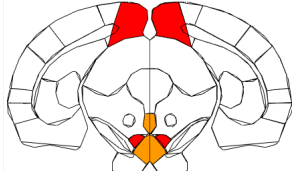
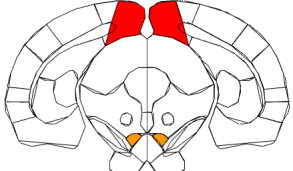
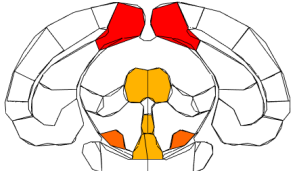
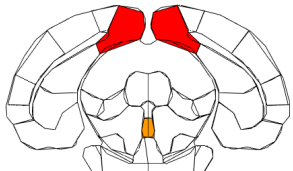
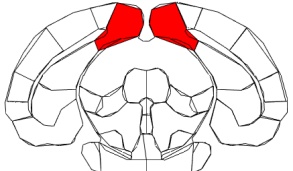
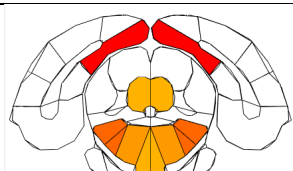
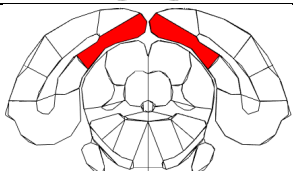
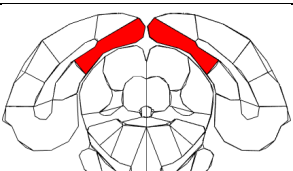
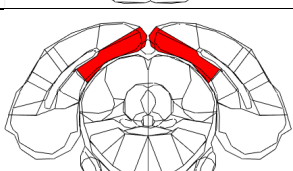
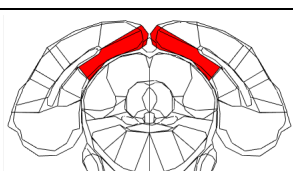
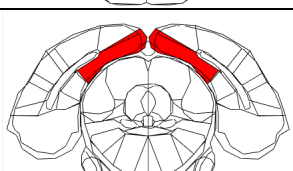
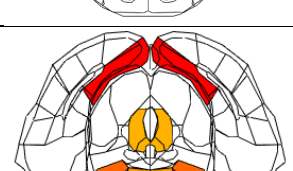
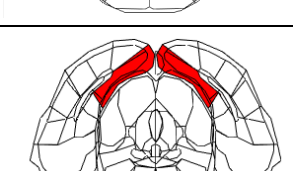
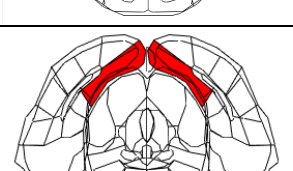
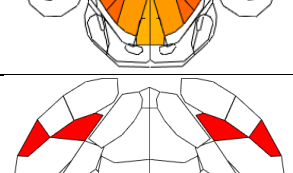
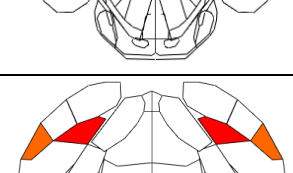
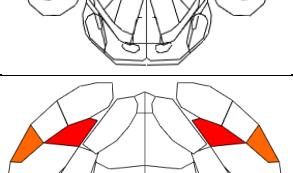
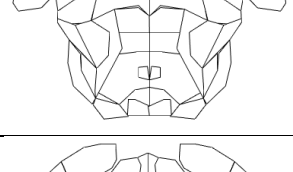
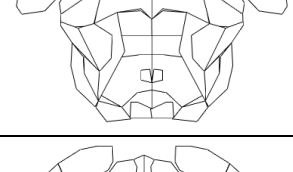
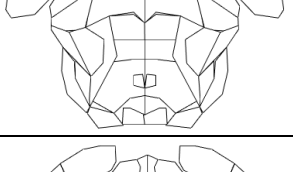
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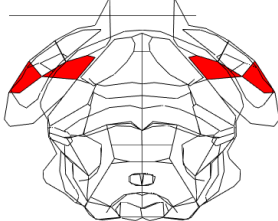
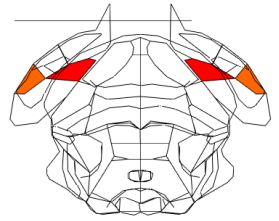
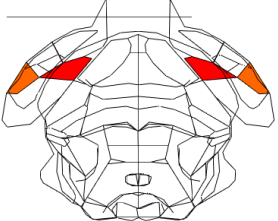
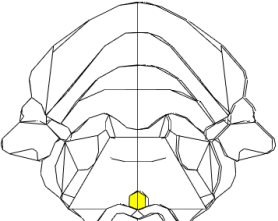
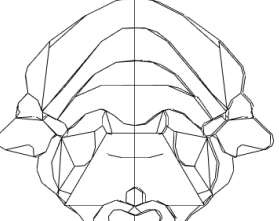
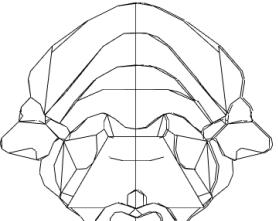
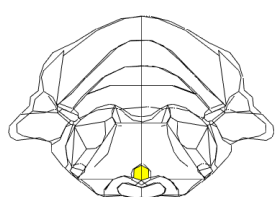
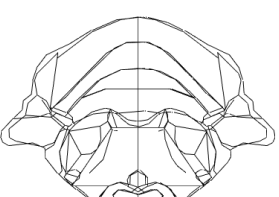
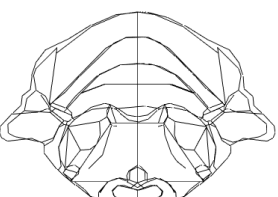
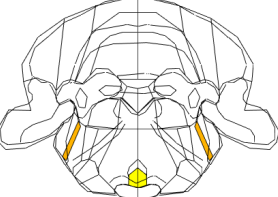
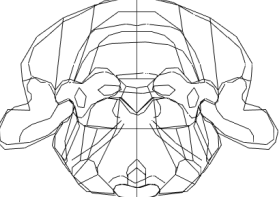
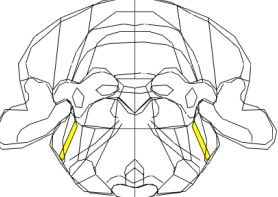
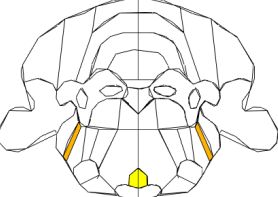
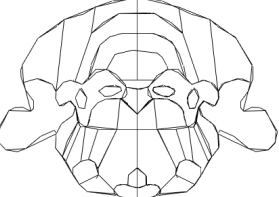
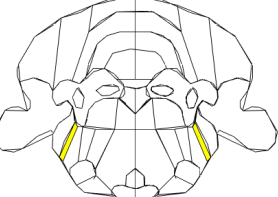
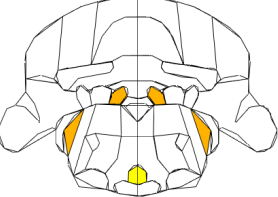
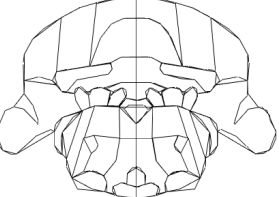
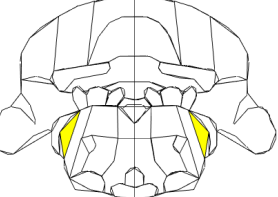
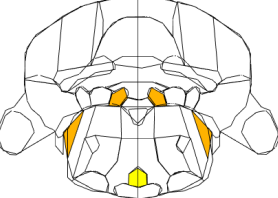
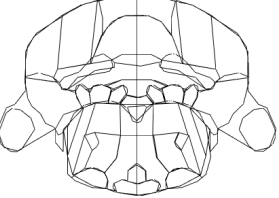
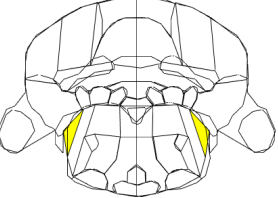
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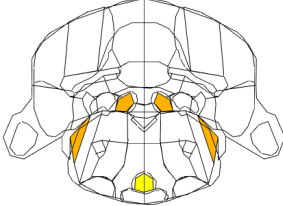
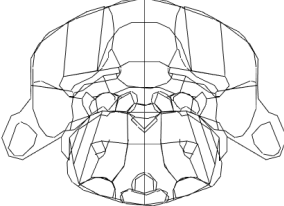
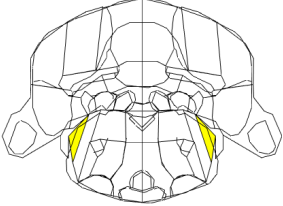
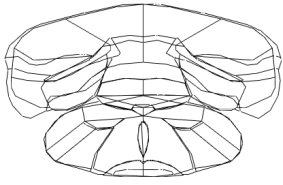
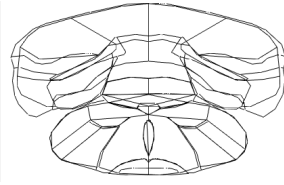
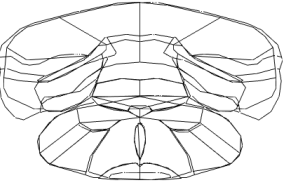
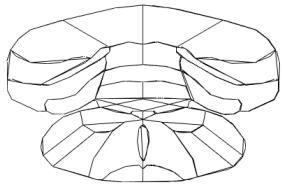
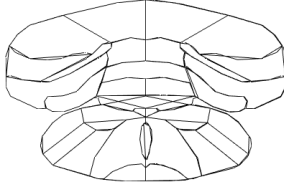
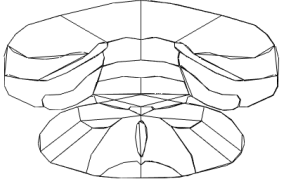
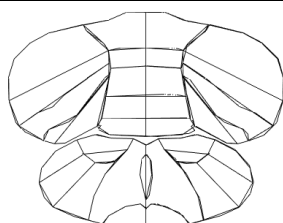
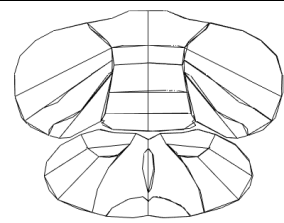
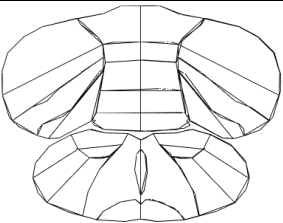
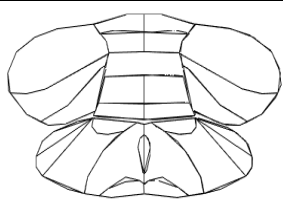
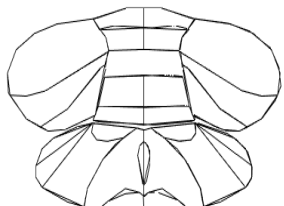
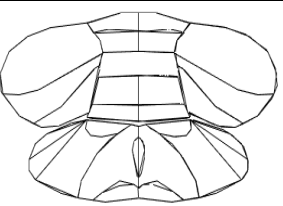
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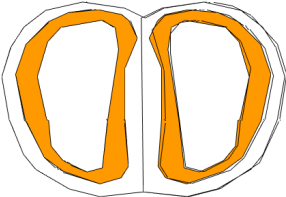
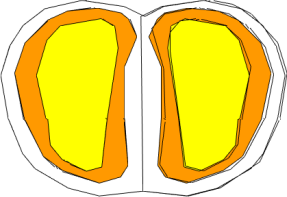
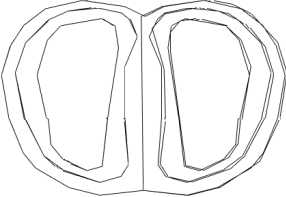
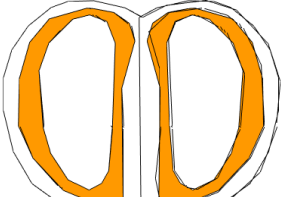

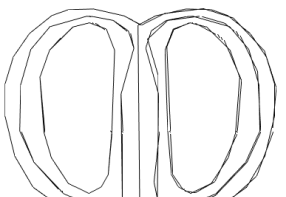
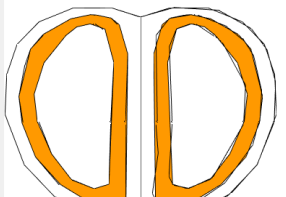
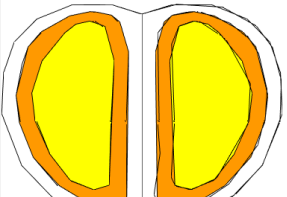
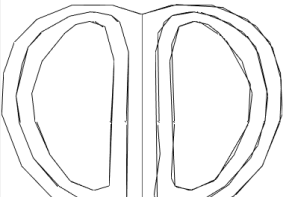
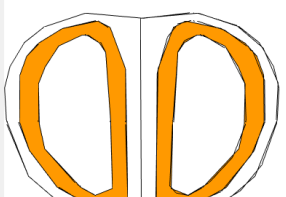
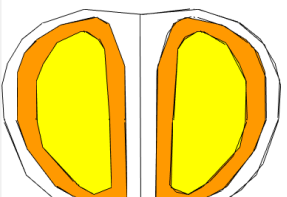
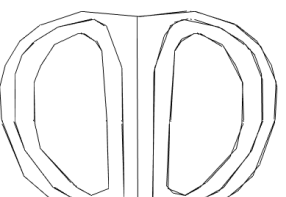
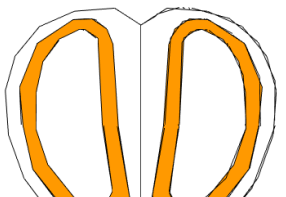
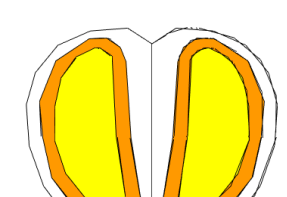
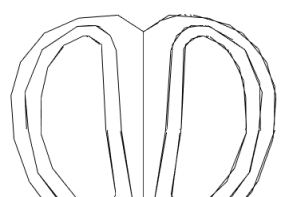
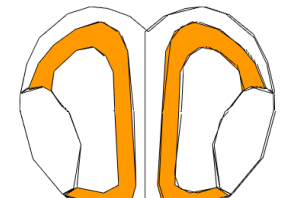
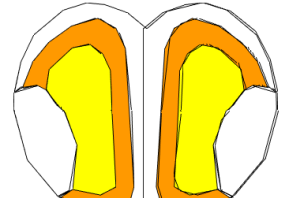
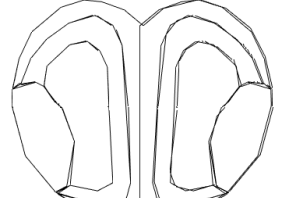
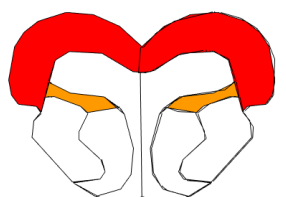
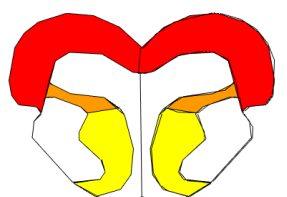
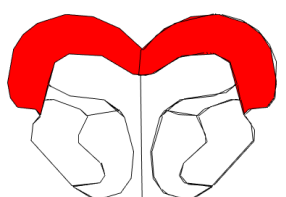
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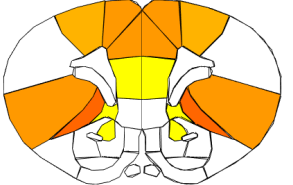
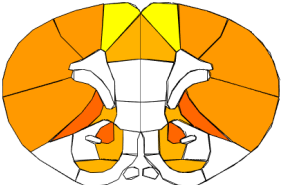
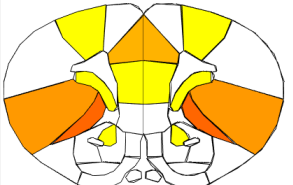
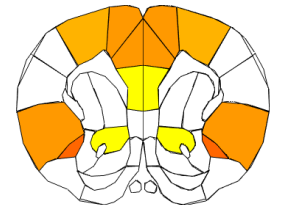
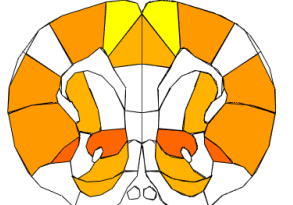

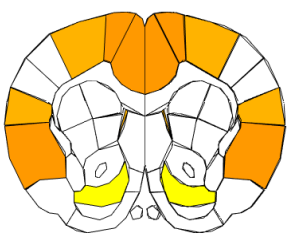
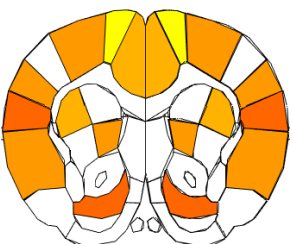
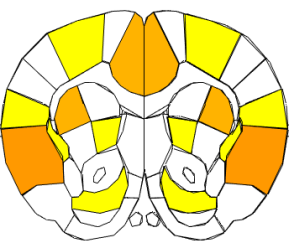
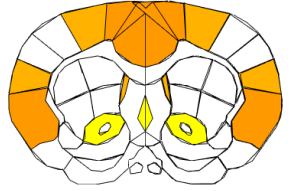
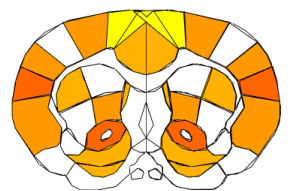
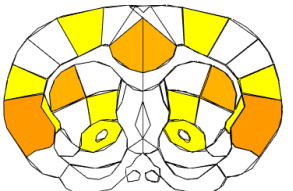
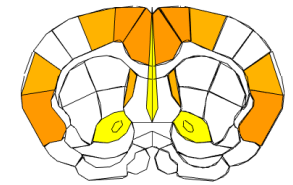
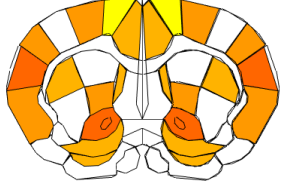
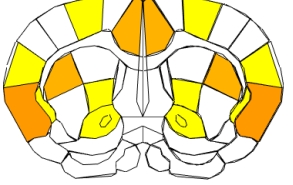
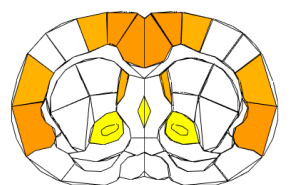
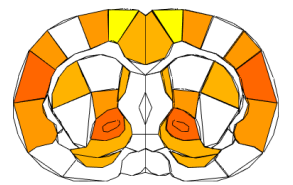
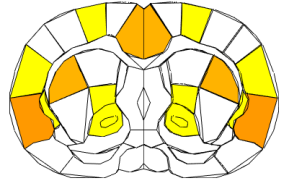
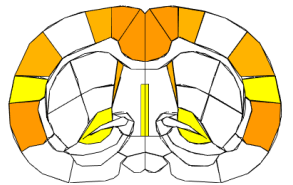
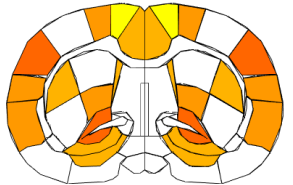
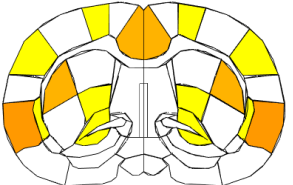
Appendix N: Candoxin Nanoemulsion Results

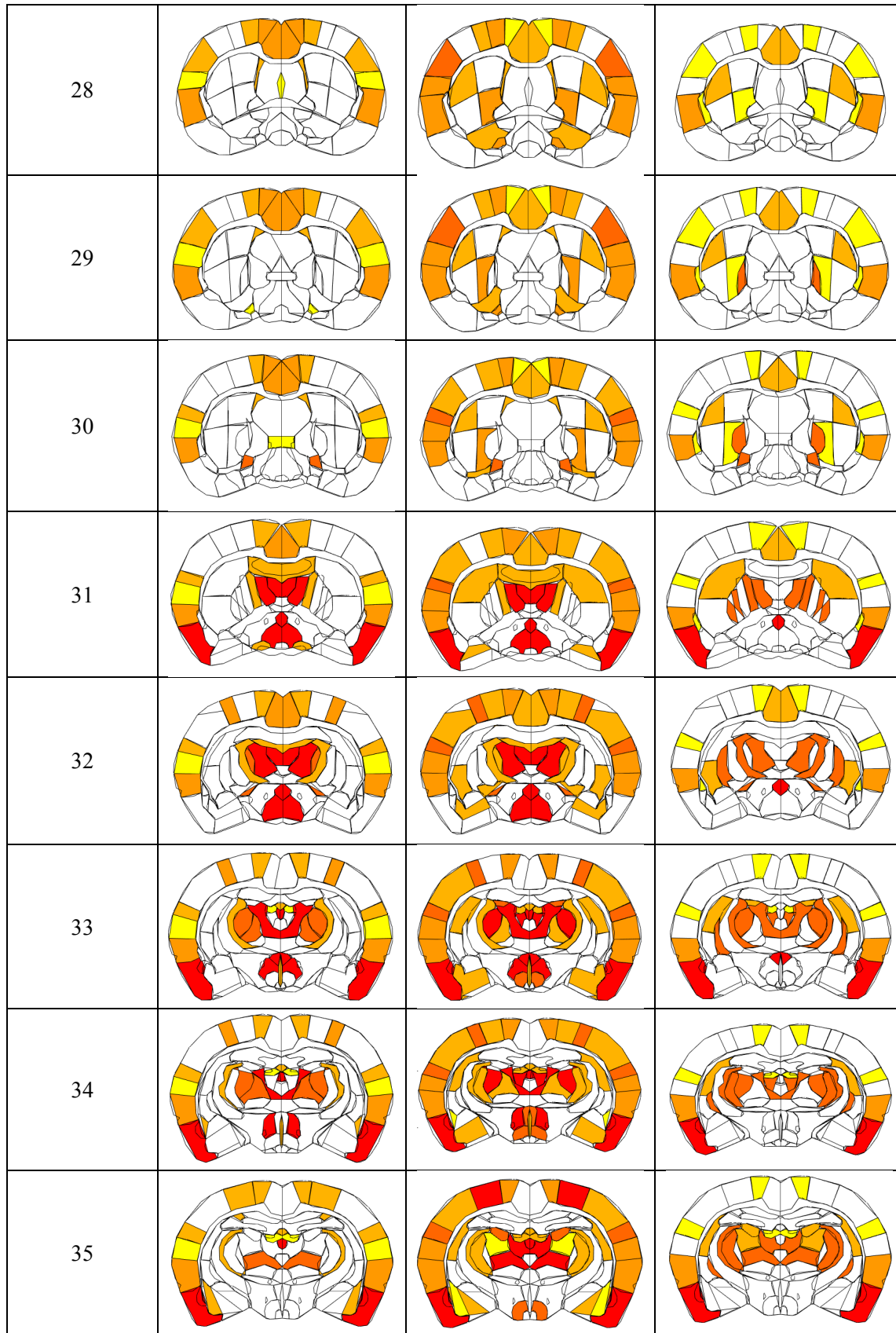


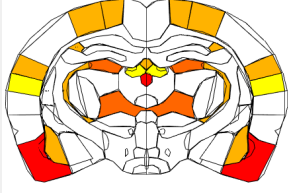
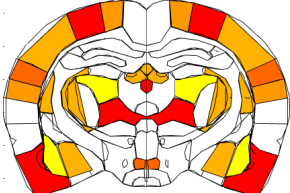
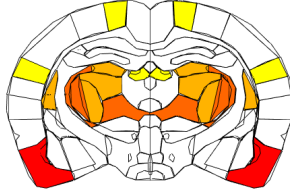
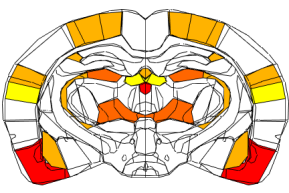
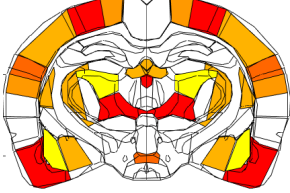
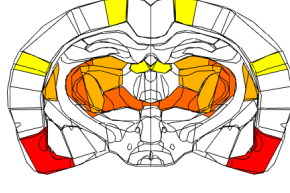
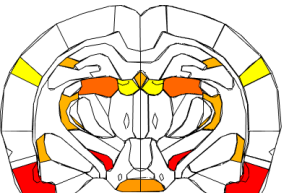
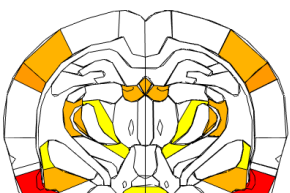
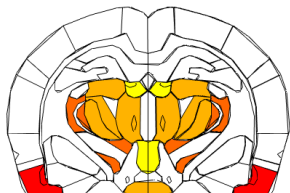
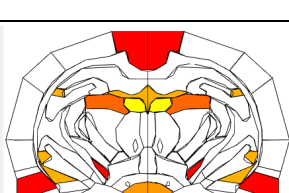
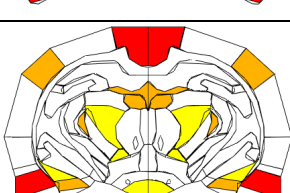
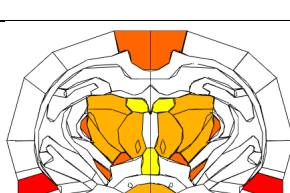
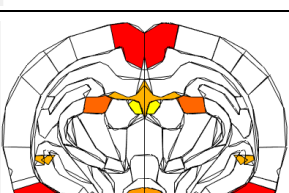
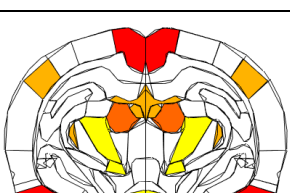
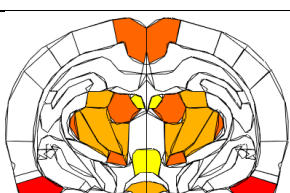
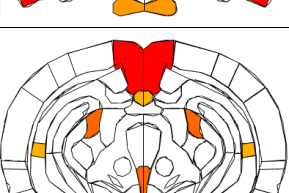
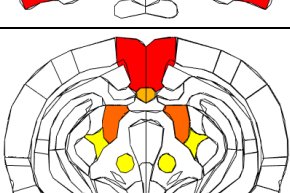
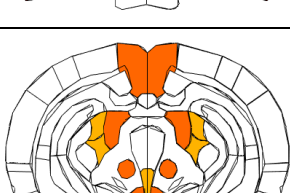
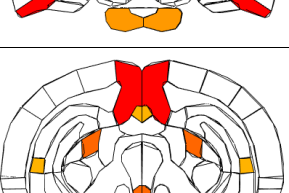
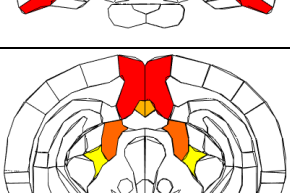
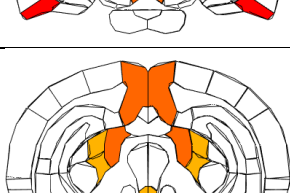
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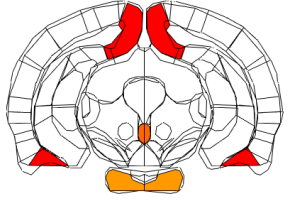
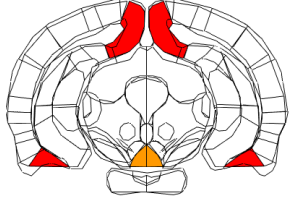
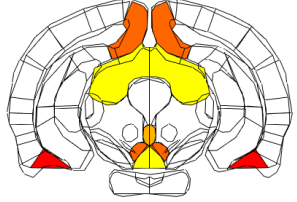
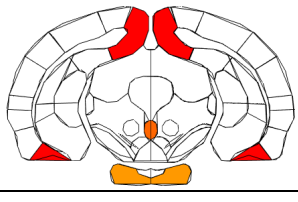
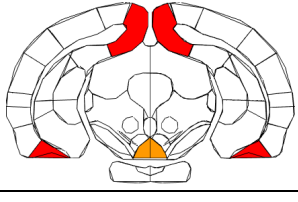
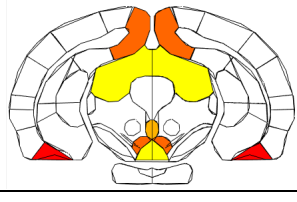
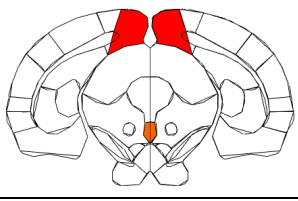
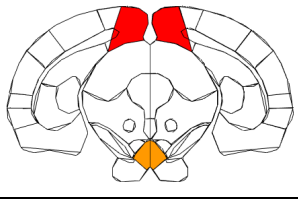
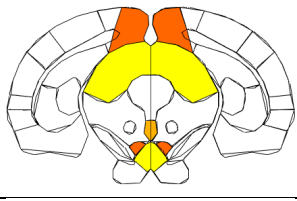
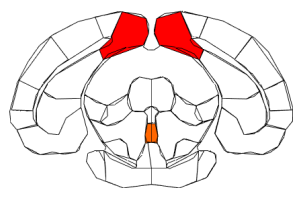
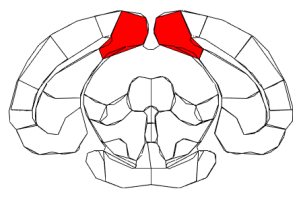
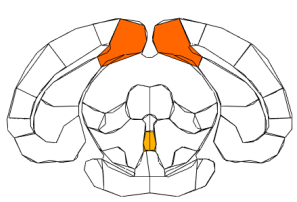
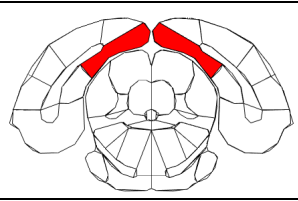
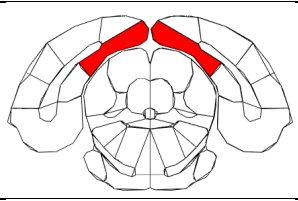
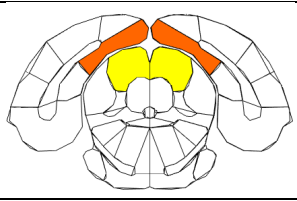
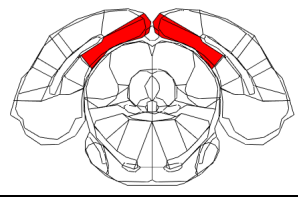
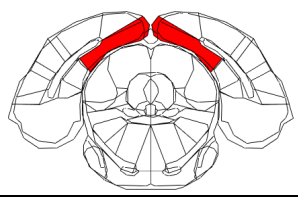
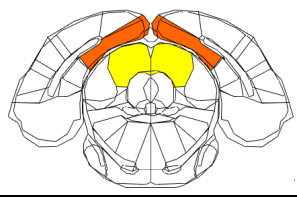
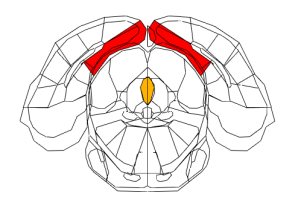
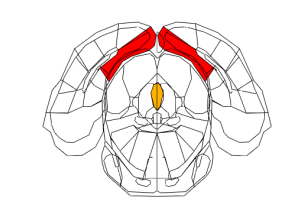
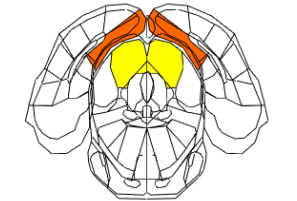
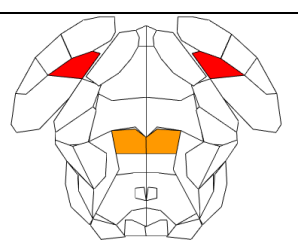
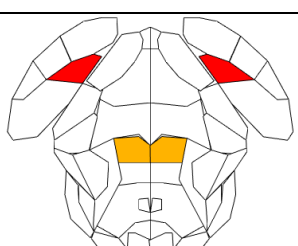
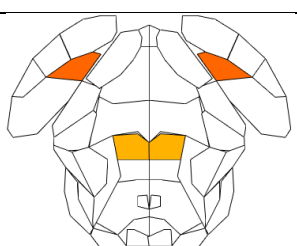
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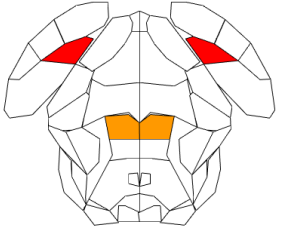
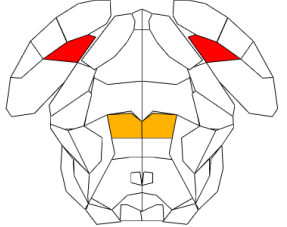
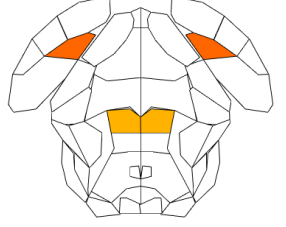
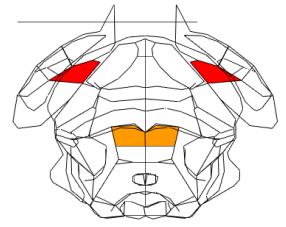
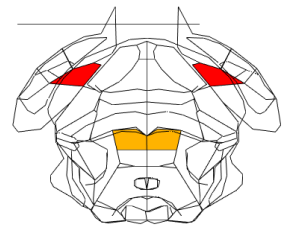
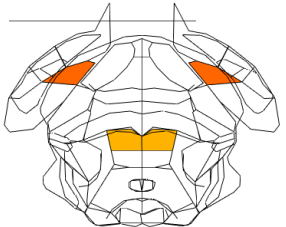
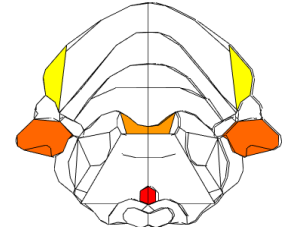
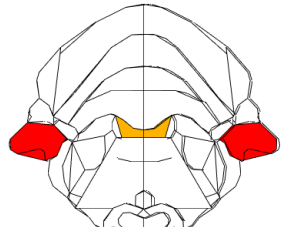
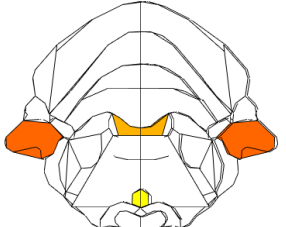
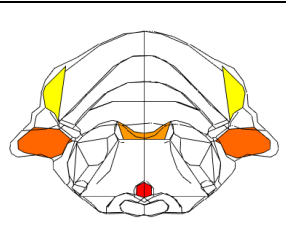
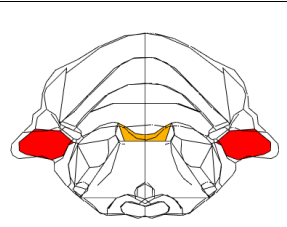
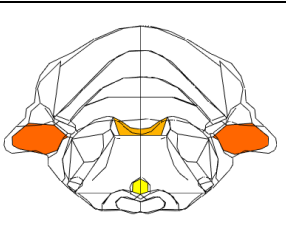
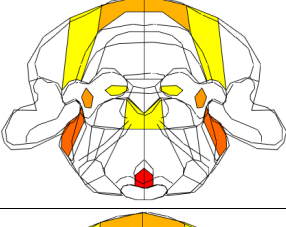
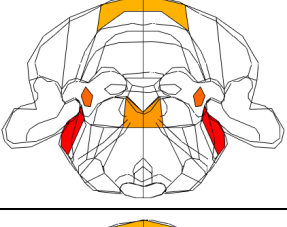
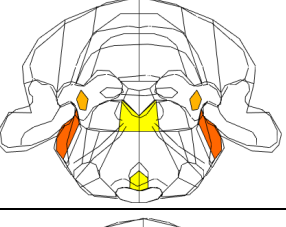
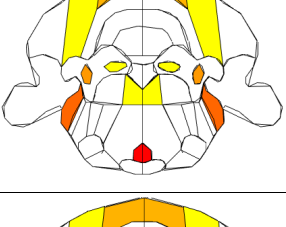
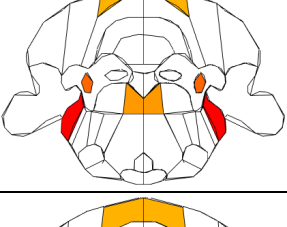
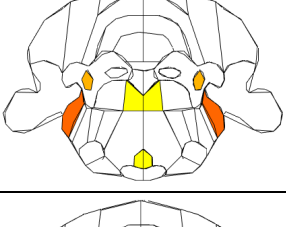
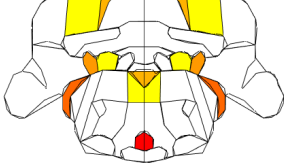
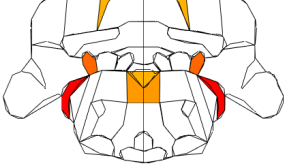
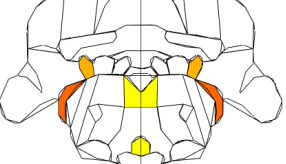
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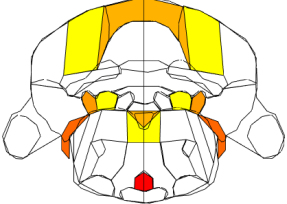
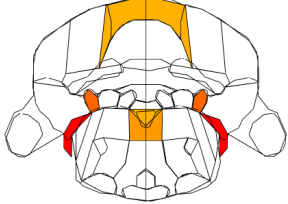
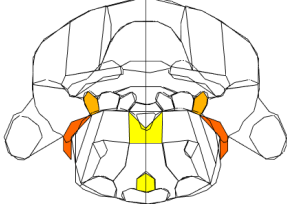
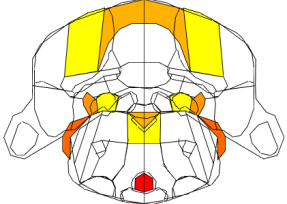
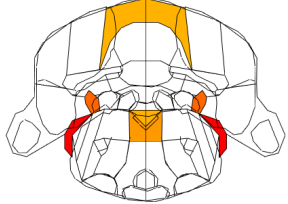
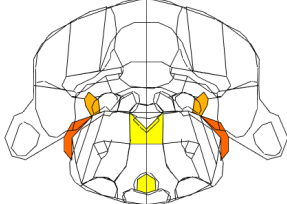
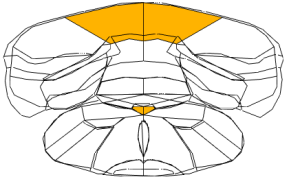
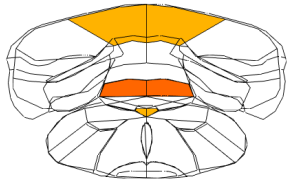
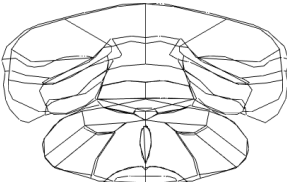
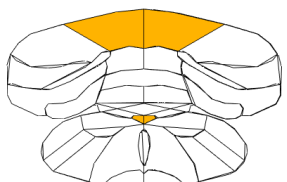
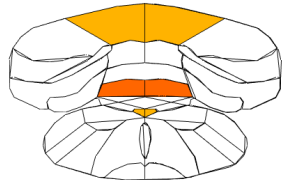
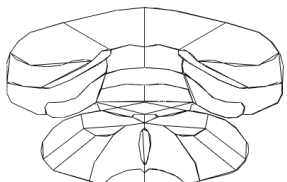
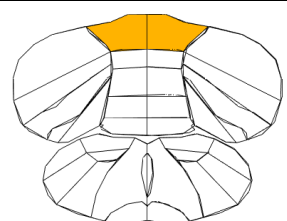
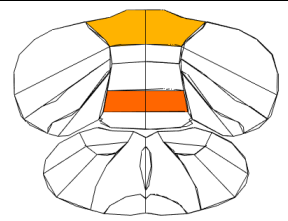
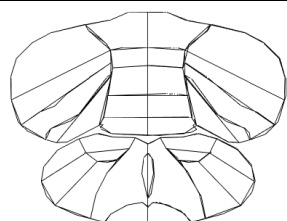
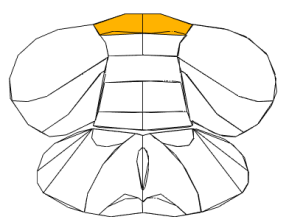
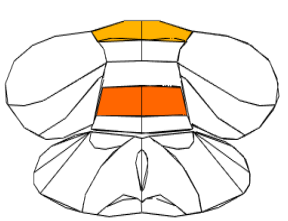
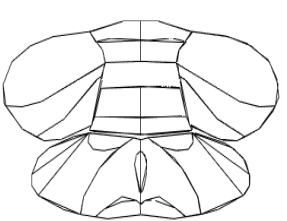
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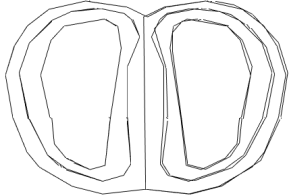
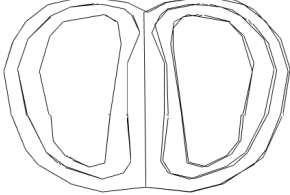
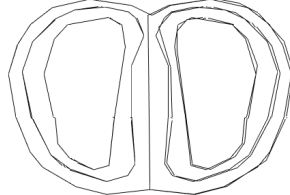
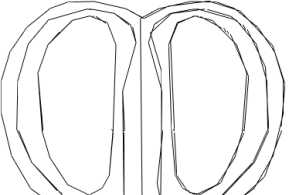
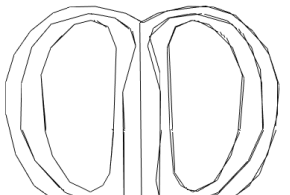
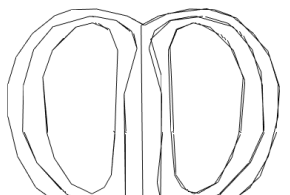
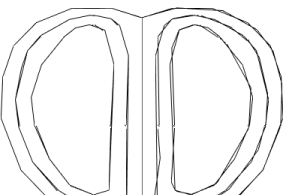
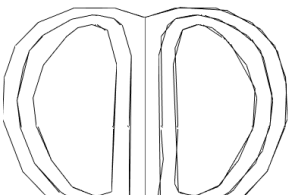
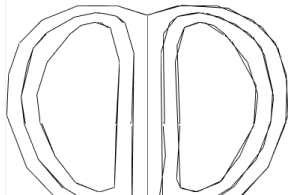
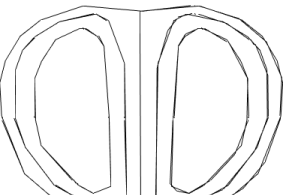
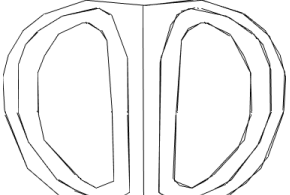
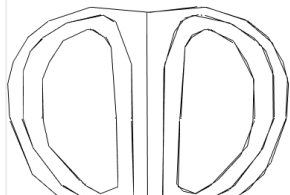
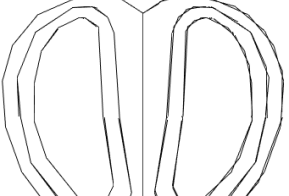
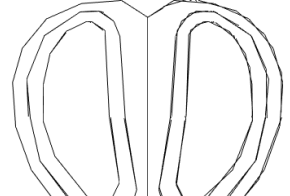
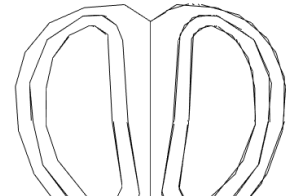
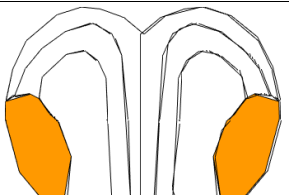
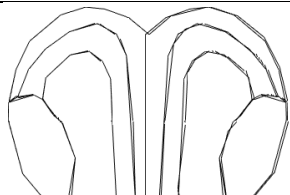
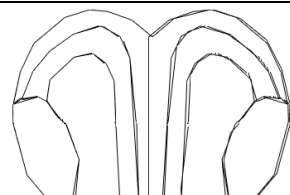
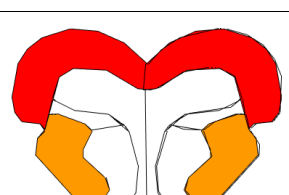
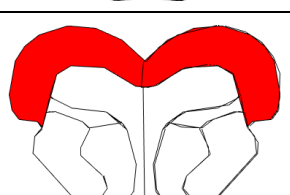
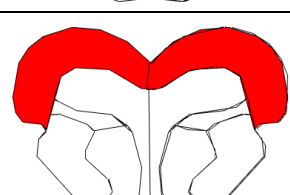
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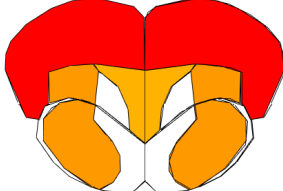
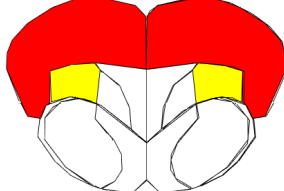
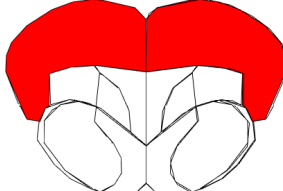
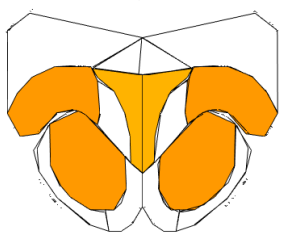
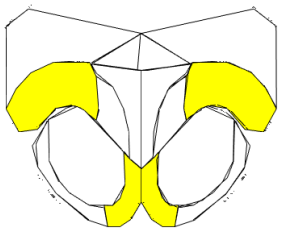
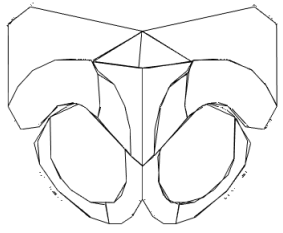
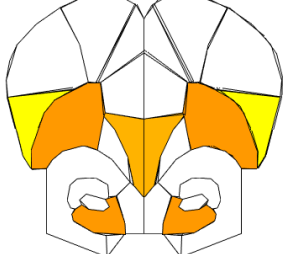
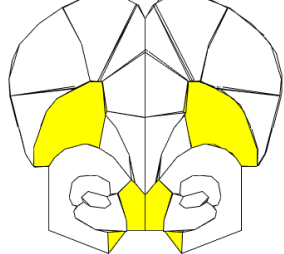
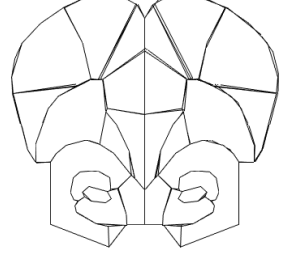
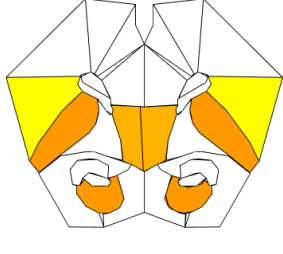
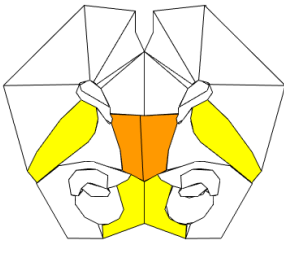
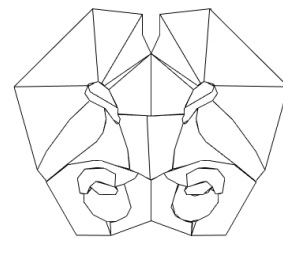
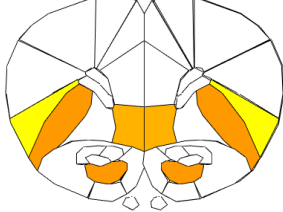
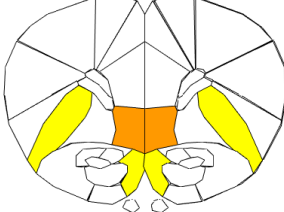
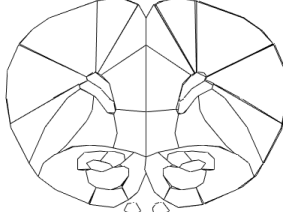
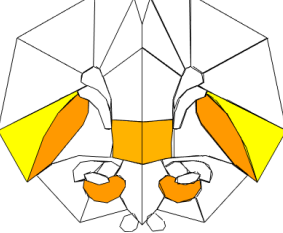
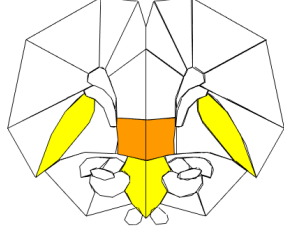
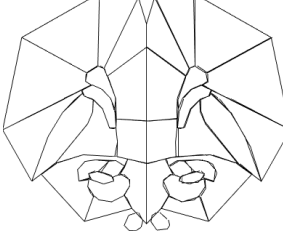
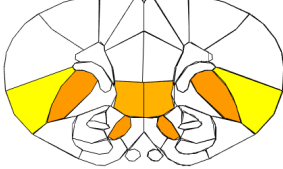
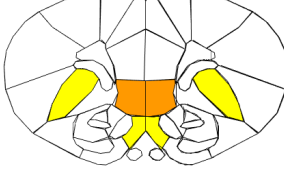
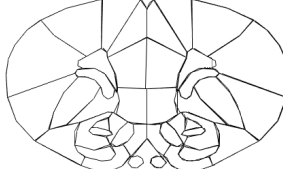
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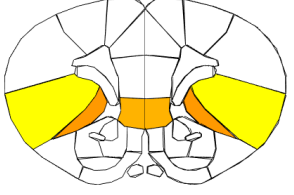
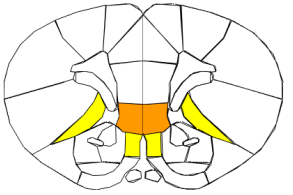
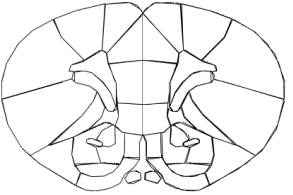
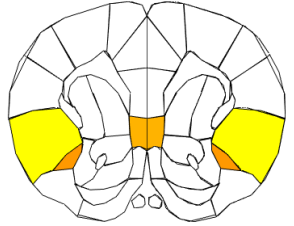
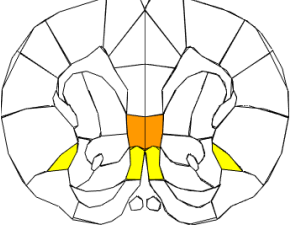
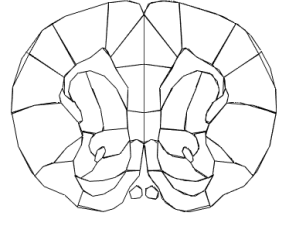
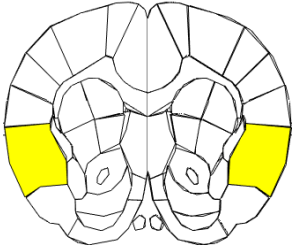
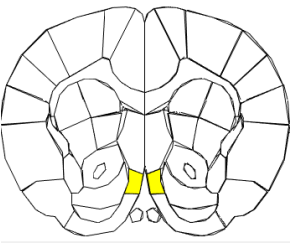
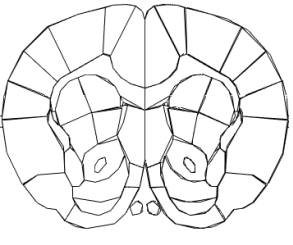
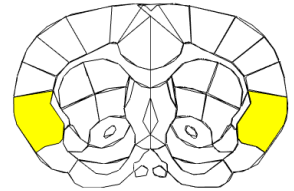
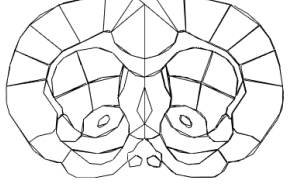
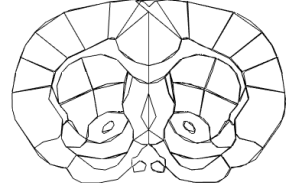
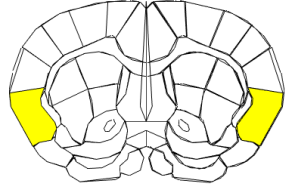
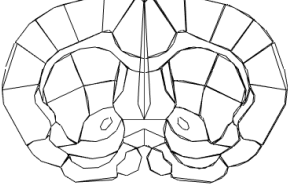
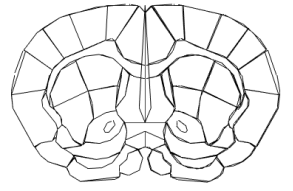
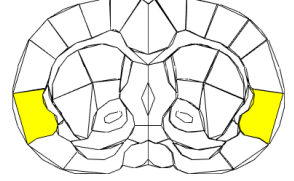
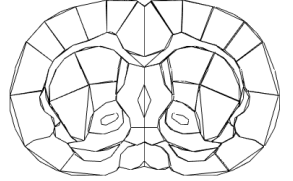
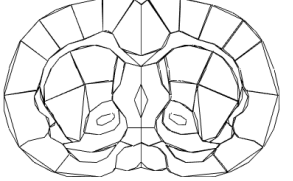
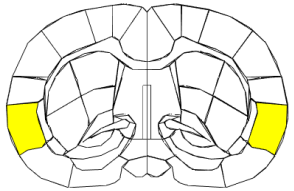
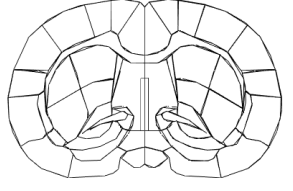
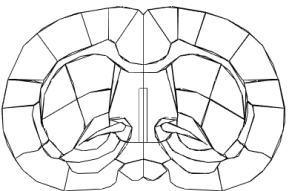
Appendix O: Cereport Nanoemulsion Results

