LONI Visualization Environment (LOVE)®

I. GENERAL DESCRIPTIONS

The Laboratory of Neuro Imaging's 3-D viewer, **LOVE**, is a versatile tool for volumetric data display and manipulation. **LOVE** is a completely portable Java-based software, which only requires a Java interpreter and a 64 MB of RAM memory to run on any computer architecture. It allows the user to interactively overlay and browse through several data volumes, zoom in and out in the axial, sagittal, and coronal views, and reports the intensities and the stereo-tactic voxel and world coordinates of the data. It also allows the expert users to delineate structures of interest, e.g., sulcal curves, on the 3 cardinal projections of the data. These curves then may be used to reconstruct surfaces representing the topological boundaries of cortical and sub-cortical regions of interest.

II. TABLE OF CONTENTS

I. GENERAL DESCRIPTION 1

II. TABLE OF CONTENTS 2

III. LOVE COPYRIGHTS 4

IV. ACKNOWLEDGEMENT 5

V. GETTING STARTED 6

A. OVERVIEW 6
B. REQUIREMENTS 6
C. INSTALLATION 7
D. RUNNING LOVE 8
E. CONTRIBUTING TO LOVE & BUGS. FAQ 8

VI. LOVE BASIC 9

A. INTERFACE OVERVIEW 9
B. LOVE MENU 9
C. LOVE TOOL BAR 10
D. TABBED PANE 10

VII. FEATURES 11

FEATURE OVERVIEW 11
A. LOADING VOLUMES 12
B. CURSOR SETTING 12
C. LAYER CONTROLS SELECTING A VOLUME COLOR MAP 12
D. 3D VIEW 14
E. HYPER GRAPH 19
F. ZOOM 20
G. MEASURE LENGTH 22
H. LATIS 23
I. HISTOGRAM & THREE COLOR MAP 24
J. SAVE MCI CONTOUR 28
K. EXIT LOVE 29
L. 30
M.
N

	O. **P.** **Q.** **R.** HELP	
VIII.	**JAVA CLASS DOCUMENTATION FOR LOVE**	**30**
IX	**DEVELOPER'S REFERENCE**	
X.	**RESULTS AND ANALYSIS**	**30**
XI.	**CONCLUSIONS AND RECOMMENDATIONS**	**30**
XII	**APPENDIX**	**30**

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IV. ACKNOWLEDGEMENT

LOVE was developed by Ivo D. Dinov, Ph.D., Laboratory of Neuro Imaging, UCLA School of Medicine and the Program in Computing, UCLA Mathematics; Michael Mega, Ph.D., M.D., Jenaro Felix, B.S., Arthur Toga, Ph.D., Department of Neurology, UCLA School of Medicine.

Partial funding for the development of **LOVE** came from NIH, NSF and NCRR resources.

The introduction of a reader of NetCDF (network Common Data Form, NC) and Montreal Net CDF (MNC) files was made possible by the Unidata Program Center in Boulder, Colorado.

ACR-NEMA, or DICOM (Digital Imaging Communication in Medicine), as being another standard for digital image networking and storage in medicine, is also implemented as allowable file format in **LOVE**. This is made possible thanks to some class libraries developed by Wayne Rasband

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This version of user's guide was written by Bae Cheol Shin

V. GETTING STARTED

A. OVERVIEW

LOVE is a 3-D viewer that allows volumetric data display and manipulation of axial, sagittal, and coronal views as well as 3D surface and volume rendering displays. It is a portable Java-based software, which only requires a Java interpreter and a 64 MB of RAM memory to run on any computer architecture.

- Application
  - LOVE is a versatile 1D, 2D and 3D data viewer geared for cross-platform visualization of stereotactic brain data. It reads Analyze, Raw-binary and NetCDF volumetric data, as well as, Multi-Contour Files (MCF), LWO/LWS/DXF surfaces, and atlas hierarchical brain-region labelings (Hyperbolic BrainGraph Model Display).
  - LOVE allows the user to interactively overlay and browse through several data volumes, zoom in and out in the axial, sagittal, and coronal views, and reports the intensities and the stereo-tactic voxel and world coordinates of the data.
  - Expert users can use LOVE to delineate structures of interest, e.g., sulcal curves, on the 3 cardinal projections of the data. These curves then may be use to reconstruct surfaces representing the topological boundaries of cortical and sub-cortical regions of interest.
- Features:
  - Region Description Database
  - Moleculo-genetic database
  - Brain anatomical data viewer
  - BrainMapper tool
  - Surface (LightWave objects/scenes) and Volume rendering tools
  - Interactive Contour Drawing tool
  - Display of 3D cortical models
  - Surface and Volume rendering tools
  - Multiple Volume Displays
  - Works with Many and Large Datasets