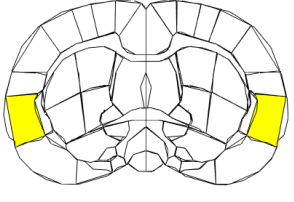
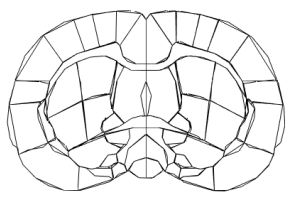
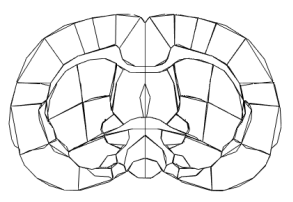
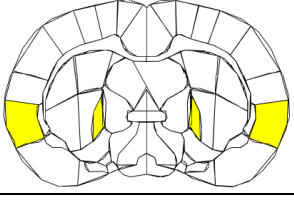
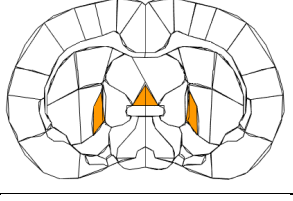
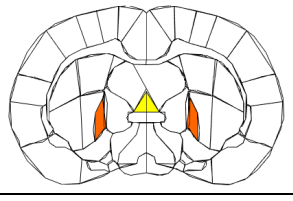
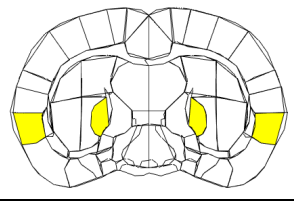
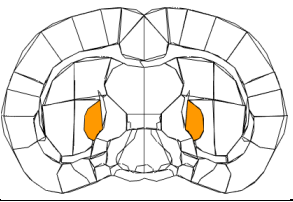
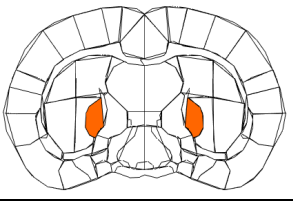
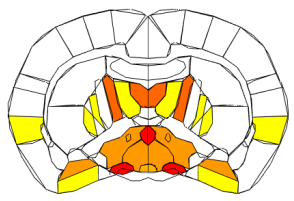
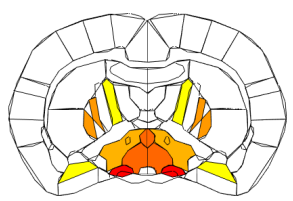
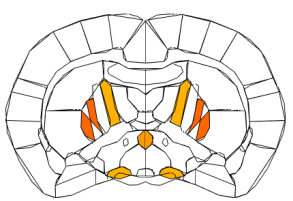
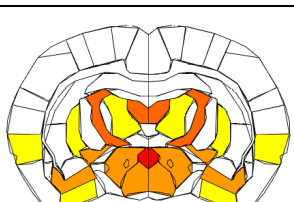
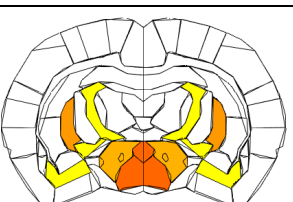
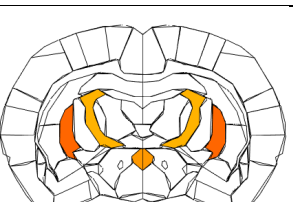
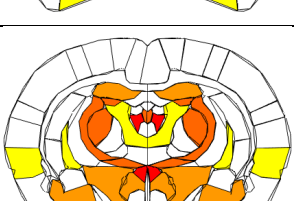
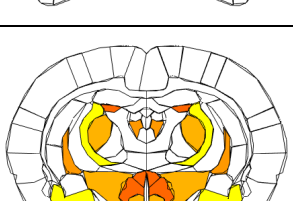
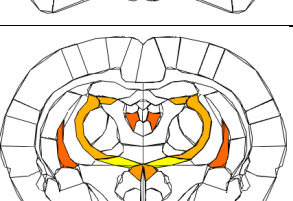
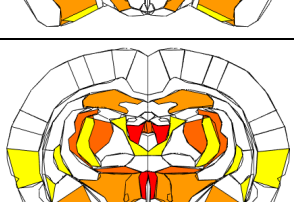
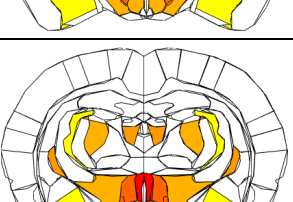
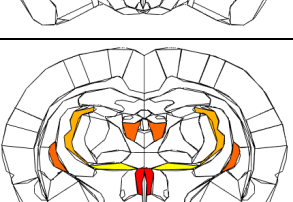
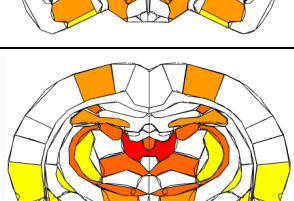
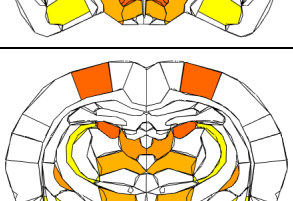
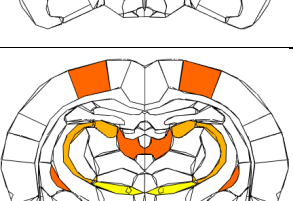


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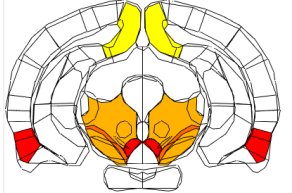
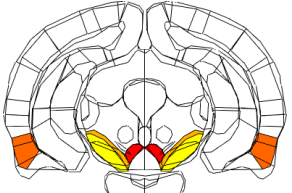
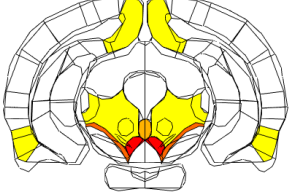
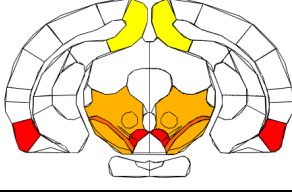
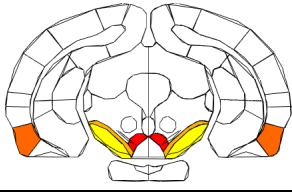
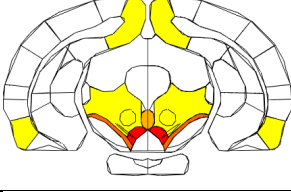
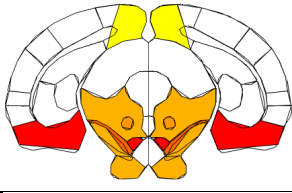
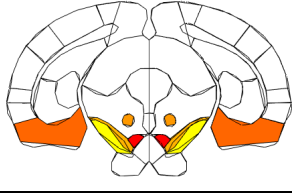
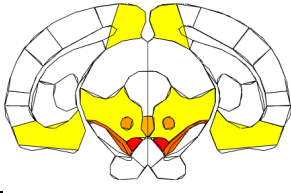
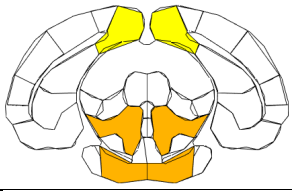
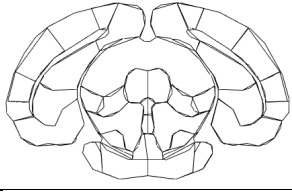
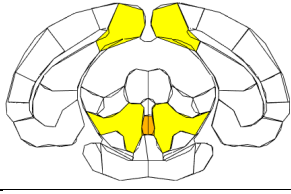
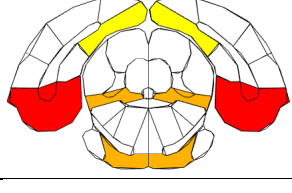
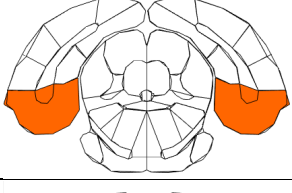
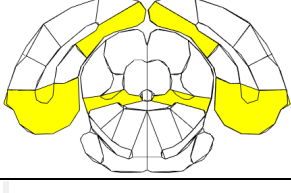
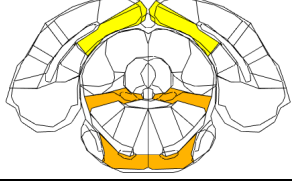
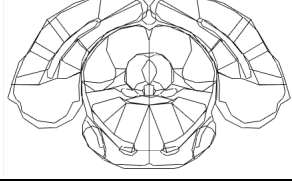
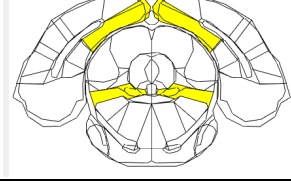
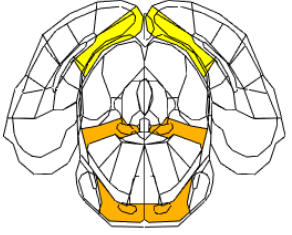
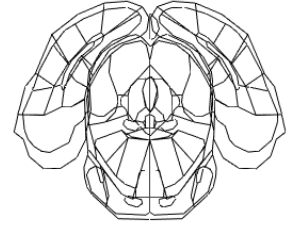
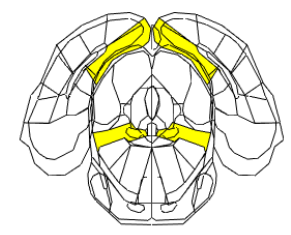
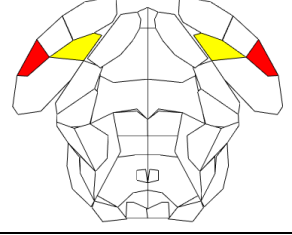
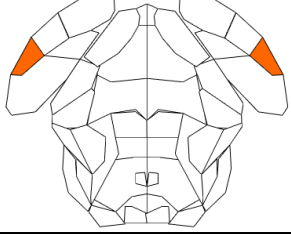
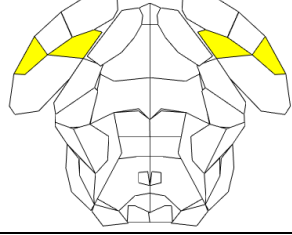
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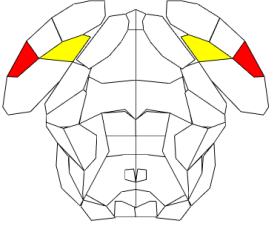
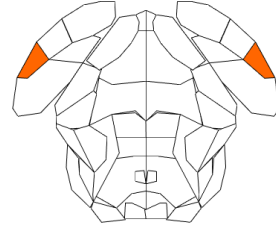
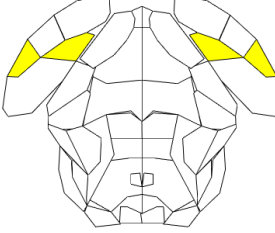
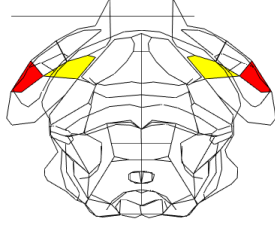
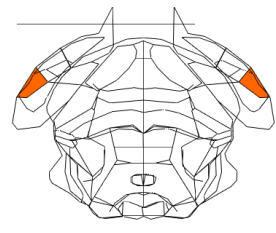
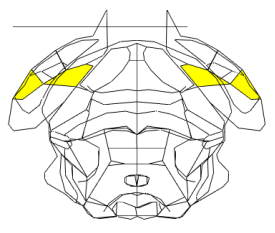
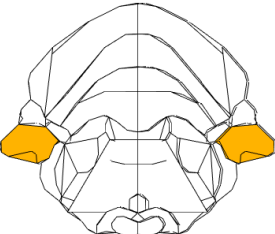
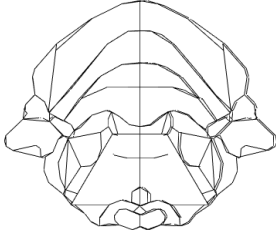
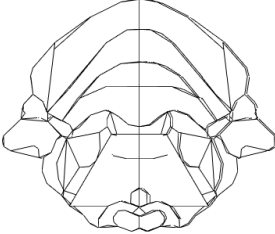
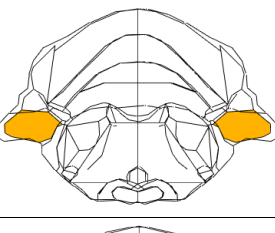
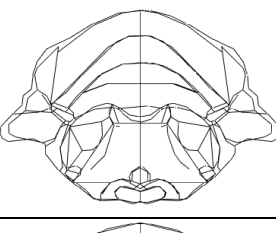
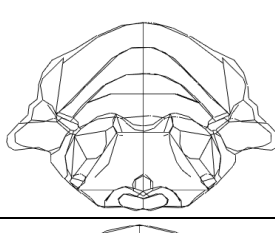
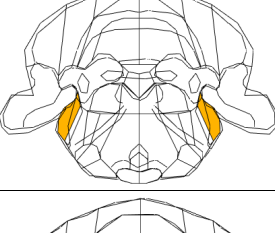
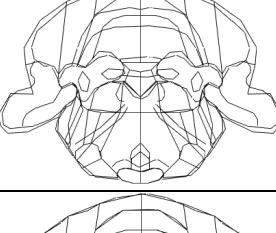
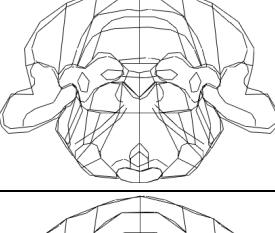
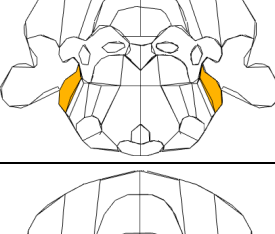
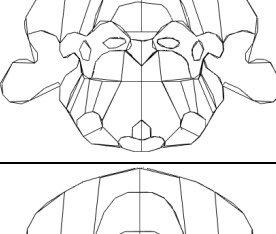
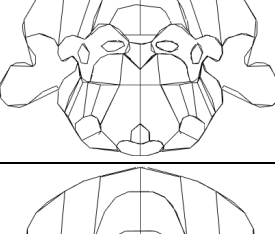
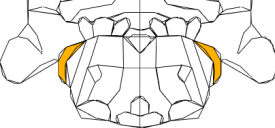
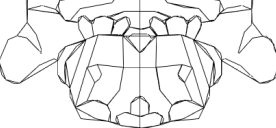
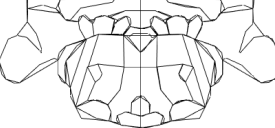
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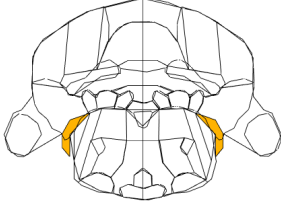
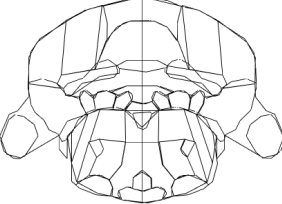
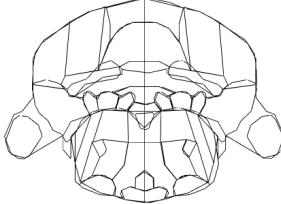
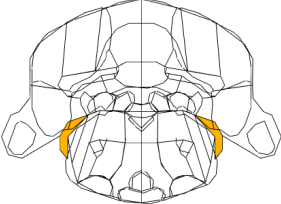
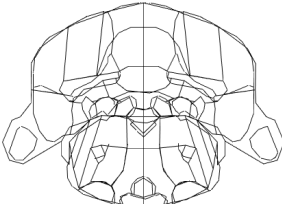
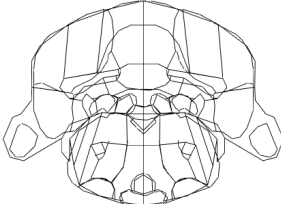
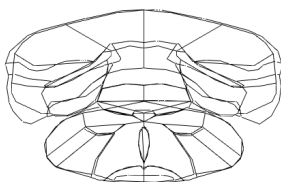
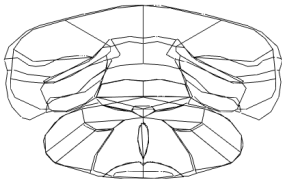
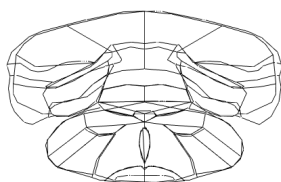
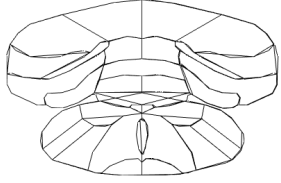
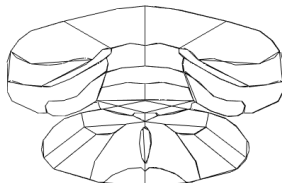
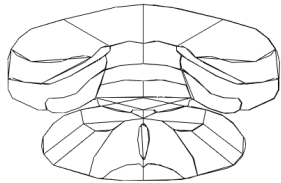
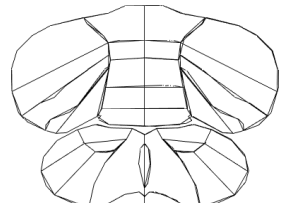
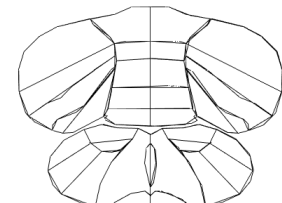
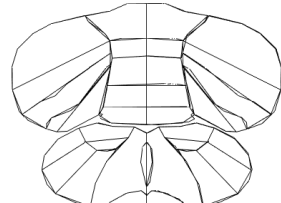
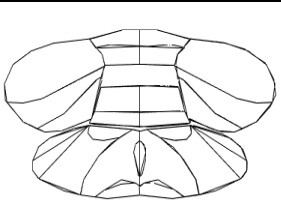
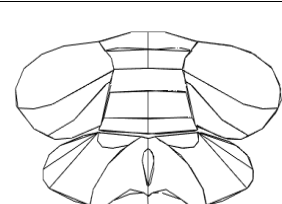
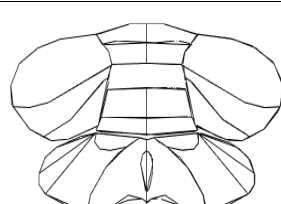
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Appendix P: How to Use the 3D Heat Mapping Program

1. Move the file containing the SPI values into the same folder as the program.
 - a. This folder should also contain the slicemap.m and plotable.mat files.
2. Select the mapping program for the number of slices (all or single) you intend to produce maps of. They are labeled appropriately.
3. When prompted by the program enter the name of the file you are imaging the SPI values from (ex. "A3_SPI.xls"), as well as the slice number (1-63), and time point (20, 40, or 60).
4. Rotate the image into the preferred orientation and save as the preferred file type.

Appendix Q: “UseableMapFeedSPI” Program

```
clear all
0
clc
%MapFeedSPI
%Slice_points
%filename =input('enter the filename you wish to image from\n','s');
filename = 'VoxelWeighted_SPI_A3.csv';
Slicenum = input('enter the index number of the slice you wish to
image:\n');
Y = Slicenum*3;
Timepoint = input('enter the timepoint you intend to image from\n
Options: 20, 40, 60 \n');
%sllicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
load('plotable.mat')
if Timepoint ==20;
valstor = xlsread(filename,'G2:G175');
end
if Timepoint ==40;
valstor = xlsread(filename,'H2:H175');
end
if Timepoint ==60;
valstor = xlsread(filename,'I2:I175');
end
%valstor = xlsread(filename,'A2:A175');%BradyNUMconvert.xlsx /
muNUMconvert.xlsx / alphaNUMconvert.xlsx
lenstor = length(valstor)+1;
specval = zeros(1,175);
for i = 1:lenstor-1;
specval(i+1)=valstor(i);
end
valstor2 = xlsread(filename,'G2:G175');
lenstor = length(valstor2)+1;
specval2 = zeros(1,175);
for i = 1:lenstor-1;
specval2(i+1)=valstor2(i);
end
3
percentile = prctile(specval2,[75,80,85,90,95]);
low = percentile(1);
medLOW =percentile(2);
MED = percentile(3);
medHIGH = percentile(4);
HIGH = percentile(5);
%Index locations for regions, list to avoid having to repetitively
find
%them
GL=2;%
EPI=3;%
Gr=4;%
TT=5;%
AO=6;%
PIRC=7;%
PirR=8;%
Cg=9;%
CG=Cg;
RSC=10;%
```

RSR=11;%Retrosplenial Rostral Ctx
Ins=12;%
V1=13;%Visual 1 Ctx
V2=14;%Visual 2 Ctx
Te=15;%
Ent=16;%Entorhinal Ctx
Au=17;%
Ect=18;%Ectorhinal Ctx
PRh=19;%
Pt=20;%Parietal Ctx
S1BF=21;%
S1FL=22;%
S1HL=23;%
S1J=24;%
S1Sh=25;%Primary Somatosensory Ctx Shoulder
S1Tr=26;%Primary Somatosensory Ctx Trunk
S1UL=27;%Primary Somatosensory Ctx Upper Lip
S2=28;%
VO=29;%
MO=30;%Medial Orbital Ctx
LO=31;%
IL=32;%
PrL=33;%
FrA=34;%Frontal Association Ctx
M1=35;%
M2=36;%
CA1D=37;%
CA1V=38;%CA1 Hippocampus Ventral
CA2=39;%CA2
CA3D=40;%CA3 Dorsal
CA3V=41;%CA3 Hippocampus Ventral
DS=42;%
VS=43;%
DgD=44;%
DgV=45;%
4
BA=46;%
Ce=47;%
AA=48;%
LA=49;%Lateral Amygdaloid Nucleus
La=49;%
I=50;%Intercalated ADygdaloid Nucleus
Co=51;%
Me=52;%
EA=53;%
DLS=54;%Dorsal Lateral Striatum
DMS=55;%Dorsal Medial Striatum
VLS=56;%Ventral Lateral Striatum
VMS=57;%
Tu=58;%
AcbC=59;%
AcbSh=60;%
AcbSH=60;% repeat for capitalization-KC
GP=61;%
VP=62;%
STh=63;%
Sth =63;%Subthalamic Nucleus
ZIR=64;%Zona Incerta

PR=65;%Prerubral Field
 EN=66;%
 SI=67;%Substantia Innominata
 Cl=68;%
 ST=69;%
 LS=70;%Lateral Septal Nucleus
 TS=71;%Triangular Septal Nucleus
 MS=72;%Medial Septum
 DB=73;%Diagonal Band of Broca
 AHA=74;%
 LH=75;%
 Lh=75;
 PM=76;%Premammillary Nucleus
 SUM=77;%Supramammillary Nucleus
 SCh=78;%Suprachiasmatic Nucleus
 PVA=79;%
 Arc=80;%Arcuate Nucleus
 DM=81;%
 PHD=82;%Posterior Hypothalamic Area
 MCPO=83;%Magnocellular Preoptic Nucleus
 MM=84;%Medial Mammillary Nucleus
 SO=85;%
 VMH=86;%
 LPO=87;%Lateral Preoptic Area
 MPA=88;%Medial Preoptic Area
 Rch=89;%Retrochiasmatic Nucleus
 AI=90;%
 AL=90;
 Al=90;
 NL=91;%
 A=92;%
 CM=93;%
 5
 LD=94;%Lateral Dorsal Thalamic Nucleus
 LP=95;%Lateral Posterior Thalamic Nucleus
 MD=96;%Medial Dorsal Thalamic Nucleus
 PF=97;%Parafascicular Thalamic Nucleus
 Re=98;%
 Va=99; VA=99;%Ventral Anterior Thalamic Nucleus
 VL=100;%Ventrolateral Thalamic Nucleus
 VM=101;%Ventromedial Thalamic Nucleus
 VPL=102;%Ventral Posteriolateral Thalamic Nucleus
 VPM=103;%Ventral Posteriolmedial Thalamic Nucleus
 Pa=104;%
 PO=105;
 Po=105;%Posterior Thalamic Nucleus
 MG=106;%
 LG=107;%Lateral Geniculate
 Rt=108;%
 HB=109;%Habenula Nucleus
 Hb=HB;
 Pi=110;%Pineal Gland
 oneCb=111;%1st Cerebellar Lobule
 twoCb=112;%2nd Cerebellar Lobule
 threeCb=113;%3rd Cerebellar Lobule
 fourCb=114;%4th Cerebellar Lobule
 fiveCb=115;%5th Cerebellar Lobule
 sixCb=116;%6th Cerebellar Lobule

sevenCb=117;%7th Cerebellar Lobule
eightCb=118;%8th Cerebellar Lobule
nineCb=119;%9th Cerebellar Lobule
tenCb=120;%10th Cerebellar Lobule
Int=121;%Interposed Nucleus
Sim=122;%Simple Lobule Cerebellum
Cop=123;%Copula of the Pyramis
Pfl=124;%Paraflocculus Cerebellum
PFI=Pfl;
Crus1=125;%Crus 1 of Ansiform Lobule
Crus2=126;%Crus 2 of Ansiform Lobule
Fl=127;%Flocculus Cerebellum
FL=Fl;
Lat=128;%Lat (Lateral Cerebellar Nucleus)
Sl=129;%Medial Cerebellar Nucleus Fastigial
PMI=130;%Paramedian Lobule
Pn=131;%Pontine Nuclei
fiveN=132;%Motor Trigeminal Nucleus
Pr5=133;%Principal Sensory Nucleus Trigeminal
Prs=Pr5;
DMTg=134;%Dorsomedial Tegmental AreaTz
Tz=135;%Trapezoid Body
LL=136;%Lemniscal Nucleus
RtTfg=137;%Reticulotegmental Nucleus
RtTg=RtTfg;
Olv=138;%Olivary Nucleus
Poi=139;%Periolivary Nucleus
POI=Poi;
PnC=140;%Pontine Reticular Nucleus Caudal
6
PnO=141;%Pontine Reticular Nucleus Oral
Gig=142;%Gigantocellular Reticular Nucleus Pons
PB=143;%Parabrachial Nucleus
fiveR=144;%Root of Trigeminal Nerve
sevenN=145;%Facial Nucleus
LC=146;%Locus Ceruleus
SubC=147;%Sub Coeruleus Nucleus
MnR=148;%Median Raphe Nucleus
IC=149;%Inferior Colliculus
Su=150;%
APT=151;%Anterior Pretectal Nucleus
MPT=152;%Medial Pretectal Area
SNC=153;%Substantia Nigra Compacta
SNR=154;%
RP=155;%
VTA=156;%
Ip=157;%
IP=57;
PAG=158;%
%=159;%Central Gray
Rt=108;
mRt=160;%Reticular Nucleus Midbrain
PTg=161;%Pedunculopontine Tegmental Area
DR=162;%Dorsal Raphe
RLi=163;%
IO=164;%Inferior Olivary Complex
Sol=165;%Solitary Tract Nucleus
VCA=166;%Cochlear Nucleus

```

Ve=167;%Vestibular Nucleus
RMg=168;%Raphe Magnus
Rob=169;%Raphe Obscurus Nucleus
PCRt=170;%PCRt
DPGi=171;%DPGi
PrCN=172;%Precuneiform Nucleus
PrCn=172;%Copied for capitalization-KC
V=173;%Ventricle
WM=174;%
Dgd = DgD;
DGd = Dgd;
Error using input
Cannot call INPUT from EVALC.
Error in UsableMapFeedSPI (line 9)
Slicenum = input('enter the index number of the slice you wish to
image:\n');

```

slice1

```

if Slicenum == 1;
Y=3;
%GL 2
GLx=[1295,1295,1310,1392,1449,1501,1527,1530,1518,1488,1440,1375,1331];
7
GLz=[1315,1200,1136,1003, 968,
991,1085,1168,1231,1282,1320,1340,1335];
%EPI 3
EPIx=[1350,1423,1478,1506,1486,1463,1415,1333,1304,1313,1332];
EPIz=[1326,1299,1251,1156,1012,998 ,1003,1123,1276,1303,1323];
%Gr 4
Grx=[1338,1337,1338,1373,1416,1455,1472,1459,1409,1341];
Grz=[1305,1300,1224,1105,1046,1032,1069,1204,1268,1307];
%%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=1
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice2

```

if Slicenum == 2;
Y=6;
Grx=[1333,1335,1413,1453,1471,1463,1426,1392,1357,1345];
Grz=[1298,1225,1003,1003,1082,1185,1261,1294,1305,1304];
GLx=[1296,1342,1396,1477,1529,1547,1520,1471,1416,1388,1343,1318,1313,1301,12
91];
GLz=[1317,1343,1349,1315,1238,1107,1000, 953, 934,
944,1003,1052,1124,1143,1149];
EPIx=[1314,1307,1329,1370,1422,1471,1492,1520,1494,1431,1358];
EPIz=[1296,1265,1130,1003, 962, 986,1002,1084,1226,1309,1319];
%receptorMap(specval(2), GLx, GLz, Y)

```

```

slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=2
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice3l
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 3

```

if Slicenum == 3;
8
Y=9;
Grx=[1373,1339,1334,1372,1397,1436,1456,1471,1465,1423,1376];
Grz=[1307,1288,1261,1003, 960, 978,1010,1082,1205,1280,1306];
GLx=[1291,1295,1397,1432,1475,1524,1548,1549,1503,1458,1405,1342];
GLz=[1317,986 , 892, 883, 911,1003,1112,1212,1300,1337,1356,1348];
EPIx=[1325,1311,1336,1353,1406,1435,1465,1492,1515,1515,1503,1412,1353];
EPIz=[1313,1251,1003,965 , 922, 922, 942,
996,1069,1178,1238,1325,1330];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=3
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice3l
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice4

```

if Slicenum == 4;
Y=12;
Grx=[1354,1354,1359,1376,1404,1441,1476,1489,1486,1462,1439,1383];
Grz=[1289, 993, 949, 922, 912, 941,1000,1066,1152,1246,1284,1310];
GLx=[1291,1387,1434,1480,1544,1570,1552,1521,1462,1332,1291];
GLz=[1321,1361,1357,1336,1251,1137,994 , 909, 866, 864, 881];
EPIx=[1312,1334,1331,1363,1462,1516,1534,1539,1519,1477,1389,1359,1327];
EPIz=[1263,1003,917, 892 , 905,
976,1046,1155,1232,1296,1333,1332,1306];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=4
%l = 1; %enter whatever slice you want

```

```

hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end
9

```

slice5

```

if Slicenum == 5;
Y=15;
Grx=[1355,1341,1365,1356,1368,1397,1458,1463,1498,1497,1462,1380];
Grz=[1306,1242,1108, 993, 922, 900, 925,1003,1134,1225,1287,1321];
GLx=[1294,1300,1400,1457,1499,1538,1573,1574,1553,1519,1469,1435,1351,1291];
GLz=[1321,1350,1365,1360,1337,1286,1183,1089,1003, 903, 846, 827, 851,
834];
EPIx=[1320,1312,1332,1332,1327,1339,1397,1462,1492,1516,1542,1528,1469,1390,1
336];
EPIz=[1312,1273,1164,1003, 911, 886, 868, 887, 920,
997,1134,1233,1322,1347,1329];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=5
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice6

```

if Slicenum == 6;
Y=18;
Grx=[1345,1335,1367,1368,1399,1443,1463,1484,1506,1497,1463,1383];
Grz=[1293,1224,1108, 875, 855, 882, 917,1002,1146,1227,1291,1314];
GLx=[1291,1282,1352,1385,1410,1514,1557,1576,1574,1559,1525,1477,1418,1328];
GLz=[1320, 798, 816, 763, 769,
888,1003,1082,1152,1240,1308,1355,1370,1349];
EPIx=[1321,1307,1332,1333,1325,1338,1384,1454,1499,1546,1544,1529,1477,1400,1
339];
EPIz=[1312,1257,1164, 993, 881, 851, 829, 851,
920,1081,1180,1236,1319,1347,1331];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=6
%l = 1; %enter whatever slice you want
10
hold all
for t = 1:plotable{1,2}%slice31

```



```

plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice7

```

if Slicenum == 7;
Y=21;
EPIx =
[1324,1307,1332,1332,1325,1340,1383,1457,1496,1534,1554,1533,1487,1447,1386,1
339];
EPIz = [1312,1257,1164,1003, 857, 821, 802, 841,
885,1000,1144,1238,1309,1337,1346,1331];
Grx=[1352,1380,1462,1489,1510,1491,1487,1482,1458,1409,1378,1367,1345,1352];
Grz=[1291,1313,1291,1246,1137,1003,1000, 920, 875, 839,
852,1003,1222,1291];
GLx=[1291,1333,1418,1493,1537,1564,1582,1567,1538,1513,1445,
1383,1295];
GLz=[1320,1351,1370,1344,1292,1228,1137,1003, 894, 847, 786, 762,
777];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=7
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice8

```

if Slicenum == 8;
Y=24;
Grx=[1368,1350,1356,1364,1379,1406,1451,1488,1504,1513,1492,1441,1405];
Grz=[1297,1236,1003, 877, 842, 823, 852, 926,
998,1158,1236,1303,1315];
GLx =[1291,1295,1320,1374,
1470,1528,1568,1589,1589,1571,1536,1487,1451,1396,1329];
GLz =[1308, 760,746 , 744, 786, 841,
931,1046,1139,1217,1284,1336,1353,1355,1335];
EPIx=[1353,1320,1308,1336,1333,1375,1461,1526,1557,1555,1533,1491,1411,1397];
EPIz=[1322,1292,1242,1109, 785, 775, 822,
913,1003,1136,1238,1304,1334,1333];
l1
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(GL), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=8
%l = 1; %enter whatever slice you want
hold all

```

```

for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice9

```

if Slicenum == 9;
Y=27;
Grx =[1355,1366,1399,1450,1494,1526,1533,1511,1462,1438,1408,1375];
Grz =[1175, 818, 805, 832, 907,1002,1082,1174,1254,1279,1288,1273];
GLx=[1295,1358,1445,1522,1571,1594,1598,1555,1487,1394,1330,1295];
GLz=[1308,1334,1335,1294,1228,1140,1023, 875, 781, 733, 727, 747];
EPIx=[1324,1328,1345,1413,1474,1530,1560,1567,1541,1513,1451,1407,1394,1361,1
343];
EPIz=[1200, 769, 759, 768, 817, 898,
998,1075,1214,1257,1303,1315,1314,1305,1286];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=9
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice10

```

if Slicenum == 10;
Y=30;
l2
Grx=[1375,1364,1360,1398,1430,1510,1522,1524,1509,1479,1427,1417,1389];
Grz=[1203,1003, 805, 785, 808, 921,
993,1111,1161,1222,1254,1254,1231];
GLx=[1292,1294,1318,1396,1478,1546,1595,1599,1587,1555,1511,1420];
GLz=[1303, 725, 712, 721, 764, 841,1005,1099,1162,1232,1278,1318];
EPIx=[1331,1326,1353,1388,1445,1482,1544,1566,1565,1550,1524,1471,1392,1365];
EPIz=[1155, 773, 752, 748, 781, 808,
916,1000,1137,1192,1230,1273,1295,1276];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l=10
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice11

```
if Slicenum == 11;
Y=33;
Grx=[1392,1382,1359,1382,
1406,1430,1505,1532,1531,1516,1480,1433,1421];
Grz=[1229,1003, 830, 776, 773, 791, 899,
992,1090,1168,1226,1252,1251];
GLx=[1559,1594,1601,1579,1524,1445,1354,1295,1295,1310,1345,1445,1504];
GLz=[864 , 977,1092,1182,1259,1299,1307,1263, 719, 705, 702, 731,
779];
EPIx=[1358,1346,1320,1331,1363,1397,1447,1475,1539,1561,1569,1529,1448,1405,1
372];
EPIz=[1213,1000, 812, 769, 743, 739, 764, 794,
887,1000,1101,1215,1277,1279,1253];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
l3
l=11
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end
```

slice12

```
if Slicenum == 12;
Y=36;
%AO - 6
AOx = [1454,1472,1499,1570,1602,1601,1545,1526,1502,1484,];%6
AOz = [ 908, 786, 770, 868,1005,1050,1069,1057,1017,1000,];
%Gr-4
Grx=[1526,1490,1454,1464,1399,1363,1372,1376,1394,1423,1465,1519];
Grz=[1057,1003, 908, 788, 773, 795, 993,1110,1155,1180,1171,1113];
%GL-2
GLx=[1291,1336,1389,1431,1486,1555,1585,1600,1585,1548,1526,1490,1454,1464,14
99,1440,1365,1316,1291];
GLz=[1223,1266,1288,1293,1273,1206,1133,1051,1065,1070,1057,1003, 908,
788, 770, 726, 697, 703, 719];
%3
EPIx=[1526,1490,1454,1464,1494,1394,1357,1331,1321,1341,1363,1405,1467,1520,1
557,1581,1548];
EPIz=[1057,1003, 908, 788, 765, 734, 733, 753,
795,1169,1224,1251,1230,1186,1134,1064,1070];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
%receptorMap(specval(6),AOx,AOz,Y)
slicemap (specval(6), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
```

```

l=12
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 13

```

if Slicenum == 13;
Y=39;
%AO14
AOx=[1518,1648,1642,1620,1607,1577,1492,1468,1497,1497,1427,1413,1429];
AOz=[ 767, 919, 975,1003,1055,1057,1024,1000, 938, 911, 843, 802,
777];
%Gr-
Grx=[1515,1444,1363,1330,1322,1351,1376,1470,1497,1497,1427,1413,1429];
Grz=[ 764, 718, 743, 792, 881, 997,1019,1003, 938, 911, 843, 802,
777];
%GLGLx=[
1290,1295,1320,1399,1444,1363,1330,1322,1351,1364,1416,1525,1584,1592,1573,15
28,1423,1324];
GLz=[1138, 719, 692, 697, 718, 743, 792, 881,
997,1017,1056,1069,1100,1109,1181,1210,1204,1142];
%EPIEPIx=[
1607,1577,1492,1470,1376,1416,1525,1584,1595];
EPIz=[1055,1057,1024,1003,1019,1056,1069,1100,1109];
%FrA-34
FrAx=[1291,1284,1324,1423,1528,1573,1618,1634,1692,1714,1723,1704,1674,1628,1
538,1450,1367];
FrAz=[1223,1138,1142,1204,1210,1181,1006,1024,1031,1062,1113,1226,1275,1313,1
343,1335,1296];
%receptorMap(specval(2), GLx, GLz, Y)
slicemap (specval(2), low,medLOW, MED, medHIGH, HIGH, GLx, GLz, Y);
%receptorMap(specval(3), EPIx, EPIz, Y)
slicemap (specval(3), low,medLOW, MED, medHIGH, HIGH, EPIx, EPIz, Y);
%receptorMap(specval(4), Grx, Grz, Y)
slicemap (specval(4), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
%receptorMap(specval(6),AOx,AOz,Y)
slicemap (specval(6), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
%receptorMap(specval(34),FrAx,FrAz,Y)%FrA
slicemap (specval(34), low,medLOW, MED, medHIGH, HIGH, FrAx, FrAz, Y);
l=13;
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice14

```

if Slicenum == 14;
Y=42;
Grx=[1295,1295,1342,1444,1400,1376,1378,1403,1466,1460];
Grz=[ 859, 728, 681, 696, 723, 763, 818, 868, 944, 995];
%receptorMap(specval(4), Grx, Grz, Y)%Gr

```

```

slicemap (specval(Gr), low,medLOW, MED, medHIGH, HIGH, Grx, Grz, Y);
AOx=[1460,1466,1403,1378,1376,1400,1444,1476,1564,1634,1633,1580,1519];
AOz=[995 , 944, 868, 818, 763, 723, 696, 707, 773, 870,
947,1003,1014];
%receptorMap(specval(6), AOx, AOz, Y)%AO
slicemap (specval(AO), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
FrAx=[1297,1331,1443,1474,1539,1608,1691,1742,1759,1761,1691,1650,1629,1616,1
616,1546,1465,1295];
15
FrAz=[1305,1343,1370,1372,1363,1336,1280,1221,1176,1119, 952, 945,
991,1000,1112,1134,1141,1118];
%receptorMap(specval(34),FrAx,FrAz,Y)%FrA
slicemap (specval(FrA), low,medLOW, MED, medHIGH, HIGH, FrAx, FrAz,
Y);
MOx=[1295,1295,1345,1351,1360,1384,1449,1465];
MOz=[1118, 859, 907, 982,1003,1061,1116,1141];
%receptorMap(specval(30), MOx, MOz, Y)%MO
slicemap (specval(MO), low,medLOW, MED, medHIGH, HIGH, MOx, MOz, Y);
VOx=[1461,1449,1384,1351,1345,1445];%plot before MO and LO
VOz=[998 ,1116,1061, 982, 907, 990];
%receptorMap(specval(29), VOx, VOz, Y)%VO
slicemap (specval(VO), low,medLOW, MED, medHIGH, HIGH, VOx, VOz, Y);
LOx=[1461,1449,1468,1546,1616,1612,1549,1514];
LOz=[998 ,1116,1140,1134,1112,1003,1021,1015];
%receptorMap(specval(31), LOx, LOz, Y)%LO
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz, Y);
WMx=[1444,1476,1564,1634,1633,1580,1519,1549,1629,1650,1657,1600,1547,1476];
WMz=[ 696, 707, 773, 870, 947,1003,1014,1021, 991, 945, 881, 794, 744,
707];
%receptorMap (specval(174), WMx, WMz, Y)
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
l=14;
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice15

```

if Slicenum == 15;
Y=45;
M2x=[1295,1295,1681,1757,1758,1724,1673,1597,1466];
M2z=[1230,1230,1304,1252,1002,1062,1111,1142,1137];
%receptorMap(specval(36), M2x, M2z, Y)%M2
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z, Y);
LOx=[1472,1449,1441,1449,1502,1526,1589,1650,1714,1758,1724,1673,1597];
LOz=[1143,1100,1003, 967,1004,1012,1003, 940,
932,1002,1062,1111,1142];
%receptorMap(specval(31), LOx, LOz, Y)%LO
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz, Y);
AOx=[1355,1490,1515,1614,1610,1574,1542,1474,1393,1350];
AOz=[872 , 998,1009, 969, 844, 782, 749, 711, 710, 774];
%receptorMap(specval(6), AOx, AOz, Y)%AO
slicemap (specval(6), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
PirRx=[1613,1610,1574,1542,1474,1422,1410,1478,1587,1649,1668];
PirRz=[ 968, 844, 782, 749, 711, 703, 646, 666, 747, 826, 890];

```

```

%receptorMap(specval(8), PirRx, PirRz, Y)%PirR
16
slicemap (specval(8), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);
TTx=[1295,1330,1368,1410,1422,1393,1368,1350,1355,1295];
TTz=[720 , 668, 646, 646, 711, 710, 731, 774, 872, 821];
%receptorMap(specval(5), TTx, TTz, Y)%TT
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz, Y);
MOx=[1295,1335,1338,1356,1392,1449,1466,1295];
MOz=[ 821, 851, 934,1003,1068,1110,1137,1117];
%receptorMap(specval(30), MOx, MOz, Y)%MO
slicemap (specval(MO), low,medLOW, MED, medHIGH, HIGH, MOx, MOz, Y);
VOx=[1449,1441,1449,1392,1356,1338,1335,1414];
VOz=[ 967,1003,1100,1068,1003, 934, 851, 930];
%receptorMap(specval(29), VOx, VOz, Y)%VO
slicemap (specval(VO), low,medLOW, MED, medHIGH, HIGH, VOx, VOz, Y);
PrLx = [1293,1466,1282];
PrLz = [1230,1137,1117];
%receptorMap(specval(33), PrLx, PrLz, Y)%PrL
slicemap (specval(33), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz, Y);
l=15;
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice16

```

if Slicenum == 16;
Y=48;
Cgx=[1295,1326,1472,1461,1295];
Cgz=[1320,1361,1135,1137,1222];
%receptorMap(specval(9), Cgx, Cgz, Y)%Cg
slicemap (specval(9), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz, Y);
M2x=[1326,1480,1509,1542,1614,1522,1425,1406];
M2z=[1361,1136,1138,1246,1352,1386,1395,1394];
%receptorMap(specval(36), M2x, M2z, Y)%M2
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z, Y);
M1x=[1617,1542,1509,1566,1818,1824,1783,1709];
M1z=[1353,1246,1138,1117,1094,1143,1245,1305];
%receptorMap(specval(35), M1x, M1z, Y)%M1
slicemap (specval(35), low,medLOW, MED, medHIGH, HIGH, M1x, M1z, Y);
Insx=[1569,1818,1760,1729,1729,1679,1638];
Insz=[1115,1094, 924, 887, 940,1048,1086];
%receptorMap(specval(12), Insx, Insz, Y)%Ins
slicemap (specval(12), low,medLOW, MED, medHIGH, HIGH, Insx, Insz, Y);
LOx=[1569,1638,1679,1729,1729,1664,1647,1607,1532,1474,1444,1463,1514];
LOz=[1115,1086,1048, 940, 887, 887, 913, 938, 953,
941,1049,1136,1134];
%receptorMap(specval(31), LOx, LOz, Y)%LO
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz, Y);
MOx=[1295,1333,1358,1405,1449,1444,1295];
17
MOz=[ 803, 834, 922, 997,1038,1049,1031];
%receptorMap(specval(30), MOx, MOz, Y)%MO
slicemap (specval(MO), low,medLOW, MED, medHIGH, HIGH, MOx, MOz, Y);

```

```

l=16;
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
VOx=[1348,1418,1474,1449,1407,1358];
VOz=[ 848, 914, 941,1038,1000, 922];
%receptorMap(specval(29), VOx, VOz, Y)%VO
slicemap (specval(VO), low,medLOW, MED, medHIGH, HIGH, VOx, VOz, Y);
PrLx=[1295,1295,1444,1461];
PrLz=[1222,1031,1049,1137];
%receptorMap(specval(33), PrLx, PrLz, Y)%PrL
slicemap (specval(33), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz, Y);
TTx=[1295,1295,1368,1437,1440,1386,1368,1400,1348,1330];
TTz=[ 803, 700,700 , 632, 694, 697, 730, 809, 848, 835];
%receptorMap(specval(5), TTx, TTz, Y)%TT
slicemap (specval(5), low,medLOW, MED, medHIGH, HIGH, TTx, TTz, Y);
PirRx=[1669,1669,1437,1440,1488,1565,1572,1561,1577,1590,1579,1552,1506,1477,
1434,1430,1403,1348,1418,1474,1524,1532,1607,1647];
PirRz=[888 , 700, 632, 694, 702, 735, 756, 771, 774, 796, 840, 858,
861, 859, 841, 806, 808, 848, 914, 941, 953, 953, 938, 913];
%receptorMap(specval(8), PirRx, PirRz, Y)%PirR
slicemap (specval(8), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);
ENx=[1436,1517,1542,1534,1558,1577,1590,1579,1552,1506,1477,1434,1430];
ENz=[ 796, 814, 797, 783, 771, 774, 796, 840, 858, 861, 859, 841,
809];
%receptorMap(specval(66), ENx, ENz, Y)%EN
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
WMx=[1444,1517,1542,1507,1451,1428];
WMz=[ 799, 814, 797, 770, 765, 777];
%receptorMap(specval(174), WMx, WMz, Y)%WM
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
AOx=[1403,1368,1366,1488,1567,1572,1559,1534,1507,1451,1428,1444];
AOz=[ 808, 730, 697, 702, 737, 756, 770, 783, 770, 765, 777, 799];
%receptorMap(specval(6), AOx, AOz, Y)%AO
slicemap (specval(AO), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
end

```

slice17

```

if Slicenum == 17;
Y=17*3;
AOx=[1405,1442,1431,1441,1507,1545,1540,1570,1569,1532,1479,1437,1395,1377];
AOz=[ 778, 774, 755, 740, 741, 768, 760, 742, 714, 671, 648,
648,666 ,697 ];
%receptorMap(specval(6), AOx, AOz, Y)%AO
slicemap (specval(6), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
ILx=[1291,1381,1391,1426,1431,1278];
18
ILz=[790 , 827, 897, 987,1018,1013];
%receptorMap(specval(32), ILx, ILz, Y)%IL
slicemap (specval(32), low,medLOW, MED, medHIGH, HIGH, ILx, ILz, Y);
l=17;
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31

```

```

plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
VOx=[1487,1436,1426,1391,1383,1514,1635,1640,1518,1491,1480,1485];
VOz=[1042, 985, 987, 897, 829, 858, 844, 844, 924, 956, 993,1040];
%receptorMap(specval(29), VOx, VOz, Y)%VO
slicemap (specval(29), low,medLOW, MED, medHIGH, HIGH, VOx, VOz, Y);
LOx=[1487,1479,1491,1518,1640,1722,1760,1723,1628,1546];
LOz=[1042,1003, 956, 924, 844, 787, 826, 890,1000,1066];
%receptorMap(specval(31), LOx, LOz, Y)%LO
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz, Y);
M2x=[1331,1497,1511,1534];
M2z=[1365,1126,1132,1384];
%receptorMap(specval(36), M2x, M2z, Y)%M2
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z, Y);
PrLx=[1295,1295,1468,1435,1433];
PrLz=[1013,1229,1104,1048,1020];
%receptorMap(specval(33), PrLx, PrLz, Y)%PrL
slicemap (specval(PrL), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz,
Y);
TTx=[1295,1295,1459,1462,1437,1395,1377,1405,1361,1347];
TTz=[ 790, 650, 599, 644, 648, 666, 697, 778, 797, 815];
%receptorMap(specval(5), TTx, TTz, Y)%TT
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz, Y);
PirRx=[1446,1408,1361,1347,1495,1528,1635,1724,1600,1459,1479,1532,1569,1570,
1586,1596,1566,1516,1486,1440];
PirRz=[ 767, 776, 797, 815, 857, 859, 844, 784, 600, 599, 648, 671,
714, 742, 746, 797, 829, 834, 832, 811];
%receptorMap(specval(8), PirRx, PirRz, Y)%PirR
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);
WMx=[1555,1513,1468,1433,1545];
WMz=[1114,1134,1104,1041,1097];
%receptorMap(specval(174), WMx, WMz, Y)%WM
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WM2x=[1445,1521,1545,1507,1441,1431];
WM2z=[ 768,786 , 768, 741, 740, 755];
%receptorMap(specval(174), WM2x, WM2z, Y)%WM
slicemap (specval(174), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z,
Y);
M1x=[1534,1511,1552,1553,1855];
M1z=[1384,1132,1123,1118,1114];
%receptorMap(specval(35), M1x, M1z, Y)%M1
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z, Y);
Cgx=[1331,1331,1497,1485,1295];
Cgz=[1295,1365,1126,1118,1229];
%receptorMap(specval(9), Cgx, Cgz, Y)%Cg
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz, Y);
19
Insx=[1855,1760,1723,1628,1546,1566,1553];
Insz=[1114, 826, 890,1000,1066,1091,1118];
%receptorMap(specval(12), Insx, Insz, Y)%Ins
slicemap (specval(12), low,medLOW, MED, medHIGH, HIGH, Insx, Insz, Y);
Clx=[1553,1545,1430,1431,1422,1426,1449,1483,1546,1566];
Clz=[1118,1097,1040,1018,1003, 987, 999,1039,1066,1091];
%receptorMap(specval(68), Clx, Clz, Y)%Cl
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
ENx=[1443,1440,1486,1566,1596,1586,1558,1545,1521,1505,1446];

```



```

ENz=[ 768, 811, 832, 829, 797, 746, 742, 768, 786, 785, 767];
%receptorMap(specval(66), ENx, ENz, Y)%EN
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
end

```

slice18

```

if Slicenum == 18;
Y=3*18;
M2x=[1330,1503,1511,1505,1409];
M2z=[1382,1103,1107,1398,1411];
%receptorMap(specval(36), M2x, M2z, Y)%M2
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z, Y);
M1x=[1511,1505,1712,1784,1841,1552];
M1z=[1107,1398,1328,1281,1223,1089];
%receptorMap(specval(35), M1x, M1z, Y)%M1
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z, Y);
S1Jx=[1546,1879,1897,1891,1843,1552];
S1Jz=[1074, 898,1002,1115,1219,1089];
%receptorMap(specval(24), S1Jx, S1Jz, Y)%S1j
slicemap (specval(S1J), low,medLOW, MED, medHIGH, HIGH, S1Jx, S1Jz,
Y);
%QCcolor (S1Jx,S1Jz,18*3)
l=18;
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
Insx=[1578,1584,1879,1876,1798,1729,1633];
Insz=[1040,1059, 898, 882, 738, 884,1003];
%receptorMap(specval(12), Insx, Insz, Y)%Ins
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);
LOx=[1520,1526,1549,1638,1682,1737,1759,1798,1729,1633,1578];
LOz=[1012, 954, 911, 810, 772, 738, 683, 738, 884,1003,1040];
%receptorMap(specval(31), LOx, LOz, Y)%LO
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz, Y);
VOx=[1434,1419,1436,1538,1615,1682,1638,1549,1526,1520,1506,1461];
VOz=[ 936, 860, 800, 811, 805, 772, 810,911 , 954,1012,1000, 943];
%receptorMap(specval(29), VOx, VOz, Y)%VO
slicemap (specval(VO), low,medLOW, MED, medHIGH, HIGH, VOx, VOz, Y);
ILx=[1295,1424,1434,1419,1436,1356,1295];
20
ILz=[ 946, 957, 936, 860, 800, 783, 763];
%receptorMap(specval(32), ILx, ILz, Y)%IL
slicemap (specval(IL), low,medLOW, MED, medHIGH, HIGH, ILx, ILz, Y);
PrLx=[1295,1295,1424,1453,1488];
PrLz=[1218, 946, 957,1062,1096];
%receptorMap(specval(33), PrLx, PrLz, Y)%PrL
slicemap (specval(PrL), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz,
Y);
Cgx=[1295,1328,1503,1488,1295];
Cgz=[1328,1383,1103,1096,1218];
%receptorMap(specval(9), Cgx, Cgz, Y)%Cg
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz, Y);
TTx=[1295,1289,1330,1371,1398,1369,1370,1411,1346];
TTz=[ 763, 712, 621, 589, 642, 688, 715, 731, 782];

```

```

%receptorMap(specval(5), TTx, TTz, Y)%TT
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz, Y);
AOx=[1369,1405,1447,1510,1542,1554,1532,1485,1438,1391,1370];
AOz=[ 688, 645, 629, 637, 659, 708, 714, 702, 720, 726, 715];
%receptorMap(specval(6), AOx, AOz, Y)%AO
slicemap (specval(AO), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
Tux=[1371,1434,1538,1510,1447,1399];
Tuz=[ 589, 558, 570, 639, 629, 638];
%receptorMap(specval(58), Tux, Tuz, Y)%Tu
slicemap (specval(Tu), low,medLOW, MED, medHIGH, HIGH, Tux, Tuz, Y);
PirRx=[1346,1473,1538,1605,1689,1737,1759,1684,1543,1510,1542,1554,1589,1589,
1560,1429,1390,1385];
PirRz=[ 782, 807, 811, 805, 772, 738, 683, 630, 574, 639, 659, 708,
712,755 , 781, 785, 774, 750];
%receptorMap(specval(8), PirRx, PirRz, Y)%PirR
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);
AcbSHx=[1438,1450,1492,1459,1429,1390,1385,1406];
AcbSHz=[ 720, 735, 747, 784, 785, 774, 750, 733];
%receptorMap(specval(60), AcbSHx, AcbSHz, Y)%AcbSh
slicemap (specval(AcbSH), low,medLOW, MED, medHIGH, HIGH, AcbSHx,
AcbSHz, Y);
ENx=[1492,1522,1551,1532,1589,1589,1560,1493,1459];
ENz=[ 747, 751, 738, 714, 712, 755, 781, 787, 784];
%receptorMap(specval(66), ENx, ENz, Y)%EN
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
WMx=[1492,1522,1551,1532,1485,1438,1450,1506];
WMz=[ 747, 751, 738, 714, 702, 720, 735, 750];
%receptorMap(specval(174), WMx, WMz, Y)%WM
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WM2x=[1431,1487,1549,1551,1522,1513,1453,1436];
WM2z=[ 978,1037,1076,1090,1107,1108,1062,1005];
%receptorMap(specval(174), WM2x, WM2z, Y)%WM
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);
WM3x=[1339,1318,1345,1390,1375];
WM3z=[ 578, 544, 523, 545, 573];
%receptorMap(specval(174), WM3x, WM3z, Y)%WM
slicemap (specval(174), low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z,
Y);
Clx=[1436,1487,1544,1582,1576,1515,1461,1426,1431];
Clz=[1005,1037,1074,1055,1041,1009, 943, 944, 978];
21
%receptorMap(specval(68), Clx, Clz, Y)%Cl
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
end

```

slice19

```

if Slicenum == 19;
Y=57;
l=19
AOx=[1420,1395,1369,1368,1394,1450,1506,1529,1556,1551,1486,1440,1444];
AOz=[ 714, 716, 698, 675, 637, 613, 620, 636, 670, 699, 680, 691,
706];
%receptorMap(specval(6), AOx, AOz, Y)%AO
slicemap (specval(AO), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
ILx=[1295,1429,1436,1295];
ILz=[ 917, 925, 783, 757];
%receptorMap(specval(32), ILx, ILz, Y)%IL

```

```

slicemap (specval(IL), low,medLOW, MED, medHIGH, HIGH, ILx, ILz, Y);
VOx=[1426,1424,1431,1459,1490,1531,1534,1557,1700,1577];
VOz=[ 783, 838, 891, 891, 963, 998, 951, 906, 758, 790];
%receptorMap(specval(29), VOx, VOz, Y)%VO
slicemap (specval(VO), low,medLOW, MED, medHIGH, HIGH, VOx, VOz, Y);
LOx=[1700,1805,1732,1668,1580,1571,1532,1534,1557];
LOz=[ 758, 690, 859, 949,1021,1011, 997, 951, 906];
%receptorMap(specval(31), LOx, LOz, Y)%LO
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz, Y);
M2x=[1484,1511,1504,1331];
M2z=[1115,1123,1398,1383];
%receptorMap(specval(36), M2x, M2z, Y)%M2
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z, Y);
PrLx=[1295,1469,1432,1429,1295,];
PrLz=[1195,1086,1003, 925, 917];
%receptorMap(specval(33), PrLx, PrLz, Y)%PrL
slicemap (specval(PrL), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz,
Y);
TTx=[1295,1378,1411,1372,1368,1394,1360,1295];
TTz=[757, 774, 718, 697, 675, 637, 588, 530];
%receptorMap(specval(5), TTx, TTz, Y)%TT
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz, Y);
PirRx=[1393,1439,1520,1568,1601,1595,1551,1556,1529,1571,1762,1692,1577,1426,
1378];
PirRz=[ 748, 768, 771, 765, 734, 691, 699,670 , 636, 539, 716, 759,
790, 783, 774];
%receptorMap(specval(8), PirRx, PirRz, Y)%PirR
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);
WMx=[1436,1432,1481,1513,1560,1566,1541,1493,1455, 1438];
WMz=[ 963,1003,1114,1125,1100,1067,1053,1037,1003, 955];
%receptorMap(specval(174), WMx, WMz, Y)%WM
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WM2x=[1440,1486,1539,1552,1524,1452];
WM2z=[ 691, 680, 696, 719, 729, 713];
%receptorMap(specval(174), WM2x, WM2z, Y)%WM
22
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);
WM3x=[1330,1374,1394,1372,1338,1311];
WM3z=[572 , 562, 524, 505, 506, 542];
%receptorMap(specval(174), WM3x, WM3z, Y)%WM
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);
M1x=[1504,1849,1559,1511];
M1z=[1398,1232,1098,1123];
%receptorMap(specval(35), M1x, M1z, Y)%M1
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z, Y);
Cgx=[1295,1331,1484,1469,1295];
Cgz=[1283,1383,1115,1086,1195];
%receptorMap(specval(9), Cgx, Cgz, Y)%Cg
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz, Y);
Insx=[1582,1934,1805,1732,1668,1608,1580];
Insz=[1034, 884, 690, 859, 949,1002,1021];
%receptorMap(specval(12), Insx, Insz, Y)%Ins
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);
ENx=[1462,1520,1568,1601,1595,1547,1552,1508,1496];
ENz=[ 766, 771, 765, 734, 691, 703, 719, 728, 725];
%receptorMap(specval(66), ENx, ENz, Y)%EN

```

```

slicemap (specval(66), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
Clx=[1459,1430,1436,1455,1493,1536,1582,1571,1535,1490];
Clz=[ 891, 892, 963,1003,1037,1053,1034,1011,1000, 963];
%receptorMap(specval(68), Clx, Clz, Y)%Cl
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
Tux=[1360,1571,1529,1506,1450,1394];
Tuz=[ 588, 539, 636, 620, 613, 637];
%receptorMap(specval(58), Tux, Tuz, Y)%Tu
slicemap (specval(Tu), low,medLOW, MED, medHIGH, HIGH, Tux, Tuz, Y);
S1Jx=[1849,1559,1566,1541,1934];
S1Jz=[1232,1098,1067,1053, 884];
%receptorMap(specval(24), S1Jx, S1Jz, Y)%S1j
slicemap (specval(S1J), low,medLOW, MED, medHIGH, HIGH, S1Jx, S1Jz,
Y);
AcbShx=[1393,1420,1444,1508,1462,1431];
AcbShz=[ 748, 714, 706, 728, 766, 768];
%receptorMap(specval(60), AcbShx, AcbShz, Y)%AcbSh
slicemap (specval(60), low,medLOW, MED, medHIGH, HIGH, AcbShx, AcbShz,
Y);
l=19;
%l = 1; %enter whatever slice you want
hold all
for t =1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice20

```

if Slicenum == 20;
23
Y=60;
l=20
AOx=[1361,1385,1427,1470,1469,1439,1385,1356];
AOz=[ 728, 740, 698, 619, 612, 607, 637, 680];
%receptorMap(specval(6), AOx, AOz, Y)%AO
slicemap (specval(6), low,medLOW, MED, medHIGH, HIGH, AOx, AOz, Y);
AcbCx=[1480,1472,1534,1559,1533];
AcbCz=[ 765, 693, 711, 709, 740];
%receptorMap(specval(59), AcbCx, AcbCz, Y)%AcbC
slicemap (specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz,
Y);
Cgx=[1295,1326,1484,1482,1295];
Cgz=[1345,1394,1114,1085,1192];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz, Y);
%receptorMap(specval(9), Cgx, Cgz, Y)%Cg
ILx=[1295,1434,1435,1425,1440,1387,1364,1295];
ILz=[ 917, 925, 901, 853, 781, 742, 735, 725];
%receptorMap(specval(32), ILx, ILz, Y)%IL
slicemap (specval(IL), low,medLOW, MED, medHIGH, HIGH, ILx, ILz, Y);
Insx=[1638,1956,1915,1828,1758,1736,1690,1620];
Insz=[1000, 871, 746, 639, 700, 794, 896, 982];
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);
%receptorMap(specval(12), Insx, Insz, Y)%Ins
VOx=[1435,1425,1452,1481,1616,1676,1547,1515,1503,1480,1455,1447];
VOz=[ 901, 853, 790, 793, 737, 723, 865, 929, 882, 862, 876, 912];
%receptorMap(specval(29), VOx, VOz, Y)%VO

```

```

slicemap (specval(VO), low,medLOW, MED, medHIGH, HIGH, VOx, VOz, Y);
LOx=[1515,1547,1679,1758,1736,1690,1620,1579,1541];
LOz=[ 929, 865, 723, 700, 794, 896, 982, 980, 964];
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz, Y);
%receptorMap(specval(31), LOx, LOz, Y)%LO
ENx=[1571,1552,1488,1470,1545,1637,1626,1612,1481,1452,1476,1533];
ENZ=[ 692, 674, 659, 619, 589, 614, 693, 737, 793, 790, 760, 740];
%receptorMap(specval(66), ENx, ENz, Y)%EN
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
Clx=[1515,1541,1586,1620,1638,1625,1544,1496,1448,1455,1480,1503];
Clz=[ 929, 964, 982, 982,1000,1020,1028,1000, 914, 876, 862, 882];
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
%receptorMap(specval(68), Clx, Clz, Y)%Cl
M2x=[1326,1484,1513,1505,1385];
M2z=[1394,1114,1134,1398,1411];
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
Tux=[1470,1439,1406,1373,1412,1482,1524,1618,1587,1509,1465,1443];
Tuz=[629 , 607, 618, 561, 504, 470, 474, 511, 552, 531, 537, 568];
%receptorMap(specval(58), Tux, Tuz, Y)%Tu
slicemap (specval(Tu), low,medLOW, MED, medHIGH, HIGH, Tux, Tuz, Y);
PrLx=[1295,1482,1443,1434,1288];
PrLz=[1192,1085, 995, 925, 917];
%receptorMap(specval(33), PrLx, PrLz, Y)%PrL
slicemap (specval(PrL), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz,
Y);
24
AcbShx=[1470,1484,1486,1458,1474,1476,1457,1385,1427,1467];
AcbShz=[ 619, 650, 663, 673, 694, 760, 792, 740, 698, 626];
slicemap (specval(AcbSh), low,medLOW, MED, medHIGH, HIGH, AcbShx,
AcbShz, Y);
%receptorMap(specval(60), AcbShx, AcbShz, Y)%AcbSh
TTx=[1295,1295,1361,1356,1385,1407,1369,];
TTz=[ 650,728 , 728, 680, 637, 620, 549,];
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz, Y);
%receptorMap(specval(5), TTx, TTz, Y)%TT
S1Jx=[1582,1736,1798,1864,1922,1952,1963,1956,1638,1625,1600,1623,1620];
S1Jz=[1091,1204,1285,1232,1151,1078, 993,
871,1000,1020,1029,1041,1067];
slicemap (specval(S1J), low,medLOW, MED, medHIGH, HIGH, S1Jx, S1Jz,
Y);
%receptorMap(specval(24), S1Jx, S1Jz, Y)%S1j
PirRx=[1616,1758,1825,1607,1589,1623,1637,1636,1614];
PirRz=[ 737, 700, 637, 508, 554, 580, 614, 693, 737];
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);
%receptorMap(specval(8), PirRx, PirRz, Y)%PirR
VPx=[1469,1443,1465,1509,1587,1623,1637,1629,1545];
VPz=[ 609, 568, 537, 531, 552, 580, 614, 615, 589];
slicemap (specval(VP), low,medLOW, MED, medHIGH, HIGH, VPx, VPz, Y);
%receptorMap(specval(62), VPx, VPz, Y)%VP
WMx=[1435,1493,1544,1598,1623,1620,1513,1485,1482,1449];
WMz=[ 901, 997,1028,1027,1041,1067,1134,1113,1083,1003];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap(specval(174), WMx, WMz, Y)%WM
WM2x=[1458,1487,1552,1571,1559,1534,1474];
WM2z=[ 673, 665, 674, 692, 709, 711, 693];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);

```

```

%receptorMap(specval(174), WM2x, WM2z, Y)%WM
WM3x=[1339,1370,1385,1367,1342,1311,1316];
WM3z=[ 559, 551, 521, 497, 493, 521, 544];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z, Y);
%receptorMap(specval(174), WM3x, WM3z, Y)%WM
M1x=[1509,1511,1582,1736,1798,1677];
M1z=[1397,1134,1091,1204,1285,1349];
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z, Y);
%receptorMap(specval(35), M1x, M1z, Y)%M1
%l = 1; %enter whatever slice you want
%%Slicefeed(1);
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
%BREAKBREAKBREAKBREAKBREAKBREAK
end

```

slice21

```

if Slicenum == 21;
25
Y=21*3;
Cgx=[1295,1471,1463,1295];
Cgz=[1356,1149,1095,1113];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz,
Y);%receptorMap(specval(), x, z, Y)
PrLx=[1295,1295,1419,1431,1461,];
PrLz=[1113, 884, 892,1003,1093];
slicemap (specval(PrL), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz,
Y);%receptorMap(specval(33), PrLx, PrLz, Y)%PrL
ILx=[1295,1295,1396,1440,1413,1419];
ILz=[884 , 725, 741, 781, 824, 892];
slicemap (specval(IL), low,medLOW, MED, medHIGH, HIGH, ILx, ILz,
Y);%receptorMap(specval(), x, z, Y)
VOx=[1419,1413,1430,1463,1558,1497,1481,1443];
VOz=[ 863, 824, 774, 793, 756, 819, 869, 847];
slicemap (specval(VO), low,medLOW, MED, medHIGH, HIGH, VOx, VOz,
Y);%receptorMap(specval(29), VOx, VOz, Y)%VO
LOx=[1481,1497,1558,1635,1750,1590,1539,1516];
LOz=[ 869, 819, 756, 716, 673, 829, 899, 950];
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz,
Y);%receptorMap(specval(31), LOx, LOz, Y)%LO
S1Jx=[1642,1986,1985,1961,1905,1835,1734,1694,1581,1645,1655,1633];
S1Jz=[1016, 910,1000,1097,1196,1265,1323,1232,1113,1088,1057,1054];
slicemap (specval(S1J), low,medLOW, MED, medHIGH, HIGH, S1Jx, S1Jz,
Y);%receptorMap(specval(24), S1Jx, S1Jz, Y)%S1j
M1x=[1480,1622,1730,1694,1581,1504,1494];
M1z=[1404,1368,1325,1232,1113,1164,1164];
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z,
Y);%receptorMap(specval(), x, z, Y)
M2x=[1494,1471,1295,1307,1359,1478];
M2z=[1164,1149,1356,1375,1410,1401];
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z,
Y);%receptorMap(specval(36), M2x, M2z, Y)%M2
WMx=[1494,1592,1645,1655,1627,1584,1545,1489,1452,1426,1425,1465,1473];
WMz=[1164,1103,1088,1057,1051,1058,1049,1000, 945, 872,
994,1096,1149];

```

```

slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap(specval(), x, z, Y)
WM2x=[1545,1491,1496,1569,1569];
WM2z=[ 711, 686, 666, 687, 703];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z,
Y);%receptorMap(specval(), x, z, Y)
WM3x=[1368,1383,1361,1336,1306,1304];
WM3z=[ 479, 503, 536, 542, 532, 498];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z,
Y);%receptorMap(specval(), x, z, Y)
Clx=[1426,1443,1467,1516,1557,1629,1629,1584,1545,1491,1452];
Clz=[ 872, 847, 852, 950, 980, 998,1055,1058,1049, 999, 945];
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz,
Y);%receptorMap(specval(68), Clx, Clz, Y)%Cl
Insx=[1516,1539,1590,1760,1846,1887,1955,1986,1642,1626,1557];
Insz=[ 950, 899, 829, 672, 621, 660, 781, 912,1016, 998, 980];
26
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);%receptorMap(specval(Ins), Insx, Insz, Y)
TTx=[1297,1382,1385,1388,1312,1311];
TTz=[ 725, 739, 630, 611, 612, 687];
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz,
Y);%receptorMap(specval(5), TTx, TTz, Y)%TT
Tux=[1388,1409,1441,1486,1543,1596,1622,1572,1525,1457,1406,1384,1336,1311];
Tuz=[ 611, 574, 536, 515, 512, 533, 467, 443, 438, 452, 478, 522, 562,
601];
slicemap (specval(Tu), low,medLOW, MED, medHIGH, HIGH, Tux, Tuz,
Y);%receptorMap(specval(58), Tux, Tuz, Y)%Tu
AcbCx=[1440,1495,1522,1491,1492,1459,1429,1431];
AcbCz=[ 781, 749, 705, 686, 671, 665, 683, 773];
slicemap (specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz,
Y);%receptorMap(specval(), x, z, Y)
AcbShx=[1431,1429,1459,1492,1524,1500,1406,1385,1382,1396,];
AcbShz=[ 773, 683, 665, 671, 664, 583, 578, 630, 739, 741,];
slicemap (specval(AcbSh), low,medLOW, MED, medHIGH, HIGH, AcbShx,
AcbShz, Y);%receptorMap(specval(60), AcbShx, AcbShz, Y)%AcbSh
ENx=[1440,1479,1631,1642,1628,1500,1524,1569,1569,1545,1523,1495];
ENZ=[ 781, 791, 718, 626, 577, 583, 664, 687, 703, 711, 700, 749];
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz,
Y);%receptorMap(specval(66), ENx, ENz, Y)%EN
VPx=[1409,1500,1628,1601,1543,1486,1441,1409];
VPz=[ 574, 583, 570, 534, 512, 515, 536, 574];
slicemap (specval(VP), low,medLOW, MED, medHIGH, HIGH, VPx, VPz,
Y);%receptorMap(specval(62), VPx, VPz, Y)%VP
PirRx=[1622,1800,1846,1760,1635,1642,1628,1601];
PirRz=[ 467, 580, 621, 672, 716, 626, 577, 534];
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);%receptorMap(specval(8), PirRx, PirRz, Y)%PirR
%QCcolor (Insx,Insz,21*3)
l=21;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice22

```
if Slicenum == 22;
Y=22*3;
Cgx=[1295,1474,1447,1295 ];
Cgz=[1346,1146,1096,1113 ];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz,
Y);%receptorMap(specval(), x, z, Y)
PrLx=[1295,1447,1381,1386,1295];
PrLz=[1113,1096, 993, 895, 884];
27
slicemap (specval(PrL), low,medLOW, MED, medHIGH, HIGH, PrLx, PrLz,
Y);%receptorMap(specval(), x, z, Y)
ILx=[1295,1386,1383,1370,1333,1295];
ILz=[ 884, 895, 811, 751, 758, 737];
slicemap (specval(IL), low,medLOW, MED, medHIGH, HIGH, ILx, ILz,
Y);%receptorMap(specval(), x, z, Y)
TTx=[1295,1333,1370,1366,1391,1316];
TTz=[ 737, 758, 751, 677, 613, 612];
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz,
Y);%receptorMap(specval(), x, z, Y)
Tux=[1316,1390,1451,1511,1570,1621,1652,1512,1458,1410,1371,1320];
Tuz=[ 612, 608, 531, 500, 491, 519, 449, 418, 432, 461, 533, 588];
slicemap (specval(Tu), low,medLOW, MED, medHIGH, HIGH, Tux, Tuz,
Y);%receptorMap(specval(), x, z, Y)
PirRx=[1652,1720,1831,1881,1837,1784,1675,1664,1621];
PirRz=[ 440, 496, 537, 586, 630, 649, 657, 591, 519];
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);%receptorMap(specval(), x, z, Y)
LOx=[1675,1778,1711,1625,1630];
LOz=[ 657, 647, 719, 774, 733];
slicemap (specval(LO), low,medLOW, MED, medHIGH, HIGH, LOx, LOz,
Y);%receptorMap(specval(), x, z, Y)
Insx=[1778,1837,1881,1969,2003,1883,1739,1648,1625,1711];
Insz=[ 647, 630, 586, 725, 879, 919, 930, 838, 774, 719];
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);%receptorMap(specval(), x, z, Y)
S1Jx=[1739,1731,1723,1912,2000,2007,1883];
S1Jz=[ 930,1000,1051,1160,1003, 884, 919];
slicemap (specval(S1J), low,medLOW, MED, medHIGH, HIGH, S1Jx, S1Jz,
Y);%receptorMap(specval(), x, z, Y)
S1FLx=[1723,1909,1841,1788,1664];
S1FLz=[1051,1162,1272,1304,1108];
slicemap (specval(S1FL), low,medLOW, MED, medHIGH, HIGH, S1FLx, S1FLz,
Y);%receptorMap(specval(), x, z, Y)
M1x=[1664,1788,1717,1485,1501,1518,1581,1658];
M1z=[1108,1304,1339,1403,1184,1190,1145,1113];
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z,
Y);%receptorMap(specval(), x, z, Y)
M2x=[1501,1483,1391,1319,1295,1474];
M2z=[1184,1402,1412,1397,1346,1146];
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z,
Y);%receptorMap(specval(36), M2x, M2z, Y)%M2
WMx=[1474,1447,1379,1385,1445,1507,1583,1650,1689,1700,1674,1719,1723,1660,15
81,1518];
WMz=[1146,1092,1000,899 ,1000,1057,1082,1070,1032, 985, 934,
967,1051,1112,1145,1190];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz,
```



```

Y);%receptorMap(specval(), x, z, Y)
WM2x=[1545,1556,1559,1545,1520,1500,1509];
WM2z=[ 707, 677, 658, 650, 670, 703, 723];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z,
Y);%receptorMap(specval(), x, z, Y)
WM3x=[1335,1307,1304,1317,1361,1373];
WM3z=[ 540, 523, 496, 483, 478, 511];
28
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z,
Y);%receptorMap(specval(), x, z, Y)
DMSx=[1388,1442,1507,1583,1607,1577,1527,1512,1520,1383];
DMSz=[ 897, 997,1057,1082,1078,1003, 899, 820, 797, 811];
slicemap (specval(DMS), low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz,
Y);%receptorMap(specval(), x, z, Y)
DLSx=[1607,1577,1527,1512,1511,1552,1629,1644,1624,1666,1700,1689,1650];
DLSz=[1078,1003, 899, 820, 799, 787, 797, 831, 847, 891,
985,1032,1070];
slicemap (specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz,
Y);%receptorMap(specval(), x, z, Y)
Clx=[1666,1719,1733,1749,1739,1648,1624,1634,1646];
Clz=[ 933, 967, 999, 965, 930, 838, 847, 891, 906];
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz,
Y);%receptorMap(specval(), x, z, Y)
AcbCx=[1383,1371,1423,1518,1500,1509,1545,1557,1580,1591,1578,1552,1510];
AcbCz=[ 811, 755, 690, 668, 703, 723, 707, 679, 698, 727, 764, 787,
801];
slicemap (specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz,
Y);%receptorMap(specval(), x, z, Y)
AcbShx=[1371,1423,1518,1545,1572,1636,1586,1517,1450,1391,1366];
AcbShz=[ 754, 690, 672, 650, 611, 575, 561, 564, 579, 613, 677];
slicemap (specval(AcbSh), low,medLOW, MED, medHIGH, HIGH, AcbShx,
AcbShz, Y);%receptorMap(specval(), x, z, Y)
ENx=[1545,1572,1636,1664,1674,1630,1625,1564,1578,1591,1580,1556,1559];
ENz=[650 ,611 , 575, 591, 658, 733, 794, 783, 764, 727, 698,
677,658 ];
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz,
Y);%receptorMap(specval(), x, z, Y)
VPx=[1390,1451,1511,1570,1621,1664,1586,1517,1450];
VPz=[ 608, 531, 500, 491, 519, 585, 561, 564, 579];
slicemap (specval(VP), low,medLOW, MED, medHIGH, HIGH, VPx, VPz,
Y);%receptorMap(specval(), x, z, Y)
S1FLx=[1660,1723,1912,1841,1788];
S1FLz=[1112,1051,1160,1272,1304];
slicemap (specval(S1FL), low,medLOW, MED, medHIGH, HIGH, S1FLx, S1FLz,
Y);%receptorMap(specval(), x, z, Y)
%QCcolor (S1FLx,S1FLz,3*22)
l=22;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 23

```
if Slicenum == 23;
```

```

Y=23*3;
29
Cgx=[1295,1307,1341,1472,1456,1416,1366,1295];
Cgz=[1343,1381,1405,1178,1124,1082,1054,1035];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz,
Y);%receptorMap(specval(Cg), Cgx, Cgz, Y)
WMx=[1472,1456,1416,1366,1295,1295,1422,1447,1546,1597,1683,1725,1753,1731,17
61,1778,1760,1724,1504];
WMz=[1178,1124,1082,1054,1035, 935,1000,1043,1095,1096,1065,1024, 937,
868, 892, 983,1041,1080,1191];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz,
Y);%receptorMap(specval(WM), WMx, WMz, Y)
WM2x=[1498,1531,1551,1552,1533,1492];
WM2z=[ 723, 713, 683, 659, 653, 695];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z,
Y);%receptorMap(specval(WM), WM2x, WM2z, Y)
WM3x=[1336,1371,1357,1317,1305];
WM3z=[ 526, 498, 463, 470, 511];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z,
Y);%receptorMap(specval(WM), WM3x, WM3z, Y)
Vx=[1383,1394,1437,1404];
Vz=[ 958, 967, 826, 881];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz,
Y);%receptorMap(specval(V), Vx, Vz, Y)
LSx=[1295,1302,1371,1437,1383,1295,];
LSz=[ 707, 675, 699, 824, 958, 936];
slicemap (specval(LS), low,medLOW, MED, medHIGH, HIGH, LSx, LSz,
Y);%receptorMap(specval(LS), LSx, LSz, Y)
TTx=[1302,1321,1398,1376,1375];
TTz=[ 675, 586, 590, 643, 699];
slicemap (specval(TT), low,medLOW, MED, medHIGH, HIGH, TTx, TTz,
Y);%receptorMap(specval(TT), TTx, TTz, Y)
Tux=[1323,1393,1449,1594,1704,1651,1619,1530,1469,1420,1398];
Tuz=[ 588, 470, 424, 402, 437, 513, 480, 461, 483, 540, 590];
slicemap (specval(Tu), low,medLOW, MED, medHIGH, HIGH, Tux, Tuz, Y);
%receptorMap(specval(58), Tux, Tuz, Y)%Tu
l=23;
PirRx=[1651,1704,1748,1793,1846,1915,1842,1704,1664,1663];
PirRz=[ 513, 437, 488, 493, 519, 598, 644, 654, 590, 540];
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);%receptorMap(specval(PirR), PirRx, PirRz, Y)
Insx=[1704,1710,1790,1793,2025,2000,1921,1842];
Insz=[ 654, 771, 879, 908, 890, 743, 601, 644];
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);%receptorMap(specval(Ins), Insx, Insz, Y)
S1ULx=[1793,1779,1778,1995,2026];
S1ULz=[ 908, 943, 987,1067, 894];
slicemap (specval(S1UL), low,medLOW, MED, medHIGH, HIGH, S1ULx, S1ULz,
Y);%receptorMap(specval(S1UL), S1ULx, S1ULz, Y)
S1Jx=[1778,1995,1913,1741,1760];
S1Jz=[ 987,1067,1202,1063,1041];
slicemap (specval(S1J), low,medLOW, MED, medHIGH, HIGH, S1Jx, S1Jz,
Y);%receptorMap(specval(S1J), S1Jx, S1Jz, Y)
S1FLx=[1741,1913,1788,1674,1724];
S1FLz=[1063,1202,1311,1104,1080];
slicemap (specval(S1FL), low,medLOW, MED, medHIGH, HIGH, S1FLx, S1FLz,
Y);%receptorMap(specval(S1FL), S1FLx, S1FLz, Y)
30

```

```

M1x=[1674,1788,1637,1496,1509];
M1z=[1104,1311,1367,1398,1188];
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z,
Y);%receptorMap(specval(M1), M1x, M1z, Y)
M2x=[1472,1341,1391,1457,1496,1509];
M2z=[1178,1405,1412,1409,1398,1188];
slicemap (specval(M2), low,medLOW, MED, medHIGH, HIGH, M2x, M2z,
Y);%receptorMap(specval(36), M2x, M2z, Y)%M2
DMSx=[1419,1420,1447,1546,1597,1636,1566];
DMSz=[ 949, 997,1043,1095,1096,1082, 924];
slicemap (specval(DMS), low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz,
Y);%receptorMap(specval(DMS), DMSx, DMSz, Y)
DLSx=[1636,1566,1728,1753,1725,1683];
DLSz=[1082, 924, 863, 937,1024,1065];
slicemap (specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz,
Y);%receptorMap(specval(DLS), DLSx, DLSz, Y)
VMSx=[1411,1566,1535,1437,1437];
VMSz=[ 944, 924, 783, 824,826];
slicemap (specval(VMS), low,medLOW, MED, medHIGH, HIGH, VMSx, VMSz,
Y);%receptorMap(specval(VMS), VMSx, VMSz, Y)
VLSx=[1535,1566,1728,1616,1602];
VLSz=[ 783, 926, 863, 696, 740];
slicemap (specval(VLS), low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz,
Y);%receptorMap(specval(VLS), VLSx, VLSz, Y)
Clx=[1779,1790,1705,1677,1683,1731,1761];
Clz=[943 , 879, 745, 768, 820, 868, 892];
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz,
Y);%receptorMap(specval(Cl), Clx, Clz, Y)
ENx=[1677,1705,1704,1666,1629,1605,1616,1651];
ENZ=[ 766, 745, 654, 592, 593, 621, 696, 748];
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz,
Y);%receptorMap(specval(EN), ENx, ENz, Y)
AcbCx=[1396,1427,1481,1547,1602,1629,1664,1662,1519,1420,1376];
AcbCz=[ 730, 673, 629, 611, 620, 593, 590, 541, 521, 544, 643];
slicemap (specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz,
Y);%receptorMap(specval(AcbC), AcbCx, AcbCz, Y)
VPx=[1420,1519,1662,1619,1530,1469];
VPz=[ 544, 521, 541, 480, 461, 483];
slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, VPx, VPz,
Y);%receptorMap(specval(VP), VPx, VPz, Y)
%%Slicefeed(1);
%l = ; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice24

```

if Slicenum == 24;
Y=24*3;
31
Cgx=[1295,1336,1473,1455,1364,1295];
Cgz=[1370,1402,1187,1130,1061,1042];slicemap (specval(Cg), low,medLOW,
MED, medHIGH, HIGH, Cgx, Cgz, Y);
WMx=[1473,1455,1364,1295,1295,1342,1379,1465,1552,1660,1786,1821,1799,1734,15
18];

```

```

WMz=[1187,1130,1061,1042, 942, 950, 980,1075,1105,1086, 836,
923,1007,1086,1192];slicemap (specval(WM), low,medLOW, MED, medHIGH,
HIGH, WMx, WMz, Y);
WM2x=[1502,1538,1546,1497,1482,1488];
WM2z=[733 , 704, 673, 686, 711, 731];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);
WM3x=[1342,1380,1374,1317,1307];
WM3z=[ 512, 480, 448, 457,491];slicemap (specval(WM), low,medLOW, MED,
medHIGH, HIGH, WM3x, WM3z, Y);
Vx=[1409,1381,1405,1436];
Vz=[1003, 982, 884, 829];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
LSx=[1381,1405,1436,1428,1376,1333,1295,1295];
LSz=[ 982, 884, 829,775 , 627, 604, 602, 942];slicemap (specval(LS),
low,medLOW, MED, medHIGH, HIGH, LSx, LSz, Y);
Tux=[1300,1330,1356,1383,1387,1462,1562,1657,1705,1737,1686,1589,1530,1465,14
11,1379,1333];
Tuz=[600 , 578, 536, 525, 478, 408, 389, 389, 414, 469, 545, 468,
461,486 , 556, 631, 604];slicemap (specval(Tu), low,medLOW, MED,
medHIGH, HIGH, Tux, Tuz, Y);
%receptorMap(specval(58), Tux, Tuz, Y)%Tu
l=24;
PirRx=[1686,1769,1788,1866,1914,1828,1737];
PirRz=[ 545, 660, 636, 617, 583,492 , 469];slicemap (specval(PirR),
low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz, Y);
Insx=[1769,1788,1866,1914,2018,2034,2035,1822,1836,1762,1769];
Insz=[ 660, 636, 617, 583, 740, 801, 891, 927, 856, 743, 660];slicemap
(specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz, Y);
S1Jx=[1809,1990,1963,1909,1733];
S1Jz=[1005,1089,1156,1228,1083];slicemap (specval(S1J), low,medLOW,
MED, medHIGH, HIGH, S1Jx, S1Jz, Y);
S1FLx=[1637,1754,1909,1733];
S1FLz=[1129,1339,1228,1083];slicemap (specval(S1FL), low,medLOW, MED,
medHIGH, HIGH, S1FLx, S1FLz, Y);
M1x=[1637,1754,1503,1516];
M1z=[1129,1339,1399,1190];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
M2x=[1503, 1516,1486,1476,1226,1374];
M2z=[1399, 1190,1198,1187,1402,1411];slicemap (specval(M2),
low,medLOW, MED, medHIGH, HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
DMSx=[1427,1409,1465,1552,1660,1598,1522];
DMSz=[ 949,1011,1075,1105,1086, 906, 940];slicemap (specval(DMS),
low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz, Y);
DLSx=[1595,1658,1728,1766,1792,1782,];
DLSz=[ 907,1084,1047,1003, 930, 829];slicemap (specval(DLS),
low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
VMSx=[1427,1595,1571,1431,1436,1427];
32
VMSz=[ 949, 907, 756, 787, 829, 949];slicemap (specval(VMS),
low,medLOW, MED, medHIGH, HIGH, VMSx, VMSz, Y);
VLSx=[1596,1571,1621,1627,1672,1712,1730,1736,1775];
VLSz=[ 907, 756, 709,629 ,660 , 732, 737, 773, 821];slicemap
(specval(VLS), low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
Clx=[1821,1775,1736,1730,1760,1762, 1836];
Clz=[ 923, 821, 773, 737, 708, 743, 856];slicemap (specval(Cl),
low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
ENx=[1739,1672,1627,1666,1742,1768,1760];

```

```

ENz=[ 737, 660, 629, 587, 588, 637, 708];slicemap (specval(EN),
low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
AcbCx=[1401,1428,1519,1571,1621,1635,1559,1439];
AcbCz=[ 737, 775, 784, 756, 709, 619, 608, 668];slicemap
(specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz, Y);
WM2x=[1502,1538,1546,1497,1482,1488];
WM2z=[733 , 704, 673, 686, 711, 731];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);
AcbShx=[1404,1378,1376,1409,1545,1681,1738,1666,1627,1559,1439,1401];
AcbShz=[ 742, 684, 627, 561, 521, 540, 588, 587, 629, 608, 668,
737];slicemap (specval(AcbSh), low,medLOW, MED, medHIGH, HIGH,
AcbShx, AcbShz, Y);
VPx=[1411,1545,1681,1589,1530,1465];
VPz=[556 , 521, 540, 468, 461, 486];slicemap (specval(VP), low,medLOW,
MED, medHIGH, HIGH, VPx, VPz, Y);
MSx=[1295,1336,1295];
MSz=[888 , 757, 684];slicemap (specval(MS), low,medLOW, MED, medHIGH,
HIGH, MSx, MSz, Y);
DBx=[1376,1333,1295,1295];
DBz=[ 627, 604,602 ,684];slicemap (specval(DB), low,medLOW, MED,
medHIGH, HIGH, DBx, DBz, Y);
%l = ; %enter whatever slice you wa
S1ULx=[1799,1822,2034,2017,1990];
S1ULz=[1007, 934, 892,1003,1089];slicemap (specval(S1UL), low,medLOW,
MED, medHIGH, HIGH, S1ULx, S1ULz, Y);
%QCcolor (S1ULx,S1ULz,3*24)
l=24;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice25

```

if Slicenum == 25;
Y=25*3;
DLSx=[1614,1809,1828,1768,1716,1684,1655];
33
DLSz=[910 , 817, 893,1033,1076,1087,1003];slicemap (specval(DLS),
low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
%receptorMap(specval(), x, z, Y)
%QCcolor (DLSx,DLSz,25*3)
Cgx=[1295,1328,1463,1415,1369,1295];
Cgz=[1365,1403,1199,1102,1075,1059];slicemap (specval(Cg), low,medLOW,
MED, medHIGH, HIGH, Cgx, Cgz, Y);
%receptorMap(specval(), x, z, Y)
WMx=[1295,1415,1465,1480,1518,1750,1806,1832,1850,1830,1828,1789,1768,1632,15
37,1474,1418,1359,1344,1295];
WMz=[1059,1102,1199,1213,1204,1100,1049,1000, 898, 824, 893,
999,1033,1112,1121,1099,1046, 993, 991, 982];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap(specval(), x, z, Y)
WM2x=[1482,1508,1526,1498,1463,1474];
WM2z=[ 737, 725, 690, 673, 715, 741];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);