B. REQUIREMENT

Platform	Platform-Independent
Processor	600 MHz Pentium chip or better
Operating System	Any OS that has Java
Memory	512 Mb
Disk Space	
Display	800 x 600
Software	Java 2(Runtime or SDK) version 1.3.1 or

	later, Java 3D™ version 1.3.1

- This version of LOVE for Windows 98/2000/XP and Unix/Linux/Mac OS 10.3+ requires the following:
  - Java 2 (Runtime or SDK) version 1.3.1 or later from Sun Microsystems (http://java.sun.com/j2se/index.jsp)
  - Java 3D™ version 1.3.1 from Sun Microsystems (http://java.sun.com/products/java-media/3D/)

- **General**:
  - **LOVE** only requires a Java 1.2+ interpreter and a Java 3D plug-in. Both are freely available from Sun Microsystems, for a variety of platforms, including Mac OS, Windows, Unix, Linux, BDF, etc.
- **PATH** setting:
  - To run **LOVE**, once you have downloaded the JAR, ZIP, or TAR file, you need to make sure your java virtual machine **knows** where to look for the class path of the **LOVE** package, namely the directory where you installed **LOVE**.
  - UNIX: machine%> setenv CLASSPATH .:/LOVE_instalation_diir/:/other_java_class_dirs/:/usr/java/bin/java/
  - Windows:
    - Windows 2000: Start > Settings > System > Advanced Settings > Variables > Set PATH variable to include the directory where you installed **LOVE**
    - Windows XP: Start > Control Panel > System > Advanced > Environment Variables > Set PATH variable to include the directory where you installed **LOVE**
- **Specific Features**:
  - CPU equivalent or better than 600 MHz Pentium Chip
  - RAM 128 MB +
  - 3-key Mouse
  - Web-Browser
  - OpenGL (SGI) or DirectX (Microsoft) graphics library,
  - Java virtual machine (Java 1.2+, JDK+JRE),
  - Java3D

C. INSTALLATION

- The LOVE package is available at no charge for educational and research purposes on a collaborative basis. To obtain a license and password to download and use LOVE please complete this request form http://www.loni.ucla.edu/Software/Download_UserSignIn.jsp?software_id=7
- You will receive your license agreement and password by return email (please make sure that your email return address is correct).

- Unzip the zip file into a LOVE_dir folder. In windows, LOVE does not update your registry, so if you want to uninstall it, just delete all the directories and files that correspond to LOVE. Follow the same procedure for unix/linux.

D. RUNNING LOVE

- For windows, create a batch file, like the RUN - type files (e.g., run.bat).
- For unix/linux, create an executable shell file to run it, like the one provided (written for the c shell, e.g., runMouseAtlas.csh).
- LOVE can load .img files representing 2D brain slices that will preferably be zipped, since they take up a lot of space. These img filenames should be explicitly given in the batch file after invoking edu.ucla.loni.LOVE.LOVE (LOVE stands for LONI Visualization Environment, an older name for this software package). After the filename, the user should write the minimum and maximum dimensions for x, y and z and then the subsampling ratios in the three dimensions, a total of 9 numbers. These img files can be other read as 8 bits/pixel(e.g. MAP_Nissl.img.gz), 16 bits/pixel (e.g. MAP_Labels.img.gz) or 24 bits/pixel (e.g. mapBlock_rgb.img.gz). The LONI header file specifies information regarding this parameter, as well as parameters like modality, x,y and z dimensions, steps and start points.
- However, all the above images are static images, independent of time. If someone wants to load an img file representing the development of a brain through time, e.g., an fMRI image (e.g. 4D_SD_FLICKER_A.img.gz), he/she should clarify the fMRI modality in the *.lhd file. Note that the img 16-bit file which will represent the labels of the nodes of the hypergraph should have the string "Labels" somewhere in its filename (e.g.: MAP_Labels, Mouse_Labels_2003, etc.). Correspondingly, the img file which will represent the 2D textured slice in the 3D world, should have the string "MRI" somewhere in its filename (e.g.: Mouse_MRI_2003, MAP_MRI, etc.).
- Now, if someone wants to load lightwave objects on the 3D world, he/she should provide their names in the batch file, preceding them with -lws (e.g. -lws BR.lws). The same principle applies for dxf objects, only that now their filenames should be preceded with -dxf (e.g. -dxf BR.dxf).
- The gml file that the hypergraph needs as its input should be a tree and not a graph with loops. You should precede its name with -graph in the batch file (e.g. -graph MAP_BrainGraph.gml).