```

```

%receptorMap(specval(), x, z, Y)
WM3x=[1337,1391,1397,1441,1437,1386,1327,1308];
WM3z=[ 573, 549, 516, 476, 438, 423, 453, 524];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z, Y);
%receptorMap(specval(), x, z, Y)
Vx=[1459,1407,1384,1421,1461];
Vz=[ 813, 884,1006,1049, 815];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
%receptorMap(specval(), x, z, Y)
LSx=[1295,1344,1381,1407,1460,1448,1409,1295];
LSz=[ 982, 991,1007, 884, 813, 774, 729, 729];slicemap (specval(LS),
low,medLOW, MED, medHIGH, HIGH, LSx, LSz, Y);
%receptorMap(specval(), x, z, Y)
Tux=[1330,1391,1397,1441,1437,1438,1658,1716,1736,1687,1679,1616,1538,1479,14
33,1406];
Tuz=[ 573, 549, 516, 476, 438, 415, 388, 425, 468, 528, 504, 463, 467,
496, 560, 604];slicemap (specval(Tu), low,medLOW, MED, medHIGH, HIGH,
Tux, Tuz, Y);
%receptorMap(specval(58), Tux, Tuz, Y)%Tu
PirRx=[1694,1799,1881,1912,1882,1837,1736];
PirRz=[ 535, 641, 610, 585, 538, 501, 468];slicemap (specval(PirR),
low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz, Y);
%receptorMap(specval(), x, z, Y)
Insx=[1815,1881,1917,2037,2045,1853,1874,1869,1795,1785];
Insz=[ 623, 610, 588, 812, 889, 920, 858, 818, 723, 690];slicemap
(specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz, Y);
%receptorMap(specval(), x, z, Y)
S1ULx=[1853,2045,1965,1816];
S1ULz=[ 920, 889,1142,1033];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
%receptorMap(specval(), x, z, Y)
S1Jx=[1816,1750,1869,1901,1975];
S1Jz=[1033,1100,1272,1248,1148];slicemap (specval(S1J), low,medLOW,
MED, medHIGH, HIGH, S1Jx, S1Jz, Y);
%receptorMap(specval(), x, z, Y)
S1FLx=[1872,1771,1720,1639,1750];
34
S1FLz=[1271,1336,1354,1148,1100];slicemap (specval(S1FL), low,medLOW,
MED, medHIGH, HIGH, S1FLx, S1FLz, Y);
%receptorMap(specval(), x, z, Y)
M1x=[1720,1505,1516,1639];
M1z=[1354,1405,1204,1148];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
%receptorMap(specval(), x, z, Y)
M2x=[1516,1463,1333,1505];
M2z=[1204,1199,1404,1405];slicemap (specval(M2), low,medLOW, MED,
medHIGH, HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
DMSx=[1684,1614,1450,1421,1474,1554,1632];
DMSz=[1087, 910, 941,1049,1099,1122,1112];slicemap (specval(DMS),
low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz, Y);
%receptorMap(specval(), x, z, Y)
%DLsx=[];
%DLsz=[];
VMSx=[1614,1450,1460,1456,1512,1583];
VMSz=[ 912, 941, 813, 797, 787,748];slicemap (specval(VMS),
low,medLOW, MED, medHIGH, HIGH, VMSx, VMSz, Y);
%receptorMap(specval(), x, z, Y)

```

```

VLSx=[1583,1614,1809,1761,1694,1646,1614];
VLSz=[ 748, 912, 817, 715, 625, 598, 712];slicemap (specval(VLS),
low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
%receptorMap(specval(), x, z, Y)
Clx=[1852,1874,1869,1795,1786,1761,1769,1795,1830];
Clz=[ 901, 858, 818, 723, 690, 715, 762, 797, 824];slicemap
(specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
%receptorMap(specval(), x, z, Y)
ENx=[1761,1786,1796,1756,1652,1697,1735];
ENZ=[ 715, 690, 618, 577, 594, 624, 697];slicemap (specval(EN),
low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
%receptorMap(specval(), x, z, Y)
AcbCx=[1456,1512,1583,1614,1635,1550,1489,1441,1409,1448];
AcbCz=[ 797, 787, 748, 712, 617, 608, 627, 668, 729, 774];slicemap
(specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz, Y);
%receptorMap(specval(), x, z, Y)
AcbShx=[1413,1397,1405,1433,1501,1569,1698,1750,1646,1629,1550,
1489,1441];
AcbShz=[ 731, 678, 626, 560, 526, 515, 542, 577, 598, 614, 608, 627 ,
668];slicemap (specval(AcbSh), low,medLOW, MED, medHIGH, HIGH,
AcbShx, AcbShz, Y);
%receptorMap(specval(), x, z, Y)
VPx=[1435,1501,1569,1699,1678,1616,1538,1479];
VPz=[ 554, 526, 515, 538, 501, 463, 467, 496];slicemap (specval(VP),
low,medLOW, MED, medHIGH, HIGH, VPx, VPz, Y);
%receptorMap(specval(), x, z, Y)
MSx=[1295,1328,1295];
MSz=[1407, 813, 729];slicemap (specval(MS), low,medLOW, MED, medHIGH,
HIGH, MSx, MSz, Y);
%receptorMap(specval(), x, z, Y)
DBx=[1295,1404,1406,1337,1295];
35
DBz=[ 678, 628,604 , 573, 587];slicemap (specval(DB), low,medLOW, MED,
medHIGH, HIGH, DBx, DBz, Y);
%receptorMap(specval(), x, z, Y)
%l = ; %enter whatever slice you wa
%QCcolor (S1ULx,S1ULz,3*24)
l=25;
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice26

```

if Slicenum ==26 ;
Y=26*3;
Cgx=[1295,1331,1459,1415,1295];
Cgz=[1372,1400,1206,1121,1076];slicemap (specval(Cg), low,medLOW, MED,
medHIGH, HIGH, Cgx, Cgz, Y);
%receptorMap(specval(), x, z, Y)
M2x=[1333,1459,1508,1515];
M2z=[1404,1206,1219,1408];slicemap (specval(M2), low,medLOW, MED,
medHIGH, HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
M1x=[1508,1515,1688,1616];

```

```

M1z=[1219,1408,1370,1172];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
%receptorMap(specval(), x, z, Y)
S1FLx=[1688,1616,1747,1868];
S1FLz=[1370,1172,1114,1283];slicemap (specval(S1FL), low,medLOW, MED,
medHIGH, HIGH, S1FLx, S1FLz, Y);
%receptorMap(specval(), x, z, Y)
S1Jx=[1747,1868,1971,1820];
S1Jz=[1114,1283,1164,1046];slicemap (specval(S1J), low,medLOW, MED,
medHIGH, HIGH, S1Jx, S1Jz, Y);
%receptorMap(specval(), x, z, Y)
S1ULx=[1971,1820,1882,2065];
S1ULz=[1164,1046, 874, 847];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
%receptorMap(specval(), x, z, Y)
Insx=[1882,2065,1981,1929,1838,1818,1809];
36
Insz=[ 874, 847, 547,583 ,605 ,631 ,663 ];slicemap (specval(Ins),
low,medLOW, MED, medHIGH, HIGH, Insx, Insz, Y);
%receptorMap(specval(), x, z, Y)
PirRx=[1981,1929,1838,1818,1804,1736,1696,1779];
PirRz=[ 547,583 ,605 ,631 , 603, 565, 510, 403];slicemap
(specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz, Y);
%receptorMap(specval(), x, z, Y)
Tux=[1696,1779,1523,1454,1342,1411];
Tuz=[ 510, 403, 376, 405, 554, 582];slicemap (specval(Tu), low,medLOW,
MED, medHIGH, HIGH, Tux, Tuz, Y);
%receptorMap(specval(), x, z, Y)
WMx=[1295,1390,1430,1440,1373,1295];
WMz=[ 574, 544, 500, 427, 410, 430];slicemap (specval(WM), low,medLOW,
MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap(specval(), x, z, Y)
WM2x=[1451,1545,1540,1513,1443];
WM2z=[ 740, 705, 677, 673, 722];slicemap (specval(WM), low,medLOW,
MED, medHIGH, HIGH, WM2x, WM2z, Y);
%receptorMap(specval(), x, z, Y)
WM3x=[1294,1382,1470,1541,1633,1753,1840,1841,1865,1842,1812,1706,1613,1509,1
453,1412];
WM3z=[1013,1036,1115,1137,1128,1064, 901, 810,
901,1003,1059,1142,1170,1219,1202,1122];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z, Y);
%receptorMap(specval(), x, z, Y)
DBx=[1295,1371,1411,1335,1295];
DBz=[659, 659, 582, 554, 572];slicemap (specval(DB), low,medLOW, MED,
medHIGH, HIGH, DBx, DBz, Y);
%receptorMap(specval(), x, z, Y)
Vx=[1460,1412,1382,1429];
Vz=[ 850, 911,1036,1073];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
%receptorMap(specval(), x, z, Y)
LSx=[1295,1371,1381,1456,1460,1412,1382,1295];
LSz=[659, 659, 716, 820, 850, 911,1036,1013];slicemap (specval(LS),
low,medLOW, MED, medHIGH, HIGH, LSx, LSz, Y);
%receptorMap(specval(), x, z, Y)
MSx=[1295,1333,1295];
MSz=[911 , 820, 716];slicemap (specval(MS), low,medLOW, MED, medHIGH,
HIGH, MSx, MSz, Y);
%receptorMap(specval(), x, z, Y)

```



```

DMSx=[1425,1452,1610,1695,1557,1470];
DMSz=[1071, 929, 912,1101,1138,1115];slicemap (specval(DMS),
low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz, Y);
%receptorMap(specval(), x, z, Y)
DLSx=[1615,1841,1840,1798,1753,1695];
DLSz=[ 907, 810, 901,1004,1064,1101];slicemap (specval(DLS),
low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
%receptorMap(specval(), x, z, Y)
VLSx=[1610,1841,1716,1640,];
VLSz=[ 912, 810, 607, 582,];slicemap (specval(VLS), low,medLOW, MED,
medHIGH, HIGH, VLSx, VLSz, Y);
%receptorMap(specval(), x, z, Y)
VMSx=[1455,1452,1610,1584];
37
VMSz=[ 815, 929, 912, 748];slicemap (specval(VMS), low,medLOW, MED,
medHIGH, HIGH, VMSx, VMSz, Y);
%receptorMap(specval(), x, z, Y)
AcbCx=[1584,1614,1528,1447,1414,1420,1456,1515];
AcbCz=[ 750, 629, 619, 647, 688, 766, 820, 804];slicemap
(specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz, Y);
%receptorMap(specval(), x, z, Y)
AcbShx=[1420,1381,1371,1411,1573,1716,1738,1640,1614,1528,1447,1414];
AcbShz=[ 766, 716, 659, 582, 517, 539, 567, 582, 629, 619, 647,
688];slicemap (specval(AcbSh), low,medLOW, MED, medHIGH, HIGH,
AcbShx, AcbShz, Y);
%receptorMap(specval(), x, z, Y)
VPx=[1434,1573,1718,1639,1545,1486];
VPz=[558 , 517, 541, 463, 459, 487];slicemap (specval(VP), low,medLOW,
MED, medHIGH, HIGH, VPx, VPz, Y);
%receptorMap(specval(), x, z, Y)
ENx=[1680,1736,1804,1809,1774,1712];
ENz=[ 577,565, 603 , 663, 694, 598];slicemap (specval(EN), low,medLOW,
MED, medHIGH, HIGH, ENx, ENz, Y);
%receptorMap(specval(), x, z, Y)
Clx=[1774,1809,1816,1867,1896,1864,1837];
Clz=[ 694, 665, 715, 753, 839, 896, 786];slicemap (specval(Cl),
low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
%receptorMap(specval(), x, z, Y)
%QCcolor (VMSx,VMSz,26*3)
l=26;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice27

```

if Slicenum == 27;
Y=27*3;
M1x=[1483,1584,1643,1487];
M1z=[1238,1201,1391,1418];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
%receptorMap(specval(), x, z, Y)
STx=[1482,1484,1431,1388,1357,1499];
STz=[ 786, 738, 664, 646, 733, 784];slicemap (specval(ST), low,medLOW,

```

```

MED, medHIGH, HIGH, STx, STz, Y);
%receptorMap(specval(), x, z, Y)
AcbCx=[1488,1484,1476,1499,1554,1631,1682,1570, 1487];
AcbCz=[ 810, 738, 707, 657, 610, 598, 612, 788, 819];slicemap
(specval(AcbC), low,medLOW, MED, medHIGH, HIGH, AcbCx, AcbCz, Y);
%receptorMap(specval(), x, z, Y)
38
LSx=[1393,1295,1295,1376,1420,1488,1485,1400,1357,1364];
LSz=[ 647, 647,1049,1049,1071, 820, 775, 784, 733, 678];slicemap
(specval(LS), low,medLOW, MED, medHIGH, HIGH, LSx, LSz, Y);
%receptorMap(specval(), x, z, Y)
Vx=[1420,1452,1488,];
Vz=[1071,1101, 820,];slicemap (specval(V), low,medLOW, MED, medHIGH,
HIGH, Vx, Vz, Y);
%receptorMap(specval(), x, z, Y)
WMx=[1295,1407,1452,1491,1772,1869,1866,1848,1812,1733,1643,1552,1503,1376,12
95];
WMz=[1092,1123,1217,1239,1115, 953, 754,
920,1003,1095,1141,1153,1144,1049,1049];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap(specval(), x, z, Y)
WM2x=[1629,1552,1422,1391,1407,1550];
WM2z=[ 649, 709, 763, 742, 713, 686];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);
%receptorMap(specval(), x, z, Y)
WM3x=[1295,1295,1319,1358,1429,1395];
WM3z=[551 , 449, 431, 430, 483, 526];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM3x, WM3z, Y);
%receptorMap(specval(), x, z, Y)
Cgx=[1295,1321,1450,1430,1367,1295];
Cgz=[1378,1408,1213,1149,1104,1092];slicemap (specval(Cg), low,medLOW,
MED, medHIGH, HIGH, Cgx, Cgz, Y);
%receptorMap(specval(), x, z, Y)
M2x=[1321,1450,1489,1487,1421];
M2z=[1408,1213,1234,1418,1423];slicemap (specval(M2), low,medLOW, MED,
medHIGH, HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
S1FLx=[1643,1582,1693,1773,1889,1763,1643];
S1FLz=[1391,1200,1161,1110,1272,1353,1391];slicemap (specval(S1FL),
low,medLOW, MED, medHIGH, HIGH, S1FLx, S1FLz, Y);
%receptorMap(specval(), x, z, Y)
S1ULx=[1773,1852,2051,1965,1889];
S1ULz=[1110,1003,1010,1200,1272];slicemap (specval(S1UL), low,medLOW,
MED, medHIGH, HIGH, S1ULx, S1ULz, Y);
%receptorMap(specval(), x, z, Y)
S2x=[1859,2051,2084,1906,1877,1869];
S2z=[ 986,1010, 843, 862, 884, 953];slicemap (specval(S2), low,medLOW,
MED, medHIGH, HIGH, S2x, S2z, Y);
%receptorMap(specval(), x, z, Y)
Insx=[1906,2084,2079,2011,1966,1885,1861,1917];
Insz=[ 858, 843, 715, 550, 584, 600, 636, 806];slicemap (specval(Ins),
low,medLOW, MED, medHIGH, HIGH, Insx, Insz, Y);
%receptorMap(specval(), x, z, Y)
PirRx=[1861,1885,1966,2014,1968,1892,1738,1708,1727,1767,1809,1861];
PirRz=[ 623, 600, 584, 552, 487, 423, 368, 509, 536, 553, 560,
623];slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx,
PirRz, Y);
%receptorMap(specval(), x, z, Y)

```

```

Clx=[1861,1917,1906,1875,1863,1818];
Clz=[ 623, 806, 858, 880, 747, 667];slicemap (specval(Cl), low,medLOW,
MED, medHIGH, HIGH, Clx, Clz, Y);
39
%receptorMap(specval(), x, z, Y)
ENx=[1861,1809,1767,1748,1773,1802,1821];
ENZ=[ 623, 560, 553, 585, 611, 649, 661];slicemap (specval(EN),
low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
%receptorMap(specval(), x, z, Y)
AcbShx=[1481,1452,1414,1459,1553,1656,1727,1767,1682,1631,1554,1499];
AcbShz=[ 705, 698, 654, 600, 553, 532, 536, 553, 612, 598, 610,
657];slicemap (specval(AcbSh), low,medLOW, MED, medHIGH, HIGH,
AcbShx, AcbShz, Y);
%receptorMap(specval(), x, z, Y)
VPx=[1425,1388,1439,1551,1659,1692,1727,1656,1553,1459];
VPz=[ 660, 646, 562, 472, 468, 481, 536, 532, 553, 600];slicemap
(specval(VP), low,medLOW, MED, medHIGH, HIGH, VPx, VPz, Y);
%receptorMap(specval(), x, z, Y)
VLSx=[1667,1862,1852,1821,1742,1691,1618,1623];
VLSz=[ 894, 777, 727, 661, 574, 603, 730, 763];slicemap (specval(VLS),
low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
%receptorMap(specval(), x, z, Y)
VMSx=[1667,1623,1618,1570,1488,1475,1595];
VMSz=[ 894, 763, 730, 788, 820, 950, 933];slicemap (specval(VMS),
low,medLOW, MED, medHIGH, HIGH, VMSx, VMSz, Y);
%receptorMap(specval(), x, z, Y)
DMSx=[1664,1733,1570,1503,1454,1473,1595];
DMSz=[ 896,1095,1154,1144,1100, 955, 933];slicemap (specval(DMS),
low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz, Y);
%receptorMap(specval(), x, z, Y)
DLSx=[1664,1862,1848,1812,1733];
DLSz=[ 896, 777, 920,1003,1095];slicemap (specval(DLS), low,medLOW,
MED, medHIGH, HIGH, DLSx, DLSz, Y);
%receptorMap(specval(), x, z, Y)
MSx=[1295,1317,1317,1295];
MSz=[ 956, 956, 647, 647];slicemap (specval(MS), low,medLOW, MED,
medHIGH, HIGH, MSx, MSz, Y);
%receptorMap(specval(), x, z, Y)
DBx=[1393,1295,1295,1400,1451];
DBz=[ 647, 647,550 , 523, 550];slicemap (specval(DB), low,medLOW, MED,
medHIGH, HIGH, DBx, DBz, Y);
%receptorMap(specval(), x, z, Y)
%QCcolor (Mlx,Mlz,27*3)
l=27;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end
slice28
if Slicenum == 28;
Y=28*3;
40
Cgx=[1295,1321,1448,1430,1351,1295];

```

```

Cgz=[1372,1408,1217,1152,1106,1105];slicemap (specval(Cg), low,medLOW,
MED, medHIGH, HIGH, Cgx, Cgz, Y);
M2x=[1321,1448,1471,1468];
M2z=[1408,1217,1238,1423];slicemap (specval(M2), low,medLOW, MED,
medHIGH, HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
M1x=[1471,1468,1609,1567];
M1z=[1238,1423,1404,1211];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
S1HLx=[1609,1567,1653,1717];
S1HLz=[1404,1211,1183,1370];slicemap (specval(S1HL), low,medLOW, MED,
medHIGH, HIGH, S1HLx, S1HLz, Y);
S1FLx=[1653,1717,1894,1781];
S1FLz=[1183,1370,1279,1116];slicemap (specval(S1FL), low,medLOW, MED,
medHIGH, HIGH, S1FLx, S1FLz, Y);
S1ULx=[1894,1781,1858,2059];
S1ULz=[1279,1116,1003,1006];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
S2x=[1858,2059,2094,1913,1881];
S2z=[1003,1006, 862, 877, 899];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, S2x, S2z, Y);
Insx=[2094,1913,1869,2040];
Insz=[ 862, 877, 633, 564];slicemap (specval(Ins), low,medLOW, MED,
medHIGH, HIGH, Insx, Insz, Y);
PirRx=[1869,2040,2014,1941,1777,1694,1685,1746];
PirRz=[ 633, 564, 503, 424, 350, 348, 493, 549];slicemap
(specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz, Y);
Tux=[1694,1685,1642,1595,1512,1487];
Tuz=[ 348, 493, 481, 436, 431, 416];slicemap (specval(Tu), low,medLOW,
MED, medHIGH, HIGH, Tux, Tuz, Y);
MCPOx=[1642,1595,1512,1487,1497];
MCPOz=[ 481, 436, 431, 416, 481];slicemap (specval(MCPO), low,medLOW,
MED, medHIGH, HIGH, MCPOx, MCPOz, Y);
DBx=[1487,1497,1457,1421,1407];
DBz=[ 416, 481, 516, 499, 461];slicemap (specval(DB), low,medLOW, MED,
medHIGH, HIGH, DBx, DBz, Y);
Slx=[1457,1520,1566,1518,1469];
Slz=[ 516, 488, 488, 559, 567];slicemap (specval(S1J), low,medLOW,
MED, medHIGH, HIGH, Slx, Slz, Y);
LPOx=[1469,1457,1421,1399,1295,1295,1366,1395,1389];
41
LPOz=[ 567, 516, 500, 597, 683, 725, 725, 718, 667];slicemap
(specval(LPO), low,medLOW, MED, medHIGH, HIGH, LPOx, LPOz, Y);
MPAx=[1295,1399,1421,1407,1366,1295];
MPAz=[ 683, 597, 500, 461, 522, 544];slicemap (specval(MPA),
low,medLOW, MED, medHIGH, HIGH, MPAx, MPAz, Y);
STx=[1481,1395,1389,1408,1513,1554,1546];
STz=[ 814, 718, 667, 624, 633, 712, 759];slicemap (specval(ST),
low,medLOW, MED, medHIGH, HIGH, STx, STz, Y);
LSx=[1295,1425,1466,1489,1422,1295];
LSz=[1087,1087,1003, 829, 753, 753];slicemap (specval(LS), low,medLOW,
MED, medHIGH, HIGH, LSx, LSz, Y);
MSx=[1295,1295,1326];
MSz=[745 ,1003, 917];slicemap (specval(MS), low,medLOW, MED, medHIGH,
HIGH, MSx, MSz, Y);
WM1x=[1295,1326,1380,1450,1626,1533,1366,1295];
WM1z=[795 , 795, 780, 733, 652, 682, 725, 725];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM1x, WM1z, Y);

```

```

WM2x=[1295,1384,1529,1623,1767,1822,1861,1871,1892,1858,1779,1696,1469,1448,1
430,1402,1351,1295];
WM2z=[1070,1070,1155,1147,1078,1003, 904, 763,
819,1003,1115,1169,1236,1217,1152,1121,1106,1106];slicemap
(specval(WM), low,medLOW, MED, medHIGH, HIGH, WM2x, WM2z, Y);
WM3x=[1295,1366,1395,1337,1295];
WM3z=[ 544, 522, 469, 424, 423];slicemap (specval(WM), low,medLOW,
MED, medHIGH, HIGH, WM3x, WM3z, Y);
Vx=[1425,1462,1503,1494,1466];
Vz=[1087,1116, 888, 834,1003];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
VPx=[1537,1752,1746,1685,1611,1566,1518,1469,1442,1519];
VPz=[ 674, 585, 549, 493, 476, 488, 559, 567, 601, 638];slicemap
(specval(VP), low,medLOW, MED, medHIGH, HIGH, VPx, VPz, Y);
DMSx=[1464,1507,1611,1665,1703,1623,1537];
DMSz=[1123, 927, 911, 885,1116,1147,1155];slicemap (specval(DMS),
low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz, Y);
DLSx=[1699,1665,1870,1882,1822,1767];
DLSz=[1118, 885, 779, 897,1003,1078];slicemap (specval(DLS),
low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
VMSx=[1504,1663,1638,1537,1556,1547,1483,1503];
VMSz=[ 926, 886, 865, 645, 686, 728, 764, 810, 888];slicemap (specval(VMS),
low,medLOW, MED, medHIGH, HIGH, VMSx, VMSz, Y);
VLSx=[1670,1638,1753,1820,1870];
VLSz=[887, 645, 585, 665, 779];slicemap (specval(VLS), low,medLOW,
MED, medHIGH, HIGH, VLSx, VLSz, Y);
Clx=[1882,1929,1869,1820,1840,1892];
42
Clz=[ 897, 840, 637, 665, 726, 819];slicemap (specval(Cl), low,medLOW,
MED, medHIGH, HIGH, Clx, Clz, Y);
ENx=[1820,1869,1834,1746,1764];
ENz=[665 , 633, 584, 549, 619];slicemap (specval(), low,medLOW, MED,
medHIGH, HIGH, ENx, ENz, Y);
%QCcolor (DMSx,DMSz,3*28)
l=28;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice29

```

if Slicenum == 29;
Y=29*3;
Cgx=[1295,1295,1352,1392,1449,1314];
Cgz=[1398,1108,1108,1120,1217,1416];slicemap (specval(Cg), low,medLOW,
MED, medHIGH, HIGH, Cgx, Cgz, Y);
%receptorMap(specval(), x, z, Y)
M2x=[1449,1314,1464,1469];
M2z=[1217,1416,1440,1237];slicemap (specval(M2), low,medLOW, MED,
medHIGH, HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
M1x=[1464,1469,1552,1597];
M1z=[1440,1237,1211,1412];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);

```

```

%receptorMap(specval(), x, z, Y)
S1HLx=[1552,1597,1721,1653];
S1HLz=[1211,1412,1381,1184];slicemap (specval(S1HL), low,medLOW, MED,
medHIGH, HIGH, S1HLx, S1HLz, Y);
%receptorMap(specval(), x, z, Y)
S1FLx=[1721,1653,1781,1901];
S1FLz=[1381,1184,1116,1290];slicemap (specval(S1FL), low,medLOW, MED,
medHIGH, HIGH, S1FLx, S1FLz, Y);
%receptorMap(specval(), x, z, Y)
S1ULx=[1781,1901,2072,1869];
S1ULz=[1116,1290,1022, 965];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
%receptorMap(specval(), x, z, Y)
S2x=[2072,1869,1901,1921,2118];
S2z=[1022, 965, 827, 820,848 ];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, S2x, S2z, Y);
%receptorMap(specval(), x, z, Y)
Insx=[1901,1921,2118,2110,2056,1890];
Insz=[ 827, 820,848 , 685, 560, 622];slicemap (specval(Ins),
low,medLOW, MED, medHIGH, HIGH, Insx, Insz, Y);
%receptorMap(specval(), x, z, Y)
PirRx=[2056,1890,1747,1685,1696,1805,1906];
43
PirRz=[ 560, 622, 545, 490, 340, 334, 374];slicemap (specval(PirR),
low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz, Y);
%receptorMap(specval(), x, z, Y)
Tux=[1685,1696,1516,1546,1630,1655];
Tuz=[ 490, 340, 410, 424, 422, 480];slicemap (specval(Tu), low,medLOW,
MED, medHIGH, HIGH, Tux, Tuz, Y);
%receptorMap(specval(), x, z, Y)
MCPOx=[1516,1546,1630,1655,1584,1529];
MCPOz=[ 410, 424, 422, 480, 478, 454];slicemap (specval(MCPO),
low,medLOW, MED, medHIGH, HIGH, MCPOx, MCPOz, Y);
%receptorMap(specval(), x, z, Y)
DBx=[1529,1490,1456,1516];
DBz=[ 454, 483, 438, 410];slicemap (specval(DB), low,medLOW, MED,
medHIGH, HIGH, DBx, DBz, Y);
%receptorMap(specval(), x, z, Y)
Slx=[1529,1490,1515,1582];
Slz=[454 , 483, 544, 478];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, Slx, Slz, Y);
%receptorMap(specval(), x, z, Y)
LPOx=[1375,1498,1513,1501,1469,1459,1355,1335];
LPOz=[ 721, 648, 613, 486, 461, 524, 644, 716];slicemap (specval(LPO),
low,medLOW, MED, medHIGH, HIGH, LPOx, LPOz, Y);
%receptorMap(specval(), x, z, Y)
MPAx=[1469,1459,1355,1335,1295,1295,1343,1353];
MPAz=[ 461, 524, 644, 716, 716, 531, 504, 463];slicemap (specval(MPA),
low,medLOW, MED, medHIGH, HIGH, MPAx, MPAz, Y);
%receptorMap(specval(), x, z, Y)
STx=[1559,1534,1501,1431,1388,1373,1416,1511,1538];
STz=[ 919, 679, 649, 666, 694, 783, 854, 910, 936];slicemap
(specval(ST), low,medLOW, MED, medHIGH, HIGH, STx, STz, Y);
%receptorMap(specval(), x, z, Y)
LSx=[1373,1416,1511,1538,1527,1491,1418,1370,1215];
LSz=[ 783, 854, 910, 936, 997,1059,1098,1079,1079];slicemap
(specval(LS), low,medLOW, MED, medHIGH, HIGH, LSx, LSz, Y);
%receptorMap(specval(), x, z, Y)

```

```

TSx=[1373,1295,1295];
TSz=[783 , 783, 910];slicemap (specval(TS), low,medLOW, MED, medHIGH,
HIGH, TSx, TSz, Y);
%receptorMap(specval(), x, z, Y)
WM1x=[1292,1370,1518,1631,1785,1859,1874,1894,1898,1812,1763,1686,1554,1483,1
447,1429,1352,
1295];
WM1z=[1077,1079,1146,1140,1057, 933, 696,
738,889 ,1082,1132,1173,1211,1240,1218,1157,1108, 1108];slicemap
(specval(WM), low,medLOW, MED, medHIGH, HIGH, WM1x, WM1z, Y);
%receptorMap(specval(), x, z, Y)
WM2x=[1537,1531,1548,1550];
WM2z=[ 676, 838, 912,689];slicemap (specval(WM), low,medLOW, MED,
medHIGH, HIGH, WM2x, WM2z, Y);
%receptorMap(specval(), x, z, Y)
WM3x=[1183,1185,1295,1295];
WM3z=[783 ,718, 718, 783];slicemap (specval(WM), low,medLOW, MED,
medHIGH, HIGH, WM3x, WM3z, Y);
%receptorMap(specval(), x, z, Y)
WM4x=[1295,1343,1353,1460,1426,1390,1295];
44
WM4z=[531 , 504, 463, 433, 402, 391, 406];slicemap (specval(WM),
low,medLOW, MED, medHIGH, HIGH, WM4x, WM4z, Y);
%receptorMap(specval(), x, z, Y)
Vx=[1418,1490,1528,1491,1421];
Vz=[1098,1138,1006,1059,1102];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
%receptorMap(specval(), x, z, Y)
VPx=[1538,1735,1677,1582,1515,1513,1498];
VPz=[ 682, 536, 488, 478, 544, 613, 648];slicemap (specval(VP),
low,medLOW, MED, medHIGH, HIGH, VPx, VPz, Y);
%receptorMap(specval(), x, z, Y)
DMSx=[1490,1551,1695,1723,1536];
DMSz=[1138, 923, 882,1109,1147];slicemap (specval(DMS), low,medLOW,
MED, medHIGH, HIGH, DMSx, DMSz, Y);
%receptorMap(specval(), x, z, Y)
DLSx=[1695,1723,1822,1882,1882];
DLSz=[ 882,1109,1003, 846, 783];slicemap (specval(DLS), low,medLOW,
MED, medHIGH, HIGH, DLSx, DLSz, Y);
%receptorMap(specval(), x, z, Y)
GPx=[1560,1539,1607,1603];
GPz=[ 868, 694, 603, 779];slicemap (specval(GP), low,medLOW, MED,
medHIGH, HIGH, GPx, GPz, Y);
%receptorMap(specval(), x, z, Y)
VMSx=[1607,1603, 1560,1548,1695,1679];
VMSz=[ 603, 779, 868 , 912, 882, 553];slicemap (specval(VMS),
low,medLOW, MED, medHIGH, HIGH, VMSx, VMSz, Y);
%receptorMap(specval(), x, z, Y)
VLSx=[1695,1679,1738,1771,1848,1881,1882];
VLSz=[ 882, 553, 539, 601, 650, 726, 783];slicemap (specval(VLS),
low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
%receptorMap(specval(), x, z, Y)
Clx=[1901,1922,1930,1887,1856,1894,1901];
Clz=[ 827, 818, 741, 632, 678, 738, 827];slicemap (specval(Cl),
low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
%receptorMap(specval(), x, z, Y)
ENx=[1848,1890,1879,1842,1787,1747,1771];
ENz=[ 650, 622, 592, 566, 565,545 , 601];slicemap (specval(EN),

```

```

low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
%receptorMap(specval(), x, z, Y)
%QCcolor (Cgx,Cgz,3*29)
l=29;
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice30

```

if Slicenum == 30;
45
Y=30*3;
DBx=[1574,1505,1489,1498,1545,1587,1593];
DBz=[ 388, 423, 423, 474, 496, 473, 438];slicemap (specval(DB),
low,medLOW, MED, medHIGH, HIGH, DBx, DBz, Y);
%receptorMap(specval(), x, z, Y)
%QCcolor (DBx,DBz,3*30)
Cgx=[1295,1442,1426 ,1295];
Cgz=[1398, 1224,1161,1116];slicemap (specval(Cg), low,medLOW, MED,
medHIGH, HIGH, Cgx, Cgz, Y);
%receptorMap(specval(), x, z, Y)
M2x=[1295,1442,1425];
M2z=[1398,1224,1442];slicemap (specval(M2), low,medLOW, MED, medHIGH,
HIGH, M2x, M2z, Y);
%receptorMap(specval(36), M2x, M2z, Y)%M2
M1x=[1442,1425,1552,1503];
M1z=[1224,1442,1433,1214];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
%receptorMap(specval(), x, z, Y)
S1HLx=[1552,1503,1652,1723];
S1HLz=[1433,1214,1181,1388];slicemap (specval(S1HL), low,medLOW, MED,
medHIGH, HIGH, S1HLx, S1HLz, Y);
%receptorMap(specval(), x, z, Y)
S1FLx=[1652,1723,1905,1782];
S1FLz=[1181,1388,1297,1118];slicemap (specval(S1FL), low,medLOW, MED,
medHIGH, HIGH, S1FLx, S1FLz, Y);
%receptorMap(specval(), x, z, Y)
S1BFx=[1905,1782,1887,2067];
S1BFz=[1297,1118, 976,1054];slicemap (specval(S1BF), low,medLOW, MED,
medHIGH, HIGH, S1BFx, S1BFz, Y);
%receptorMap(specval(), x, z, Y)
S1ULx=[1887,2067,2106,1910];
S1ULz=[ 976,1054, 948, 898];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
%receptorMap(specval(), x, z, Y)
S2x=[2106,1910,1918,1947,2126];
S2z=[ 948, 898, 819, 783, 784];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, S2x, S2z, Y);
%receptorMap(specval(), x, z, Y)
Insx=[1947,2126,2071,1982,1926];
Insz=[ 783, 784, 582, 594, 631];slicemap (specval(Ins), low,medLOW,
MED, medHIGH, HIGH, Insx, Insz, Y);
%receptorMap(specval(), x, z, Y)

```



```

PirRx=[2071,1982,1926,1888,1835,1782,1811,1776,1877,1956,2008];
PirRz=[ 582, 594, 631, 558, 515, 490, 432, 313, 333, 389,
449];slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx,
PirRz, Y);
%receptorMap(specval(), x, z, Y)
AAx=[1782,1811,1776,1614,1634,1708,1730];
AAz=[ 490, 432, 313, 373, 405, 459, 497];slicemap (specval(AA),
low,medLOW, MED, medHIGH, HIGH, AAx, AAz, Y);
%receptorMap(specval(), x, z, Y)
MCPOx=[1614,1634,1708,1730,1661,1620,1574];
MCPOz=[ 373, 405, 459, 497, 527, 521, 388];slicemap (specval(MCPO),
low,medLOW, MED, medHIGH, HIGH, MCPOx, MCPOz, Y);
46
%receptorMap(specval(), x, z, Y)
DBx=[1574,1588,1537,1498,1489];
DBz=[388 , 471, 496, 474, 423];slicemap (specval(DB), low,medLOW, MED,
medHIGH, HIGH, DBx, DBz, Y);
%receptorMap(specval(), x, z, Y)
Slx=[1620,1588,1521,1514];
Slz=[ 521, 471, 490, 573];
slicemap (specval(Sl), low,medLOW, MED, medHIGH, HIGH, Slx, Slz, Y);
%receptorMap(specval(), x, z, Y)
LPOx=[1514,1521,1498,1452,1460,1450,1354,1335,1397,1438,1490];
LPOz=[ 573, 490, 474, 491, 523, 552, 646, 705, 699, 658, 644];slicemap
(specval(LPO), low,medLOW, MED, medHIGH, HIGH, LPOx, LPOz, Y);
%receptorMap(specval(), x, z, Y)
MPAx=[1295,1343,1354,1452,1419,1295];
MPAz=[ 708, 703,730, 491, 459, 438];
slicemap (specval(MPA), low,medLOW, MED, medHIGH, HIGH, MPAx, MPAz,
Y);
%receptorMap(specval(), x, z, Y)
STx=[1511,1583,1545,1518,1537,1515,1400,1397,1438];
STz=[ 628, 652, 701, 809, 895, 915,801 , 699, 658];
slicemap (specval(ST), low,medLOW, MED, medHIGH, HIGH, STx, STz, Y);
%receptorMap(specval(), x, z, Y)
EAx=[1511,1583, 1610,1514];
EAz=[628 , 652, 537, 573];slicemap (specval(EA), low,medLOW, MED,
medHIGH, HIGH, EAx, EAz, Y);
%receptorMap(specval(), x, z, Y)
LSx=[1395,1295,1295,1389,1416,1481,1530,1512,1395];
LSz=[ 797, 797,1080,1092,1106,1070, 973, 914, 797];slicemap
(specval(LS), low,medLOW, MED, medHIGH, HIGH, LSx, LSz, Y);
%receptorMap(specval(), x, z, Y)
MSx=[1395,1295,1295,1397];
MSz=[797, 797 , 707, 699];slicemap (specval(MS), low,medLOW, MED,
medHIGH, HIGH, MSx, MSz, Y);
%receptorMap(specval(), x, z, Y)
WMx=[1271,
1426,1444,1678,1778,1834,1910,1882,1902,1897,1832,1707,1635,1489,1389,1295];
WMz=[1116, 1161,1224,1175,1122,1077, 898, 664,764 ,
847,1004,1109,1140,1140,1092,1080];slicemap (specval(WM), low,medLOW,
MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap(specval(), x, z, Y)
VPx=[1603,1781,1784,1717,1661,1610];
VPz=[ 598, 540, 501, 500, 527, 537];
slicemap (specval(VP), low,medLOW, MED, medHIGH, HIGH, VPx, VPz, Y);
%receptorMap(specval(), x, z, Y)
Vx=[1416,1481,1528,1489];

```

```

Vz=[1106,1070, 973,1140];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
%receptorMap(specval(), x, z, Y)
47
DMSx=[1528,1489,1707,1710,1512];
DMSz=[973,1140 ,1109, 885, 914];
slicemap (specval(DMS), low,medLOW, MED, medHIGH, HIGH, DMSx, DMSz,
Y);
%receptorMap(specval(), x, z, Y)
DLSx=[1710,1885,1837,1707];
DLSz=[ 885, 845, 999,1109];
slicemap (specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz,
Y);
%receptorMap(specval(), x, z, Y)
VMSx=[1703,1718,1645,1606,1554];
VMSz=[ 882,543 , 568, 594, 883];
slicemap (specval(VMS), low,medLOW, MED, medHIGH, HIGH, VMSx, VMSz,
Y);
%receptorMap(specval(), x, z, Y)
VLSx=[1703,1718,1781,1879,1897];
VLSz=[ 882, 543, 540, 668, 847];slicemap (specval(VLS), low,medLOW,
MED, medHIGH, HIGH, VLSx, VLSz, Y);
%receptorMap(specval(), x, z, Y)
Clx=[1921,1911,1869,1926,1949];
Clz=[ 820, 727, 654, 631, 748];slicemap (specval(Cl), low,medLOW, MED,
medHIGH, HIGH, Clx, Clz, Y);
%receptorMap(specval(), x, z, Y)
ENx=[1926,1875,1788,1795,1888];
ENz=[ 631, 662, 551, 500, 558];slicemap (specval(EN), low,medLOW, MED,
medHIGH, HIGH, ENx, ENz, Y);
%receptorMap(specval(), x, z, Y)
GPx=[1590,1562,1539,1554,1628,1645,1650,1624];
GPz=[ 635, 680, 703,883 , 827, 787, 700, 649];slicemap (specval(GP),
low,medLOW, MED, medHIGH, HIGH, GPx, GPz, Y);
%receptorMap(specval(), x, z, Y)
l=30;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice31

```

if Slicenum == 31;
Y=31*3;
Cgx=[1295,1433,1409,1295];
Cgz=[1408,1230,1155,1146];slicemap (specval(Cg), low,medLOW, MED,
medHIGH, HIGH, Cgx, Cgz, Y);
M1x=[1310,1431,1493,1522];
M1z=[1415,1231,1234,1449];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
S1HLx=[1493,1522,1692,1624];
48
S1HLz=[1234,1449,1410,1203];slicemap (specval(S1HL), low,medLOW, MED,
medHIGH, HIGH, S1HLx, S1HLz, Y);

```

```

S1FLx=[1692,1624,1750,1857];
S1FLz=[1410,1203,1154,1341];slicemap (specval(S1FL), low,medLOW, MED,
medHIGH, HIGH, S1FLx, S1FLz, Y);
S1BFx=[1750,1857,1999,2072,1891,1836];
S1BFz=[1154,1341,1220,1052,1003,1091];slicemap (specval(S1BF),
low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz, Y);
S1ULx=[2072,1891,1917,2109];
S1ULz=[1052,1003, 919, 966];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
S2x=[1917,2109,2145,1929];
S2z=[ 919, 966, 788, 780];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, S2x, S2z, Y);
Insx=[2145,1929,1934,2093];
Insz=[ 788, 780, 646, 609];slicemap (specval(Ins), low,medLOW, MED,
medHIGH, HIGH, Insx, Insz, Y);
PIRCx=[1934,2093,1913,1841,1840,1810];
PIRCz=[ 646, 609, 330, 305, 385, 451];slicemap (specval(PIRC),
low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz, Y);
BAX=[1597,1844,1777,1638];
BAZ=[ 482, 380, 502, 523];slicemap (specval(BA), low,medLOW, MED,
medHIGH, HIGH, BAX, BAZ, Y);
Cox=[1597,1598,1741,1841,1844];
Coz=[482 , 387, 321, 305,380 ];slicemap (specval(Co), low,medLOW, MED,
medHIGH, HIGH, Cox, Coz, Y);
Cex=[1777,1638,1702,1767,1784];
Cez=[ 502, 523, 578, 579, 534];slicemap (specval(Ce), low,medLOW, MED,
medHIGH, HIGH, Cex, Cez, Y);
Mex=[1597,1598,1488];
Mez=[482 , 387, 422];slicemap (specval(Me), low,medLOW, MED, medHIGH,
HIGH, Mex, Mez, Y);
MCPOx=[1665,1591,1546,1543,1597];
MCPOz=[531 , 562, 532, 457, 482];slicemap (specval(MCPO), low,medLOW,
MED, medHIGH, HIGH, MCPOx, MCPOz, Y);
SOx=[1448,1379,1386,1435,1510,1533];
SOz=[ 422, 447, 475, 499, 474,440 ];
slicemap (specval(SO), low,medLOW, MED, medHIGH, HIGH, SOx, SOz, Y);
LHx=[1295,1329,1405,1463,1562,1591,1546,1543,1452,1449,1414,1333,1344];
LHz=[ 725, 725, 715, 654, 620, 562, 532, 457, 497, 537, 589, 640,
682];
slicemap (specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
AHAx=[1295,1333,1414,1449,1450,1427,1386,1379,1351,1295];
AHAz=[ 604, 640, 589, 537, 496, 499, 475, 447, 440, 440];
slicemap (specval(AHA), low,medLOW, MED, medHIGH, HIGH, AHAx, AHAz,
Y);
SCHx=[1351,1295,1295,1337];
SCHz=[ 440, 440, 488, 479];
slicemap (specval(SCh), low,medLOW, MED, medHIGH, HIGH, SCHx, SCHz,
Y);
Rex=[1295,1357,1390,1342,1295];
Rez=[ 765, 787, 765, 728, 728];
slicemap (specval(Re), low,medLOW, MED, medHIGH, HIGH, Rex, Rez, Y);
CMx=[1295,1357,1338,1295];
49
CMz=[ 765, 787, 841, 839];
slicemap (specval(CM), low,medLOW, MED, medHIGH, HIGH, CMx, CMz, Y);
PVAx=[1338,1295,1295,1345,1412,1402];
PVAz=[ 841, 839, 951, 987, 997, 920];
slicemap (specval(PVA), low,medLOW, MED, medHIGH, HIGH, PVAx, PVAz,

```

```

Y);
Ax=[1412,1402,1339,1345,1412,1478,1504];
Az=[ 997, 920, 845, 803,770 , 859,1003];
slicemap (specval(A), low,medLOW, MED, medHIGH, HIGH, Ax, Az, Y);
Rtx=[1504,1447,1508,1572,1546];
Rtz=[1003, 776, 747,1010,1042];
slicemap (specval(Rt), low,medLOW, MED, medHIGH, HIGH, Rtx, Rtz, Y);
Vx=[1295,1345,1506,1549,1555,1462,1398,1295];
Vz=[951 ,987 ,1022,1041,1160,1147,1111,1111];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
%WMx=[];
%WMz=[];slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
%WM2x=[];
%WM2z=[];slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z,
Y);
%WM3x=[];
%WM3z=[];slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z,
Y);
DLSx=[1556,1549,1682,1903,1848,1728];
DLSz=[1161,1054, 852, 845,1003,1113];
slicemap (specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz,
Y);
VLSx=[1683,1903,1911,1870,1787,1602,1659,1687];
VLSz=[ 849, 845, 715, 619, 547, 659, 690, 744];
slicemap (specval(VLS), low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz,
Y);
GPx=[1602,1659,1687,1683,1551,1587,1611,1654];
GPz=[ 659, 690, 744, 849, 699, 784, 925, 908];
slicemap (specval(GP), low,medLOW, MED, medHIGH, HIGH, GPx, GPz, Y);
Clx=[1926,1946,1903,1878];
Clz=[ 745, 694, 593, 635];
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
ENx=[1903,1878,1787,1777,1805,1846,1880];
ENz=[ 593, 635, 547, 502, 450, 459,505 ];
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
Pax=[1294,1333,1344,1303,1294];
Paz=[ 604, 640, 682, 725,727];
slicemap (specval(Pa), low,medLOW, MED, medHIGH, HIGH, Pax, Paz, Y);
%QCcolor (Pax,Paz,31*3)
l=31;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end
50

```

slice32

```

if Slicenum ==32 ;
Y=32*3;
S1BFx=[1414,1270,1968,2078,1900,1838];
S1BFz=[1181,1373,1262,1077, 984,1098];
slicemap (specval(S1BF), low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz,
Y);
Cgx=[1295,1354,1433,1427,1407,1295];

```