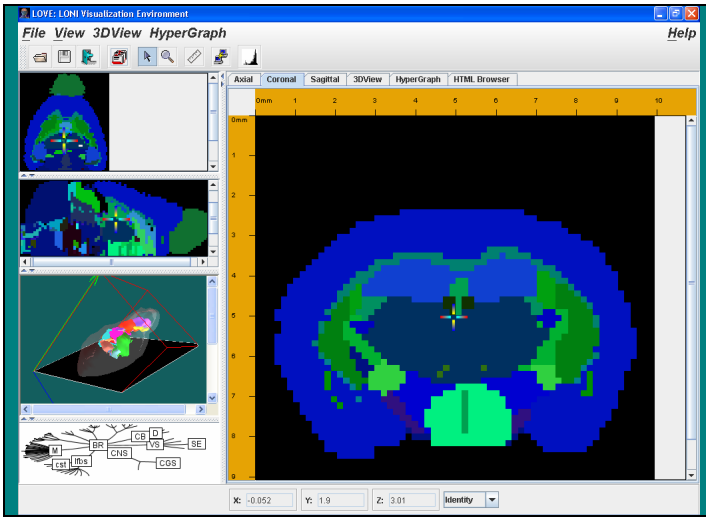
E. CONTRIBUTING LOVE & BUGS.FAQ

- For code development and the implementation of several plug-ins to LOVE, please closely follow the API. For questions on code or style, email: dinov@loni.ucla.edu. or baecheol.shin@loni.ucla.edu.
- If you discover any bugs, please email baecheol.shin@loni.ucla.edu.

VI. LOVE BASICS

A. INTERFACE OVERVIEW

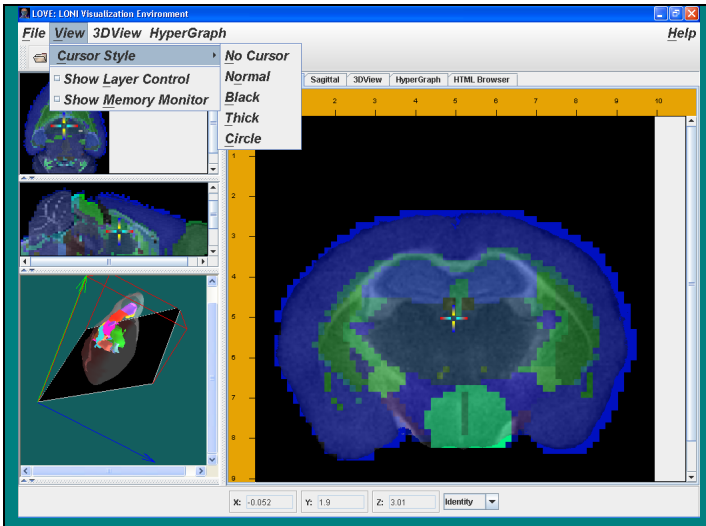
The LOVE viewer allows interactive conrol and syncronous display of: sectional 2D anatomy, 3D object views, Brain Ontology (BrainGraph) and various online databases (genetics and high resolution anatomy). Stereotactic and voxel coordinates may be displayed.



Stereotactic Display
BrainMapping Functionality
External DB interactivity
3D Object Model display
Image Processing
Quantitative Volumetric Analysis

B. LOVE MENU

Main menu items consist of "File", "View", "3DView", and "HyperGraph"



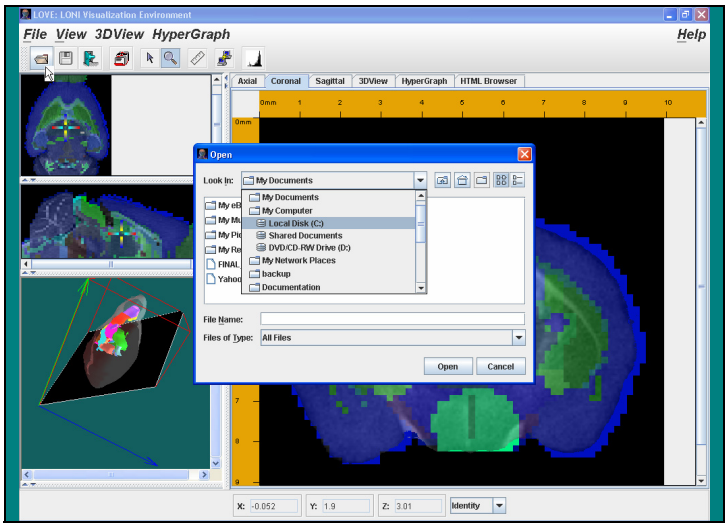
- File Menu Item – allows access to "Open" and "Exit"
- View Menu Item – allows access to layer and cursor control manager
- 3DView Menu Item – allows access to "File", "Transform", "Color", "Add/Remove", "Objects View"
- HyperGraph Menu Item – allows access to "Find Node", "Find an Edge", "Create a Node", and "Create an Edge"

C. TOOLS BARS

Plug-in achitechrute allows quick import of new data processing tools and visulization applications.

Icon	Name	Description
	Open File	
	Save MCF Contour	
	Exit LOVE	
	Show Layer Control	Allows control of image colormaps, opacities and volume properties (point to Layer-Contrl Section above)
	Normal Tool	Default Tool
	Zoom	Tool for pixel-based image magnification
	Measure Length	Eucleadian measure of (shortest) distance between two selected co-planar voxels
	Draw Free Drawing	Start and end the free drawing
	Edit Free Drawing	Add or substract an original drawing
	Undo Edit	Start over your editing
	LATIS	(Internet-connection required) retrieval of high-resolution imaging data via LONI online server
	Show Histogram	

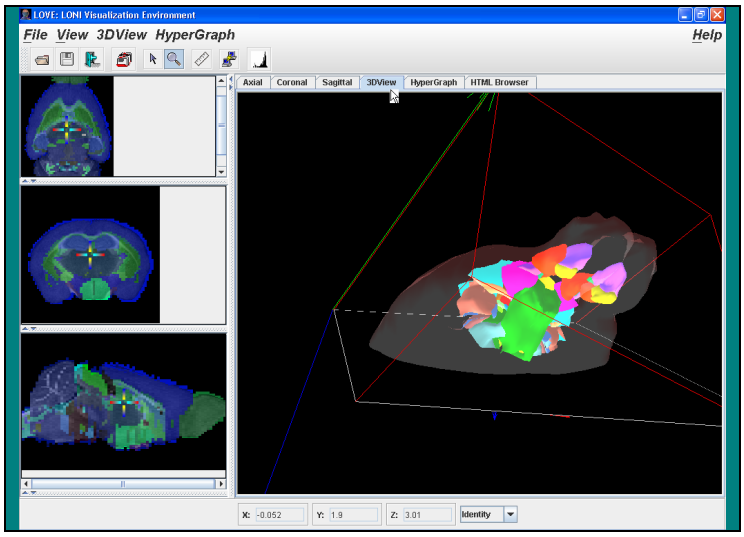
Example of usage



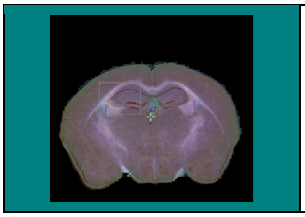
D. TABBED PANES

The main LOVE display windows include: Axial, Coronal, Sagittal, 3DView, HyperGraph, and HTML Browser tabbed pane.

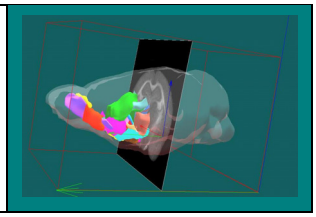
Example of usage



VII. FEATURES



Features Overview



1. Display of 3D cortical models
LOVE includes a SurfaceViewer and a full real-time VolumeRenderer. These allow the user to view the relative positions of different anatomical or functional regions, which are not co-planar in any of the axial, sagittal or coronal 2D projection planes.

2. Surface and Volume rendering tools
LOVE features a region drawing module used for manual delineation of regions of interest. A series of 2D contours describing the boundary of a region in projection planes (axial, sagittal or coronal) can be used to reconstruct the surface-representation of the 3D outer shell of the region. The 3D shell can be resliced in directions complementary to the drawing-direction and these complementary contours can be loaded in all tree cardinal views. In addition the surface object can be displayed using the SurfaceViewer.

3. BrainMapper tool
A semi-intelligent tool (BrainMapper) provides the real interaction between the anatomical (voxel/world) atlas coordinates, the brain-tree (region hierarchical labeling nomenclature), the region description data-base and the moleculo-genetic data-base. This allows the user to synchronously query these sources of information and continuously map results between these different entities.

4. Multiple Volume Displays
LOVE permits overlay of several volume on top of each other. The user could overlay several pre-registered volumes, change intensity colors and ranges and the inter-volume opacities to visually inspect similarities and differences between the different subjects/modalities. Several image-processing aids provide histogram plotting and image-smoothing.