```

Cgz=[1406,1451,1245,1187,1166,1156];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, Cgx, Cgz, Y);
M1x=[1350,1436,1493,1522];
M1z=[1447,1245,1244,1458];
slicemap (specval(M1), low,medLOW, MED, medHIGH, HIGH, M1x, M1z, Y);
S1HLx=[1493,1522,1696,1624];
S1HLz=[1244,1458,1414,1207];
slicemap (specval(S1HL), low,medLOW, MED, medHIGH, HIGH, S1HLx, S1HLz,
Y);
S1Shx=[1696,1624,1713,1797];
S1Shz=[1414,1207,1181,1373];
slicemap (specval(S1Sh), low,medLOW, MED, medHIGH, HIGH, S1Shx, S1Shz,
Y);
S1ULx=[2078,1900,1921,2121];
S1ULz=[1077, 984, 921, 966];
slicemap (specval(S1UL), low,medLOW, MED, medHIGH, HIGH, S1ULx, S1ULz,
Y);
S2x=[1921,2121,2153,1943];
S2z=[ 921, 966, 785, 781];
slicemap (specval(S2), low,medLOW, MED, medHIGH, HIGH, S2x, S2z, Y);
Insx=[2153,1943,1939,2096];
Insz=[ 785, 781, 627, 591];
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);
PirRx=[1939,2096,1914,1839,1827,1928];
PirRz=[ 627, 591, 310, 304, 406, 523];
slicemap (specval(PirR), low,medLOW, MED, medHIGH, HIGH, PirRx, PirRz,
Y);
Cox =[1838,1827,1594,1554];
Coz=[ 299 , 406, 516, 414];
slicemap (specval(Co), low,medLOW, MED, medHIGH, HIGH, Cox, Coz, Y);
Cex=[1802,1648,1688,1721,1794,1830];
Cez=[ 494, 593, 629, 637, 621, 562];
slicemap (specval(Ce), low,medLOW, MED, medHIGH, HIGH, Cex, Cez, Y);
AAx=[1630,1604,1552,1566];
AAz=[ 547, 382, 412, 472];
slicemap (specval(AA), low,medLOW, MED, medHIGH, HIGH, AAx, AAz, Y);
EAx=[1657,1563,1483];
EAz=[ 600, 608, 702];
slicemap (specval(EA), low,medLOW, MED, medHIGH, HIGH, EAx, EAz, Y);
S1
BAx=[1594,1827,1885,1876,1802,1648,1510,1552,1716,1702];
BAz=[ 516, 406, 472, 611, 494, 593, 716, 716, 677, 637];
slicemap (specval(BA), low,medLOW, MED, medHIGH, HIGH, BAx, BAz, Y);
ENx=[1878,1931,1928,1885];
ENZ=[ 615, 603, 523, 476];
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
Clx=[1878,1931,1925,1889];
Clz=[ 615, 603, 705, 642];
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
DLSx=[1830,1945,1917,1797,1795,1751,1806];
DLSz=[ 562, 743, 839, 850, 735, 642, 616];
slicemap (specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz,
Y);
VLSx=[1917,1797,1763,1657,1683,1576,1740,1789,1894];
VLSz=[ 839, 850, 938,1028,1037,1167,1116,1082, 928];
slicemap (specval(VLS), low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz,
Y);

```

```

GPx=[1714,1763,1793,1795,1748,1686,1716,1669,1702,1717,1714];
GPz=[ 975, 938, 868, 735, 651, 626, 677, 708, 751, 810, 970];
slicemap (specval(GP), low,medLOW, MED, medHIGH, HIGH, GPx, GPz, Y);
MCPOx=[1562,1650,1633,1560,1533,1535];
MCPOz=[ 602, 589, 551, 539, 564, 581];
slicemap (specval(MCPO), low,medLOW, MED, medHIGH, HIGH, MCPOx, MCPOz,
Y);
LHx=[1560,1562,1483,1304,1467];
LHz=[ 539, 602, 702, 697, 441];
slicemap (specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
Rchx=[1443,1295,1295,1345];
Rchz=[ 391, 426, 390, 370];
slicemap (specval(Rch), low,medLOW, MED, medHIGH, HIGH, Rchx, Rchz,
Y);
AHAx=[1443,1295,1295,1351,1429,1461];
AHAz=[ 391, 426, 564,613 , 545, 440];
slicemap (specval(AHA), low,medLOW, MED, medHIGH, HIGH, AHAx, AHAz,
Y);
Pax=[1295,1351,1362,1305,1295];
Paz=[ 564,613 , 650, 701, 701];
slicemap (specval(Pa), low,medLOW, MED, medHIGH, HIGH, Pax, Paz, Y);
Rex=[1295,1406,1446,1362,1295];
Rez=[701 , 704, 750, 786, 750];
slicemap (specval(Re), low,medLOW, MED, medHIGH, HIGH, Rex, Rez, Y);
CMx=[1362,1295,1295,1346];
CMz=[ 786, 750, 847, 847];
slicemap (specval(CM), low,medLOW, MED, medHIGH, HIGH, CMx, CMz, Y);
PVAx=[1295,1346,1425,1423,1349,1295];
PVAz=[ 847, 847, 941,1003, 988, 946];
slicemap (specval(PVA), low,medLOW, MED, medHIGH, HIGH, PVAx, PVAz,
Y);
Ax=[1346,1336,1446,1514,1516,1573,1517,1423,1425,1382];
Az=[ 847, 812, 750, 776, 890,1006,1037,1003, 941, 879];
slicemap (specval(A), low,medLOW, MED, medHIGH, HIGH, Ax, Az, Y);
VAX=[1514,1516,1573,1595,1549,1522];
VAz=[ 776, 890,1006, 952, 814, 779];
slicemap (specval(VA), low,medLOW, MED, medHIGH, HIGH, VAX, VAz, Y);
52
Rtx=[1573,1595,1549,1522,1401,1484,1552,1638,1639,1684,1564,1517];
Rtz=[1006, 952, 814, 779, 720, 703, 716, 851, 953,1011,1068,1037];
slicemap (specval(Rt), low,medLOW, MED, medHIGH, HIGH, Rtx, Rtz, Y);
Vx=[1564,1462,1349,1295,1295,1347,1475,1547];
Vz=[1068,1009, 988, 946,1020,1021,1065,1056];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
CMx=[1282,1362,1336,1346,1233];
CMz=[ 766, 786, 812, 847,851];
slicemap (specval(CM), low,medLOW, MED, medHIGH, HIGH, CMx, CMz, Y);
WMx=[1019,924 ,906,1027 ,1118,1250,1295,1295,1198,1111];
WMz=[1161,1080,1036,1068,1064,1020,1020,1110,1119,1164];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WMx=[1295,1391,1478,1575,1740,1864,1923,1868,1856,1803,1870,1880,1945,1921,18
38,1713,1445,1427,1407,1295];
WMz=[1110,1119,1164,1167,1116, 928, 734, 652, 588, 512, 577, 642, 743,
924,1098,1181,1250,1187,1166,1156];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WMx=[1639,1638,1554,1587,1650,1702,1713,1677];
WMz=[ 953, 851, 725, 680, 692, 751,1000,1018];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);

```

```

WMx=[1443,1554,1633,1598,1560,1461];
WMz=[ 391, 414, 549, 559, 539, 440];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%QCcolor (CMx,CMz,3*32)
l=32;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 33

```

if Slicenum == 33;
Y=33*3
WMx=[1295,1404,1875,1949,1933,1876,1835,1718,1459,1435,1401,1295];
WMz=[373, 359 , 611, 779, 920,1072,1120,1198,1275,1271,1186,1186];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
RSRx=[1295,1324,1361,1435,1423,1401,1249];
RSRz=[1415,1445,1462,1271,1208,1186,1177];
slicemap (specval(RSR), low,medLOW, MED, medHIGH, HIGH, RSRx, RSRz,
Y);
Mlx=[1361,1433,1494,1521];
Mlz=[1462,1264,1262,1459];
slicemap (specval(Ml), low,medLOW, MED, medHIGH, HIGH, Mlx, Mlz, Y);
S1HLx=[1521,1496,1538,1625,1694];
S1HLz=[1459,1263,1241,1229,1421];
slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, S1HLx, S1HLz, Y);
S1Shx=[1625,1694,1790,1715];
S1Shz=[1229,1421,1390,1196];
53
slicemap (specval(S1Sh), low,medLOW, MED, medHIGH, HIGH, S1Shx, S1Shz,
Y);
S1BFx=[1790,1715,1835,1916,2079,1976];
S1BFz=[1390,1196,1120,1002,1079,1257];
slicemap (specval(S1BF), low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz,
Y);
S1ULx=[1916,2079,2125,1933];
S1ULz=[1002,1076, 976, 920];
slicemap (specval(S1UL), low,medLOW, MED, medHIGH, HIGH, S1ULx, S1ULz,
Y);
S2x=[2125,1933,1947,2156];
S2z=[ 976, 920, 781, 787];
slicemap (specval(S2), low,medLOW, MED, medHIGH, HIGH, S2x, S2z, Y);
Insx=[1947,2156,2097,1986,1911];
Insz=[ 781, 787, 591, 601, 637];
slicemap (specval(Ins), low,medLOW, MED, medHIGH, HIGH, Insx, Insz,
Y);
PIRCx=[2097,1957,1902,1825,1807,1820,1911,1986];
PIRCz=[ 591, 330, 296, 301, 351, 413, 637, 601];
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,
Y);
Clx=[1910,1939,1929,1895,1875];
Clz=[ 607, 687, 715, 670, 611];
slicemap (specval(Cl), low,medLOW, MED, medHIGH, HIGH, Clx, Clz, Y);
ENx=[1910,1875,1895,1929,1939];

```

```

ENz=[607 , 611, 670, 715, 687];
slicemap (specval(EN), low,medLOW, MED, medHIGH, HIGH, ENx, ENz, Y);
BAx=[1634,1868,1888,1820,1825,1563,1566];
BAz=[ 554, 588, 492, 404, 301, 421, 454];
slicemap (specval(BA), low,medLOW, MED, medHIGH, HIGH, BAx, BAz, Y);
Cox=[1566,1809,1739,1563];
Coz=[ 454, 335, 326, 421];
slicemap (specval(Co), low,medLOW, MED, medHIGH, HIGH, Cox, Coz, Y);
Mex=[1592,1563,1566,1634];
Mez=[ 405, 421, 454, 554];
slicemap (specval(Me), low,medLOW, MED, medHIGH, HIGH, Mex, Mez, Y);
Cex=[1797,1829,1810,1766,1690,1653];
Cez=[ 509, 605, 642, 660, 639, 558];
slicemap (specval(Ce), low,medLOW, MED, medHIGH, HIGH, Cex, Cez, Y);
VLSx=[1829,1907,1915,1817,1809,1785];
VLSz=[ 605, 713, 842, 821, 725, 656];
slicemap (specval(VLS), low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz,
Y);
DLSx=[1663,1817,1915,1864,1755];
DLSz=[1101, 821, 842,1000,1125];
slicemap (specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz,
Y);
GPx=[1771,1812,1809,1791,1720,1687,1737,1778];
GPz=[ 950, 885, 725, 654, 650, 664, 712, 814];
slicemap (specval(GP), low,medLOW, MED, medHIGH, HIGH, GPx, GPz, Y);
DGdx=[1295,1324,1374,1446,1375,1316,1295];
DGdz=[1131,1139,1091,1075,1036,1066,1066];
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
54
CA3Dx=[1324,1388,1466,1538,1599,1629,1596,1536,1446,1374];
CA3Dz=[1139,1140,1182,1190,1173,1117,1093,1094,1075,1091];
slicemap (specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz,
Y);
Vx=[1316,1295,1295,1360];
Vz=[1066,1066,1007,1037];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
PVAx=[1295,1295,1314,1327,1317];
PVAz=[1007, 933, 948,1003,1025];
slicemap (specval(PVA), low,medLOW, MED, medHIGH, HIGH, PVAx, PVAz,
Y);
Hbx=[1340,1375,1407,1415,1362,1327,1321];
Hbz=[1050,1036,1051,1003, 986,1003,1030];
slicemap (specval(Hb), low,medLOW, MED, medHIGH, HIGH, Hbx, Hbz, Y);
MDx=[1327,1362,1406,1352,1335,1314];
MDz=[1003, 986, 989, 874, 937, 948];
slicemap (specval(MD), low,medLOW, MED, medHIGH, HIGH, MDx, MDz, Y);
CMx=[1314,1295,1295,1352,1335];
CMz=[ 948, 933, 846, 874, 937];
slicemap (specval(CM), low,medLOW, MED, medHIGH, HIGH, CMx, CMz, Y);
Ax=[1295,1354,1403,1392,1446,1493,1551,1530,1469,1449,1430,1295];
Az=[ 846, 876, 955,1042,1075,1043,1051,1004, 951, 906, 802, 784];
slicemap (specval(A), low,medLOW, MED, medHIGH, HIGH, Ax, Az, Y);
LDx=[1466,1446,1493,1554,1575,1495];
LDz=[1084,1075,1043,1052,1094,1087];
slicemap (specval(LD), low,medLOW, MED, medHIGH, HIGH, LDx, LDz, Y);
Rex=[1295,1439,1412,1419,1295];
Rez=[ 673, 722, 752, 794, 784];

```



```

slicemap (specval(Re), low,medLOW, MED, medHIGH, HIGH, Rex, Rez, Y);
VMx=[1436,1414,1412,1439,1514,1558,1486];
VMz=[ 812, 787, 752, 722, 729, 753, 766];
slicemap (specval(VM), low,medLOW, MED, medHIGH, HIGH, VMx, VMz, Y);
VAX=[1436,1486,1558,1614,1540,1517,1499,1469,1449,1453];
VAz=[ 812, 766, 753, 793, 855, 895, 980, 951, 906, 845];
slicemap (specval(VA), low,medLOW, MED, medHIGH, HIGH, VAX, VAz, Y);
VLx=[1507,1548,1616,1658,1652,1605,1540,1517];
VLz=[ 979,1030,1003, 928, 855, 788, 855, 895];
slicemap (specval(VL), low,medLOW, MED, medHIGH, HIGH, VLx, VLz, Y);
Rtx=[1554,1575,1622,1632,1684,1708,1695,1657,1582,1439,1514,1608,1652,1658,16
16,1562,1557];
Rtz=[1052,1094,1112,1063,1003, 948, 841, 774, 703, 722, 729, 787, 855,
928,1003,1029,1071];
slicemap (specval(Rt), low,medLOW, MED, medHIGH, HIGH, Rtx, Rtz, Y);
ZIRx=[1305,1377,1466,1578,1439];
ZIRz=[ 673, 652, 667, 701, 722];
slicemap (specval(ZIR), low,medLOW, MED, medHIGH, HIGH, ZIRx, ZIRz,
Y);
Pax=[1295,1311,1380,1353,1288];
Paz=[655 , 567, 629, 663, 676];
slicemap (specval(Pa), low,medLOW, MED, medHIGH, HIGH, Pax, Paz, Y);
Vx=[1295,1308,1311,1295];
Vz=[655 , 566, 436, 396];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
AHAX=[1308,1309,1355,1401,1410,1466,1450,1407,1380,1311];
AHAz=[ 566, 511, 525, 500, 451, 505, 588, 629, 629, 567];
55
slicemap (specval(AHA), low,medLOW, MED, medHIGH, HIGH, AHAX, AHAz,
Y);
VMHx=[1309,1311,1346,1402,1418,1401,1339];
VMHz=[ 511, 436, 398, 423, 450, 500, 525];
slicemap (specval(VMH), low,medLOW, MED, medHIGH, HIGH, VMHx, VMHz,
Y);
Arcx=[1295,1311,1321,1338,1230,1295];
Arcz=[ 396, 436, 437, 396,373 , 373];
slicemap (specval(Arc), low,medLOW, MED, medHIGH, HIGH, Arcx, Arcz,
Y);
Rchx=[1295,1338,1392,1463,1404,1317];
Rchz=[ 373, 396, 410, 387, 359, 367];
slicemap (specval(Rch), low,medLOW, MED, medHIGH, HIGH, Rchx, Rchz,
Y);
LHx=[1392,1410,1466,1407,1380,1377,1466,1605,1686,1656,1615,1540,1498,1463];
LHz=[410 , 451, 505, 629, 629, 652, 667, 668, 674, 560, 550, 486, 435,
387];
slicemap (specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
l=33;
load('plotable.mat')
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
PVAX=[1291,1314,1327,1317,1293];
PVAz=[ 933, 948,1003,1025,1007];
slicemap (specval(PVA), low,medLOW, MED, medHIGH, HIGH, PVAX, PVAz,
Y);

```

```

%QCcolor(PVax,PVAz,33*3)
l=33;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

Slice34

```

if Slicenum == 34;
Rex=[1292,1329,1436,1401,1375,1215];
Rez=[ 694, 683, 722, 750, 789,792];slicemap (specval(Re), low,medLOW,
MED, medHIGH, HIGH, Rex, Rez, Y);
%receptorMap(specval(), x, z, Y)
RSRx=[1295,1362,1434,1385,1295,];
RSRz=[1425,1462,1270,1200,1177];slicemap (specval(RSR), low,medLOW,
MED, medHIGH, HIGH, RSRx, RSRz, Y);
56
%receptorMap(specval(), x, z, Y)
M1x=[1362,1429,1494,1520];
M1z=[1462,1275,1276,1466];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
%receptorMap(specval(), x, z, Y)
S1HLx=[1494,1520,1693,1626];
S1HLz=[1276,1466,1429,1243];slicemap (specval(S1HL), low,medLOW, MED,
medHIGH, HIGH, S1HLx, S1HLz, Y);
%receptorMap(specval(), x, z, Y)
S1Shx=[1693,1626,1717,1790];
S1Shz=[1429,1243,1210,1392];slicemap (specval(S1Sh), low,medLOW, MED,
medHIGH, HIGH, S1Shx, S1Shz, Y);
%receptorMap(specval(), x, z, Y)
S1BFx=[1717,1790,1896,2015,2082,1913,1874,1822];
S1BFz=[1210,1392,1336,1207,1081,1000,1087,1146];slicemap
(specval(S1BF), low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz, Y);
%receptorMap(specval(), x, z, Y)
S1ULx=[2082,1913,1944,2136];
S1ULz=[1081,1000, 920, 976];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
%receptorMap(specval(), x, z, Y)
S2x=[1944,2136,2165,1968];
S2z=[920, 976 , 836, 815];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, S2x, S2z, Y);
%receptorMap(specval(), x, z, Y)
Insx=[2165,1968,1945,2096];
Insz=[ 836, 815, 628, 580];slicemap (specval(Ins), low,medLOW, MED,
medHIGH, HIGH, Insx, Insz, Y);
%receptorMap(specval(), x, z, Y)
PIRCx=[1945,2096,1956,1884,1796];
PIRCz=[ 628, 580, 310, 284, 321];slicemap (specval(PIRC), low,medLOW,
MED, medHIGH, HIGH, PIRCx, PIRCz, Y);
%receptorMap(specval(), x, z, Y)
Cox=[1792,1589,1574,1788];
Coz=[321 , 421, 471, 356];slicemap (specval(Co), low,medLOW, MED,
medHIGH, HIGH, Cox, Coz, Y);
%receptorMap(specval(), x, z, Y)

```

```

Cex=[1714,1755,1809,1865];
Cez=[ 623, 654, 663, 607];slicemap (specval(Ce), low,medLOW, MED,
medHIGH, HIGH, Cex, Cez, Y);
%receptorMap(specval(), x, z, Y)
BAx=[1574,1788,1868,1888,1865,1699];
BAz=[ 471, 356, 366, 445, 607,620 ];slicemap (specval(BA), low,medLOW,
MED, medHIGH, HIGH, BAx, BAz, Y);
%receptorMap(specval(), x, z, Y)
Mex=[1698,1607,1574];
Mez=[ 607, 411, 471];slicemap (specval(Me), low,medLOW, MED, medHIGH,
HIGH, Mex, Mez, Y);
%receptorMap(specval(), x, z, Y)
Cex=[1694,1888,1865,1792];
Cez=[ 604, 470, 607, 671];slicemap (specval(Ce), low,medLOW, MED,
medHIGH, HIGH, Cex, Cez, Y);
%receptorMap(specval(), x, z, Y)
Lax=[1888,1865,1904,1938];
57
Laz=[ 470, 607, 656, 670];slicemap (specval(La), low,medLOW, MED,
medHIGH, HIGH, Lax, Laz, Y);
%receptorMap(specval(), x, z, Y)
VLSx=[1793,1844,1879,1868,1929,1947,1865];
VLSz=[ 671, 699, 796, 836, 827, 678,607 ];slicemap (specval(VLS),
low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
%receptorMap(specval(), x, z, Y)
GPx=[1779,1844,1879,1868,1837,1834,1816,1763];
GPz=[ 666, 699, 796, 836, 864, 801, 743, 663];slicemap (specval(GP),
low,medLOW, MED, medHIGH, HIGH, GPx, GPz, Y);
%receptorMap(specval(), x, z, Y)
DLSx=[1790,1881,1929,1878,1868,1837,1808,1760,1674,1667];
DLSz=[1126,1000, 827, 823, 836, 864,1015,1077,1094,1177];slicemap
(specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
%receptorMap(specval(), x, z, Y)
LHx=[1718,1562,1541,1536,1424,1389,1597];
LHz=[ 631, 524, 486, 439, 359, 677, 678];slicemap (specval(LH),
low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
%receptorMap(specval(), x, z, Y)
VMHx=[1307,1337,1383,1417,1431,1419,1302];
VMHz=[ 511, 518, 507, 472, 427, 384,421 ];slicemap (specval(VMH),
low,medLOW, MED, medHIGH, HIGH, VMHx, VMHz, Y);
%receptorMap(specval(), x, z, Y)
AHAx=[1338,1337,1417,1443,1431,1389];
AHAz=[ 683, 518, 472, 504, 628, 677];slicemap (specval(AHA),
low,medLOW, MED, medHIGH, HIGH, AHAx, AHAz, Y);
%receptorMap(specval(), x, z, Y)
Rchx=[1326,1424,1419,1372];
Rchz=[ 362, 359, 384, 396];slicemap (specval(Rch), low,medLOW, MED,
medHIGH, HIGH, Rchx, Rchz, Y);
%receptorMap(specval(), x, z, Y)
Arcx=[1326,1372,1306,1295,1295];
Arcz=[ 362, 396, 426, 426, 362];slicemap (specval(Arc), low,medLOW,
MED, medHIGH, HIGH, Arcx, Arcz, Y);
%receptorMap(specval(), x, z, Y)
DMx=[1295,1338,1352,1331,1308,1295];
DMz=[ 698, 683, 653, 518, 511, 511];slicemap (specval(DM), low,medLOW,
MED, medHIGH, HIGH, DMx, DMz, Y);
%receptorMap(specval(), x, z, Y)
Vx=[1295,1309,1302,1295];

```

```

Vz=[ 658, 593, 421,421 ];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
ZIRx=[1338,1436,1631,1579,1389];
ZIRz=[ 683, 722, 702, 682, 677];slicemap (specval(ZIR), low,medLOW,
MED, medHIGH, HIGH, ZIRx, ZIRz, Y);
%receptorMap(specval(), x, z, Y)
VMx=[1373,1435,1556,1585,1584,1436];
VMz=[ 789, 805, 788, 749, 716, 722];slicemap (specval(VM), low,medLOW,
MED, medHIGH, HIGH, VMx, VMz, Y);
%receptorMap(specval(), x, z, Y)
VPLx=[1584,1642,1727,1738,1676,1634,1625,1660,1653];
VPLz=[ 716, 725, 809, 859,1037,1045, 993, 885, 841];slicemap
(specval(VPL), low,medLOW, MED, medHIGH, HIGH, VPLx, VPLz, Y);
%receptorMap(specval(), x, z, Y)
58
VLx=[1676,1634,1625,1660,1653,1624,1536,1509,1507];
VLz=[1037,1045, 993, 885, 841, 797, 875, 945, 995];slicemap
(specval(VL), low,medLOW, MED, medHIGH, HIGH, VLx, VLz, Y);
%receptorMap(specval(), x, z, Y)
VAX=[1373,1435,1556,1585,1624,1536,1509,1524,1450];
VAZ=[ 789, 805, 788, 749, 797, 875, 945,1002, 951];slicemap
(specval(VA), low,medLOW, MED, medHIGH, HIGH, VAX, VAZ, Y);
%receptorMap(specval(), x, z, Y)
Rtx=[1600,1725,1785,1777,1631,1642,1727,1738,1676,1607];
Rtz=[1086,1058, 896, 826, 702, 725, 809, 859,1037,1054];slicemap
(specval(Rt), low,medLOW, MED, medHIGH, HIGH, Rtx, Rtz, Y);
%receptorMap(specval(), x, z, Y)
LDx=[1607,1633,1569,1460,1471,1533];
LDz=[1054,1097,1097,1054,1027,1024];slicemap (specval(), low,medLOW,
MED, medHIGH, HIGH, LDx, LDz, Y);
%receptorMap(specval(), x, z, Y)
Ax=[1295,1375,1447,1530,1432,1422,1295];
Az=[ 792, 789, 951,1013,1042, 919, 816];slicemap (specval(A),
low,medLOW, MED, medHIGH, HIGH, Ax, Az, Y);
%receptorMap(specval(), x, z, Y)
Rex=[1295,1295,1330,1436,1375];
Rez=[792, 690 , 685, 722, 789];slicemap (specval(Re), low,medLOW, MED,
medHIGH, HIGH, Rex, Rez, Y);
%receptorMap(specval(), x, z, Y)
CMx=[1295,1356,1355,1295];
CMz=[ 816, 861, 938, 915];slicemap (specval(CM), low,medLOW, MED,
medHIGH, HIGH, CMx, CMz, Y);
%receptorMap(specval(), x, z, Y)
PVAX=[1335,1292,1281,1313];
PVAZ=[ 938, 932,1011,1003];slicemap (specval(PVA), low,medLOW, MED,
medHIGH, HIGH, PVAX, PVAZ, Y);
%receptorMap(specval(), x, z, Y)
MDx=[1313,1335,1356,1404,1430,1354,];
MDz=[1003, 938, 861, 888, 987, 981];slicemap (specval(MD), low,medLOW,
MED, medHIGH, HIGH, MDx, MDz, Y);
%receptorMap(specval(), x, z, Y)
Hbx=[1354,1430,1416,1383,1350,1302];
Hbz=[ 981, 987,1025,1030,1039,1017];slicemap (specval(Hb), low,medLOW,
MED, medHIGH, HIGH, Hbx, Hbz, Y);
%receptorMap(specval(), x, z, Y)Hb
Vx=[1295,1341,1316,1295];
Vz=[1011,1043,1066,1066];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);

```

```

%receptorMap(specval(), x, z, Y)
DGdx=[1316,1295,1293,1317,1359,1431,1468,1475,1432,1417,1425,1455,1358];
DGdz=[1066,1066,1129,1143,1118,1133,1127,1111,1094,1074,1058,1052,1037];slice
map
(specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz, Y);
%receptorMap(specval(), x, z, Y)
CA3Dx=[1293,1317,1359,1431,1468,1475,1432,1417,1425,1539,1695,1700,1650,1503,
1391];
CA3Dz=[1129,1143,1118,1133,1127,1111,1094,1074,1058,1091,1100,1137,1189,1213,
1161];(specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz, Y);
%receptorMap(specval(), x, z, Y)
WMx=[1295,1391,1503,1667,1790,1883,1943,1928,1885,1960,1968,1874,1715,1459,14
29,1385,1294];
59
WMz=[1129,1161,1213,1177,1126,1003, 824, 667, 481, 676,
815,1087,1209,1291,1275,1200,1177];slicemap (specval(WM), low,medLOW,
MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap (specval(174), WMx, WMz, Y)
WMx=[1540,1589,1574,1720,1562,1541];
WMz=[ 440, 421, 471, 625, 524, 486];slicemap (specval(WM), low,medLOW,
MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap (specval(174), WMx, WMz, Y)
WMx=[1607,1720,1755,1834,1808,1760,1666,1725,1749,1740,1785,1777,1715,1597];
WMz=[ 632, 637, 654, 801,1015,1077,1094,1058,1003, 942,896 , 826, 748,
678];slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz,
Y);
%receptorMap (specval(174), WMx, WMz, Y)
%QCcolor (Rex,Rez,34*3)
l=34;
%%Slicefeed(l);
%template\ (0.0)/
% %receptorMap (specval(index), x, z, Y)
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice35

```

if Slicenum == 35;
S2x=[1967,2167,2134,2055,1938,1968];
S2z=[ 827, 849,1021,1000, 961, 832];slicemap (specval(S2), low,medLOW,
MED, medHIGH, HIGH, S2x, S2z, Y);
%QCcolor (S2x,S2z,35*3)
l=35;
RSRx=[1295,1376,1443,1383,1295];
RSRz=[1438,1474,1300,1215,1193];slicemap (specval(RSR), low,medLOW,
MED, medHIGH, HIGH, RSRx, RSRz, Y);
M1x=[1376,1443,1504,1534];
M1z=[1474,1300,1284,1475];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
S1Trx=[1504,1534,1765,1700];
S1Trz=[1284,1475,1411,1233];slicemap (specval(S1Tr), low,medLOW, MED,
medHIGH, HIGH, S1Trx, S1Trz, Y);
S1BFx=[1765,1700,1796,1893,2067,1863];
S1BFz=[1411,1233,1182,1059,1144,1362];slicemap (specval(S1BF),

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low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz, Y);
S1ULx=[1893,2067,2134,1938];
S1ULz=[1059,1144,1021, 961];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
Insx=[1967,2167,2173,2102,1943];
Insz=[ 827, 849, 792, 566, 619];slicemap (specval(Ins), low,medLOW,
MED, medHIGH, HIGH, Insx, Insz, Y);
60
PIRCx=[2102,1943,1878,1825,1768,1776,1903,1970];
PIRCz=[ 566, 619, 399, 382, 387, 341, 291, 301];slicemap
(specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz, Y);
Cox=[1768,1776,1560,1552,1570,1784];
Coz=[ 392, 341, 444, 475, 517, 392];slicemap (specval(Co), low,medLOW,
MED, medHIGH, HIGH, Cox, Coz, Y);
Cex=[1867,1867,1666,1723,1777,1828];
Cez=[ 617, 580, 580, 639, 654, 646,];slicemap (specval(Ce),
low,medLOW, MED, medHIGH, HIGH, Cex, Cez, Y);
Mex=[1867,1666,1567,1552,1560,1608];
Mez=[ 580, 580, 543, 475, 444, 415];slicemap (specval(Me), low,medLOW,
MED, medHIGH, HIGH, Mex, Mez, Y);
BAX=[1608,1867,1940,1866,1825,1789];
BAZ=[ 415, 617, 618, 391, 382, 390];slicemap (specval(BA), low,medLOW,
MED, medHIGH, HIGH, BAX, BAZ, Y);
Lax=[1867,1768,1844,1877,1929];
Laz=[ 617, 392, 383, 406, 677];slicemap (specval(La), low,medLOW, MED,
medHIGH, HIGH, Lax, Laz, Y);
VLSx=[1784,1874,1926,1945,1864,1874,1863,1830];
VLSz=[ 660, 616, 679, 836, 825, 769, 727, 683];slicemap (specval(VLS),
low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
GPx=[1864,1874,1863,1830,1784,1740,1817,1855];
GPz=[ 825, 769, 727, 683, 660, 644, 729, 843];slicemap (specval(GP),
low,medLOW, MED, medHIGH, HIGH, GPx, GPz, Y);
DLSx=[1855,1870,1938,1928,1815,1768,1709,1788,1771,1822,1854];
DLSz=[ 843, 829, 836, 918,1118,1160,1179,1110,1072,1003, 917];slicemap
(specval(DLS), low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
LHx=[1594,1536,1425,1334,1362,1468];
LHz=[ 677, 440, 363, 508, 627, 636];slicemap (specval(LH), low,medLOW,
MED, medHIGH, HIGH, LHx, LHz, Y);
WMx=[1536,
1594,1730,1791,1794,1771,1704,1609,1771,1854,1870,1817,1740,1669,1570,1560];
WMz=[440 , 677 , 757, 835, 938,1003,1070,1082,1072, 917, 829, 729,
644, 579, 517, 444];slicemap (specval(WM), low,medLOW, MED, medHIGH,
HIGH, WMx, WMz, Y);
WMx=[1295,1390,1488,1618,1768,1815,1928,1945,1926,1967,1939,1872,1796,1666,14
40,1383,1294];
WMz=[1153,1181,1232,1216,1160,1118, 918, 836, 502, 827,
959,1103,1182,1248,1302,1215,1193];slicemap (specval(WM), low,medLOW,
MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap (specval(174), WMx, WMz, Y)
VMHx=[1325,1293,1350,1391,1426,1435,1424,1384];
VMHz=[ 510, 367, 353, 350, 357, 415, 462, 500];slicemap (specval(VMH),
low,medLOW, MED, medHIGH, HIGH, VMHx, VMHz, Y);
Arcx=[1295,1305,1313,1345,1350,1295];
Arcz=[ 418, 418, 427, 412, 353, 359];slicemap (specval(Arc),
low,medLOW, MED, medHIGH, HIGH, Arcx, Arcz, Y);
VPMx=[1641,1066,1585,1573];
VPMz=[ 948, 874, 746, 796];slicemap (specval(VPM), low,medLOW, MED,
medHIGH, HIGH, VPMx, VPMz, Y);

```

```

CMx=[1295,1303,1350,1340,1295];
CMz=[ 786, 786, 840, 881, 881];slicemap (specval(CM), low,medLOW, MED,
medHIGH, HIGH, CMx, CMz, Y);
ZIRx=[1295,1364,1468,1618,1583,1437,1366];
61
ZIRz=[ 644, 627, 636, 696, 711, 698, 675];slicemap (specval(ZIR),
low,medLOW, MED, medHIGH, HIGH, ZIRx, ZIRz, Y);
VMx=[1335,1374,1585,1590,1435];
VMz=[ 755, 676, 711, 751, 796];slicemap (specval(VM), low,medLOW, MED,
medHIGH, HIGH, VMx, VMz, Y);
VLx=[1293,1335,1435,1585,1609,1442,1415,1350];
VLz=[ 776, 755, 796, 746, 860, 906, 877, 840];slicemap (specval(VL),
low,medLOW, MED, medHIGH, HIGH, VLx, VLz, Y);
VPLx=[1657,1753,1762,1706,1661,1585,1590,1666,1635];
VPLz=[1051, 946, 873, 771, 734, 711, 751, 874,1007];slicemap
(specval(VPL), low,medLOW, MED, medHIGH, HIGH, VPLx, VPLz, Y);
Rtx=[1657,1753,1762,1706,1661,1585,1590,1624,1730,1791,1794,1771,1704,1604,16
16];
Rtz=[1051, 946, 873, 771, 734, 711, 751, 699, 757, 835,
938,1003,1070,1087,1059];slicemap (specval(Rt), low,medLOW, MED,
medHIGH, HIGH, Rtx, Rtz, Y);
LDx=[1615,1599,1519,1490,1466,1460,1562];
LDz=[1090,1051, 989, 986,1003,1054,1096];slicemap (specval(LD),
low,medLOW, MED, medHIGH, HIGH, LDx, LDz, Y);
Rex=[1294,1374,1335,1295];
Rez=[ 638, 676, 755, 763];slicemap (specval(Re), low,medLOW, MED,
medHIGH, HIGH, Rex, Rez, Y);
MDx=[1448,1466,1450,1416,1368,1335,1321,1295,1295,1340,1359,1415];
MDz=[ 913,1003,1049, 987, 975, 992, 939, 920, 887, 881, 850,
877];slicemap (specval(MD), low,medLOW, MED, medHIGH, HIGH, MDx, MDz,
Y);
Pox=[1448,1466,1490,1519,1599,1657,1631,1641,1606];
Poz=[ 913,1003, 986, 989,1051,1051, 993, 948, 861];slicemap
(specval(Po), low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
PVAx=[1295,1324,1335,1295];
PVAz=[ 920, 938, 992,1009];slicemap (specval(PVA), low,medLOW, MED,
medHIGH, HIGH, PVAx, PVAz, Y);
Hbx=[1295,1368,1416,1432,1359,1335,1295];
Hbz=[1009, 975, 987,1042,1036,1058,1032];slicemap (specval(Hb),
low,medLOW, MED, medHIGH, HIGH, Hbx, Hbz, Y);
Vx=[1295,1341,1323,1295];
Vz=[1032,1050,1084,1088];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
DGdx=[1295,1323,1363,1443,1448,1417,1440,1604,1611,1565,1372,1330,1312,1295];
DGdz=[1088,1084,1035,1045,1070,1089,1109,1134,1174,1180,1131,1133,1147,1140];
slicemap
(specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz, Y);
CA1Dx=[1312,1330,1372,1565,1619,1488,1390,1308];
CA1Dz=[1147,1133,1131,1180,1217,1232,1181,1160];slicemap
(specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz, Y);
CA2x=[1587,1618,1687,1626];
CA2z=[1178,1216,1194,1155];slicemap (specval(CA2), low,medLOW, MED,
medHIGH, HIGH, CA2x, CA2z, Y);
CA3Dx=[1418,1490,1562,1772,1782,1705,1604,1487,1440,1417];
CA3Dz=[1069,1075,1096,1090,1120,1185,1134,1126,1109,1089];slicemap
(specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want

```

```

hold all
62
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice36

```

if Slicenum == 36;
PHDx=[1290,1348,1368,1353,1332,1295];
PHDz=[ 513, 525, 614, 680, 689, 676];
%QCcolor (PHDx,PHDz,36*3)
l=36;
WMx=[1295,1379,1442,1551,1724,1829,1905,1964,1912,1295];
WMz=[1206,1226,1320,1287,1234,1165,1041, 851, 450, 450];slicemap
(specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap (specval(174), WMx, WMz, Y)
RSRx=[1295,1333,1402,1435,1442,1379,1295];
RSRz=[1424,1460,1481,1480,1320,1226,1206];slicemap (specval(RSR),
low,medLOW, MED, medHIGH, HIGH, RSRx, RSRz, Y);
M1x=[1435,1449,1551,1583];
M1z=[1480,1322,1287,1466];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
S1Trx=[1551,1583,1788,1727];
S1Trz=[1287,1466,1399,1234];slicemap (specval(S1Tr), low,medLOW, MED,
medHIGH, HIGH, S1Trx, S1Trz, Y);
S1BFx=[1788,1727,1829,1906,2086,];
S1BFz=[1399,1234,1165,1042,1123,];slicemap (specval(S1BF), low,medLOW,
MED, medHIGH, HIGH, S1BFx, S1BFz, Y);
S1ULx=[1906,2086,2143,1944];
S1ULz=[1042,1123,1003, 953];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
S2x=[2143,1944,1964,2164];
S2z=[1003, 953, 851, 887];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, S2x, S2z, Y);
Aux=[1964,2164,2164,1958];
Auz=[ 851, 887, 730, 734];slicemap (specval(Au), low,medLOW, MED,
medHIGH, HIGH, Aux, Auz, Y);
PRhx=[2164,1958,1935,1992,2106];
PRhz=[ 730, 734, 621, 572, 536];slicemap (specval(PRh), low,medLOW,
MED, medHIGH, HIGH, PRhx, PRhz, Y);
PIRCx=[1935,1992,2106,1993,1934,1762,1761,1783,1912,1931];
PIRCz=[ 621, 572, 536, 309, 298, 352, 380, 409, 450, 497];slicemap
(specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz, Y);
Cox=[1781,1762,1551,1567];
Coz=[ 405, 352, 450, 505];slicemap (specval(Co), low,medLOW, MED,
medHIGH, HIGH, Cox, Coz, Y);
Mex=[1738,1634,1567,1551,1630];
Mez=[ 613, 563, 505, 450, 412];slicemap (specval(Me), low,medLOW, MED,
medHIGH, HIGH, Mex, Mez, Y);
Cex=[1717,1843,1836,1783];
63
Cez=[ 605, 591, 617, 622];slicemap (specval(Ce), low,medLOW, MED,
medHIGH, HIGH, Cex, Cez, Y);
BAX=[1630,1743,1829,1843,1775];
BAZ=[450 , 614, 621, 591, 402];slicemap (specval(BA), low,medLOW, MED,
medHIGH, HIGH, BAX, BAZ, Y);

```



```

Lax=[1781,1853,1899,1932,1931,1878];
Laz=[ 405, 595, 649, 667, 497, 426];slicemap (specval(La), low,medLOW,
MED, medHIGH, HIGH, Lax, Laz, Y);
VLSx=[1738,1791,1846,1918,1958,1934,1813];
VLSz=[ 618, 623, 609, 662, 729, 798, 673];slicemap (specval(VLS),
low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
DLSx=[1950,1965,1868,1862,1883,1872];
DLSz=[ 800, 850,1046,1003, 873, 788];slicemap (specval(DLS),
low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
LHx=[1573,1551,1503,1443,1421,1367,1357,1368,1427];
LHz=[ 631, 450, 431, 369, 431, 451, 525, 614, 580];slicemap
(specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
DMx=[1295,1356,1376,1367,1295];
DMz=[ 507, 523, 503, 451, 451];slicemap (specval(DM), low,medLOW, MED,
medHIGH, HIGH, DMx, DMz, Y);
PMx=[1295,1305,1367,1421,1443,1381,1296];
PMz=[457, 457 , 451, 431, 369, 350, 350];slicemap (specval(PM),
low,medLOW, MED, medHIGH, HIGH, PMx, PMz, Y);
Arcx=[1295,1332,1372,1381,1295];
Arcz=[ 401, 408, 390, 350, 350];slicemap (specval(Arc), low,medLOW,
MED, medHIGH, HIGH, Arcx, Arcz, Y);
ZIRx=[1360,1523,1615,1656,1578,1427,1392];
ZIRz=[ 656, 656, 700, 678, 633, 580, 587];slicemap (specval(ZIR),
low,medLOW, MED, medHIGH, HIGH, ZIRx, ZIRz, Y);
VMx=[1360,1523,1615,1460,1365];
VMz=[ 656, 656, 700, 753, 720];slicemap (specval(VM), low,medLOW, MED,
medHIGH, HIGH, VMx, VMz, Y);
Rex=[1365,1353,1324,1293,1295,1330];
Rez=[ 720, 680, 689, 677, 759, 759];slicemap (specval(Re), low,medLOW,
MED, medHIGH, HIGH, Rex, Rez, Y);
VLx=[1292,1373,1418,1468,1588,1598,1452,1365,1330,1295];
VLz=[ 773, 797, 832, 889, 847, 711, 753, 720, 759, 759];slicemap
(specval(VL), low,medLOW, MED, medHIGH, HIGH, VLx, VLz, Y);
VPLx=[1730,1662,1780,1783];
VPLz=[1012, 711, 821, 958];slicemap (specval(VPL), low,medLOW, MED,
medHIGH, HIGH, VPLx, VPLz, Y);
VPMx=[1730,1662,1598,1581,1629,1673];
VPMz=[1012, 711, 711, 797, 931, 969];slicemap (specval(VPM),
low,medLOW, MED, medHIGH, HIGH, VPMx, VPMz, Y);
Rtx=[1658,1782,1822,1814,1656,1615,1705,1780,1783,1732,1652];
Rtz=[1075,1003, 932, 835, 678, 700, 732, 821, 958,1019,1029];slicemap
(specval(Rt), low,medLOW, MED, medHIGH, HIGH, Rtx, Rtz, Y);
LPx=[1652,1658,1546,1437,1471,1519];
LPz=[1029,1075,1092,1043,1002,1004];slicemap (specval(LP), low,medLOW,
MED, medHIGH, HIGH, LPx, LPz, Y);
Pox=[1470,1652,1732,1727,1673,1629,1588,1469];
Poz=[ 996,1029,1019, 984, 969, 931, 847, 900];slicemap (specval(Po),
low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
64
CMx=[1295,1350,1366,1295];
CMz=[ 866, 847, 800, 773];slicemap (specval(CM), low,medLOW, MED,
medHIGH, HIGH, CMx, CMz, Y);
PVAx=[1295,1326,1332,1286,1295];
PVAz=[ 914, 936, 984,1007,1024];slicemap (specval(PVA), low,medLOW,
MED, medHIGH, HIGH, PVAx, PVAz, Y);
Hbx=[1286,1332,1384,1429,1412,1380,1336,];
Hbz=[1007, 984, 974,1003,1037,1036,1060,];slicemap (specval(Hb),
low,medLOW, MED, medHIGH, HIGH, Hbx, Hbz, Y);

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```

Vx=[1295,1336,1313,1295];
Vz=[1024,1060,1091,1095];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
DGdx=[1295,1313,1375,1437,1546,1670,1696,1637,1305,1295];
DGdz=[1095,1091,1037,1043,1092,1115,1136,1185,1166,1166];slicemap
(specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz, Y);
CA1Dx=[1305,1322,1364,1589,1683,1716,1610,1507,1449,1379];
CA1Dz=[1166,1137,1130,1192,1164,1203,1238,1251,1237,1178];slicemap
(specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz, Y);
CA2x=[1683,1720,1788,1703];
CA2z=[1164,1202,1164,1136];slicemap (specval(CA2), low,medLOW, MED,
medHIGH, HIGH, CA2x, CA2z, Y);
CA3Dx=[1420,1425,1532,1605,1670,1703,1780,1833,1803,1761,1523,1455];
CA3Dz=[1085,1111,1148,1144,1115,1136,1163,1114,1070,1059,1104,1075];slicemap
(specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice37

```

if Slicenum == 37;
PHDx=[1290,1348,1368,1353,1332,1295];
PHDz=[ 513, 525, 614, 680, 689, 676];
%QCcolor (PHDx,PHDz,36*3)
l=37;
WMx=[1295,1379,1442,1551,1724,1829,1905,1964,1912,1295];
WMz=[1206,1226,1320,1287,1234,1165,1041, 851, 450, 450];slicemap
(specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap (specval(174), WMx, WMz, Y)
RSRx=[1295,1333,1402,1435,1442,1379,1295];
RSRz=[1424,1460,1481,1480,1320,1226,1206];slicemap (specval(RSR),
low,medLOW, MED, medHIGH, HIGH, RSRx, RSRz, Y);
M1x=[1435,1449,1551,1583];
M1z=[1480,1322,1287,1466];slicemap (specval(M1), low,medLOW, MED,
medHIGH, HIGH, M1x, M1z, Y);
S1Trx=[1551,1583,1788,1727];
65
S1Trz=[1287,1466,1399,1234];slicemap (specval(S1Tr), low,medLOW, MED,
medHIGH, HIGH, S1Trx, S1Trz, Y);
S1BFx=[1788,1727,1829,1906,2086,];
S1BFz=[1399,1234,1165,1042,1123,];slicemap (specval(S1BF), low,medLOW,
MED, medHIGH, HIGH, S1BFx, S1BFz, Y);
S1ULx=[1906,2086,2143,1944];
S1ULz=[1042,1123,1003, 953];slicemap (specval(S1UL), low,medLOW, MED,
medHIGH, HIGH, S1ULx, S1ULz, Y);
S2x=[2143,1944,1964,2164];
S2z=[1003, 953, 851, 887];slicemap (specval(S2), low,medLOW, MED,
medHIGH, HIGH, S2x, S2z, Y);
Aux=[1964,2164,2164,1958];
Auz=[ 851, 887, 730, 734];slicemap (specval(Au), low,medLOW, MED,
medHIGH, HIGH, Aux, Auz, Y);
PRhx=[2164,1958,1935,1992,2106];
PRhz=[ 730, 734, 621, 572, 536];slicemap (specval(PRh), low,medLOW,