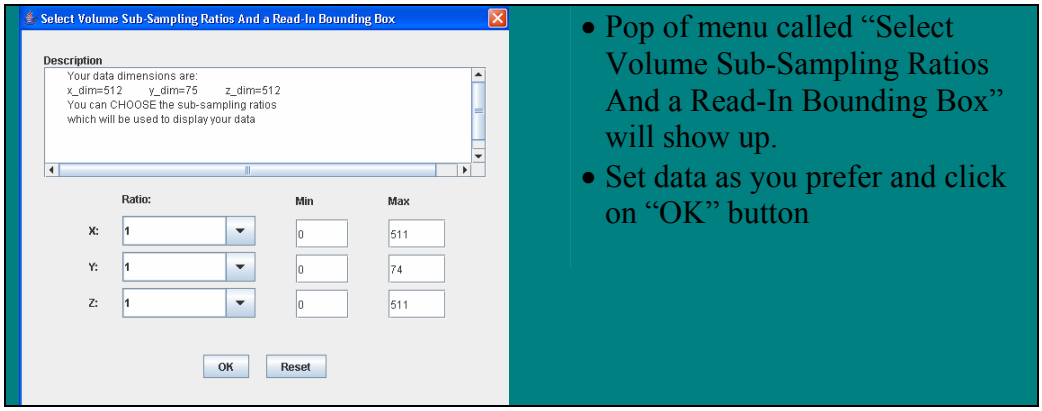
5. Works with Large Datasets
A pre-loading data crop and sub-sampling module allows the user to load and view practically data of any size. This is especially important when viewing cryotome, histological or stained data-sets which may reach 1GB (109 bytes) in size. LOVE allows the user to select independent sub-sampling rations and ranges for each dimension index of the data once the header file (*.LHD) is parsed out. These choices significantly improve on the speed of the viewer and decrease the resource requirements.

6. Versatile Implementation
The software is available as both an applet and a standalone application. The applet can be used to browse data from within the LONI database, but it does have restrictions on file-size, Internet connection and network-bandwidth and client/server file access. The application requires a local install and configuration of the LOVE software.

A. Loading Volumes

LOVE allows you to overlay several volumes on top of each other. You also can load more volumes on top of volumes that you initialy loaded during running time.

To display another voulume on top of volumes either click on “Open File” icon or click on “File” Choose “Open” from the top down menu. Locate volume you want to load. (To check appropriate volume file, see a section Input Data & File Formats)

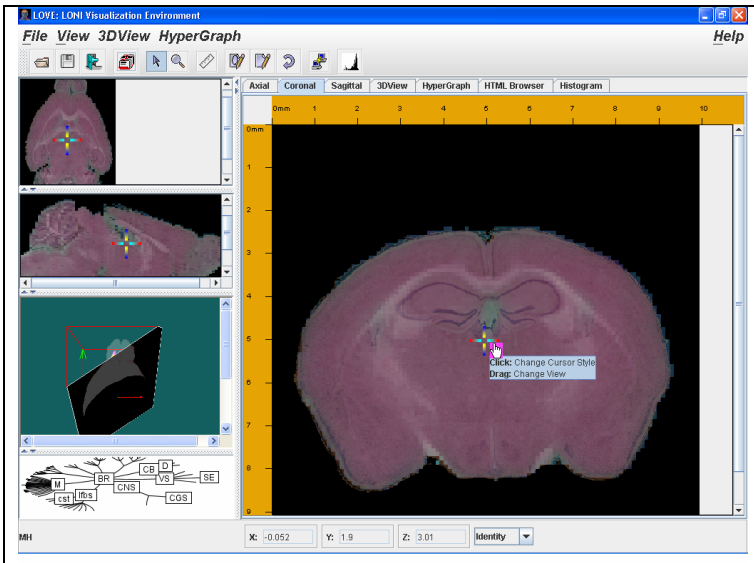
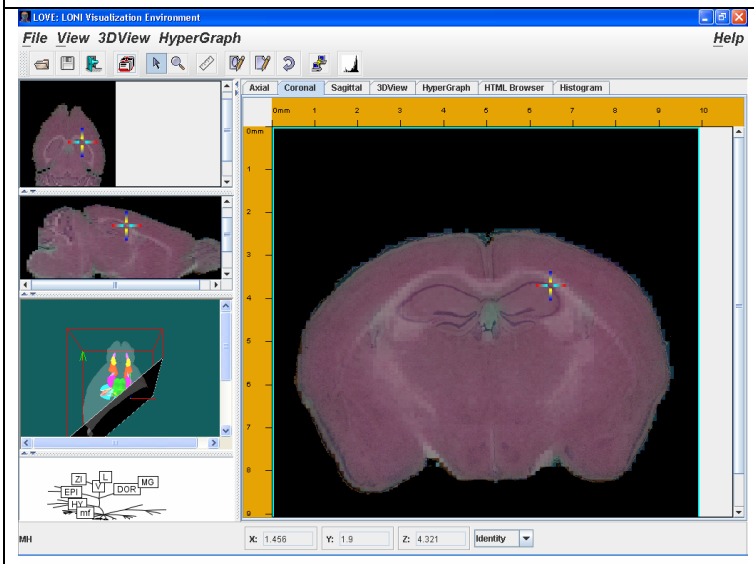
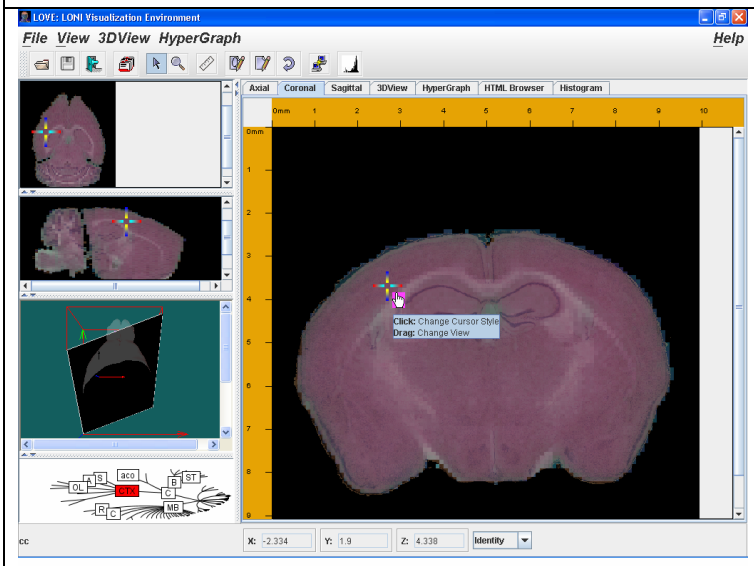