```

MED, medHIGH, HIGH, PRhx, PRhz, Y);
PIRCx=[1935,1992,2106,1993,1934,1762,1761,1783,1912,1931];
PIRCz=[621, 572, 536, 309, 298, 352, 380, 409, 450, 497];slicemap
(specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz, Y);
Cox=[1781,1762,1551,1567];
Coz=[405, 352, 450, 505];slicemap (specval(Co), low,medLOW, MED,
medHIGH, HIGH, Cox, Coz, Y);
Mex=[1738,1634,1567,1551,1630];
Mez=[613, 563, 505, 450, 412];slicemap (specval(Me), low,medLOW, MED,
medHIGH, HIGH, Mex, Mez, Y);
Cex=[1717,1843,1836,1783];
Cez=[605, 591, 617, 622];slicemap (specval(Ce), low,medLOW, MED,
medHIGH, HIGH, Cex, Cez, Y);
BAX=[1630,1743,1829,1843,1775];
BAz=[450 , 614, 621, 591, 402];slicemap (specval(BA), low,medLOW, MED,
medHIGH, HIGH, BAX, BAz, Y);
Lax=[1781,1853,1899,1932,1931,1878];
Laz=[405, 595, 649, 667, 497, 426];slicemap (specval(La), low,medLOW,
MED, medHIGH, HIGH, Lax, Laz, Y);
VLSx=[1738,1791,1846,1918,1958,1934,1813];
VLSz=[618, 623, 609, 662, 729, 798, 673];slicemap (specval(VLS),
low,medLOW, MED, medHIGH, HIGH, VLSx, VLSz, Y);
DLSx=[1950,1965,1868,1862,1883,1872];
DLSz=[800, 850,1046,1003, 873, 788];slicemap (specval(DLS),
low,medLOW, MED, medHIGH, HIGH, DLSx, DLSz, Y);
LHx=[1573,1551,1503,1443,1421,1367,1357,1368,1427];
LHz=[631, 450, 431, 369, 431, 451, 525, 614, 580];slicemap
(specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
DMx=[1295,1356,1376,1367,1295];
DMz=[507, 523, 503, 451, 451];slicemap (specval(DM), low,medLOW, MED,
medHIGH, HIGH, DMx, DMz, Y);
PMx=[1295,1305,1367,1421,1443,1381,1296];
PMz=[457 , 457 , 451, 431, 369, 350, 350];slicemap (specval(PM),
low,medLOW, MED, medHIGH, HIGH, PMx, PMz, Y);
Arcx=[1295,1332,1372,1381,1295];
Arcz=[401, 408, 390, 350, 350];slicemap (specval(Arc), low,medLOW,
MED, medHIGH, HIGH, Arcx, Arcz, Y);
66
ZIRx=[1360,1523,1615,1656,1578,1427,1392];
ZIRz=[656, 656, 700, 678, 633, 580, 587];slicemap (specval(ZIR),
low,medLOW, MED, medHIGH, HIGH, ZIRx, ZIRz, Y);
VMx=[1360,1523,1615,1460,1365];
VMz=[656, 656, 700, 753, 720];slicemap (specval(VM), low,medLOW, MED,
medHIGH, HIGH, VMx, VMz, Y);
Rex=[1365,1353,1324,1293,1295,1330];
Rez=[720, 680, 689, 677, 759, 759];slicemap (specval(Re), low,medLOW,
MED, medHIGH, HIGH, Rex, Rez, Y);
VLx=[1292,1373,1418,1468,1588,1598,1452,1365,1330,1295];
VLz=[773, 797, 832, 889, 847, 711, 753, 720, 759, 759];slicemap
(specval(VL), low,medLOW, MED, medHIGH, HIGH, VLx, VLz, Y);
VPLx=[1730,1662,1780,1783];
VPLz=[1012, 711, 821, 958];slicemap (specval(VPL), low,medLOW, MED,
medHIGH, HIGH, VPLx, VPLz, Y);
VPMx=[1730,1662,1598,1581,1629,1673];
VPMz=[1012, 711, 711, 797, 931, 969];slicemap (specval(VPM),
low,medLOW, MED, medHIGH, HIGH, VPMx, VPMz, Y);
Rtx=[1658,1782,1822,1814,1656,1615,1705,1780,1783,1732,1652];
Rtz=[1075,1003, 932, 835, 678, 700, 732, 821, 958,1019,1029];slicemap

```

(specval(Rt), low,medLOW, MED, medHIGH, HIGH, Rtx, Rtz, Y);
LPx=[1652,1658,1546,1437,1471,1519];
LPz=[1029,1075,1092,1043,1002,1004];slicemap (specval(LP), low,medLOW,
MED, medHIGH, HIGH, LPx, LPz, Y);
Pox=[1470,1652,1732,1727,1673,1629,1588,1469];
Poz=[ 996,1029,1019, 984, 969, 931, 847, 900];slicemap (specval(Po),
low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
CMx=[1295,1350,1366,1295];
CMz=[ 866, 847, 800, 773];slicemap (specval(CM), low,medLOW, MED,
medHIGH, HIGH, CMx, CMz, Y);
PVAx=[1295,1326,1332,1286,1295];
PVAz=[ 914, 936, 984,1007,1024];slicemap (specval(PVA), low,medLOW,
MED, medHIGH, HIGH, PVAx, PVAz, Y);
Hbx=[1286,1332,1384,1429,1412,1380,1336,];
Hbz=[1007, 984, 974,1003,1037,1036,1060,];slicemap (specval(Hb),
low,medLOW, MED, medHIGH, HIGH, Hbx, Hbz, Y);
Vx=[1295,1336,1313,1295];
Vz=[1024,1060,1091,1095];slicemap (specval(V), low,medLOW, MED,
medHIGH, HIGH, Vx, Vz, Y);
DGdx=[1295,1313,1375,1437,1546,1670,1696,1637,1305,1295];
DGdz=[1095,1091,1037,1043,1092,1115,1136,1185,1166,1166];slicemap
(specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz, Y);
CA1Dx=[1305,1322,1364,1589,1683,1716,1610,1507,1449,1379];
CA1Dz=[1166,1137,1130,1192,1164,1203,1238,1251,1237,1178];slicemap
(specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz, Y);
CA2x=[1683,1720,1788,1703];
CA2z=[1164,1202,1164,1136];slicemap (specval(CA2), low,medLOW, MED,
medHIGH, HIGH, CA2x, CA2z, Y);
CA3Dx=[1420,1425,1532,1605,1670,1703,1780,1833,1803,1761,1523,1455];
CA3Dz=[1085,1111,1148,1144,1115,1136,1163,1114,1070,1059,1104,1075];slicemap
(specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
67
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice38

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 38;
PAGx=[1294,1325,1345,1342,1301,1294];
PAGz=[ 703, 710, 750, 967,1003, 992];
%QCcolor (PAGx,PAGz,3*38)
l=38;
RSRx=[1292,1324, 1421,1456,1465,1432,1376,1294];
RSRz=[1431,1463, 1495,1492,1335,1340,1241,1223];
slicemap (specval(RSR), low,medLOW, MED, medHIGH, HIGH, RSRx, RSRz,
Y);
Ptx=[1456,1465,1517,1636,1753,1832,1662,1496];
Ptz=[1492,1335,1313,1292,1237,1385,1447,1489];
slicemap (specval(Pt), low,medLOW, MED, medHIGH, HIGH, Ptx, Ptz, Y);
S1BFx=[1832,1753,1919,2064];
S1BFz=[1385,1237,1072,1191];
slicemap (specval(S1BF), low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz,

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Y);
S2x=[1919,2064,2124,1947];
S2z=[1072,1191,1095,1014];
slicemap (specval(S2), low,medLOW, MED, medHIGH, HIGH, S2x, S2z, Y);
Aux=[2124,1947,1984,2183,2166];
Auz=[1095,1014, 750, 751, 997];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
PRhx=[1983,2183,2128,1959];
PRhz=[ 754, 751, 568, 612];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[2128,1959,1955,2115];
Entz=[ 568, 612, 573, 527];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
PIRCx=[1955,2115,2018,1836,1839,1890,1944,];
PIRCz=[ 573, 527, 322, 368, 434, 450, 494,];
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,
Y);
Cox=[1839,1650,1596,1688,1766,1819];
Coz=[ 434, 506, 476, 403, 352, 346];
slicemap (specval(Co), low,medLOW, MED, medHIGH, HIGH, Cox, Coz, Y);
BAX=[1839,1650,1864,1938,1928,1895,1850];
BAZ=[ 434, 506, 583, 567, 459, 449, 445];
slicemap (specval(BA), low,medLOW, MED, medHIGH, HIGH, BAX, BAZ, Y);
Lax=[1864,1938,1960,1907,1910,1894];
Laz=[ 583, 567, 698, 738, 688, 622];
68
slicemap (specval(La), low,medLOW, MED, medHIGH, HIGH, Lax, Laz, Y);
CA3Vx=[1907,1910,1894,1864,1651,1617,1598,1804,1862];
CA3Vz=[ 738, 688, 622, 583, 510, 514, 554, 716, 741];
slicemap (specval(CA3V), low,medLOW, MED, medHIGH, HIGH, CA3Vx, CA3Vz,
Y);
DGvx=[1592,1617,1647,1596,1554,1557];
DGvz=[ 546, 514, 504, 476, 478, 507];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
WMx=[
1558,1557,1596,1804,1877,1907,1960,1938,1983,1977,1946,1919,1824,1824,1636,15
17,1432,1376,1295,1295];
WMz=[ 476, 507, 553, 716, 742, 738, 698, 567, 691,
913,1016,1072,1188,1188,1292,1313,1340,1241,1223, 476];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
LGx=[1676,1780,1791,1744,1669];
LGz=[1053,1003, 968, 955,1017];
slicemap (specval(LG), low,medLOW, MED, medHIGH, HIGH, LGx, LGz, Y);
Rtx=[1693,1653,1761,1800,1814,1797,1744];
Rtz=[ 981, 770, 759, 810,917 , 973, 955];
slicemap (specval(Rt), low,medLOW, MED, medHIGH, HIGH, Rtx, Rtz, Y);
WMx=[1679,1742,1748,1710,1595,1680,1745,1770,1739];
WMz=[ 950, 892, 852, 799, 727, 762, 807, 870, 926];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
ZIRx=[1422,1488,1758,1683,1579];
ZIRz=[ 629, 516,757 , 760, 719];
slicemap (specval(ZIR), low,medLOW, MED, medHIGH, HIGH, ZIRx, ZIRz,
Y);
SThx=[1512,1533,1637,1503,1475,1469,1488];
SThz=[ 516,568 , 646, 607, 580, 539, 516];

```

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slicemap (specval(STh), low,medLOW, MED, medHIGH, HIGH, STHx, STHz,
Y);
LHx=[1511,1512,1469,1387,1367,1356,1369,1338,1383,1379,1427,1455];
LHz=[ 466, 516, 538, 699, 710, 670, 580, 532, 496, 469, 445, 408];
slicemap (specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
PRx=[1422,1579,1535,1474,1446,1399,1395];
PRz=[629 , 719, 710,715 , 724, 695, 671];
slicemap (specval(PR), low,medLOW, MED, medHIGH, HIGH, PRx, PRz, Y);
VPMx=[1464,1579,1656,1698,1695,1655,1621,1558];
VPMz=[ 717, 719, 769, 866, 936, 955, 935, 785];
slicemap (specval(VPM), low,medLOW, MED, medHIGH, HIGH, VPMx, VPMz,
Y);
VPLx=[1653,1698,1695,1742,1748];
VPLz=[ 770, 866, 936, 892, 852];
slicemap (specval(VPL), low,medLOW, MED, medHIGH, HIGH, VPLx, VPLz,
Y);
LPx=[1690,1688,1588,1484,1438,1432,1493,1615,1676,1669,1693];
LPz=[ 965, 966, 975, 950,1000,1057,1075,1066,1053,1017, 981];
slicemap (specval(LP), low,medLOW, MED, medHIGH, HIGH, LPx, LPz, Y);
Pox=[1690,1688,1588,1501,1458,1464,1555,1587,1621,1655,1692];
Poz=[ 965, 966, 975, 837, 734, 717, 785, 828, 935, 955, 938];
slicemap (specval(Po), low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
Hbx=[1443,1436,1420,1382,1344,1301,1348,1411];
Hbz=[1064, 998, 978, 962, 973,1003,1058,1052];
slicemap (specval(Hb), low,medLOW, MED, medHIGH, HIGH, Hbx, Hbz, Y);
PFx=[1342,1345,1325,1402,1446,1485,1501,1484,1436,1422,1382,1342];
69
PFz=[ 967, 750, 710, 695, 724, 773, 837, 950, 998, 975, 962, 967];
slicemap (specval(PF), low,medLOW, MED, medHIGH, HIGH, PFx, PFz, Y);
Vx=[1295,1334,1310,1295];
Vz=[1003,1067,1104,1104];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
PAGx=[1295,1342,1345,1321,1295,];
PAGz=[1003, 967, 750, 710, 710];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
PHDx=[1295,1321,1367,1356,1369,1338,1295];
PHDz=[710 ,710 , 710, 670, 580, 532,515 ];
slicemap (specval(PHD), low,medLOW, MED, medHIGH, HIGH, PHDx, PHDz,
Y);
SUMx=[1295,1338,1383,1379,1295];
SUMz=[515, 532 , 496, 469, 469];
slicemap (specval(SUM), low,medLOW, MED, medHIGH, HIGH, SUMx, SUMz,
Y);
MMx=[1295,1379,1427,1449,1408,1295];
MMz=[ 469, 469, 445, 406, 394, 394];
slicemap (specval(MM), low,medLOW, MED, medHIGH, HIGH, MMx, MMz, Y);
DGdx=[1422,1502,1555,1613,1715,1689,1617,1595,1493];
DGdz=[1057,1190,1210,1198,1142,1112,1097,1066,1075];
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
CA1Dx=[1295,1348,1412,1502,1555,1613,1684,1759,1652,1521,1472,1379,1295];
CA1Dz=[1106,1058,1054,1190,1210,1198,1166,1188,1250,1271,1253,1161,1161];
slicemap (specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz,
Y);
CA2x=[1683,1715,1721,1821,1762];
CA2z=[1160,1142,1124,1142,1190];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,

```

```

Y);
CA3Dx=[1689,1821,1884,1883,1845,1748,1595,1617,1553,1564,1643];
CA3Dz=[1112,1142,1066,1006,1003,1052,1066,1097,1109,1139,1136];
slicemap (specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz,
Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice39

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 39;
LPx=[1303,1311,1319,1351,1445,1448,1404,1341];
LPz=[ 955,1004,1025,1046,1044, 998, 959, 950];
70
slicemap (specval(LP), low,medLOW, MED, medHIGH, HIGH, LPx, LPz, Y);
%QCcolor(LPx,LPz,39*3)
l=39;
%%Slicefeed(1);
WMx=[1295,1339,1410,1435,1534,1685,1810,1894,1972,2010,2014,1986,1892,1295];
WMz=[1216,1224,1269,1349,1312,1288,1221,1145,1004, 850, 709, 605, 498,
498];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
RSCx=[1295,1521,1487,1435,1412,1339,1295];
RSCz=[1472,1472,1335,1349,1270,1224,1224];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
Ptx=[1521,1492,1534,1685,1808,1901];
Ptz=[1472,1332,1312,1288,1221,1337];
slicemap (specval(Pt), low,medLOW, MED, medHIGH, HIGH, Ptx, Ptz, Y);
S1BFx=[1808,1901,2077,1946];
S1BFz=[1221,1337,1174,1072];
slicemap (specval(S1BF), low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz,
Y);
Aux=[2077,1946,1975,2010,2014,2185];
Auz=[1174,1072, 997, 850, 774, 773];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
PRhx=[2014,2185,2130,1986];
PRhz=[ 774, 773, 570, 605];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[2130,1986,1961,2116];
Entz=[ 570, 605, 570, 522];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
PIRCx=[1961,2116,2116,1847];
PIRCz=[570, 522 , 380, 471];
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,
Y);
Cox=[1822,1844,1655];
Coz=[ 376, 431, 459];
slicemap (specval(Co), low,medLOW, MED, medHIGH, HIGH, Cox, Coz, Y);
BAX=[1844,1655,1725,1879];

```

```

BAz=[ 431, 459,515 , 492];
slicemap (specval(BA), low,medLOW, MED, medHIGH, HIGH, BAx, BAz, Y);
Lax=[1725,1879,1981];
Laz=[515 , 492, 636];
slicemap (specval(La), low,medLOW, MED, medHIGH, HIGH, Lax, Laz, Y);
VSx=[1655,1623,1658,1713];
VSz=[ 459, 498, 525, 506];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
CA1Vx=[1658,1713,1950,1942,1913];
CA1Vz=[ 525, 506, 608, 731, 746];
slicemap (specval(CA1V), low,medLOW, MED, medHIGH, HIGH, CA1Vx, CA1Vz,
Y);
CA2x=[1939,1899,1960,1985,1983,1931];
CA2z=[ 706, 670, 618, 678, 698, 703];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,
Y);
71
CA3Vx=[1931,1983,1961,1933,1844,1737,1631,1658,1824,1913,1942];
CA3Vz=[ 703, 698, 780, 804, 736, 686, 574, 525, 652, 746, 731];
slicemap (specval(CA3V), low,medLOW, MED, medHIGH, HIGH, CA3Vx, CA3Vz,
Y);
DGvx=[1631,1658,1623,1571];
DGvz=[ 574, 525, 498, 486];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
LGx=[1693,1774,1815,1783,1717,1749,1754,1710,1681,1695];
LGz=[1058,1009, 902, 800, 792, 829, 875, 938,1003,1057];
slicemap (specval(LG), low,medLOW, MED, medHIGH, HIGH, LGx, LGz, Y);
ZIRx=[1524,1663,1786,1765,1688,1650,1540];
ZIRz=[ 617, 765, 796, 766, 715, 664, 581];
slicemap (specval(ZIR), low,medLOW, MED, medHIGH, HIGH, ZIRx, ZIRz,
Y);
SThx=[1537,1650,1625,1548];
SThz=[ 570, 657, 603, 516];
slicemap (specval(STh), low,medLOW, MED, medHIGH, HIGH, SThx, SThz,
Y);
PRx=[1545,1477,1446,1402];
PRz=[ 606, 695, 697, 647];
slicemap (specval(PR), low,medLOW, MED, medHIGH, HIGH, PRx, PRz, Y);
VPMx=[1531,1663,1688,1675,1647,1610,1546,1477];
VPMz=[ 632, 765, 873, 947, 935, 832, 752, 700];
slicemap (specval(VPM), low,medLOW, MED, medHIGH, HIGH, VPMx, VPMz,
Y);
VPLx=[1686,1688,1660,1730,1723,1675];
VPLz=[ 939, 873,775 , 856, 897, 947];
slicemap (specval(VPL), low,medLOW, MED, medHIGH, HIGH, VPLx, VPLz,
Y);
LPx=[1683,1695,1586,1535,1475,1435,1404,1435,1547];
LPz=[ 973,1057,1065,1070,1049,1044, 959, 937, 973];
slicemap (specval(LP), low,medLOW, MED, medHIGH, HIGH, LPx, LPz, Y);
Pox=[1435,1496,1489,1446,1477,1555,1610,1684,1683,1576,1532];
Poz=[ 937, 845, 762, 697, 700, 758, 832, 939, 973, 975, 972];
slicemap (specval(Po), low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
PFx=[1339,1346,1320,1343,1402,1489,1496,1435,1404];
PFz=[ 948,811 , 726, 683, 647, 762, 845, 937, 959];
slicemap (specval(PF), low,medLOW, MED, medHIGH, HIGH, PFx, PFz, Y);
Hbx=[1306,1341,1404,1446,1435,1337,1311,1297];
Hbz=[ 956, 950, 959,1000,1044,1037,1004, 944];

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slicemap (specval(Hb), low,medLOW, MED, medHIGH, HIGH, Hbx, Hbz, Y);
PAGx=[1295,1305,1339,1346,1320,1295];
PAGz=[ 937, 961, 948, 811,726 , 726];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
PHDx=[1320,1343,1353,1345,1295,1295];
PHDz=[ 726, 683, 593, 552, 552, 728];
slicemap (specval(PHD), low,medLOW, MED, medHIGH, HIGH, PHDx, PHDz,
Y);
LHx=[1343,1353,1345,1451,1524,1571,1532,1545,1343];
LHz=[ 683, 593, 552, 538, 473, 486, 533, 606, 683];
slicemap (specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
SUMx=[1295,1348,1451,1524,1457,1378,1295];
72
SUMz=[ 558, 558,538 , 473, 438, 491, 505];
slicemap (specval(SUM), low,medLOW, MED, medHIGH, HIGH, SUMx, SUMz,
Y);
MMx=[1457,1378,1295,1295,1395];
MMz=[ 438, 491, 505, 414, 408];
slicemap (specval(MM), low,medLOW, MED, medHIGH, HIGH, MMx, MMz, Y);
NLx=[1295,1395,1295];
NLz=[ 414, 408, 373];
slicemap (specval(NL), low,medLOW, MED, medHIGH, HIGH, NLx, NLz, Y);
ALx=[1395,1295,1405];
ALz=[ 408, 373, 380];
slicemap (specval(AL), low,medLOW, MED, medHIGH, HIGH, ALx, ALz, Y);
CA1Dx=[1295,1295,1411,1480,1706,1866,1544,1454,1295];
CA1Dz=[1125,1165,1166,1245,1234,1107,1078,1045,1045];
slicemap (specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz,
Y);
Vx=[1548,1460,1347,1311,1295,1295,1348,1398,1482,1539];
Vz=[1076,1046,1041,1004, 939,1125,1077,1062,1095,1085];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
DGdx=[1533,1551,1635,1818,1814,1657,1586];
DGdz=[1084,1140,1177,1094,1048,1066,1065];
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
CA2x=[1818,1866,1898,1816];
CA2z=[1094,1107,1063,1048];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,
Y);
CA3Dx=[1898,1816,1761,1647,1618,1665,1657,1850,1890,1938,1926,1901];
CA3Dz=[1063,1048,1096,1139,1112,1086,1066, 958, 898, 924,1005,1063];
slicemap (specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz,
Y);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice40 next 3

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 40; Y=Slicenum*3;
PFx=[1430,1411,1401,1482,1535,1491,1450,1448];
PFz=[ 684, 712, 892, 872, 905, 797, 739, 696];

```

```

slicemap (specval(PF), low,medLOW, MED, medHIGH, HIGH, PFx, PFz, Y);
%QCcolor(PFx,PFz,40*3)
l=40;
%%Slicefeed(l);
WMx=[1295,1430,1481,1525,1681,1774,1894,1948,1977,2013,1994,1952,1815,1563,12
95];
WMz=[1221,1351,1344,1319,1294,1249,1149,1074,1000, 711, 630, 571,
507,483 , 483];
73
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
RSCx=[1295,1403,1510,1479,1441,1412,1295];
RSCz=[1434,1495,1483,1342,1356,1276,1221];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V2x=[1510,1479,1718,1769];
V2z=[1483,1342,1279,1414];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Ptx=[1718,1769,1913,1835];
Ptz=[1279,1414,1313,1204];
slicemap (specval(Pt), low,medLOW, MED, medHIGH, HIGH, Ptx, Ptz, Y);
S1BFx=[1913,1835,1948,2070];
S1BFz=[1313,1204,1074,1183];
slicemap (specval(S1BF), low,medLOW, MED, medHIGH, HIGH, S1BFx, S1BFz,
Y);
Aux=[1948,2070,2171,2185,2014,2010,1977];
Auz=[1074,1183,1003, 776,772 , 849,1000];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
PRhx=[2185,2014,1981,2130];
PRhz=[ 776,772 , 606, 568];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[1981,2130,2121,1952];
Entz=[ 606, 568, 523, 571];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
PIRCx=[2121,1952,1810,1866,1961,2059];
PIRCz=[ 523, 571, 494, 429, 414, 374];
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,
Y);
Cox=[1866,1815,1668,1700,1814];
Coz=[ 437, 507, 475, 442, 404];
slicemap (specval(Co), low,medLOW, MED, medHIGH, HIGH, Cox, Coz, Y);
VSx=[1724,1678,1644,1688];
VSz=[ 491, 543, 502, 475];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
CA1Vx=[1724,1678,1859,1871,1881,1930,1986,1950,1810];
CA1Vz=[ 491, 543, 651, 706, 753, 753, 666, 570, 494];
slicemap (specval(CA1V), low,medLOW, MED, medHIGH, HIGH, CA1Vx, CA1Vz,
Y);
CA2x=[1932,1925,1986,1981];
CA2z=[ 729, 671, 699, 723];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,
Y);
CA3Vx=[1626,1797,1837,1983,1962,1909,1810];
CA3Vz=[564 , 647, 730, 724, 786, 809,773 ];
slicemap (specval(CA3V), low,medLOW, MED, medHIGH, HIGH, CA3Vx, CA3Vz,
Y);
DGvx=[1626,1797,1837,1895,1898,1859,1830,1678,1644,1571];

```

```

DGvz=[564 , 647, 730, 746, 745, 651, 615, 543, 502, 488];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
DGdx=[1546,1566,1630,1784,1862,1901,1887];
DGdz=[1080,1142,1176,1132,1063, 995, 962];
74
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
CA3Dx=[1665,1632,1660,1788,1887,1899,1945,1969,1956,1921,1878,1834,1825,1787]
;
CA3Dz=[1062,1111,1138,1088, 962, 995, 992, 933, 846, 824, 882, 922,
961,1003];
slicemap (specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz,
Y);
CA2x=[1857,1901,1945,1906];
Ca2z=[1067, 995, 992,1066];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,
Y);
CA1Dx=[1857,1906,1769,1576,1525,1471,1295,1295,1348,1398,1542,1549,1630,1784]
;
CA1Dz=[1067,1066,1207,1268,1247,1188,1166,1300,1077,1062,1073,1112,1176,1132]
;
slicemap (specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz,
Y);
Vx=[1295,1322,1379,1454,1527,1482,1398,1348,1295];
Vz=[ 937,1023,1047,1045,1070,1095,1062,1077,1166];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
Hbx=[1306,1328,1368,1398,1353,];
Hbz=[ 965,1030,1046,1023, 966,];
slicemap (specval(Hb), low,medLOW, MED, medHIGH, HIGH, Hbx, Hbz, Y);
APTx=[1326,1405,1482,1550,1546,1496,1412,1383,1353];
APTz=[ 964, 884, 872, 943, 977,1055,1050,1000, 966];
slicemap (specval(APT), low,medLOW, MED, medHIGH, HIGH, APTx, APTz,
Y);
LPx=[1496,1544,1682,1665,1586,1542];
LPz=[1055, 969, 973,1062,1065,1073];
slicemap (specval(LP), low,medLOW, MED, medHIGH, HIGH, LPx, LPz, Y);
LGx=[1665,1682,1778,1790,1735,1808,1841,1825,1745];
LGz=[1062, 973, 935, 821, 774, 791, 904, 961,1035];
slicemap (specval(LG), low,medLOW, MED, medHIGH, HIGH, LGx, LGz, Y);
ZIRx=[1547,1543,1583,1735,1805,1759,1651,1561];
ZIRz=[ 637, 678, 715, 774, 787, 717, 670, 645];
slicemap (specval(ZIR), low,medLOW, MED, medHIGH, HIGH, ZIRx, ZIRz,
Y);
VPLx=[1750,1720,1782,1776];
VPLz=[ 941, 776, 862,905 ];
slicemap (specval(VPL), low,medLOW, MED, medHIGH, HIGH, VPLx, VPLz,
Y);
VPMx=[1750,1720,1543,1522,1600,1718];
VPMz=[ 941, 776, 678, 718, 766, 952];
slicemap (specval(VPM), low,medLOW, MED, medHIGH, HIGH, VPMx, VPMz,
Y);
Pox=[1718,1597,1532,1448,1544,1682];
Poz=[952 , 767, 720, 696, 969, 973];
slicemap (specval(Po), low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
PRx=[1548,1522,1430,1418];
PRz=[ 652, 718, 684, 629];
slicemap (specval(PR), low,medLOW, MED, medHIGH, HIGH, PRx, PRz, Y);

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PFx=[1418,1405,1527];
PFz=[ 629, 878, 883];
slicemap (specval(PF), low,medLOW, MED, medHIGH, HIGH, PFx, PFz, Y);
PAGx=[1295,1405,1411,1387,1381,1358,1295];
PAGz=[941 , 887, 716, 656, 699, 725, 725];
75
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
PHDx=[1387,1381,1358,1295,1295,1337,1367];
PHDz=[ 656, 699, 725, 725, 589, 589, 571];
slicemap (specval(PHD), low,medLOW, MED, medHIGH, HIGH, PHDx, PHDz,
Y);
SUMx=[1295,1337,1426,1442,1388,1316,1295];
SUMz=[589 , 589, 527, 471, 523, 538, 538];
slicemap (specval(SUM), low,medLOW, MED, medHIGH, HIGH, SUMx, SUMz,
Y);
MMx=[1295,1315,1388,1431,1393,1368,1295];
MMz=[ 538, 538, 523, 483, 481,452 , 452];
slicemap (specval(MM), low,medLOW, MED, medHIGH, HIGH, MMx, MMz, Y);
NLx=[1295,1368,1388,1295];
NLz=[ 452, 452, 434, 390];
slicemap (specval(NL), low,medLOW, MED, medHIGH, HIGH, NLx, NLz, Y);
ALx=[1388,1295,1295,1449,1494,1494,1463];
ALz=[ 434, 390, 351, 322, 341, 391, 422];
slicemap (specval(AL), low,medLOW, MED, medHIGH, HIGH, ALx, ALz, Y);
LHx=[1367,1387,1439,1554,1484,1503,1442,1426];
LHz=[ 571,656 , 620, 625, 568, 466, 471, 527];
slicemap (specval(LH), low,medLOW, MED, medHIGH, HIGH, LHx, LHz, Y);
SNCx=[1486,1504,1594,1529,1484];
SNCz=[ 511, 563, 655, 621, 568];
slicemap (specval(SNC), low,medLOW, MED, medHIGH, HIGH, SNCx, SNCz,
Y);
SNRx=[1486,1504,1594,1631,1618,1559,1563,1503];
SNRz=[ 511, 563, 655, 661, 592, 524, 484, 466];
slicemap (specval(SNR), low,medLOW, MED, medHIGH, HIGH, SNRx, SNRz,
Y);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice41

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 41;
CA2x=[2002,1912,1909,1989];
CA2z=[ 812, 806, 885, 894];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,
Y);
%QCcolor(CA2x,CA2z,41*3)
l=41;
RSCx=[1105,1110,1179,1232,1258,1295,1295,1239];
RSCz=[1490,1343,1201,1169,1194,1194,1433,1477];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V2x=[1492,1479,1521,1649,1717,1769];

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V2z=[1484,1342,1320,1303,1279,1414];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V1x=[1717,1769,1897,1826];
V1z=[1279,1414,1356,1213];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
Ptx=[1897,1826,1922,2061];
Ptz=[1356,1213,1126,1216];
slicemap (specval(Pt), low,medLOW, MED, medHIGH, HIGH, Ptx, Ptz, Y);
Aux=[1922,2061,2146,2190,2190,2040,2018,1988];
Auz=[1126,1216,1084, 888, 789, 783, 894,1003];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
Tex=[2190,2040,2022,2179];
Tez=[ 789, 783, 737, 741];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
PRhx=[2022,2179,2135,1991];
PRhz=[ 737, 741, 587, 626];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[2135,1991,1924,2099];
Entz=[ 587, 626, 550, 442];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
PIRCx=[1924,2099,2057,1904,1845];
PIRCz=[ 550, 442, 405, 453, 503];
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,
Y);
Cox=[1904,1845,1668,1737];
Coz=[ 453, 503, 475, 434];
slicemap (specval(Co), low,medLOW, MED, medHIGH, HIGH, Cox, Coz, Y);
VSx=[1845,1751,1678,1640,1668,1696];
VSz=[ 503, 573, 543, 498, 475, 490];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
CA1Vx=[1845,1751,1884,1912,2001,2004,1975,1924];
CA1Vz=[ 503, 573, 668, 806, 818, 705, 616, 550];
slicemap (specval(CA1V), low,medLOW, MED, medHIGH, HIGH, CA1Vx, CA1Vz,
Y);
CA2x=[1914,2001,1989,1909];
CA2z=[ 805, 818, 894, 887];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,
Y);
CA1Dx=[1989,1909,1879,1771,1635,1573,1553,1415,1370,1359,1437,1498,1534,1531,
1583,1704,1786,1957];
CA1Dz=[ 894,
887,1003,1122,1165,1139,1093,1091,1112,1143,1122,1125,1171,1227,1261,1236,119
7,1004];
slicemap (specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz,
Y);
DSx=[1359,1437,1498,1534,1531,1472,1407];
DSz=[1154,1122,1125,1171,1227,1179,1201];
slicemap (specval(DS), low,medLOW, MED, medHIGH, HIGH, DSx, DSz, Y);
DGdx=[1550,1663,1791,1807,1867,1909,1899,1837,1771,1635,1573];
DGdz=[1092,1054, 919, 837, 829, 829, 955,1064,1122,1165,1139];
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
CA3Dx=[1662,1791,1807,1867,1861,1818,1743,1640,1636];
CA3Dz=[1054, 919, 837, 829, 912,1003,1083,1125,1099];
```

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```

slicemap (specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz,
Y);
CA3Vx=[1807,1873,1829,1770,1696,1625,1643];
CA3Vz=[ 837, 833, 730, 646, 580, 558, 599];
slicemap (specval(CA3V), low,medLOW, MED, medHIGH, HIGH, CA3Vx, CA3Vz,
Y);
DGvx=[1640,1884,1907,1909,1867,1770,1696,1613];
DGvz=[ 500,668 , 715, 829, 829, 646, 580, 537];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
WMx=[1437,1391,1407,1472,1583,1704,1861,];
WMz=[1330,1226,1201,1179,1261,1236,1139,];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
mRtx=[1295,1401,1439,1465,1480,1566,1653,1647,1295];
mRtz=[1060,1059,1038,1000, 903, 839, 730, 662, 551];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
PAGx=[1295,1327,1404,1394,1338,1312,1295];
PAGz=[ 996,1011, 961, 859, 736, 640, 564];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
RLix=[1295,1321,1338,1320,1308,1295];
RLiz=[ 757, 755, 736, 651, 551, 551];
slicemap (specval(RLi), low,medLOW, MED, medHIGH, HIGH, RLix, RLiz,
Y);
VTAx=[1320,1308,1387,1420,1362];
VTAz=[ 651, 551, 498, 594, 644];
slicemap (specval(VTA), low,medLOW, MED, medHIGH, HIGH, VTAx, VTAz,
Y);
PRx=[1423,1471,1484,1458,1422,1381,1369,1384];
PRz=[ 810, 788, 749, 703, 697, 718, 747, 793];
slicemap (specval(PR), low,medLOW, MED, medHIGH, HIGH, PRx, PRz, Y);
SNCx=[1411,1624,1566,1420,1396];
SNCz=[ 536, 657, 671, 594, 552];
slicemap (specval(SNC), low,medLOW, MED, medHIGH, HIGH, SNCx, SNCz,
Y);
NLx=[1200,1213,1291,1372,1391];
NLz=[ 460, 432, 403, 431, 462];
slicemap (specval(NL), low,medLOW, MED, medHIGH, HIGH, NLx, NLz, Y);
ALx=[1295,1295,1408,1497,1528,1536,1513,1387,1372];
ALz=[ 403, 352, 323, 340, 383, 433, 459, 460, 431];
slicemap (specval(AL), low,medLOW, MED, medHIGH, HIGH, ALx, ALz, Y);
SNRx=[1401,1405,1485,1592,1624,1526];
SNRz=[ 524, 485, 495, 542, 657, 627];
slicemap (specval(SNR), low,medLOW, MED, medHIGH, HIGH, SNRx, SNRz,
Y);
Vx=[1295,1352,1354,1329,1295];
Vz=[1104,1139,1170,1194,1194];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
MPTx=[1295,1352,1370,1415,1401,1350,1295];
MPTz=[1104,1139,1112,1091,1059,1049,1060];
slicemap (specval(MPT), low,medLOW, MED, medHIGH, HIGH, MPTx, MPTz,
Y);
78
LGx=[1657,1649,1652,1681,1649,1661,1783,1807,1791,1657];
LGz=[1041,1003, 951, 903, 734, 679, 768, 837, 919,1041];
slicemap (specval(LG), low,medLOW, MED, medHIGH, HIGH, LGx, LGz, Y);
MGx=[1653,1736,1749,1690,1625,1609,1628];

```

```

MGz=[ 730, 809, 856, 907, 865, 801, 754];
slicemap (specval(MG), low,medLOW, MED, medHIGH, HIGH, MGx, MGz, Y);
LPx=[1673,1634,1569,1550,1593,1657,1649,1652];
LPz=[ 922, 919, 962,1092,1084,1041,1003, 951];
slicemap (specval(LP), low,medLOW, MED, medHIGH, HIGH, LPx, LPz, Y);
Pox=[1569,1562,1529,1566,1604,1609,1625,1690,1675,1634,1589];
Poz=[ 966, 902, 866, 839, 770, 801, 865, 907, 920, 919, 940];
slicemap (specval(Po), low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
APTx=[1550,1571,1569,1562,1529,1480,1465,1401,1415];
APTz=[1092,1003, 963, 902, 866, 903,1000,1059,1091];
slicemap (specval(APT), low,medLOW, MED, medHIGH, HIGH, APTx, APTz,
Y);
%%Sl=[];icefeed(1);
%l = 1;; %enter whatever slice you want
hold all;
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice42

```

if Slicenum == 42;
MGx=[1631,1664,1665,1697,1772,1794,1748,1691,1625,1609];
MGz=[ 754, 714, 677, 718, 775, 829, 892, 903, 865, 801];
%QCcolor(MGx,MGz,42*3)
l=42;
RSCx=[1295,1311,1467,1455,1424,1482,1442,1378,1328,1295];
RSCz=[1424,1450,1488,1365,1334,1189,1109,1143,1223,1219];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V2x=[1468,1455,1522,1658,1710];
V2z=[1489,1365,1328,1299,1433];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V2x=[1926,1839,1928,2056];
V2z=[1335,1217,1139,1214];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V1x=[1658,1710,1926,1839,1764];
V1z=[1299,1433,1335,1217,1266];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
Aux=[1928,2056,2129,2170,2194,2042,2001];
Auz=[1139,1214,1118,1003, 797, 805,1000];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
Tex=[2035,2194,2182,2030];
Tez=[ 804, 797, 737, 739];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
79
PRhx=[2182,2030,2002,2140];
PRhz=[ 737, 739, 642, 607];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[2002,2140,2104,1930];
Entz=[ 642, 607, 470, 554];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
PIRCx=[2104,1930,1842,1897,2049];
PIRCz=[ 470, 554,514 ,482 , 425];
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,

```

```

Y);
Cox=[1842,1897,1715,1687];
Coz=[514 ,482 , 440, 478];
slicemap (specval(Co), low,medLOW, MED, medHIGH, HIGH, Cox, Coz, Y);
VSx=[1687,1662,1746,1830];
VSz=[ 478, 527, 570, 516];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
CA1Vx=[1746,1830,1954,2005,2006,1914,1913,1889];
CA1Vz=[ 570, 516,568 , 670, 835, 824, 729, 668];
slicemap (specval(CA1V), low,medLOW, MED, medHIGH, HIGH, CA1Vx, CA1Vz,
Y);
CA2x=[1914,2006,1984,1912];
CA2z=[ 824, 835, 919, 913];
slicemap (specval(CA2), low,medLOW, MED, medHIGH, HIGH, CA2x, CA2z,
Y);
CA1Dx=[1984,1912,1814,1748,1699,1650,1579,1567,1756,1930,1973];
CA1Dz=[ 919, 913,1096,1145,1166,1170,1145,1217,1225,1085,1003];
slicemap (specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz,
Y);
DSx=[1570,1579,1566,1506,1477,1452];
DSz=[1090,1145,1215,1185,1193,1108];
slicemap (specval(DS), low,medLOW, MED, medHIGH, HIGH, DSx, DSz, Y);
DGdx=[1570,1692,1864,1919,1912,1814,1699,1650,1579];
DGdz=[1090,1031, 836, 825, 916,1096,1166,1170,1145];
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
CA3Dx=[1692,1693,1663,1689,1820,1861,1856,1806,1791];
CA3Dz=[1031,1062,1116,1128,1003, 874, 832, 837,919 ];
slicemap (specval(CA3D), low,medLOW, MED, medHIGH, HIGH, CA3Dx, CA3Dz,
Y);
DGvx=[1659,1684,1889,1913,1914,1864,1841,1768,1722];
DGvz=[ 609, 551, 668, 729, 824, 836, 771, 666,630,];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
CA3Vx=[1864,1841,1768,1722,1659];
CA3Vz=[ 836, 771, 666, 630, 609];
slicemap (specval(CA3V), low,medLOW, MED, medHIGH, HIGH, CA3Vx, CA3Vz,
Y);
LGx=[1678,1791,1794,1748,1691,1660];
LGz=[1026, 919, 829, 892, 903, 948];
slicemap (specval(LG), low,medLOW, MED, medHIGH, HIGH, LGx, LGz, Y);
LPx=[1551,1678,1674,1645,1569];
LPz=[1091,1026, 924, 917, 967];
80
slicemap (specval(LP), low,medLOW, MED, medHIGH, HIGH, LPx, LPz, Y);
Pox=[1569,1693,1625,1609,1629,1529];
Poz=[ 963, 903, 865, 801, 754, 866];
slicemap (specval(Po), low,medLOW, MED, medHIGH, HIGH, Pox, Poz, Y);
MGx=[1625,1609,1629,1665,1772,1807,1748];
MGz=[ 865, 801, 754, 677, 775, 865, 892];
slicemap (specval(MG), low,medLOW, MED, medHIGH, HIGH, MGx, MGz, Y);
APTx=[1529,1571,1571,1551,1442,1437,1401,1439,1465,1480];
APTz=[ 866, 924,1003,1091,1109,1079,1058,1038,1000, 903];
slicemap (specval(APT), low,medLOW, MED, medHIGH, HIGH, APTx, APTz,
Y);
MPTx=[1295,1364,1420,1437,1401,1350,1295];
MPTz=[1127,1167,1116,1079,1058,1049,1060];
slicemap (specval(MPT), low,medLOW, MED, medHIGH, HIGH, MPTx, MPTz,

```



```

Y);
Vx=[1295,1362,1328,1295];
Vz=[1124,1171,1223,1223];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
mRtx=[1350,1295,1295,1654,1664,1604,1566,1480,1465,1439];
mRtz=[1049,1060, 619, 662, 714, 770, 839, 903,1000,1038];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
RPx=[1418,1450,1470,1445,1411,1370,1377,1410];
RPz=[ 762, 753, 712, 671, 669, 703, 741, 765];
slicemap (specval(RP), low,medLOW, MED, medHIGH, HIGH, RPx, RPz, Y);
PAGx=[1299,1354,1401,1423,1425,1370,1352,1311,1295];
PAGz=[1014,1003, 969, 936, 899, 804, 728, 757, 757];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
RLix=[1352,1311,1295,1295,1322,1335];
RLiz=[ 728, 757, 757, 500, 500, 619];
slicemap (specval(RLi), low,medLOW, MED, medHIGH, HIGH, RLix, RLiz,
Y);
VTAx=[1322,1335,1394,1416,1400,1389];
VTAz=[ 500, 619, 620, 592, 526, 499];
slicemap (specval(VTA), low,medLOW, MED, medHIGH, HIGH, VTAx, VTAz,
Y);
SNCx=[1400,1469,1622,1558,1486,1416];
SNCz=[ 526, 589, 658, 673, 652, 592];
slicemap (specval(SNC), low,medLOW, MED, medHIGH, HIGH, SNCx, SNCz,
Y);
SNRx=[1389, 1469,1625,1654,1577];
SNRz=[499 , 589, 657, 662, 495];
slicemap (specval(SNR), low,medLOW, MED, medHIGH, HIGH, SNRx, SNRz,
Y);
NLx=[1295,1337,1386,1373,1295];
NLz=[ 462, 475, 472, 436, 403];
slicemap (specval(NL), low,medLOW, MED, medHIGH, HIGH, NLx, NLz, Y);
ALx=[1386,1373,1295,1295,1435,1523,1542,1528];
ALz=[ 472, 436, 403, 352, 327, 367, 409, 453];
slicemap (specval(AL), low,medLOW, MED, medHIGH, HIGH, ALx, ALz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
8l
hold all
for t = 1:plotable{1,2}%slice3l
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 43

```

% slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 43;
PAGx=[1235,1339,1390,1424,1434,1416,1334,1326,1293];
PAGz=[1034,1037,1024, 996, 930, 875, 813, 748, 756];
%QCcolor(PAGx,PAGz,3*44)
l=43;
RSCx=[1404,1463,1437,1507,1561,1529,1406,1341,1308,1308,1332];
RSCz=[1478,1348,1313,1237,1216,1140,1179,1237,1330,1418,1450];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);

```

```

V1x=[1627,1568,1620,1738,1826,1929];
V1z=[1447,1312,1282,1245,1188,1318];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1627,1568,1525,1462,1417];
V2z=[1447,1312,1339,1346,1478];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V2x=[1929,1826,1941,2073];
V2z=[1318,1188,1079,1164];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Aux=[1941,2073,2172,2022];
Auz=[1079,1164, 918, 901];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
Tex=[2172,2022,2032,2180];
Tez=[ 918, 901, 820, 826];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
PRhx=[2032,2180,2181,2141,2019,2033];
PRhz=[ 820, 826, 764, 687, 718, 788];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[2141,2019,1965,2046,2095,2119];
Entz=[ 687, 718, 613, 505, 522, 590];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
PIRCx=[2046,1965,1813,1785];
PIRCz=[ 505, 613, 542, 500];
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,
Y);
VSx=[1785,1970,2014,2009,1894,1892,1803,1758,1716,1665,1734];
VSz=[ 500, 624, 744, 862, 864, 806, 716, 712, 731, 618, 501];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
CA1Vx=[1894,2007,2013,1892];
CA1Vz=[ 864, 859, 739, 806];
82
slicemap (specval(CA1V), low,medLOW, MED, medHIGH, HIGH,CA1Vx, CA1Vz,
Y);
DSx=[1800,1691,1611,1534,1561,1686,];
DSz=[1159,1011,1111,1141,1216,1210,];
slicemap (specval(DS), low,medLOW, MED, medHIGH, HIGH, DSx, DSz, Y);
CA1Dx=[1894,2007,1956,1800,1739,1847,1893,1770];
CA1Dz=[ 864, 859,1000,1159,1079,1003, 911,1180];
slicemap (specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz,
Y);
DGdx=[1691,1698,1749,1847,1893,1894,1742];
DGdz=[1011,1058,1077,1003, 911, 864, 869];
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
DGvx=[1742,1894,1892,1803,1758,1716,1746];
DGvz=[ 869, 864, 806, 716, 712, 731, 813];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
MGx=[1674,1650,1647,1696,1701];
MGz=[ 936, 903, 825, 791, 892];
slicemap (specval(MG), low,medLOW, MED, medHIGH, HIGH, MGx, MGz, Y);
Sux=[1436,1504,1565,1652,1677,1642,1406,1341,1324,1295,1295,1339,1390,1424];
Suz=[ 930, 877, 872, 909, 936,1088,1179,1237,1211,1211,1037,1037,1024,
996];
slicemap (specval(Su), low,medLOW, MED, medHIGH, HIGH, Sux, Suz, Y);

```

```

mRtx=[1436,1504,1565,1652,1647,1670,1695,1670,1616,1423,1369,1324,1337,1334,1
416];
mRtz=[ 930, 877, 872, 909, 825, 796, 790, 725, 735, 590, 650, 652,
688, 813, 875];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
SNRx=[1668,1626,1460,1397,1452,1554,1638];
SNRz=[ 711, 619, 493, 491, 583, 678, 714];
slicemap (specval(SNR), low,medLOW, MED, medHIGH, HIGH, SNRx, SNRz,
Y);
VTAx=[1295,1365,1388,1421,1410,1369,1324];
VTAz=[ 632, 573, 534, 582, 617, 650, 652];
slicemap (specval(VTA), low,medLOW, MED, medHIGH, HIGH, VTAx, VTAz,
Y);
SNCx=[1388,1426,1546,1616,1670,1668,1638,1554,1452,1400];
SNCz=[ 534, 590, 699, 735, 725, 711, 714, 678, 583, 497];
slicemap (specval(SNC), low,medLOW, MED, medHIGH, HIGH, SNCx, SNCz,
Y);
IPx=[1295,1365,1388,1401,1295];
IPz=[ 632, 573, 534, 500, 500];
slicemap (specval(IP), low,medLOW, MED, medHIGH, HIGH, IPx, IPz, Y);
RLix=[1295,1324,1337,1331,1306,1295];
RLiz=[ 632, 652, 688, 736, 756, 756];
slicemap (specval(RLi), low,medLOW, MED, medHIGH, HIGH, RLix, RLiz,
Y);
PAGx=[1306,1295,1295,1339,1390,1424,1434,1416,1334];
PAGz=[ 756, 756,1037,1037,1024, 996, 930, 875, 813];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
ALx=[1385,1371,1295,1295,1519,1546,1527,1498];
ALz=[ 449, 418, 390, 352,353 , 433, 471, 480];
83
slicemap (specval(AL), low,medLOW, MED, medHIGH, HIGH, ALx, ALz, Y);
NLx=[1385,1371,1295,1295,1325];
NLz=[ 449, 418, 390, 451, 439];
slicemap (specval(NL), low,medLOW, MED, medHIGH, HIGH, NLx, NLz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 44

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 44;
PAGx=[1235,1339,1390,1424,1434,1416,1334,1326,1293];
PAGz=[1034,1037,1024, 996, 930, 875, 813, 748, 756];
%QCcolor(PAGx,PAGz,3*44)
l=44;
RSCx=[1404,1463,1437,1507,1561,1529,1406,1341,1308,1308,1332];
RSCz=[1478,1348,1313,1237,1216,1140,1179,1237,1330,1418,1450];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V1x=[1627,1568,1620,1738,1826,1929];
V1z=[1447,1312,1282,1245,1188,1318];