B. Cursor Setting

1. Changing Cursor Shape: LOVE allows you to use 5 types of cursor displays. The default cursor is “Thick” cursor. Other cursors are “No cursor”, “Normal”, “Black”, and “Circle” cursor. Users need to go back-and-forth between these types of cursor display because under different color-maps and at different scalings, either cursor display may look better. Particullary the “Circle” cursor has its own function of drawings “ThreeColorMap” within a given radius (See “Circle Cursor” under “Histogram and ThreeColorMap ” section for more detail).

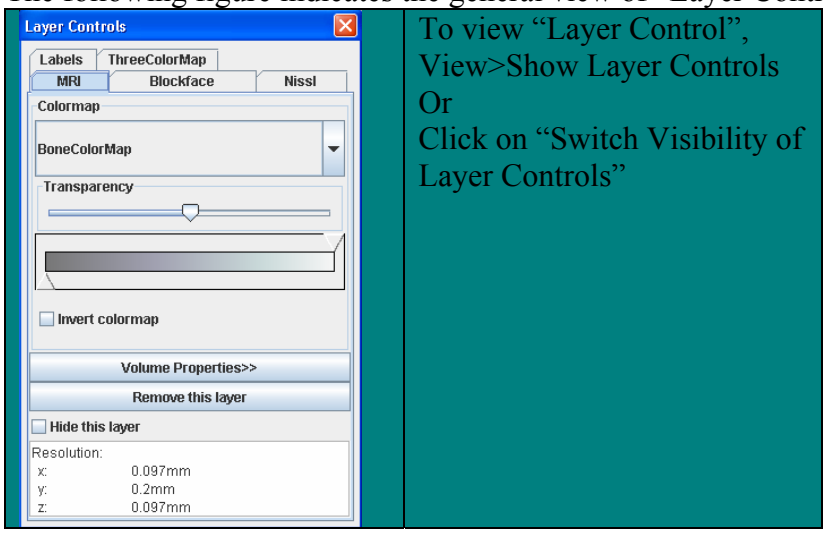
   The cursor apperance is changed by View>Cursor Style menu-option.

2. Basic Cursor move:

	• Move the mouse over the cursor • Mouse will change from to • Drage the mouse and release it where you want to the cursor go
	• All brain images are updated accordingly
	• You can change a view of brain one slice up or down • Move the mouse over the cursor • LEFT Click(RIGTH Click) on the mouse while holding down CTRL key will change the brain view one slice up(down)

C. Layer Controls

The “Layer Controls” provides various controls over volumes.
The following figure indicates the general view of “Layer Controls” pop up menu.



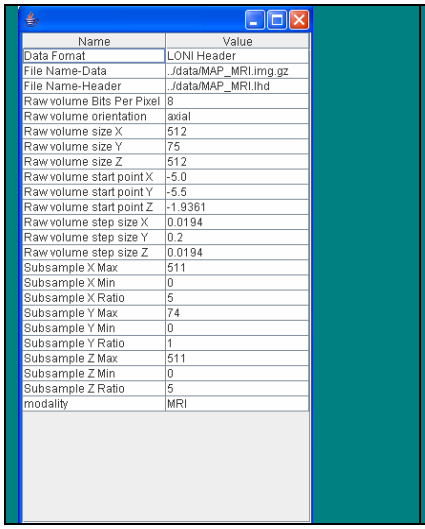
1. Changing Color Map
   - Click on a tab that you want to change its color map
   - Click on the arrow button of the combo box.
   - Select desired color map from a drop-down list.

2. Transparency
   By controlling “Transparency” slider, selected image can be shown in different levels of opaque or transparency. For example, when the slider is at the most left or the most right, the image is completely opaque with an alpha value of 1.0 or completely transparent with an alpha value of 0.0, respectfully.

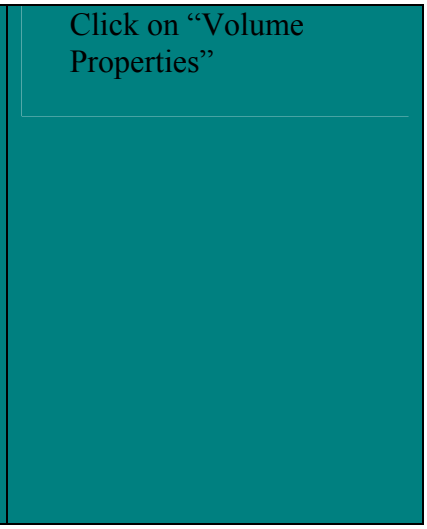
3. Upper & Lower Limit
   Except “ThreeColorMap”

4. Invert colormap
   - Check a check box “Invert Color Map”

5. Volume Properties



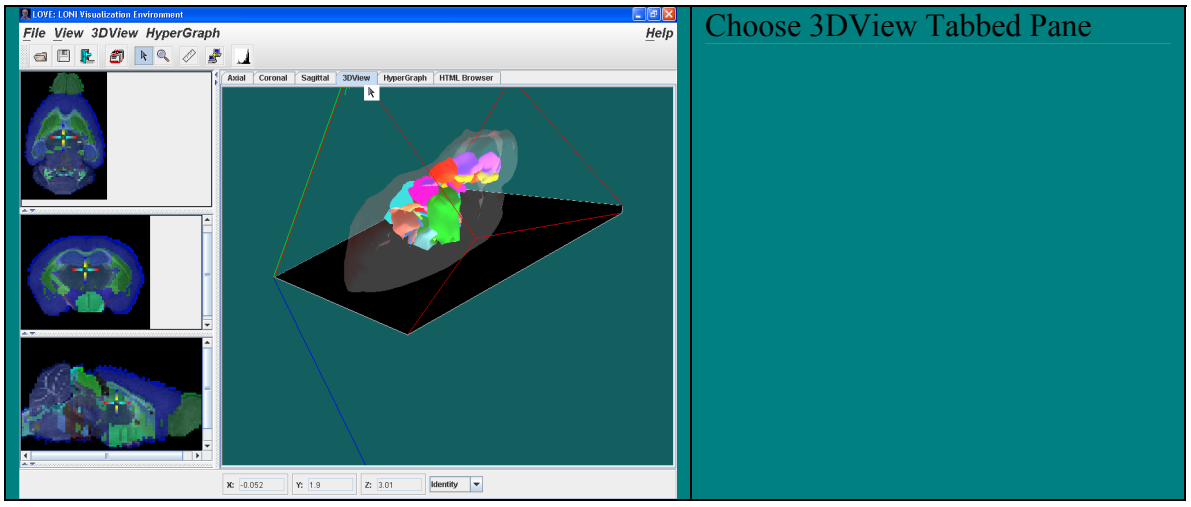
Name	Value
Data Fomat	LONI Header
File Name-Data	./data/MAP_MRI.img.gz
File Name-Header	./data/MAP_MRI.lhd
Raw volume Bits Per Pixel	8
Raw volume orientation	axial
Raw volume size X	512
Raw volume size Y	75
Raw volume size Z	512
Raw volume start point X	-5.0
Raw volume start point Y	-5.5
Raw volume start point Z	-1.9361
Raw volume step size X	0.0194
Raw volume step size Y	0.2
Raw volume step size Z	0.0194
Subsample X Max	511
Subsample X Min	0
Subsample X Ratio	5
Subsample Y Max	74
Subsample Y Min	0
Subsample Y Ratio	1
Subsample Z Max	511
Subsample Z Min	0
Subsample Z Ratio	5
modality	MRI