```

```

slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1627,1568,1525,1462,1417];
V2z=[1447,1312,1339,1346,1478];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V2x=[1929,1826,1941,2073];
V2z=[1318,1188,1079,1164];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Aux=[1941,2073,2172,2022];
Auz=[1079,1164, 918, 901];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
Tex=[2172,2022,2032,2180];
Tez=[ 918, 901, 820, 826];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
PRhx=[2032,2180,2181,2141,2019,2033];
PRhz=[ 820, 826, 764, 687, 718, 788];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[2141,2019,1965,2046,2095,2119];
Entz=[ 687, 718, 613, 505, 522, 590];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
PIRCx=[2046,1965,1813,1785];
PIRCz=[ 505, 613, 542, 500];
84
slicemap (specval(PIRC), low,medLOW, MED, medHIGH, HIGH, PIRCx, PIRCz,
Y);
VSx=[1785,1970,2014,2009,1894,1892,1803,1758,1716,1665,1734];
VSz=[ 500, 624, 744, 862, 864, 806, 716, 712, 731, 618, 501];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
CA1Vx=[1894,2007,2013,1892];
CA1Vz=[ 864, 859, 739, 806];
slicemap (specval(CA1V), low,medLOW, MED, medHIGH, HIGH,CA1Vx, CA1Vz,
Y);
DSx=[1800,1691,1611,1534,1561,1686,];
DSz=[1159,1011,1111,1141,1216,1210,];
slicemap (specval(DS), low,medLOW, MED, medHIGH, HIGH, DSx, DSz, Y);
CA1Dx=[1894,2007,1956,1800,1739,1847,1893,1770];
CA1Dz=[ 864, 859,1000,1159,1079,1003, 911,1180];
slicemap (specval(CA1D), low,medLOW, MED, medHIGH, HIGH, CA1Dx, CA1Dz,
Y);
DGdx=[1691,1698,1749,1847,1893,1894,1742];
DGdz=[1011,1058,1077,1003, 911, 864, 869];
slicemap (specval(DGd), low,medLOW, MED, medHIGH, HIGH, DGdx, DGdz,
Y);
DGvx=[1742,1894,1892,1803,1758,1716,1746];
DGvz=[ 869, 864, 806, 716, 712, 731, 813];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
MGx=[1674,1650,1647,1696,1701];
MGz=[ 936, 903, 825, 791, 892];
slicemap (specval(MG), low,medLOW, MED, medHIGH, HIGH, MGx, MGz, Y);
Sux=[1436,1504,1565,1652,1677,1642,1406,1341,1324,1295,1295,1339,1390,1424];
Suz=[ 930, 877, 872, 909, 936,1088,1179,1237,1211,1211,1037,1037,1024,
996];
slicemap (specval(Su), low,medLOW, MED, medHIGH, HIGH, Sux, Suz, Y);
mRtx=[1436,1504,1565,1652,1647,1670,1695,1670,1616,1423,1369,1324,1337,1334,1
416];
mRtz=[ 930, 877, 872, 909, 825, 796, 790, 725, 735, 590, 650, 652,

```

```

688, 813, 875];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
SNRx=[1668,1626,1460,1397,1452,1554,1638];
SNRz=[ 711, 619, 493, 491, 583, 678, 714];
slicemap (specval(SNR), low,medLOW, MED, medHIGH, HIGH, SNRx, SNRz,
Y);
VTAx=[1295,1365,1388,1421,1410,1369,1324];
VTAz=[ 632, 573, 534, 582, 617, 650, 652];
slicemap (specval(VTA), low,medLOW, MED, medHIGH, HIGH, VTAx, VTAz,
Y);
SNCx=[1388,1426,1546,1616,1670,1668,1638,1554,1452,1400];
SNCz=[ 534, 590, 699, 735, 725, 711, 714, 678, 583, 497];
slicemap (specval(SNC), low,medLOW, MED, medHIGH, HIGH, SNCx, SNCz,
Y);
IPx=[1295,1365,1388,1401,1295];
IPz=[ 632, 573, 534, 500, 500];
slicemap (specval(IP), low,medLOW, MED, medHIGH, HIGH, IPx, IPz, Y);
RLix=[1295,1324,1337,1331,1306,1295];
RLiz=[ 632, 652, 688, 736, 756, 756];
85
slicemap (specval(RLi), low,medLOW, MED, medHIGH, HIGH, RLix, RLiz,
Y);
PAGx=[1306,1295,1295,1339,1390,1424,1434,1416,1334];
PAGz=[ 756, 756,1037,1037,1024, 996, 930, 875, 813];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
ALx=[1385,1371,1295,1295,1519,1546,1527,1498];
ALz=[ 449, 418, 390, 352,353 , 433, 471, 480];
slicemap (specval(AL), low,medLOW, MED, medHIGH, HIGH, ALx, ALz, Y);
NLx=[1385,1371,1295,1295,1325];
NLz=[ 449, 418, 390, 451, 439];
slicemap (specval(NL), low,medLOW, MED, medHIGH, HIGH, NLx, NLz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice45

```

if Slicenum == 45;
DGvx=[1731,1796,1858,1877,1860,1775,1729,1722,1741,1738];
DGvz=[ 815, 786, 817, 885, 956,1021, 997, 957, 902, 835];
%QCcolor (DGvx,DGvz,45*3)
l=45;
RSCx=[1555,1330,1338,1306,1311,1363,1472,1517];
RSCz=[1176,1251,1272,1356,1415,1453,1465,1326];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH,RSCx, RSCz, Y);
V2x=[1472,1517,1572,1625];
V2z=[1465,1326,1315,1442];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V1x=[1572,1625,1744,1876,1920,1819];
V1z=[1315,1442,1410,1347,1314,1179];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1920,1819,1940,2057];

```

```

V2z=[1314,1179,1071,1186];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Aux=[1940,2057,2103,2141,2154,2019,1985];
Auz=[1071,1186,1104,1005, 915, 901,1003];
slicemap (specval(Au), low,medLOW, MED, medHIGH, HIGH, Aux, Auz, Y);
Tex=[2154,2019,2029,2177];
Tez=[ 915, 901, 821, 821];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
PRhx=[2029,2177,2136,1987];
PRhz=[ 821, 821,686, 728];
slicemap (specval(PRh), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz,
Y);
Entx=[2136,1987,1721,1678,1725,2093];
86
Entz=[686, 728, 794, 664, 542, 575];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
VSx=[1731,1723,1781,1928,1978,2011,1968,1860,1877,1858,1796];
VSz=[ 815, 796, 728, 686, 722, 781, 976, 956, 885, 817, 786];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
DSx=[1722,1555,1574,1752,1844,1918,1966,1871];
DSz=[ 957,1176,1234,1176,1125,1059, 980, 956];
slicemap (specval(DS), low,medLOW, MED, medHIGH, HIGH, DSx, DSz, Y);
DGvx=[1871,1877,1858,1796,1731,1741,1724,1753,1775];
DGvz=[ 956, 885, 817, 786, 815, 902, 959,1021,1021];
slicemap (specval(DGv), low,medLOW, MED, medHIGH, HIGH, DGvx, DGvz,
Y);
Sux=[1295,1330,1449,1555,1628,1710,1553,1440,1410,1350,1295];
Suz=[1222,1251,1231,1176,1094, 935, 864, 948,1003,1039,1039];
slicemap (specval(Su), low,medLOW, MED, medHIGH, HIGH, Sux, Suz, Y);
mRtx=[1325,1333,1405,1440,1498,1553,1624,1710,1711,1674,1614,1545,1426,1359,1
311,1303,1336];
mRtz=[ 751, 811, 862, 948, 883, 864, 880, 935, 838, 732, 727, 692,
594, 622, 620, 629, 675];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
RPx=[1449,1462,1456,1403,1389,1416];
RPz=[ 741, 710, 685, 674, 733, 752];
slicemap (specval(RP), low,medLOW, MED, medHIGH, HIGH, RPx, RPz, Y);
SNCx=[1392,1426,1545,1614,1674,1655,1627,1555,1452,1404];
SNCz=[ 536, 594, 692, 727, 732, 711, 714, 680, 538, 507];
slicemap (specval(SNC), low,medLOW, MED, medHIGH, HIGH, SNCx, SNCz,
Y);
SNRx=[1655,1627,1555,1452,1404,1422,1496,1605];
SNRz=[ 711, 714, 680, 538, 507, 477, 509, 629];
slicemap (specval(SNR), low,medLOW, MED, medHIGH, HIGH, SNRx, SNRz,
Y);
VTAx=[1385,1428,1395,1359,1325];
VTAz=[ 532, 587, 617, 622, 605];
slicemap (specval(VTA), low,medLOW, MED, medHIGH, HIGH, VTAx, VTAz,
Y);
IPx=[1295,1325,1404,1315,1295];
IPz=[ 620, 605, 507,430 , 451];
slicemap (specval(IP), low,medLOW, MED, medHIGH, HIGH, IPx, IPz, Y);
Pnx=[1315,1387,1491,1527,1527,1471,1359];
Pnz=[ 430, 495, 504, 443, 392, 355, 363];
slicemap (specval(Pn), low,medLOW, MED, medHIGH, HIGH, Pnx, Pnz, Y);
RLix=[1295,1325,1336,1295];

```

```

RLiz=[ 757, 751, 675, 620];
slicemap (specval(RLi), low,medLOW, MED, medHIGH, HIGH, RLix, RLiz,
Y);
PAGx=[1440,1410,1350,1295,1295,1325,1333,1405];
PAGz=[ 948,1003,1039,1039, 757, 751, 811, 862];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
87
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice46 next 3

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 46;
ICx=[1565,1569,1636,1706,1711,1676,1612];
ICz=[ 798, 862, 886, 936, 874, 779, 763];
%QCcolor (ICx,ICz,46*3)
l=46;
RSCx=[1616,1592,1345,1313,1327,1475,1546];
RSCz=[1221,1156,1248,1320,1417,1461,1289];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V2x=[1475,1546,1590,1642];
V2z=[1461,1289,1294,1427];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V1x=[1590,1642,1746,1915,1808];
V1z=[1294,1427,1398,1302,1158];
slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1915,1808,1874,1989,2111];
V2z=[1302,1158,1110, 964,1025];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Tex=[2111,1989,2027,2158];
Tez=[1025, 964, 833, 837];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
PRhx=[2027,2158,2124,1998];
PRhz=[ 833, 837, 712, 737];
slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, PRhx, PRhz, Y);
Entx=[2124,1998,1728,1686,1762,1979,2077];
Entz=[ 712, 737, 850, 689, 568, 553,605 ];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
VSx=[1729,1821,1867,1930,2003,2004,1962,1882,1731];
VSz=[ 853, 785, 679, 687, 745, 844, 955, 907, 912];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
DSx=[1962,1882,1731,1702,1592 ,1616,1885,1937];
DSz=[ 955, 907, 912, 999, 1156,1221,1060,1003];
slicemap (specval(DS), low,medLOW, MED, medHIGH, HIGH, DSx, DSz, Y);
PAGx=[1295,1369,1419,1445,1428,1395,1341,1295];
PAGz=[1031,1046,1004, 887, 846, 825, 827, 861];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
DRx=[1341,1295,1295,1319,1320];

```

```

DRz=[ 827, 861, 750, 750, 802];
slicemap (specval(DR), low,medLOW, MED, medHIGH, HIGH, DRx, DRz, Y);
RLx=[1295,1319,1334,1332,1295];
RLz=[ 750, 750, 677, 626, 626];
slicemap (specval(RLi), low,medLOW, MED, medHIGH, HIGH, RLx, RLz, Y);
88
mRtx=[1341,1320,1334,1332,1352,1385,1430,1447,1493,1584,1676,1568,1470,1414];
mRtz=[ 827, 802, 677, 626, 556, 514, 535, 621, 654, 625, 779, 737,
774, 831];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
PrCnx=[1414,1470,1568,1612,1569,1440];
PrCnz=[ 831, 774, 737, 763, 862, 939];
slicemap (specval(PrCn), low,medLOW, MED, medHIGH, HIGH, PrCnx, PrCnz,
Y);
ICx=[1569,1612,1676,1711,1708];
ICz=[ 862, 763, 779, 874, 932];
slicemap (specval(IC), low,medLOW, MED, medHIGH, HIGH, ICx, ICz, Y);
MnRx=[1273,1332,1385,1390,1295];
MnRz=[ 634, 626, 514, 469, 469];
slicemap (specval(MnR), low,medLOW, MED, medHIGH, HIGH, MnRx, MnRz,
Y);
Pnx=[1295,1390,1588,1574,1468,1295];
Pnz=[469 , 469, 578, 383, 342, 365];
slicemap (specval(Pn), low,medLOW, MED, medHIGH, HIGH, Pnx, Pnz, Y);
PTgx=[1430,1522,1587,1493,1447];
PTgz=[ 530, 556, 628, 654, 621];
slicemap (specval(PTg), low,medLOW, MED, medHIGH, HIGH, PTgx, PTgz,
Y);
fiveRx=[1588,1574,1634,1696,1686,1644];
fiveRz=[ 578, 383, 406, 509, 562, 578];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice47 star

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 47;
DRx=[1295,1326,1340,1322,1291];
DRz=[ 861, 849, 828, 791,788];
%QCcolor (DRx,DRz,47*3)
l=47;
RSCx=[1343,1592, 1608,1754,1665,1559,1494,1358,1314,1301];
RSCz=[1415, 1265,1232,1135,1059,1190,1222,1260,1292,1359];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V2x=[1343,1592,1611,1590,1443];
V2z=[1415,1265,1282,1434,1443];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V1x=[1590,1611,1668,1823,1933,1761];
89

```



```

V1z=[1434,1282,1258,1126,1270,1376];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1823,1915,2038,1930];
V2z=[1126,1007,1070,1272];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Tex=[1915,2035,2103,2151,1982];
Tez=[1007,1072,1003, 859, 858];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
Entx=[2149,1981,1865,1808,1718,1709,1770,1872,1983,2078,2115,2175];
Entz=[ 860, 856, 900, 898, 937, 734, 637, 584, 580, 645, 733, 770];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
VSx=[1866,1808,1719,1702,1665,1735,1849];
VSz=[ 899, 898, 941,1003,1059,1147,1003];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
Sux=[1548,1466,1353,1317,1295,1295,1326,1374,1423,1437,1507,1560];
Suz=[1170,1220,1240,1217,1140,1031,1045,1045,1003, 957, 962,1077];
slicemap (specval(Su), low,medLOW, MED, medHIGH, HIGH, Sux, Suz, Y);
ICx=[1548,1560,1507,1501,1519,1583,1689,1704,1685,1623];
ICz=[1170,1077, 962, 925, 873, 821, 806, 938,1003,1094];
slicemap (specval(IC), low,medLOW, MED, medHIGH, HIGH, ICx, ICz, Y);
PrCnx=[1437,1436,1514,1583,1519,1501,1507];
PrCnz=[ 957, 862, 803, 821, 873, 925, 962];
slicemap (specval(PrCn), low,medLOW, MED, medHIGH, HIGH, PrCnx, PrCnz,
Y);
PAGx=[1437,1436,1406,1338,1295,1295,1326,1374,1423];
PAGz=[ 957, 862, 831, 820, 861,1031,1045,1045,1003];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
DRx=[1295,1322,1326,1295];
DRz=[ 788, 791, 849, 862];
slicemap (specval(DR), low,medLOW, MED, medHIGH, HIGH, DRx, DRz, Y);
mRtx=[1322,1444,1478,1653,1689,1583,1433,1406,1338];
mRtz=[ 791, 758, 779, 695, 806, 821, 862, 831, 820];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
WMx=[1295,1322,1441,1413,1295];
WMz=[ 788, 791, 761, 745, 728];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WMx=[1653,1504,1456,1388,1407,1478,1639];
WMz=[ 695, 539, 502, 480, 425, 450, 625];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
PTgx=[1478,1644,1653,1581,1436];
PTgz=[ 779, 731, 702,612 , 740];
slicemap (specval(PTg), low,medLOW, MED, medHIGH, HIGH, PTgx, PTgz,
Y);
LLx=[1581,1436,1513];
LLz=[612 , 740, 541];
slicemap (specval(LL), low,medLOW, MED, medHIGH, HIGH, LLx, LLz, Y);
PnOx=[1436,1513,1456,1388,1295];
PnOz=[ 740, 541, 502, 480, 728];
slicemap (specval(PnO), low,medLOW, MED, medHIGH, HIGH, PnOx, PnOz,
Y);
90
MnRx=[1295,1295,1384,1388];
MnRz=[ 728, 436, 436, 480];
slicemap (specval(MnR), low,medLOW, MED, medHIGH, HIGH, MnRx, MnRz,
Y);

```

```

Pnx=[1295,1384,1407,1478,1597,1562,1579,1515,1324,1295];
Pnz=[ 436, 436, 425, 450, 574, 440, 395, 350, 343, 356];
slicemap (specval(Pn), low,medLOW, MED, medHIGH, HIGH, Pnx, Pnz, Y);
fiveRx=[1597,1562,1579,1673,1705,1687,1646];
fiveRz=[ 574, 440, 395, 463, 549, 578, 595];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice48

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 48;
DRx=[1295,1326,1340,1322,1291];
DRz=[ 861, 849, 828, 791,788];
%QCcolor (DRx,DRz,47*3)
l=48;
Y=48*3;
RSCx=[1343,1592, 1608,1754,1665,1559,1494,1358,1314,1301];
RSCz=[1415, 1265,1232,1135,1059,1190,1222,1260,1292,1359];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V2x=[1343,1592,1611,1590,1443];
V2z=[1415,1265,1282,1434,1443];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V1x=[1590,1611,1668,1823,1933,1761];
V1z=[1434,1282,1258,1126,1270,1376];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1823,1915,2038,1930];
V2z=[1126,1007,1070,1272];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Tex=[1915,2035,2103,2151,1982];
Tez=[1007,1072,1003, 859, 858];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
Entx=[2149,1981,1865,1808,1718,1709,1770,1872,1983,2078,2115,2175];
Entz=[ 860, 856, 900, 898, 937, 734, 637, 584, 580, 645, 733, 770];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
VSx=[1866,1808,1719,1702,1665,1735,1849];
VSz=[ 899, 898, 941,1003,1059,1147,1003];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
Sux=[1548,1466,1353,1317,1295,1295,1326,1374,1423,1437,1507,1560];
9l
Suz=[1170,1220,1240,1217,1140,1031,1045,1045,1003, 957, 962,1077];
slicemap (specval(Su), low,medLOW, MED, medHIGH, HIGH, Sux, Suz, Y);
ICx=[1548,1560,1507,1501,1519,1583,1689,1704,1685,1623];
ICz=[1170,1077, 962, 925, 873, 821, 806, 938,1003,1094];
slicemap (specval(IC), low,medLOW, MED, medHIGH, HIGH, ICx, ICz, Y);
PrCnx=[1437,1436,1514,1583,1519,1501,1507];
PrCnz=[ 957, 862, 803, 821, 873, 925, 962];
slicemap (specval(PrCn), low,medLOW, MED, medHIGH, HIGH, PrCnx, PrCnz,
Y);

```

```

PAGx=[1437,1436,1406,1338,1295,1295,1326,1374,1423];
PAGz=[ 957, 862, 831, 820, 861,1031,1045,1045,1003];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
DRx=[1295,1322,1326,1295];
DRz=[ 788, 791, 849, 862];
slicemap (specval(DR), low,medLOW, MED, medHIGH, HIGH, DRx, DRz, Y);
mRtx=[1322,1444,1478,1653,1689,1583,1433,1406,1338];
mRtz=[ 791, 758, 779, 695, 806, 821, 862, 831, 820];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
WMx=[1295,1322,1441,1413,1295];
WMz=[ 788, 791, 761, 745, 728];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WMx=[1653,1504,1456,1388,1407,1478,1639];
WMz=[ 695, 539, 502, 480, 425, 450, 625];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
PTgx=[1478,1644,1653,1581,1436];
PTgz=[ 779, 731, 702,612 , 740];
slicemap (specval(PTg), low,medLOW, MED, medHIGH, HIGH, PTgx, PTgz,
Y);
LLx=[1581,1436,1513];
LLz=[612 , 740, 541];
slicemap (specval(LL), low,medLOW, MED, medHIGH, HIGH, LLx, LLz, Y);
PnOx=[1436,1513,1456,1388,1295];
PnOz=[ 740, 541, 502, 480, 728];
slicemap (specval(PnO), low,medLOW, MED, medHIGH, HIGH, PnOx, PnOz,
Y);
MnRx=[1295,1295,1384,1388];
MnRz=[ 728, 436, 436, 480];
slicemap (specval(MnR), low,medLOW, MED, medHIGH, HIGH, MnRx, MnRz,
Y);
Pnx=[1295,1384,1407,1478,1597,1562,1579,1515,1324,1295];
Pnz=[ 436, 436, 425, 450, 574, 440, 395, 350, 343, 356];
slicemap (specval(Pn), low,medLOW, MED, medHIGH, HIGH, Pnx, Pnz, Y);
fiveRx=[1597,1562,1579,1673,1705,1687,1646];
fiveRz=[ 574, 440, 395, 463, 549, 578, 595];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
%%Slicefeed(1);
%1 = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
92
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice49

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 49;
DRx=[1295,1326,1340,1322,1291];
DRz=[ 861, 849, 828, 791,788];
%QCcolor (DRx,DRz,47*3)
l=49;
Y=49*3;
RSCx=[1343,1592, 1608,1754,1665,1559,1494,1358,1314,1301];

```

```

RSCz=[1415, 1265,1232,1135,1059,1190,1222,1260,1292,1359];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
V2x=[1343,1592,1611,1590,1443];
V2z=[1415,1265,1282,1434,1443];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
V1x=[1590,1611,1668,1823,1933,1761];
V1z=[1434,1282,1258,1126,1270,1376];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1823,1915,2038,1930];
V2z=[1126,1007,1070,1272];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Tex=[1915,2035,2103,2151,1982];
Tez=[1007,1072,1003, 859, 858];
slicemap (specval(Te), low,medLOW, MED, medHIGH, HIGH, Tex, Tez, Y);
Entx=[2149,1981,1865,1808,1718,1709,1770,1872,1983,2078,2115,2175];
Entz=[ 860, 856, 900, 898, 937, 734, 637, 584, 580, 645, 733, 770];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
VSx=[1866,1808,1719,1702,1665,1735,1849];
VSz=[ 899, 898, 941,1003,1059,1147,1003];
slicemap (specval(VS), low,medLOW, MED, medHIGH, HIGH, VSx, VSz, Y);
Sux=[1548,1466,1353,1317,1295,1295,1326,1374,1423,1437,1507,1560];
Suz=[1170,1220,1240,1217,1140,1031,1045,1045,1003, 957, 962,1077];
slicemap (specval(Su), low,medLOW, MED, medHIGH, HIGH, Sux, Suz, Y);
ICx=[1548,1560,1507,1501,1519,1583,1689,1704,1685,1623];
ICz=[1170,1077, 962, 925, 873, 821, 806, 938,1003,1094];
slicemap (specval(IC), low,medLOW, MED, medHIGH, HIGH, ICx, ICz, Y);
PrCnx=[1437,1436,1514,1583,1519,1501,1507];
PrCnz=[ 957, 862, 803, 821, 873, 925, 962];
slicemap (specval(PrCn), low,medLOW, MED, medHIGH, HIGH, PrCnx, PrCnz,
Y);
PAGx=[1437,1436,1406,1338,1295,1295,1326,1374,1423];
PAGz=[ 957, 862, 831, 820, 861,1031,1045,1045,1003];
slicemap (specval(PAG), low,medLOW, MED, medHIGH, HIGH, PAGx, PAGz,
Y);
DRx=[1295,1322,1326,1295];
DRz=[ 788, 791, 849, 862];
93
slicemap (specval(DR), low,medLOW, MED, medHIGH, HIGH, DRx, DRz, Y);
mRtx=[1322,1444,1478,1653,1689,1583,1433,1406,1338];
mRtz=[ 791, 758, 779, 695, 806, 821, 862, 831, 820];
slicemap (specval(mRt), low,medLOW, MED, medHIGH, HIGH, mRtx, mRtz,
Y);
WMx=[1295,1322,1441,1413,1295];
WMz=[ 788, 791, 761, 745, 728];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
WMx=[1653,1504,1456,1388,1407,1478,1639];
WMz=[ 695, 539, 502, 480, 425, 450, 625];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
PTgx=[1478,1644,1653,1581,1436];
PTgz=[ 779, 731, 702,612 , 740];
slicemap (specval(PTg), low,medLOW, MED, medHIGH, HIGH, PTgx, PTgz,
Y);
LLx=[1581,1436,1513];
LLz=[612 , 740, 541];
slicemap (specval(LL), low,medLOW, MED, medHIGH, HIGH, LLx, LLz, Y);
PnOx=[1436,1513,1456,1388,1295];

```

```

PnOz=[ 740, 541, 502, 480, 728];
slicemap (specval(PnO), low,medLOW, MED, medHIGH, HIGH, PnOx, PnOz,
Y);
MnRx=[1295,1295,1384,1388];
MnRz=[ 728, 436, 436, 480];
slicemap (specval(MnR), low,medLOW, MED, medHIGH, HIGH, MnRx, MnRz,
Y);
Pnx=[1295,1384,1407,1478,1597,1562,1579,1515,1324,1295];
Pnz=[ 436, 436, 425, 450, 574, 440, 395, 350, 343, 356];
slicemap (specval(Pn), low,medLOW, MED, medHIGH, HIGH, Pnx, Pnz, Y);
fiveRx=[1597,1562,1579,1673,1705,1687,1646];
fiveRz=[ 574, 440, 395, 463, 549, 578, 595];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Vx=[1295,1322,1343,1318,1295];
Vz=[1054,1038, 985, 898,873 ];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice50 star

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum ==50 ;
Y = 50*3;
Cbx =[1437,1295,1294,1385,1450,1503,1507];
Cbz =[991 , 991, 785, 785, 812, 886, 926];
94
%QCcolor (Cbx,Cbz,50*3)
V1x=[1470,1549,1643,1765,1705,1591,1490,1465];
V1z=[1376,1376,1359,1292,1174,1209,1261,1301];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1707,1766,1906,1837];
V2z=[1173,1291,1178,1092];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Ectx=[1906,1837,1957,2015];
Ectz=[1178,1092,1000,1003];
slicemap (specval(Ect), low,medLOW, MED, medHIGH, HIGH, Ectx, Ectz,
Y);
Entx=[1837,1957,2015,2039,2010,1884,1697,1648];
Entz=[1092,1000,1003, 853, 814, 830,1002,1075];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
RSCx=[1648,1837,1705,1591,1548];
RSCz=[1075,1092,1174,1209,1198];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
fourCbx=[1295,1352,1333,1339,1295];
fourCbz=[1333,1311,1276,1232,1232];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1295,1339,1445,1556,1557,1485,1295];
threeCbz=[1232,1232,1103,1041,1002, 969, 986];

```

```

slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
twoCbx=[1295,1485,1557,1613,1486,1355,1295];
twoCbz=[986 , 969,1002, 760, 823, 841, 790];
slicemap (specval(twoCb), low,medLOW, MED, medHIGH, HIGH, twoCbx,
twoCbz, Y);
fiveCbx=[1544,1648,1804,1794,1588];
fiveCbz=[1043,1075, 869, 815, 939];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);
threeCbx=[1794,1588,1570,1617,1721,1796];
threeCbz=[ 815, 939, 924, 758, 753, 778];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
ICx=[1556,1627,1443,1352,1333,1339,1377,1445];
ICz=[1040,1086,1299,1311,1276,1232,1173,1103];
slicemap (specval(IC), low,medLOW, MED, medHIGH, HIGH, ICx, ICz, Y);
CGx=[1295,1512,1486,1355,1294];
CGz=[712 ,712 , 823, 831, 790];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, CGx, CGz, Y);
PBx=[1486,1615,1700,1669,1512];
PBz=[ 823, 757, 747, 703, 712];
slicemap (specval(PB), low,medLOW, MED, medHIGH, HIGH, PBx, PBz, Y);
DMTgx=[1295,1512,1519,1365,1295];
DMTgz=[ 712,712 , 601, 618, 618];
slicemap (specval(DMTg), low,medLOW, MED, medHIGH, HIGH, DMTgx, DMTgz,
Y);
PnCx=[1519,1365,1295,1295,1375,1460,1592];
95
PnCz=[ 601, 618, 618, 448, 435, 365, 431];
slicemap (specval(PnC), low,medLOW, MED, medHIGH, HIGH, PnCx, PnCz,
Y);
RtTgx=[1306,1354,1354,1295];
RtTgz=[ 548, 544, 496, 483];
slicemap (specval(RtTg), low,medLOW, MED, medHIGH, HIGH, RtTgx, RtTgz,
Y);
Tzx=[1295,1375,1460,1415,1295];
Tzz=[ 448, 435, 365, 311, 311];
slicemap (specval(Tz), low,medLOW, MED, medHIGH, HIGH, Tzx, Tzz, Y);
WMx=[1295,1415,1410,1373,1288];
WMz=[311 , 311, 389, 389, 355];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
POIx=[1409,1543,1602,1589,1460];
POIz=[ 308, 295, 363, 395, 365];
slicemap (specval(POI), low,medLOW, MED, medHIGH, HIGH, POIx, POIz,
Y);
fiveRx=[1592,1666,1673,1733,1740,1710,1607,1589];
fiveRz=[ 431, 528, 610, 676, 565, 454, 367, 395];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Prsx=[1589,1583,1665,1666];
Prsz=[ 395, 538, 611, 528];
slicemap (specval(Prs), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
SubCx=[1589,1444,1486,1613,1512,1519,1583,1592];
SubCz=[ 395, 635, 823, 769, 712, 601, 538, 431];
slicemap (specval(SubC), low,medLOW, MED, medHIGH, HIGH, SubCx, SubCz,
Y);

```

```

fiveNx=[1613,1512,1519,1583,1700];
fiveNz=[ 769, 712, 601, 538, 747];
slicemap (specval(fiveN), low,medLOW, MED, medHIGH, HIGH, fiveNx,
fiveNz, Y);
WMx=[1700,1583,1733,1797,1796];
WMz=[ 747, 538, 676, 760, 778];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
end

```

slice51

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 51;
Cbx=[1290,1337,1333,1363,1295,];
Cbz=[1257,1232,1276,1318,1333];
%QCcolor (Cbx,Cbz,51*3)
V1x=[1470,1549,1643,1765,1705,1591,1490,1465];
V1z=[1376,1376,1359,1292,1174,1209,1261,1301];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1707,1766,1906,1837];
V2z=[1173,1291,1178,1092];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
96
Ectx=[1906,1837,1957,2015];
Ectz=[1178,1092,1000,1003];
slicemap (specval(Ect), low,medLOW, MED, medHIGH, HIGH, Ectx, Ectz,
Y);
Entx=[1837,1957,2015,2039,2010,1884,1697,1648];
Entz=[1092,1000,1003, 853, 814, 830,1002,1075];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
RSCx=[1648,1837,1705,1591,1548];
RSCz=[1075,1092,1174,1209,1198];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
fourCbx=[1295,1352,1333,1339,1295];
fourCbz=[1333,1311,1276,1232,1232];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1295,1339,1445,1556,1557,1485,1295];
threeCbz=[1232,1232,1103,1041,1002, 969, 986];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
twoCbx=[1295,1485,1557,1613,1486,1355,1295];
twoCbz=[986 , 969,1002, 760, 823, 841, 790];
slicemap (specval(twoCb), low,medLOW, MED, medHIGH, HIGH, twoCbx,
twoCbz, Y);
fiveCbx=[1544,1648,1804,1794,1588];
fiveCbz=[1043,1075, 869, 815, 939];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);
threeCbx=[1794,1588,1570,1617,1721,1796];
threeCbz=[ 815, 939, 924, 758, 753, 778];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
ICx=[1556,1627,1443,1352,1333,1339,1377,1445];
ICz=[1040,1086,1299,1311,1276,1232,1173,1103];
slicemap (specval(IC), low,medLOW, MED, medHIGH, HIGH, ICx, ICz, Y);
CGx=[1295,1512,1486,1355,1294];

```

```

CGz=[712 ,712 , 823, 831, 790];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, CGx, CGz, Y);
PBx=[1486,1615,1700,1669,1512];
PBz=[ 823, 757, 747, 703, 712];
slicemap (specval(PB), low,medLOW, MED, medHIGH, HIGH, PBx, PBz, Y);
DMTgx=[1295,1512,1519,1365,1295];
DMTgz=[ 712,712 , 601, 618, 618];
slicemap (specval(DMTg), low,medLOW, MED, medHIGH, HIGH, DMTgx, DMTgz,
Y);
PnCx=[1519,1365,1295,1295,1375,1460,1592];
PnCz=[ 601, 618, 618, 448, 435, 365, 431];
slicemap (specval(PnC), low,medLOW, MED, medHIGH, HIGH, PnCx, PnCz,
Y);
RtTgx=[1306,1354,1354,1295];
RtTgz=[ 548, 544, 496, 483];
slicemap (specval(RtTg), low,medLOW, MED, medHIGH, HIGH, RtTgx, RtTgz,
Y);
Tzx=[1295,1375,1460,1415,1295];
97
Tzz=[ 448, 435, 365, 311, 311];
slicemap (specval(Tz), low,medLOW, MED, medHIGH, HIGH, Tzx, Tzz, Y);
WMx=[1295,1415,1410,1373,1288];
WMz=[311 , 311, 389, 389, 355];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
POIx=[1409,1543,1602,1589,1460];
POIz=[ 308, 295, 363, 395, 365];
slicemap (specval(POI), low,medLOW, MED, medHIGH, HIGH, POIx, POIz,
Y);
fiveRx=[1592,1666,1673,1733,1740,1710,1607,1589];
fiveRz=[ 431, 528, 610, 676, 565, 454, 367, 395];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Prsx=[1589,1583,1665,1666];
Prsz=[ 395, 538, 611, 528];
slicemap (specval(Prs), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
SubCx=[1589,1444,1486,1613,1512,1519,1583,1592];
SubCz=[ 395, 635, 823, 769, 712, 601, 538, 431];
slicemap (specval(SubC), low,medLOW, MED, medHIGH, HIGH, SubCx, SubCz,
Y);
fiveNx=[1613,1512,1519,1583,1700];
fiveNz=[ 769, 712, 601, 538, 747];
slicemap (specval(fiveN), low,medLOW, MED, medHIGH, HIGH, fiveNx,
fiveNz, Y);
l=51;
WMx=[1700,1583,1733,1797,1796];
WMz=[ 747, 538, 676, 760, 778];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
end

```

slice52

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 52;
Cbx=[1290,1337,1333,1363,1295,];
Cbz=[1257,1232,1276,1318,1333];
%QCcolor (Cbx,Cbz,51*3)

```



```

V1x=[1470,1549,1643,1765,1705,1591,1490,1465];
V1z=[1531,1376,1359,1292,1174,1209,1261,1301];
slicemap (specval(V1), low,medLOW, MED, medHIGH, HIGH, V1x, V1z, Y);
V2x=[1707,1766,1906,1837];
V2z=[1173,1291,1178,1092];
slicemap (specval(V2), low,medLOW, MED, medHIGH, HIGH, V2x, V2z, Y);
Ectx=[1906,1837,1957,2015];
Ectz=[1178,1092,1000,1003];
98
slicemap (specval(Ect), low,medLOW, MED, medHIGH, HIGH, Ectx, Ectz,
Y);
Entx=[1837,1957,2015,2039,2010,1884,1697,1648];
Entz=[1092,1000,1003, 853, 814, 830,1002,1075];
slicemap (specval(Ent), low,medLOW, MED, medHIGH, HIGH, Entx, Entz,
Y);
RSCx=[1648,1837,1705,1591,1548];
RSCz=[1075,1092,1174,1209,1198];
slicemap (specval(RSC), low,medLOW, MED, medHIGH, HIGH, RSCx, RSCz,
Y);
fourCbx=[1295,1352,1333,1339,1295];
fourCbz=[1333,1311,1276,1232,1232];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1295,1339,1445,1556,1557,1485,1295];
threeCbz=[1232,1232,1103,1041,1002, 969, 986];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
twoCbx=[1295,1485,1557,1613,1486,1355,1295];
twoCbz=[986 , 969,1002, 760, 823, 841, 790];
slicemap (specval(twoCb), low,medLOW, MED, medHIGH, HIGH, twoCbx,
twoCbz, Y);
fiveCbx=[1544,1648,1804,1794,1588];
fiveCbz=[1043,1075, 869, 815, 939];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);
threeCbx=[1794,1588,1570,1617,1721,1796];
threeCbz=[ 815, 939, 924, 758, 753, 778];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
ICx=[1556,1627,1443,1352,1333,1339,1377,1445];
ICz=[1040,1086,1299,1311,1276,1232,1173,1103];
slicemap (specval(IC), low,medLOW, MED, medHIGH, HIGH, ICx, ICz, Y);
CGx=[1295,1512,1486,1355,1294];
CGz=[712 ,712 , 823, 831, 790];
slicemap (specval(Cg), low,medLOW, MED, medHIGH, HIGH, CGx, CGz, Y);
PBx=[1486,1615,1700,1669,1512];
PBz=[ 823, 757, 747, 703, 712];
slicemap (specval(PB), low,medLOW, MED, medHIGH, HIGH, PBx, PBz, Y);
DMTgx=[1295,1512,1519,1365,1295];
DMTgz=[ 712,712 , 601, 618, 618];
slicemap (specval(DMTg), low,medLOW, MED, medHIGH, HIGH, DMTgx, DMTgz,
Y);
PnCx=[1519,1365,1295,1295,1375,1460,1592];
PnCz=[ 601, 618, 618, 448, 435, 365, 431];
slicemap (specval(PnC), low,medLOW, MED, medHIGH, HIGH, PnCx, PnCz,
Y);
RtTgx=[1306,1354,1354,1295];
RtTgz=[ 548, 544, 496, 483];

```

```

slicemap (specval(RtTg), low,medLOW, MED, medHIGH, HIGH, RtTgx, RtTgz,
Y);
Tzx=[1295,1375,1460,1415,1295];
Tzz=[ 448, 435, 365, 311, 311];
slicemap (specval(Tz), low,medLOW, MED, medHIGH, HIGH, Tzx, Tzz, Y);
99
WMx=[1295,1415,1410,1373,1288];
WMz=[311 , 311, 389, 389, 355];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
POIx=[1409,1543,1602,1589,1460];
POIz=[ 308, 295, 363, 395, 365];
slicemap (specval(POI), low,medLOW, MED, medHIGH, HIGH, POIx, POIz,
Y);
fiveRx=[1592,1666,1673,1733,1740,1710,1607,1589];
fiveRz=[ 431, 528, 610, 676, 565, 454, 367, 395];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Prsx=[1589,1583,1665,1666];
Prsz=[ 395, 538, 611, 528];
slicemap (specval(Prs), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
SubCx=[1589,1444,1486,1613,1512,1519,1583,1592];
SubCz=[ 395, 635, 823, 769, 712, 601, 538, 431];
slicemap (specval(SubC), low,medLOW, MED, medHIGH, HIGH, SubCx, SubCz,
Y);
fiveNx=[1613,1512,1519,1583,1700];
fiveNz=[ 769, 712, 601, 538, 747];
slicemap (specval(fiveN), low,medLOW, MED, medHIGH, HIGH, fiveNx,
fiveNz, Y);
l=52;
WMx=[1700,1583,1733,1797,1796];
WMz=[ 747, 538, 676, 760, 778];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice53 star = 54

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 53;
CGx=[1404,1410,1295,1291,1350];
CGz=[ 816, 726, 726, 768, 777];
%QCcolor (CGx,CGz,53*3)
l=53;
%%Slicefeed(l);
fiveCbx=[1295,1391,1551,1858,1785,1295];
fiveCbz=[1365,1350,1280,1042,838 , 838];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);
fourCbx=[1295, 1703,1782,1469,1358,1295];
fourCbz=[795 , 795, 832,1159,1220,1223];
100
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,

```

```

fourCbz, Y);
threeCbx=[1295,1392,1505,1609,1472,1295];
threeCbz=[1071,1062,1007, 901, 954, 954];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
twoCbx=[1609,1472,1295,1295,1350,1477,1551,1644,1703];
twoCbz=[ 901, 954, 954, 768, 777, 844, 822, 748, 795];
slicemap (specval(twoCb), low,medLOW, MED, medHIGH, HIGH, twoCbx,
twoCbz, Y);
Simx=[1741,1785,1857,1871,1858];
Simz=[1161, 838, 919,1003,1042];
slicemap (specval(Sim), low,medLOW, MED, medHIGH, HIGH, Simx, Simz,
Y);
PFIX=[1778,1922,1909,1857,1805,1779];
PFIZ=[ 792, 803, 871, 919, 885, 829];
slicemap (specval(PFI), low,medLOW, MED, medHIGH, HIGH, PFIx, PFIz,
Y);
FLx=[1778,1702,1733,1761,1825,1976,2012,2014,1922];
FLz=[ 792, 724, 707, 647, 623, 655, 675, 725, 803];
slicemap (specval(FL), low,medLOW, MED, medHIGH, HIGH, FLx, FLz, Y);
WMx=[1778,1751,1663,1644,1658,1702];
WMz=[ 792, 815, 778, 748, 716, 724];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
VCAx=[1680,1733,1801,1810,1784,1699,1693,1722,1732];
VCAz=[ 711, 707, 620, 562, 503, 439, 469, 523, 597];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
fiveRx=[1678,1693,1722,1732];
fiveRz=[ 712, 469, 523, 597];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Pr5x=[1678,1699,1663,1611];
Pr5z=[ 712, 439, 398, 578];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Pr5x, Pr5z,
Y);
fiveNx=[1680,1611,1558,1521,1501,1505];
fiveNz=[ 711, 578, 582, 610, 665, 741];
slicemap (specval(fiveN), low,medLOW, MED, medHIGH, HIGH, fiveNx,
fiveNz, Y);
PBx=[1505,1680,1647,1551,1477,1447,1462,1505];
PBz=[741 , 711, 749, 822, 844, 838, 768, 741];
slicemap (specval(PB), low,medLOW, MED, medHIGH, HIGH, PBx, PBz, Y);
LCx=[1447,1410,1441,1462,1463];
LCz=[ 838, 726, 733, 768, 806];
slicemap (specval(LC), low,medLOW, MED, medHIGH, HIGH, LCx, LCz, Y);
CGx=[1295,1410,1447,1404,1350,1295];
CGz=[ 726, 726, 838, 816, 777, 768];
slicemap (specval(CG), low,medLOW, MED, medHIGH, HIGH, CGx, CGz, Y);
SubCx=[1462,1441,1434,1633,1707,1611,1558,1521,1501,1505];
SubCz=[ 768, 733, 633, 398, 448, 578, 582, 610, 665, 741];
slicemap (specval(SubC), low,medLOW, MED, medHIGH, HIGH, SubCx, SubCz,
Y);
POIx=[1458,1693,1707,1589,1556,1511,1509];
POIz=[ 398, 469, 448, 355, 316, 296, 339];
101
slicemap (specval(POI), low,medLOW, MED, medHIGH, HIGH, POIx, POIz,
Y);
DMTgx=[1295,1441,1434,1358,1295];
DMTgz=[ 733, 733, 633, 618, 618];

```

```

slicemap (specval(DMTg), low,medLOW, MED, medHIGH, HIGH, DMTgx, DMTgz,
Y);
PnCx=[1295,1441,1663,1458,1295];
PnCz=[ 733, 733, 398, 398, 392];
slicemap (specval(PnC), low,medLOW, MED, medHIGH, HIGH, PnCx, PnCz,
Y);
RMgx=[1295,1339,1337,1295];
RMgz=[ 392, 407, 458, 482];
slicemap (specval(RMg), low,medLOW, MED, medHIGH, HIGH, RMgx, RMgz,
Y);
Tzx=[1295,1339,1393,1458,1509,1511,1405];
Tzz=[ 392, 407, 420, 398, 334, 296, 302];
slicemap (specval(Tz), low,medLOW, MED, medHIGH, HIGH, Tzx, Tzz, Y);
WMx=[1405,1334,1295,1295,1368,1405,1432,1428];
WMz=[ 302, 279, 294, 349, 377, 375, 344,322 ];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice54

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 54;
CGx=[1404,1410,1295,1291,1350];
CGz=[ 816, 726, 726, 768, 777];
%QCcolor (CGx,CGz,53*3)
Y=Slicenum*3;
%%Slicefeed(1);
fiveCbx=[1295,1391,1551,1858,1785,1295];
fiveCbz=[1365,1350,1280,1042,838 , 838];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);
fourCbx=[1295, 1703,1782,1469,1358,1295];
fourCbz=[795 , 795, 832,1159,1220,1223];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1295,1392,1505,1609,1472,1295];
threeCbz=[1071,1062,1007, 901, 954, 954];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
twoCbx=[1609,1472,1295,1295,1350,1477,1551,1644,1703];
102
twoCbz=[ 901, 954, 954, 768, 777, 844, 822, 748, 795];
slicemap (specval(twoCb), low,medLOW, MED, medHIGH, HIGH, twoCbx,
twoCbz, Y);
Simx=[1741,1785,1857,1871,1858];
Simz=[1161, 838, 919,1003,1042];
slicemap (specval(Sim), low,medLOW, MED, medHIGH, HIGH, Simx, Simz,
Y);
PFIX=[1778,1922,1909,1857,1805,1779];
PFIZ=[ 792, 803, 871, 919, 885, 829];
slicemap (specval(PFI), low,medLOW, MED, medHIGH, HIGH, PFIx, PFIz,
Y);
FLx=[1778,1702,1733,1761,1825,1976,2012,2014,1922];

```

```

FLz=[ 792, 724, 707, 647, 623, 655, 675, 725, 803];
slicemap (specval(FL), low,medLOW, MED, medHIGH, HIGH, FLx, FLz, Y);
WMx=[1778,1751,1663,1644,1658,1702];
WMz=[ 792, 815, 778, 748, 716, 724];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
VCax=[1680,1733,1801,1810,1784,1699,1693,1722,1732];
VCaz=[ 711, 707, 620, 562, 503, 439, 469, 523, 597];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
fiveRx=[1678,1693,1722,1732];
fiveRz=[ 712, 469, 523, 597];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Pr5x=[1678,1699,1663,1611];
Pr5z=[ 712, 439, 398, 578];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Pr5x, Pr5z,
Y);
fiveNx=[1680,1611,1558,1521,1501,1505];
fiveNz=[ 711, 578, 582, 610, 665, 741];
slicemap (specval(fiveN), low,medLOW, MED, medHIGH, HIGH, fiveNx,
fiveNz, Y);
PBx=[1505,1680,1647,1551,1477,1447,1462,1505];
PBz=[741 , 711, 749, 822, 844, 838, 768, 741];
slicemap (specval(PB), low,medLOW, MED, medHIGH, HIGH, PBx, PBz, Y);
LCx=[1447,1410,1441,1462,1463];
LCz=[ 838, 726, 733, 768, 806];
slicemap (specval(LC), low,medLOW, MED, medHIGH, HIGH, LCx, LCz, Y);
CGx=[1295,1410,1447,1404,1350,1295];
CGz=[ 726, 726, 838, 816, 777, 768];
slicemap (specval(CG), low,medLOW, MED, medHIGH, HIGH, CGx, CGz, Y);
SubCx=[1462,1441,1434,1633,1707,1611,1558,1521,1501,1505];
SubCz=[ 768, 733, 633, 398, 448, 578, 582, 610, 665, 741];
slicemap (specval(SubC), low,medLOW, MED, medHIGH, HIGH, SubCx, SubCz,
Y);
POIx=[1458,1693,1707,1589,1556,1511,1509];
POIz=[ 398, 469, 448, 355, 316, 296, 339];
slicemap (specval(POI), low,medLOW, MED, medHIGH, HIGH, POIx, POIz,
Y);
DMTgx=[1295,1441,1434,1358,1295];
DMTgz=[ 733, 733, 633, 618, 618];
slicemap (specval(DMTg), low,medLOW, MED, medHIGH, HIGH, DMTgx, DMTgz,
Y);
PnCx=[1295,1441,1663,1458,1295];
103
PnCz=[ 733, 733, 398, 398, 392];
slicemap (specval(PnC), low,medLOW, MED, medHIGH, HIGH, PnCx, PnCz,
Y);
RMgx=[1295,1339,1337,1295];
RMgz=[ 392, 407, 458, 482];
slicemap (specval(RMg), low,medLOW, MED, medHIGH, HIGH, RMgx, RMgz,
Y);
Tzx=[1295,1339,1393,1458,1509,1511,1405];
Tzz=[ 392, 407, 420, 398, 334, 296, 302];
slicemap (specval(Tz), low,medLOW, MED, medHIGH, HIGH, Tzx, Tzz, Y);
WMx=[1405,1334,1295,1295,1368,1405,1432,1428];
WMz=[ 302, 279, 294, 349, 377, 375, 344,322 ];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
l=Slicenum;
%l = 1; %enter whatever slice you want

```

```

hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice55 star

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 55;
l=55;
%%Slicefeed(l);
sixCbx=[1295,1551,1575,1406,1295];
sixCbz=[1370,1316,1174,1281,1281];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
fiveCbx=[1295,1406,1575,1702,1630,1593,1523,1463,1385,1295];
fiveCbz=[1281,1281,1174, 921, 899, 922,1111,1155,1175,1175];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);
fourCbx=[1593,1523,1463,1385,1295,1295];
fourCbz=[ 922,1111,1155,1175,1175, 922];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1295,1360,1420,1483,1430,1321,1295];
threeCbz=[ 873, 884, 951, 978,1061,1084,1084];
oneCbx=[1295,1360,1389,1295];
oneCbz=[873, 884, 823, 739];
slicemap (specval(oneCb), low,medLOW, MED, medHIGH, HIGH, oneCbx,
oneCbz, Y);
Simx=[1551,1575,1675,1791,1990,1999,1902,1741];
Simz=[1316,1174, 915, 862, 910,1003,1148,1249];
slicemap (specval(Sim), low,medLOW, MED, medHIGH, HIGH, Simx, Simz,
Y);
l04
Cruslx=[1990,1999,1902,1741,1791,1815];
Cruslz=[ 910,1003,1148,1249, 862, 900];
slicemap (specval(Crusl), low,medLOW, MED, medHIGH, HIGH, Cruslx,
Cruslz, Y);
PFIx=[1791,1815,1909,1990,1945,2080,2156,2140,2099,1977,1789,1758,1688,1672,1
710];
PFIZ=[ 862, 900, 930, 910, 755, 758, 644, 585, 546, 553, 633, 687,
732, 779, 810];
slicemap (specval(PFI), low,medLOW, MED, medHIGH, HIGH, PFIx, PFIz,
Y);
Rx=[1671,1655,1753,1795,1790,1758,1688];
Rz=[ 776, 693, 508, 557, 632, 687, 732];
slicemap (specval(Fl), low,medLOW, MED, medHIGH, HIGH, Rx, Rz, Y);
WMx=[1642,1599,1575,1489,1389,1360,1474,1546,1630,1702,1747,1791,1794,1771,17
02,1671];
WMz=[ 670, 674, 760, 819, 823, 884, 978, 982, 899, 921, 910, 862, 823,
784, 811, 776];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
Latx=[1645,1602,1616,1652, 1673];
Latz=[ 876, 828, 768, 774, 827 ];
slicemap (specval(Lat), low,medLOW, MED, medHIGH, HIGH, Latx, Latz,
Y);
Intx=[1530,1494,1448,1390,1396,1489];

```

```

Intz=[ 863, 835, 837, 865, 884, 889];
slicemap (specval(Int), low,medLOW, MED, medHIGH, HIGH, Intx, Intz,
Y);
Vex=[1389,1418,1599,1575,1536,1489];
Vez=[823 , 657, 674, 760, 800, 819];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
PCRTx=[1418,1534,1593,1534];
PCRTz=[ 657, 444, 494, 657];
slicemap (specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
Prsx=[1593,1534,1611,1639];
Prsz=[ 494, 657, 669, 484];
slicemap (specval(Prs), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
fiveRx=[1611,1639,1689,1753,1656];
fiveRz=[ 669, 484, 413, 508, 698];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
VCAx=[1753,1656,1642,1731];
VCAz=[ 508, 698, 670, 486];
slicemap (specval(VCA), low,medLOW, MED, medHIGH, HIGH, VCAx, VCAz,
Y);
sevenNx=[1687,1688,1639,1593,1554,1531,1649];
sevenNz=[ 410, 449, 484, 494, 479, 412, 360];
slicemap (specval(sevenN), low,medLOW, MED, medHIGH, HIGH, sevenNx,
sevenNz, Y);
Olvx=[1531,1649,1600,1432,1438,1531];
Olvz=[ 412, 360, 321, 309,330 , 412];
slicemap (specval(Olv), low,medLOW, MED, medHIGH, HIGH, Olvx, Olvz,
Y);
Gigx=[1295,1438,1531,1535,1418,1295];
Gigz=[ 330, 330, 412, 447, 657, 657];
105
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
DPGIx=[1418,1295,1295,1398];
DPGIz=[ 657, 657, 739, 823];
slicemap (specval(DPGi), low,medLOW, MED, medHIGH, HIGH, DPGIx, DPGIz,
Y);
RMgx=[1295,1348,1351,1295];
RMgz=[ 448, 410, 353, 340];
slicemap (specval(RMg), low,medLOW, MED, medHIGH, HIGH, RMgx, RMgz,
Y);
WMx=[1295,1371,1420,1438,1408,1338,1295];
WMz=[ 340, 361, 353, 330, 297, 279, 279];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice56 star

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 56;
Intx=[1396,1429,1489,1530,1494,1448,1390];

```

```

Intz=[ 884, 895, 889, 863, 835, 837, 865];
%QCcolor (Intx,Intz,3*56)
l=56;
%%Slicefeed(l);
sixCbx=[1295,1551,1575,1406,1295];
sixCbz=[1370,1316,1174,1281,1281];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
fiveCbx=[1295,1406,1575,1702,1630,1593,1523,1463,1385,1295];
fiveCbz=[1281,1281,1174, 921, 899, 922,1111,1155,1175,1175];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);
fourCbx=[1593,1523,1463,1385,1295,1295];
fourCbz=[ 922,1111,1155,1175,1175, 922];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1295,1360,1420,1483,1430,1321,1295];
threeCbz=[ 873, 884, 951, 978,1061,1084,1084];
oneCbx=[1295,1360,1389,1295];
oneCbz=[873, 884, 823, 739];
slicemap (specval(oneCb), low,medLOW, MED, medHIGH, HIGH, oneCbx,
oneCbz, Y);
Simx=[1551,1575,1675,1791,1990,1999,1902,1741];
106
Simz=[1316,1174, 915, 862, 910,1003,1148,1249];
slicemap (specval(Sim), low,medLOW, MED, medHIGH, HIGH, Simx, Simz,
Y);
Cruslx=[1990,1999,1902,1741,1791,1815];
Cruslz=[ 910,1003,1148,1249, 862, 900];
slicemap (specval(Crusl), low,medLOW, MED, medHIGH, HIGH, Cruslx,
Cruslz, Y);
PFIx=[1791,1815,1909,1990,1945,2080,2156,2140,2099,1977,1789,1758,1688,1672,1
710];
PFIz=[ 862, 900, 930, 910, 755, 758, 644, 585, 546, 553, 633, 687,
732, 779, 810];
slicemap (specval(PFI), low,medLOW, MED, medHIGH, HIGH, PFIx, PFIz,
Y);
Rx=[1671,1655,1753,1795,1790,1758,1688];
Rz=[ 776, 693, 508, 557, 632, 687, 732];
slicemap (specval(Fl), low,medLOW, MED, medHIGH, HIGH, Rx, Rz, Y);
WMx=[1642,1599,1575,1489,1389,1360,1474,1546,1630,1702,1747,1791,1794,1771,17
02,1671];
WMz=[ 670, 674, 760, 819, 823, 884, 978, 982, 899, 921, 910, 862, 823,
784, 811, 776];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
Latx=[1645,1602,1616,1652, 1673];
Latz=[ 876, 828, 768, 774, 827 ];
slicemap (specval(Lat), low,medLOW, MED, medHIGH, HIGH, Latx, Latz,
Y);
Intx=[1530,1494,1448,1390,1396,1489];
Intz=[ 863, 835, 837, 865, 884, 889];
slicemap (specval(Int), low,medLOW, MED, medHIGH, HIGH, Intx, Intz,
Y);
Vex=[1389,1418,1599,1575,1536,1489];
Vez=[823 , 657, 674, 760, 800, 819];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
PCRTx=[1418,1534,1593,1534];
PCRTz=[ 657, 444, 494, 657];

```



```

slicemap (specval(PCrt), low,medLOW, MED, medHIGH, HIGH, PCrtx, PCrtz,
Y);
Prsx=[1593,1534,1611,1639];
Prsz=[ 494, 657, 669, 484];
slicemap (specval(Prs), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
fiveRx=[1611,1639,1689,1753,1656];
fiveRz=[ 669, 484, 413, 508, 698];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
VCAx=[1753,1656,1642,1731];
VCAz=[ 508, 698, 670, 486];
slicemap (specval(VCA), low,medLOW, MED, medHIGH, HIGH, VCAx, VCAz,
Y);
sevenNx=[1687,1688,1639,1593,1554,1531,1649];
sevenNz=[ 410, 449, 484, 494, 479, 412, 360];
slicemap (specval(sevenN), low,medLOW, MED, medHIGH, HIGH, sevenNx,
sevenNz, Y);
Olvx=[1531,1649,1600,1432,1438,1531];
Olvz=[ 412, 360, 321, 309,330 , 412];
slicemap (specval(Olv), low,medLOW, MED, medHIGH, HIGH, Olvx, Olvz,
Y);
107
Gigx=[1295,1438,1531,1535,1418,1295];
Gigz=[ 330, 330, 412, 447, 657, 657];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
DPGIx=[1418,1295,1295,1398];
DPGIz=[ 657, 657, 739, 823];
slicemap (specval(DPGi), low,medLOW, MED, medHIGH, HIGH, DPGIx, DPGIz,
Y);
RMgx=[1295,1348,1351,1295];
RMgz=[ 448, 410, 353, 340];
slicemap (specval(RMg), low,medLOW, MED, medHIGH, HIGH, RMgx, RMgz,
Y);
WMx=[1295,1371,1420,1438,1408,1338,1295];
WMz=[ 340, 361, 353, 330, 297, 279, 279];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice57 = 58 = 59

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 57;
nx=[1485,1651,1686,1614,1543,1492,1471];
nz=[ 313, 327, 386, 421, 423, 397,360];
%QCcolor (nx,nz,57*3)
l=57;
sixCbx=[1295,1638,1578,1511,1445,1368,1295];
sixCbz=[1370,1297, 978,1135,1210,1241,1241];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
fiveCbx=[1578,1511,1445,1368,1295,1295,1385,1449];

```

```

fiveCbz=[ 978,1135,1210,1241,1241,1033,1033,1003];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCb,
fiveCbz, Y);
fourCbz=[1295,1385,1449,1463,1655,1727,1668,1476,1385,1295];
fourCbz=[1033,1033,1003, 942, 911, 844, 837, 864, 897, 897];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCb,
fourCbz, Y);
threeCbz=[1476,1385,1295,1295,1355];
threeCbz=[ 864, 897, 897, 801, 813];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCb,
threeCbz, Y);
oneCbz=[1295,1355,1397,1295];
oneCbz=[ 801, 813, 766, 766];
108
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, oneCb,
oneCbz, Y);
Medx=[1470,1450,1378,1355,1402];
Medz=[ 772, 832, 868, 813, 768];
slicemap (specval(MnR), low,medLOW, MED, medHIGH, HIGH, Medx, Medz,
Y);
Simx=[1578,1535,1638,1750,1779];
Simz=[ 985,1324,1297,1244, 954];
slicemap (specval(Sim), low,medLOW, MED, medHIGH, HIGH, Simx, Simz,
Y);
Cruslx=[1750,1779,1773,1973,1975 ,1925];
Cruslz=[1244, 954, 884, 908, 1047,1128];
slicemap (specval(Crusl), low,medLOW, MED, medHIGH, HIGH, Cruslx,
Cruslz, Y);
PFIX=[1772,1973,1976,2040,2091,2148,2106,2023,1790,1743,1619,1668,1743];
PFIZ=[ 883, 908, 838, 765, 747, 631, 534, 515, 636, 710, 748, 837,
846];
slicemap (specval(PFI), low,medLOW, MED, medHIGH, HIGH, PFIx, PFIz,
Y);
WMx=[1449,1779,1804,1749,1717,1655,1463,1440];
WMz=[1003, 954, 907, 851, 847, 911, 942, 969];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
Latx=[1574,1580,1642,1668,1662,1625];
Latz=[766, 826 , 873, 837, 802, 744];
slicemap (specval(Lat), low,medLOW, MED, medHIGH, HIGH, Latx, Latz,
Y);
Intx=[1470,1574,1586,1565,1508,1451];
Intz=[772, 766, 839, 860, 871, 850 ];
slicemap (specval(Int), low,medLOW, MED, medHIGH, HIGH, Intx, Intz,
Y);
Vx=[1295,1397,1295];
Vz=[ 677, 766, 766];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
DPGIX=[1295,1397,1393,1295];
DPGIZ=[ 677, 766, 599, 599];
slicemap (specval(DPGi), low,medLOW, MED, medHIGH, HIGH, DPGIX, DPGIZ,
Y);
Vex=[1397,1393,1551,1614,1547];
Vez=[ 766, 599, 614,599 , 772];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
FIX=[1619,1743,1744,1790,1790,1743];
FIZ=[ 748, 631, 510, 559, 636, 710];
slicemap (specval(Fl), low,medLOW, MED, medHIGH, HIGH, FIX, FIZ, Y);
VCAX=[1619,1743,1718,1547];

```

```

VCAz=[ 748, 631, 489, 772];
slicemap (specval(VCA), low,medLOW, MED, medHIGH, HIGH, VCAx, VCAz,
Y);
fiveRx=[1718,1619,1547,1686];
fiveRz=[ 489, 748, 772, 386];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Solx=[1551,1526,1537,1567,1614];
Solz=[614 , 563, 539, 518, 599];
109
slicemap (specval(Sol), low,medLOW, MED, medHIGH, HIGH, Solx, Solz,
Y);
Prsx=[1567,1614,1686,1574];
Prsz=[ 518, 599, 386, 425];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
sevenNx=[1686,1574,1491,1471,1485,1561];
sevenNz=[ 386, 425, 399, 360, 313, 327];
slicemap (specval(sevenN), low,medLOW, MED, medHIGH, HIGH, sevenNx,
sevenNz, Y);
PCRTx=[1551,1526,1537,1567,1614,1543,1492,1417,1393];
PCRTz=[614 , 563, 539, 518, 421, 423, 397, 479, 599];
slicemap(specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
Gigx=[1295,1393,1417,1491,1471,1485,1421,1295];
Gigz=[ 599, 599, 479, 399, 360, 313,300, 300];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
RMgx=[1295,1348,1351,1295];
RMgz=[440 , 410, 352, 338];
slicemap (specval(RMg), low,medLOW, MED, medHIGH, HIGH, RMgx, RMgz,
Y);
WMx=[1295,1384,1434,1416,1295];
WMz=[ 338, 361, 341, 292, 276];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice58

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 58;
nx=[1485,1651,1686,1614,1543,1492,1471];
nz=[ 313, 327, 386, 421, 423, 397,360];
%QCcolor (nx,nz,57*3)
l=58;
sixCbx=[1295,1638,1578,1511,1445,1368,1295];
sixCbz=[1370,1297, 978,1135,1210,1241,1241];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
fiveCbx=[1578,1511,1445,1368,1295,1295,1385,1449];
fiveCbz=[ 978,1135,1210,1241,1241,1033,1033,1003];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,

```

```

fiveCbz, Y);
fourCbx=[1295,1385,1449,1463,1655,1727,1668,1476,1385,1295];
110
fourCbz=[1033,1033,1003, 942, 911, 844, 837, 864, 897, 897];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1476,1385,1295,1295,1355];
threeCbz=[ 864, 897, 897, 801, 813];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
oneCbx=[1295,1355,1397,1295];
oneCbz=[ 801, 813, 766, 766];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, oneCbx,
oneCbz, Y);
Medx=[1470,1450,1378,1355,1402];
Medz=[ 772, 832, 868, 813, 768];
slicemap (specval(MnR), low,medLOW, MED, medHIGH, HIGH, Medx, Medz,
Y);
Simx=[1578,1535,1638,1750,1779];
Simz=[ 985,1324,1297,1244, 954];
slicemap (specval(Sim), low,medLOW, MED, medHIGH, HIGH, Simx, Simz,
Y);
Crus1x=[1750,1779,1773,1973,1975 ,1925];
Crus1z=[1244, 954, 884, 908, 1047,1128];
slicemap (specval(Crus1), low,medLOW, MED, medHIGH, HIGH, Crus1x,
Crus1z, Y);
PF1x=[1772,1973,1976,2040,2091,2148,2106,2023,1790,1743,1619,1668,1743];
PF1z=[ 883, 908, 838, 765, 747, 631, 534, 515, 636, 710, 748, 837,
846];
slicemap (specval(PF1), low,medLOW, MED, medHIGH, HIGH, PF1x, PF1z,
Y);
WMx=[1449,1779,1804,1749,1717,1655,1463,1440];
WMz=[1003, 954, 907, 851, 847, 911, 942, 969];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
Latx=[1574,1580,1642,1668,1662,1625];
Latz=[766, 826 , 873, 837, 802, 744];
slicemap (specval(Lat), low,medLOW, MED, medHIGH, HIGH, Latx, Latz,
Y);
Intx=[1470,1574,1586,1565,1508,1451];
Intz=[772, 766, 839, 860, 871, 850 ];
slicemap (specval(Int), low,medLOW, MED, medHIGH, HIGH, Intx, Intz,
Y);
Vx=[1295,1397,1295];
Vz=[ 677, 766, 766];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
DPG1x=[1295,1397,1393,1295];
DPG1z=[ 677, 766, 599, 599];
slicemap (specval(DPG1), low,medLOW, MED, medHIGH, HIGH, DPG1x, DPG1z,
Y);
Vex=[1397,1393,1551,1614,1547];
Vez=[ 766, 599, 614,599 , 772];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
F1x=[1619,1743,1744,1790,1790,1743];
F1z=[ 748, 631, 510, 559, 636, 710];
slicemap (specval(F1), low,medLOW, MED, medHIGH, HIGH, F1x, F1z, Y);
VCAx=[1619,1743,1718,1547];
VCAz=[ 748, 631, 489, 772];
111

```

```

slicemap (specval(VCA), low,medLOW, MED, medHIGH, HIGH, VCAx, VCAz,
Y);
fiveRx=[1718,1619,1547,1686];
fiveRz=[ 489, 748, 772, 386];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Solx=[1551,1526,1537,1567,1614];
Solz=[614 , 563, 539, 518, 599];
slicemap (specval(Sol), low,medLOW, MED, medHIGH, HIGH, Solx, Solz,
Y);
Prsx=[1567,1614,1686,1574];
Prsz=[ 518, 599, 386, 425];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
sevenNx=[1686,1574,1491,1471,1485,1561];
sevenNz=[ 386, 425, 399, 360, 313, 327];
slicemap (specval(sevenN), low,medLOW, MED, medHIGH, HIGH, sevenNx,
sevenNz, Y);
PCRTx=[1551,1526,1537,1567,1614,1543,1492,1417,1393];
PCRTz=[614 , 563, 539, 518, 421, 423, 397, 479, 599];
slicemap(specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
Gigx=[1295,1393,1417,1491,1471,1485,1421,1295];
Gigz=[ 599, 599, 479, 399, 360, 313,300, 300];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
RMgx=[1295,1348,1351,1295];
RMgz=[440 , 410, 352, 338];
slicemap (specval(RMg), low,medLOW, MED, medHIGH, HIGH, RMgx, RMgz,
Y);
WMx=[1295,1384,1434,1416,1295];
WMz=[ 338, 361, 341, 292, 276];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice59

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 59;
nx=[1485,1651,1686,1614,1543,1492,1471];
nz=[ 313, 327, 386, 421, 423, 397,360];
%QCcolor (nx,nz,57*3)
l=59;
sixCbx=[1295,1638,1578,1511,1445,1368,1295];
l12
sixCbz=[1370,1297, 978,1135,1210,1241,1241];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
fiveCbx=[1578,1511,1445,1368,1295,1295,1385,1449];
fiveCbz=[ 978,1135,1210,1241,1241,1033,1033,1003];
slicemap (specval(fiveCb), low,medLOW, MED, medHIGH, HIGH, fiveCbx,
fiveCbz, Y);

```

```

fourCbx=[1295,1385,1449,1463,1655,1727,1668,1476,1385,1295];
fourCbz=[1033,1033,1003, 942, 911, 844, 837, 864, 897, 897];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, fourCbx,
fourCbz, Y);
threeCbx=[1476,1385,1295,1295,1355];
threeCbz=[ 864, 897, 897, 801, 813];
slicemap (specval(threeCb), low,medLOW, MED, medHIGH, HIGH, threeCbx,
threeCbz, Y);
oneCbx=[1295,1355,1397,1295];
oneCbz=[ 801, 813, 766, 766];
slicemap (specval(fourCb), low,medLOW, MED, medHIGH, HIGH, oneCbx,
oneCbz, Y);
Medx=[1470,1450,1378,1355,1402];
Medz=[ 772, 832, 868, 813, 768];
slicemap (specval(MnR), low,medLOW, MED, medHIGH, HIGH, Medx, Medz,
Y);
Simx=[1578,1535,1638,1750,1779];
Simz=[ 985,1324,1297,1244, 954];
slicemap (specval(Sim), low,medLOW, MED, medHIGH, HIGH, Simx, Simz,
Y);
Crus1x=[1750,1779,1773,1973,1975 ,1925];
Crus1z=[1244, 954, 884, 908, 1047,1128];
slicemap (specval(Crus1), low,medLOW, MED, medHIGH, HIGH, Crus1x,
Crus1z, Y);
PFIx=[1772,1973,1976,2040,2091,2148,2106,2023,1790,1743,1619,1668,1743];
PFIz=[ 883, 908, 838, 765, 747, 631, 534, 515, 636, 710, 748, 837,
846];
slicemap (specval(PFI), low,medLOW, MED, medHIGH, HIGH, PFIx, PFIz,
Y);
WMx=[1449,1779,1804,1749,1717,1655,1463,1440];
WMz=[1003, 954, 907, 851, 847, 911, 942, 969];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
Latx=[1574,1580,1642,1668,1662,1625];
Latz=[766, 826 , 873, 837, 802, 744];
slicemap (specval(Lat), low,medLOW, MED, medHIGH, HIGH, Latx, Latz,
Y);
Intx=[1470,1574,1586,1565,1508,1451];
Intz=[772, 766, 839, 860, 871, 850 ];
slicemap (specval(Int), low,medLOW, MED, medHIGH, HIGH, Intx, Intz,
Y);
Vx=[1295,1397,1295];
Vz=[ 677, 766, 766];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
DPGIx=[1295,1397,1393,1295];
DPGIz=[ 677, 766, 599, 599];
slicemap (specval(DPGi), low,medLOW, MED, medHIGH, HIGH, DPGIx, DPGIz,
Y);
113
Vex=[1397,1393,1551,1614,1547];
Vez=[ 766, 599, 614,599 , 772];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
FIx=[1619,1743,1744,1790,1790,1743];
FIz=[ 748, 631, 510, 559, 636, 710];
slicemap (specval(FI), low,medLOW, MED, medHIGH, HIGH, FIx, FIz, Y);
VCAx=[1619,1743,1718,1547];
VCAz=[ 748, 631, 489, 772];
slicemap (specval(VCA), low,medLOW, MED, medHIGH, HIGH, VCAx, VCAz,
Y);

```

```

fiveRx=[1718,1619,1547,1686];
fiveRz=[ 489, 748, 772, 386];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
Solx=[1551,1526,1537,1567,1614];
Solz=[614 , 563, 539, 518, 599];
slicemap (specval(Sol), low,medLOW, MED, medHIGH, HIGH, Solx, Solz,
Y);
Prsx=[1567,1614,1686,1574];
Prsz=[ 518, 599, 386, 425];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Prsx, Prsz,
Y);
sevenNx=[1686,1574,1491,1471,1485,1561];
sevenNz=[ 386, 425, 399, 360, 313, 327];
slicemap (specval(sevenN), low,medLOW, MED, medHIGH, HIGH, sevenNx,
sevenNz, Y);
PCRTx=[1551,1526,1537,1567,1614,1543,1492,1417,1393];
PCRTz=[614 , 563, 539, 518, 421, 423, 397, 479, 599];
slicemap(specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
Gigx=[1295,1393,1417,1491,1471,1485,1421,1295];
Gigz=[ 599, 599, 479, 399, 360, 313,300, 300];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
RMgx=[1295,1348,1351,1295];
RMgz=[440 , 410, 352, 338];
slicemap (specval(RMg), low,medLOW, MED, medHIGH, HIGH, RMgx, RMgz,
Y);
WMx=[1295,1384,1434,1416,1295];
WMz=[ 338, 361, 341, 292, 276];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end
l14

```

slice 60

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 60;
Cbx=[1295,1383, 1500,1516,1231,];
Cbz=[ 877, 887, 858, 767, 784];
%receptorMap(specval(), x, z, Y)
%QCcolor (Cbx,Cbz,60*3)
l=60;
Vx=[1295,1351,1342,1295];
Vz=[ 651, 687, 704, 704];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
%receptorMap(specval(), x, z, Y)
WMx=[1446,1489,1539,1766,1724,1634,1470,1449];
WMz=[1093,1086,1022, 865, 862, 910,1037,1064];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap (specval(174), WMx, WMz, Y)
Crus1x=[1449,1665,1816,1870,1907,1814,1535,1489];

```

```

Crus1z=[1092,1257,1198,1143,1075, 999,1025,1086];
slicemap (specval(Crus1), low,medLOW, MED, medHIGH, HIGH, Crus1x,
Crus1z, Y);
%receptorMap(specval(), x, z, Y)
Crus2x=[1907,1814,1535,1766,1846,1921];
Crus2z=[1075, 999,1025, 865, 873, 892];
slicemap (specval(Crus2), low,medLOW, MED, medHIGH, HIGH, Crus2x,
Crus2z, Y);
%receptorMap(specval(), x, z, Y)
PMIx=[1766,1846,1921,1920,1901,1778,1740,1749,1735,1665,1605,1543,1472,1464,1
470,1634,1724];
PMIz=[ 865, 873, 892, 826, 775, 700, 704, 745, 773, 778, 804, 888,
953,1003,1037, 910, 862];
slicemap (specval(PMI), low,medLOW, MED, medHIGH, HIGH, PMIx, PMIz,
Y);
%receptorMap(specval(), x, z, Y)
Copx=[1473,1543,1605,1665,1735,1749,1740,1713,1663,1593,1517,1472];
Copz=[ 948, 888, 804, 778, 773, 745, 704, 685, 683, 715, 775, 946];
slicemap (specval(Cop), low,medLOW, MED, medHIGH, HIGH, Copx, Copz,
Y);
%receptorMap(specval(), x, z, Y)
sixCbx=[1449,1665,1426,1295,1295,1362,1449];
sixCbz=[1092,1257,1331,1349,1110,1124,1092];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
%receptorMap(specval(), x, z, Y)
sevenCbx=[1295,1362,1449,1449,1470,1464,1469,1401,1295];
sevenCbz=[1110,1124,1092,1064,1037,1003, 951, 975, 986];
slicemap (specval(sevenCb), low,medLOW, MED, medHIGH, HIGH, sevenCbx,
sevenCbz, Y);
%receptorMap(specval(), x, z, Y)
eightCbx=[1469,1401,1295,1295,1377,1492];
eightCbz=[ 951, 975, 986, 879, 887, 856];
115
slicemap (specval(eightCb), low,medLOW, MED, medHIGH, HIGH, eightCbx,
eightCb, Y);
%receptorMap(specval(), x, z, Y)
nineCbx=[1295,1377,1492,1516,1295];
nineCbz=[ 879, 887, 856, 777, 777];
slicemap (specval(nineCb), low,medLOW, MED, medHIGH, HIGH, nineCbx,
nineCbz, Y);
%receptorMap(specval(), x, z, Y)
tenCbx=[1516,1295,1487,1354,1342,1295];
tenCbz=[ 777, 777,726 , 686, 704, 704];
slicemap (specval(tenCb), low,medLOW, MED, medHIGH, HIGH, tenCbx,
tenCbz, Y);
%receptorMap(specval(), x, z, Y)
Solx=[1380,1572,1517,1430];
Solz=[ 636, 618, 574, 581];
slicemap (specval(Sol), low,medLOW, MED, medHIGH, HIGH, Solx, Solz,
Y);
%receptorMap(specval(), x, z, Y)
%receptorMap(specval(), x, z, Y)
Vex=[1380,1572,1585,1487,1420,1351,1295];
Vez=[ 636, 618, 704, 726, 697, 687, 651];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
%receptorMap(specval(), x, z, Y)
fiveRx=[1572,1585,1664,1713,1759,1756];

```



```

fiveRz=[ 618, 704, 667, 617, 537, 432];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
%receptorMap(specval(), x, z, Y)
Pr5x=[1572,1756,1712,1517];
Pr5z=[ 618, 432, 365, 574];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Pr5x, Pr5z,
Y);
%receptorMap(specval(), x, z, Y)
PCRTx=[1712,1517,1466,1433,1524,1546];
PCRTz=[ 365, 574, 571, 586, 411, 302];
slicemap (specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
%receptorMap(specval(), x, z, Y)
Gigx=[1433,1524,1546,1509,1295,1295,1380];
Gigz=[ 586, 411, 302, 285,285 , 651,636 ];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
%receptorMap(specval(), x, z, Y)
IOx=[1286,1313,1321,1310,1295];
IOz=[ 615, 598, 520, 432, 396];
slicemap (specval(IO), low,medLOW, MED, medHIGH, HIGH, IOx, IOz, Y);
%receptorMap(specval(), x, z, Y)
Robx=[1295,1313,1373,1444,1485,1385,1295];
Robz=[351 , 373, 366, 327, 281,270 , 270];
slicemap (specval(Rob), low,medLOW, MED, medHIGH, HIGH, Robx, Robz,
Y);
%receptorMap(specval(), x, z, Y)
%%Slicefeed(1);
116
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 61 next 3

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 61;
%QCcolor (Crus2x,Crus2z,61*3)
l=61;
Vx=[1295,1351,1342,1295];
Vz=[ 651, 687, 704, 704];
slicemap (specval(V), low,medLOW, MED, medHIGH, HIGH, Vx, Vz, Y);
%receptorMap(specval(), x, z, Y)
WMx=[1446,1489,1539,1766,1724,1634,1470,1449];
WMz=[1093,1086,1022, 865, 862, 910,1037,1064];
slicemap (specval(WM), low,medLOW, MED, medHIGH, HIGH, WMx, WMz, Y);
%receptorMap (specval(174), WMx, WMz, Y)
Crus1x=[1449,1665,1816,1870,1907,1814,1535,1489];
Crus1z=[1092,1257,1198,1143,1075, 999,1025,1086];
slicemap (specval(Crus1), low,medLOW, MED, medHIGH, HIGH, Crus1x,
Crus1z, Y);
%receptorMap(specval(), x, z, Y)
Crus2x=[1907,1814,1535,1766,1846,1921];
Crus2z=[1075, 999,1025, 865, 873, 892];

```

```

slicemap (specval(Crus2), low,medLOW, MED, medHIGH, HIGH, Crus2x,
Crus2z, Y);
%receptorMap(specval(), x, z, Y)
PMIx=[1766,1846,1921,1920,1901,1778,1740,1749,1735,1665,1605,1543,1472,1464,1
470,1634,1724];
PMIz=[ 865, 873, 892, 826, 775, 700, 704, 745, 773, 778, 804, 888,
953,1003,1037, 910, 862];
slicemap (specval(PMI), low,medLOW, MED, medHIGH, HIGH, PMIx, PMIz,
Y);
%receptorMap(specval(), x, z, Y)
Copx=[1473,1543,1605,1665,1735,1749,1740,1713,1663,1593,1517,1472];
Copz=[ 948, 888, 804, 778, 773, 745, 704, 685, 683, 715, 775, 946];
slicemap (specval(Cop), low,medLOW, MED, medHIGH, HIGH, Copx, Copz,
Y);
%receptorMap(specval(), x, z, Y)
sixCbx=[1449,1665,1426,1295,1295,1362,1449];
sixCbz=[1092,1257,1331,1349,1110,1124,1092];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
%receptorMap(specval(), x, z, Y)
sevenCbx=[1295,1362,1449,1449,1470,1464,1469,1401,1295];
sevenCbz=[1110,1124,1092,1064,1037,1003, 951, 975, 986];
117
slicemap (specval(sevenCb), low,medLOW, MED, medHIGH, HIGH, sevenCbx,
sevenCbz, Y);
%receptorMap(specval(), x, z, Y)
eightCbx=[1469,1401,1295,1295,1377,1492];
eightCbz=[ 951, 975, 986, 879, 887, 856];
slicemap (specval(eightCb), low,medLOW, MED, medHIGH, HIGH, eightCbx,
eightCb, Y);
%receptorMap(specval(), x, z, Y)
nineCbx=[1295,1377,1492,1516,1295];
nineCbz=[ 879, 887, 856, 777, 777];
slicemap (specval(nineCb), low,medLOW, MED, medHIGH, HIGH, nineCbx,
nineCbz, Y);
%receptorMap(specval(), x, z, Y)
tenCbx=[1516,1295,1487,1354,1342,1295];
tenCbz=[ 777, 777,726 , 686, 704, 704];
slicemap (specval(tenCb), low,medLOW, MED, medHIGH, HIGH, tenCbx,
tenCbz, Y);
%receptorMap(specval(), x, z, Y)
Solx=[1380,1572,1517,1430];
Solz=[ 636, 618, 574, 581];
slicemap (specval(Sol), low,medLOW, MED, medHIGH, HIGH, Solx, Solz,
Y);
%receptorMap(specval(), x, z, Y)
%receptorMap(specval(), x, z, Y)
Vex=[1380,1572,1585,1487,1420,1351,1295];
Vez=[ 636, 618, 704, 726, 697, 687, 651];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
%receptorMap(specval(), x, z, Y)
fiveRx=[1572,1585,1664,1713,1759,1756];
fiveRz=[ 618, 704, 667, 617, 537, 432];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
%receptorMap(specval(), x, z, Y)
Pr5x=[1572,1756,1712,1517];
Pr5z=[ 618, 432, 365, 574];

```

```

slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Pr5x, Pr5z,
Y);
%receptorMap(specval(), x, z, Y)
PCRTx=[1712,1517,1466,1433,1524,1546];
PCRTz=[ 365, 574, 571, 586, 411, 302];
slicemap (specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
%receptorMap(specval(), x, z, Y)
Gigx=[1433,1524,1546,1509,1295,1295,1380];
Gigz=[ 586, 411, 302, 285,285 , 651,636 ];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
%receptorMap(specval(), x, z, Y)
IOx=[1286,1313,1321,1310,1295];
IOz=[ 615, 598, 520, 432, 396];
slicemap (specval(IO), low,medLOW, MED, medHIGH, HIGH, IOx, IOz, Y);
%receptorMap(specval(), x, z, Y)
Robx=[1295,1313,1373,1444,1485,1385,1295];
Robz=[351 , 373, 366, 327, 281,270 , 270];
l18
slicemap (specval(Rob), low,medLOW, MED, medHIGH, HIGH, Robx, Robz,
Y);
%receptorMap(specval(), x, z, Y)
%%Slicefeed(1);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 62 star

```

%sllicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 62;
%receptorMap(specval(), x, z, Y)
%QCcolor (Cbx,Cbz,62*3)
Crus1x=[1460,1900,1903,1877,1807,1725,1572,1558];
Crus1z=[1141, 890,1003,1099,1178,1228,1269,1240];
slicemap (specval(Crus1), low,medLOW, MED, medHIGH, HIGH, Crus1x,
Crus1z, Y);
%receptorMap(specval(), x, z, Y)
Crus2x=[1460,1900,1856,1458];
Crus2z=[1141, 890, 764,1077];
slicemap (specval(Crus2), low,medLOW, MED, medHIGH, HIGH, Crus2x,
Crus2z, Y);
%receptorMap(specval(), x, z, Y)
PMIx=[1856,1458,1459,1600,1724,1747];
PMIz=[ 764,1077,1014, 818, 746, 690];
slicemap (specval(PMI), low,medLOW, MED, medHIGH, HIGH, PMIx, PMIz,
Y);
%receptorMap(specval(), x, z, Y)
Copx=[1699,1652,1511,1456];
Copz=[ 675, 678, 762,1012];
slicemap (specval(Cop), low,medLOW, MED, medHIGH, HIGH, Copx, Copz,
Y);
%receptorMap(specval(), x, z, Y)
sixCbx=[1295,1384,1459,1572,1481,1460,1295];

```

```

sixCbz=[1330,1330,1293,1269,1176,1141,1154];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
%receptorMap(specval(), x, z, Y)
sevenCbz=[1460,1295,1295, 1450];
sevenCbz=[1141,1154,1063, 1052];
slicemap (specval(sevenCb), low,medLOW, MED, medHIGH, HIGH, sevenCbx,
sevenCbz, Y);
%receptorMap(specval(), x, z, Y)
eightCbz=[1295, 1450,1471,1295];
eightCbz=[1063, 1052, 911, 911];
119
slicemap (specval(eightCb), low,medLOW, MED, medHIGH, HIGH, eightCbx,
eightCbz, Y);
%receptorMap(specval(), x, z, Y)
nineCbz=[1471,1295,1295,1490];
nineCbz=[ 911, 911, 800, 800];
slicemap (specval(nineCb), low,medLOW, MED, medHIGH, HIGH, nineCbx,
nineCbz, Y);
%receptorMap(specval(), x, z, Y)
tenCbz=[1295,1490,1511,1456,1295];
tenCbz=[ 800, 800, 762, 720, 711];
slicemap (specval(tenCb), low,medLOW, MED, medHIGH, HIGH, tenCbx,
tenCbz, Y);
%receptorMap(specval(), x, z, Y)
Solx=[1377,1569,1519,1430];
Solz=[ 645, 623, 580, 586];
slicemap (specval(Sol), low,medLOW, MED, medHIGH, HIGH, Solx, Solz,
Y);
%receptorMap(specval(), x, z, Y)
Vex=[1377,1569,1600,1520,1448,1350];
Vez=[ 645, 623, 694, 720, 703, 700];
slicemap (specval(Ve), low,medLOW, MED, medHIGH, HIGH, Vex, Vez, Y);
%receptorMap(specval(), x, z, Y)
fiveRx=[1569,1600,1694,1756,1767];
fiveRz=[ 623, 694, 638, 553, 480];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
%receptorMap(specval(), x, z, Y)
Pr5x=[1767,1569,1519,1706];
Pr5z=[ 480, 623, 580, 359];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Pr5x, Pr5z,
Y);
%receptorMap(specval(), x, z, Y)
PCRTx=[1519,1706,1549,1525,1475,1430,1472];
PCRTz=[ 580, 359, 293, 413, 523, 586, 576];
slicemap (specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
%receptorMap(specval(), x, z, Y)
Gigx=[1295,1350,1377,1475,1525,1549,1485,1364,1295];
Gigz=[668 , 700, 645, 523, 413, 293, 273, 265, 277];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
%receptorMap(specval(), x, z, Y)
IOx=[1364,1295,1295,1319,1385,1459,1485];
IOz=[ 265, 277, 351, 374, 361, 315, 273];
slicemap (specval(IO), low,medLOW, MED, medHIGH, HIGH, IOx, IOz, Y);
%receptorMap(specval(), x, z, Y)

```

```

Robx=[1295,1313,1321,1295];
Robz=[621 , 598, 520, 393];
slicemap (specval(Rob), low,medLOW, MED, medHIGH, HIGH, Robx, Robz,
Y);
%receptorMap(specval(), x, z, Y)
120
l=62;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end

```

slice 63

```

%slicemap (specval(), low,medLOW, MED, medHIGH, HIGH, x, z, Y);
if Slicenum == 63;
Crus2x=[1512,1457,1445,1715,1798,1867,1878,1841,1762,1666,1500];
Crus2z=[1261,1164,1092, 885, 857, 862, 977,1099,1185,1234,1263];
slicemap (specval(Crus2), low,medLOW, MED, medHIGH, HIGH, Crus2x,
Crus2z, Y);
%receptorMap(specval(Crus2), Crus2x, Crus2z, Y)
PMIx=[1445,1715,1798,1867,1797,1738,1621,1462];
PMIz=[1092, 885, 857, 862, 738, 695, 790,1019];
slicemap (specval(PMI), low,medLOW, MED, medHIGH, HIGH, PMIx, PMIz,
Y);
%receptorMap(specval(PMI), PMIx, PMIz, Y)
Copx=[1462,1503,1630,1703,1738,1621,1482,];
Copz=[1019, 756, 683, 674, 695, 790,1003,];
slicemap (specval(Cop), low,medLOW, MED, medHIGH, HIGH, Copx, Copz,
Y);
%receptorMap(specval(Cop), Copx, Copz, Y)
sixCbx=[1295,1370,1512,1481,1295];
sixCbz=[1317,1317,1261,1203,1214];
slicemap (specval(sixCb), low,medLOW, MED, medHIGH, HIGH, sixCbx,
sixCbz, Y);
%receptorMap(specval(sixCb), sixCbx, sixCbz, Y)
sevenCbx=[1481,1295,1295,1445,1457];
sevenCbz=[1203,1214,1101,1095,1164];
slicemap (specval(sevenCb), low,medLOW, MED, medHIGH, HIGH, sevenCbx,
sevenCbz, Y);
%receptorMap(specval(sevenCb), sevenCbx, sevenCbz, Y)
eightCbx=[1295,1445,1462,1295];
eightCbz=[1101,1095,956 , 967];
slicemap (specval(eightCb), low,medLOW, MED, medHIGH, HIGH, eightCbx,
eightCb, Y);
%receptorMap(specval(eightCb), eightCbx, eightCbz, Y)
nineCbx=[1462,1295,1295,1489];
nineCbz=[956 , 967, 798, 805];
slicemap (specval(nineCb), low,medLOW, MED, medHIGH, HIGH, nineCbx,
nineCbz, Y);
%receptorMap(specval(nineCb), nineCbx, nineCbz, Y)
tenCbx=[1295,1489,1512,1295];
tenCbz=[ 805,805, 731, 707];
slicemap (specval(tenCb), low,medLOW, MED, medHIGH, HIGH, tenCbx,
tenCbz, Y);

```

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```
%receptorMap(specval(tenCb), tenCbx, tenCbz, Y)
Solx=[1326,1383,1451,1497,1518,1512];
Solz=[690 , 639, 621, 629, 667, 715];
slicemap (specval(Sol), low,medLOW, MED, medHIGH, HIGH, Solx, Solz,
Y);
%receptorMap(specval(Sol), Solx, Solz, Y)
fiveRx=[1515,1681,1730,1756];
fiveRz=[ 716, 638, 582, 494];
slicemap (specval(fiveR), low,medLOW, MED, medHIGH, HIGH, fiveRx,
fiveRz, Y);
%receptorMap(specval(5R), fiveRx, fiveRz, Y)
Pr5x=[1756,1756,1730,1515];
Pr5z=[494 ,432 , 380,716 ];
slicemap (specval(Pr5), low,medLOW, MED, medHIGH, HIGH, Pr5x, Pr5z,
Y);
%receptorMap(specval(), x, z, Y)
PCRTx=[1383,1451,1497,1518,1512,1515,1730,1550,1536,1470];
PCRTz=[ 639, 621, 629, 667, 715,716 , 380, 278, 376, 527];
slicemap (specval(PCRT), low,medLOW, MED, medHIGH, HIGH, PCRTx, PCRTz,
Y);
%receptorMap(specval(PCR), PCRx, PCRz, Y)
Gigx=[1550,1536,1470,1383,1326,1295,1295,1435];
Gigz=[ 278, 376, 527, 639, 690, 680, 277, 255];
slicemap (specval(Gig), low,medLOW, MED, medHIGH, HIGH, Gigx, Gigz,
Y);
%receptorMap(specval(Gig), Gigx, Gigz, Y)
IOx=[1295,1435,1487,1449,1374,1314,1293];
IOz=[ 277, 255,266 , 307, 374, 354, 332];
slicemap (specval(IO), low,medLOW, MED, medHIGH, HIGH, IOx, IOz, Y);
%receptorMap(specval(IO), IOx, IOz, Y)
Robx=[1295,1321,1313,1295];
Robz=[ 393, 546, 598, 620];
slicemap (specval(Rob), low,medLOW, MED, medHIGH, HIGH, Robx, Robz,
Y);
%receptorMap(specval(Rob), Robx, Robz, Y)
%QCcolor (Copx,Copz,63*3)
l=63;
%%Slicefeed(l);
%l = 1; %enter whatever slice you want
hold all
for t = 1:plotable{1,2}%slice31
plot3(plotable{1,1}{t}{1}, plotable{1,1}{t}{3}, 2000-
plotable{1,1}{t}{2}, 'k-')
end
end
end
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```

Appendix R: “slicemap” Program

```
function slicemap (specval, low,medLOW, MED, medHIGH, HIGH, xpoints,
zpoints, Y)
hold all
ypoints = zpoints;
xpointmirror = xpoints;
len = length(ypoints);
for i =1:length(xpoints);
```

```

xpointmirror(i) = ((1295*2)-(xpoints(i))) ;
end
for i=1:len
ypoints(i) = Y;
end
if specval <= (low)
fill3(xpoints,ypoints,zpoints,[1,1,1])
fill3(xpointmirror,ypoints,zpoints,[1,1,1])
%<plot white color>
end
if specval >= (low)
fill3(xpoints,ypoints,zpoints,[1,1,0])
fill3(xpointmirror,ypoints,zpoints,[1,1,0])
%<plot yellow color>
end
if specval >= (medLOW)
hold all
fill3(xpoints,ypoints,zpoints,[1,0.7,0])
fill3(xpointmirror,ypoints,zpoints,[1,0.7,0])
%<plot yellow-orange color>
end
if specval >= (MED)
hold all
fill3(xpoints,ypoints,zpoints,[1,0.6,0])
fill3(xpointmirror,ypoints,zpoints,[1,0.6,0])
%<plot orange color>
end
if specval >= (medHIGH)
hold all
fill3(xpoints,ypoints,zpoints,[1,0.4,0])
fill3(xpointmirror,ypoints,zpoints,[1,0.4,0])
%<plot red-orange color>
end
if specval >= (HIGH)
hold all
fill3(xpoints,ypoints,zpoints,[1,0,0])
fill3(xpointmirror,ypoints,zpoints,[1,0,0])
%<plot red color>
end

```

Appendix S: “receptorMap” Program

```
function receptorMap (specval, xpoints, zpoints, Y)
low = 1;%0.903305;%1.269407; %1 for receptor, else use cutoff values
    from percentiles
medLOW = 2; %1.374403; %2 for receptor
MED = 3;%1.435702; %3 for receptor
medHIGH =4; %1.533658; %4 for receptor
HIGH = 5;%1.671788; %5 for receptor
hold all
%5=[0,1,1]
%4=[0,0.8,0.8]
%3=[0,0.6,0.6]
%2=[0,0.4,0.4]
%1=[0,0.2,0.2]
%0=[0,0,0]
ypoints = xpoints;
xpointmirror = xpoints;
len = length(zpoints);
for i =1:length(xpoints);
xpointmirror(i) = ((1295*2)-(xpoints(i))) ;
end
for i=1:len
ypoints(i) = Y;
end
if specval == (0)
    fill3(xpoints,ypoints,zpoints,[0,0,0])
    fill3(xpointmirror,ypoints,zpoints,[0,0,0])
%<plot black color>
end
if specval == (low)
    fill3(xpoints,ypoints,zpoints,[0,.2,.2])
    fill3(xpointmirror,ypoints,zpoints,[0,0.2,0.2])
%<plot low color>
end
    if specval==(medLOW)
        hold all
        fill3(xpoints,ypoints,zpoints,[0,0.4,0.4])
        fill3(xpointmirror,ypoints,zpoints,[0,0.4,0.4])
%<plot med-low color>
    end
    if specval == (MED)
        hold all
        fill3(xpoints,ypoints,zpoints,[0,0.6,0.6])
        fill3(xpointmirror,ypoints,zpoints,[0,0.6,0.6])
%<plot mid color>
    end
    if specval == (medHIGH)
        hold all
        fill3(xpoints,ypoints,zpoints,[0,0.8,0.8])

fill3(xpointmirror,ypoints,zpoints,[0,0.8,0.8])
```



```
%<plot med-high color>
end
    ypoints = zpoints;
xpointmirror = xpoints;
len = length(ypoints);
for i =1:length(xpoints);
xpointmirror(i) = ((1295*2)-(xpoints(i))) ;
end
for i=1:len
ypoints(i) = Y;
end
    if specval == (HIGH)
        hold all
fill3(xpoints,ypoints,zpoints,[0,1,1])
fill3(xpointmirror,ypoints,zpoints,[0,1,1])
%<plot high color>
end
low = 1
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```