6. Removing volume
   - Click on “Remove This Layer” button
   - When a dialog box appears, click on “yes” button

7. Hiding volume
   - Check a check box “Hide This Layer”

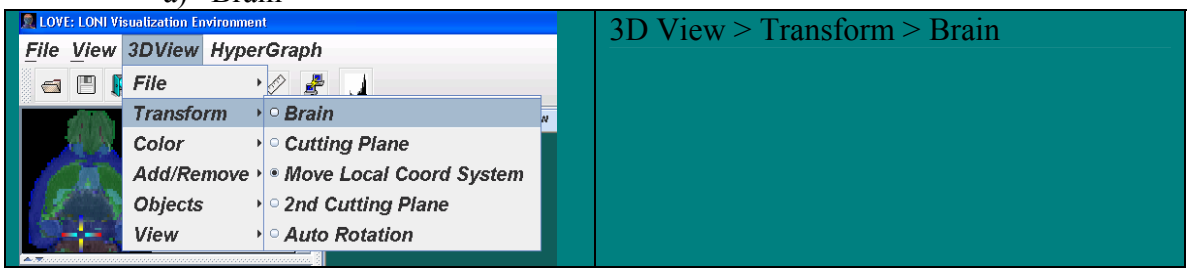
D. 3D View



1. File
   a) Loading Data File
   b) Loading Mask Data File

c) Changing Background
d) Exit

2. Transform
   a) Brain

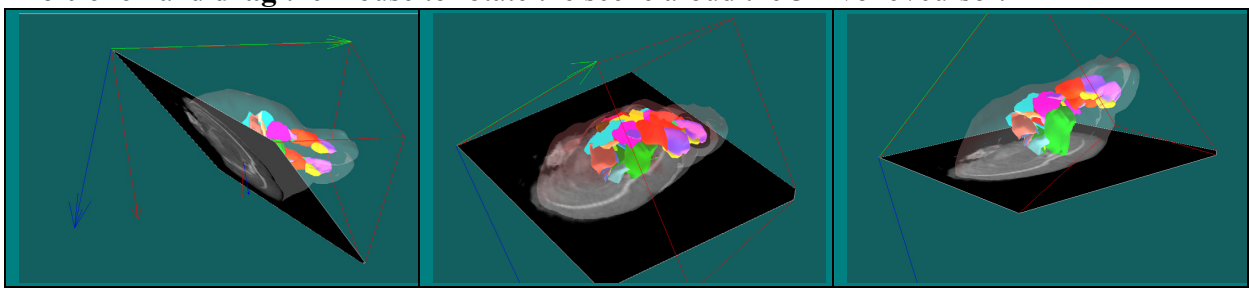


In "Brain" mode you can do following

- Rotating 3D view
- Moving the objects in space
- Zooming in and out

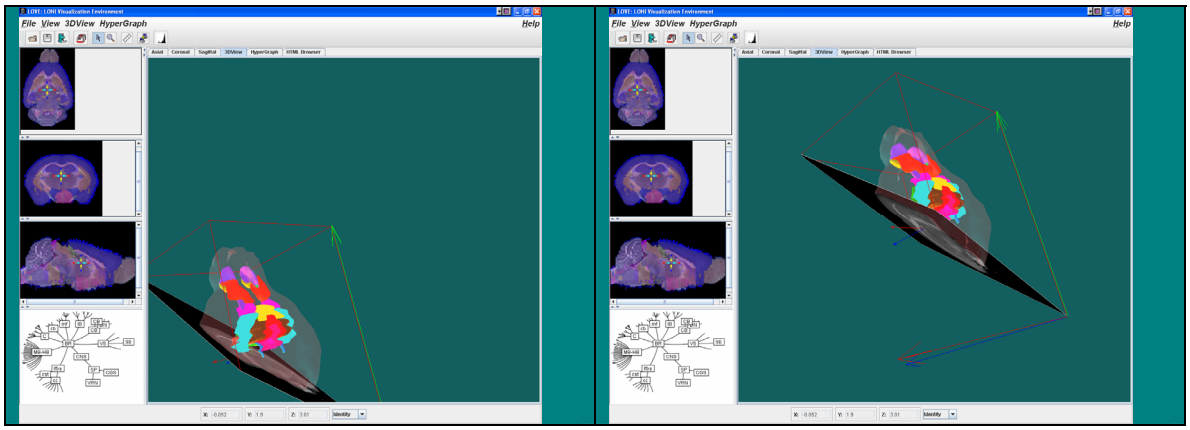
Rotate 3D view

Left-click and **drag** the mouse to rotate the scene aroud the 3D voxel/cursor.



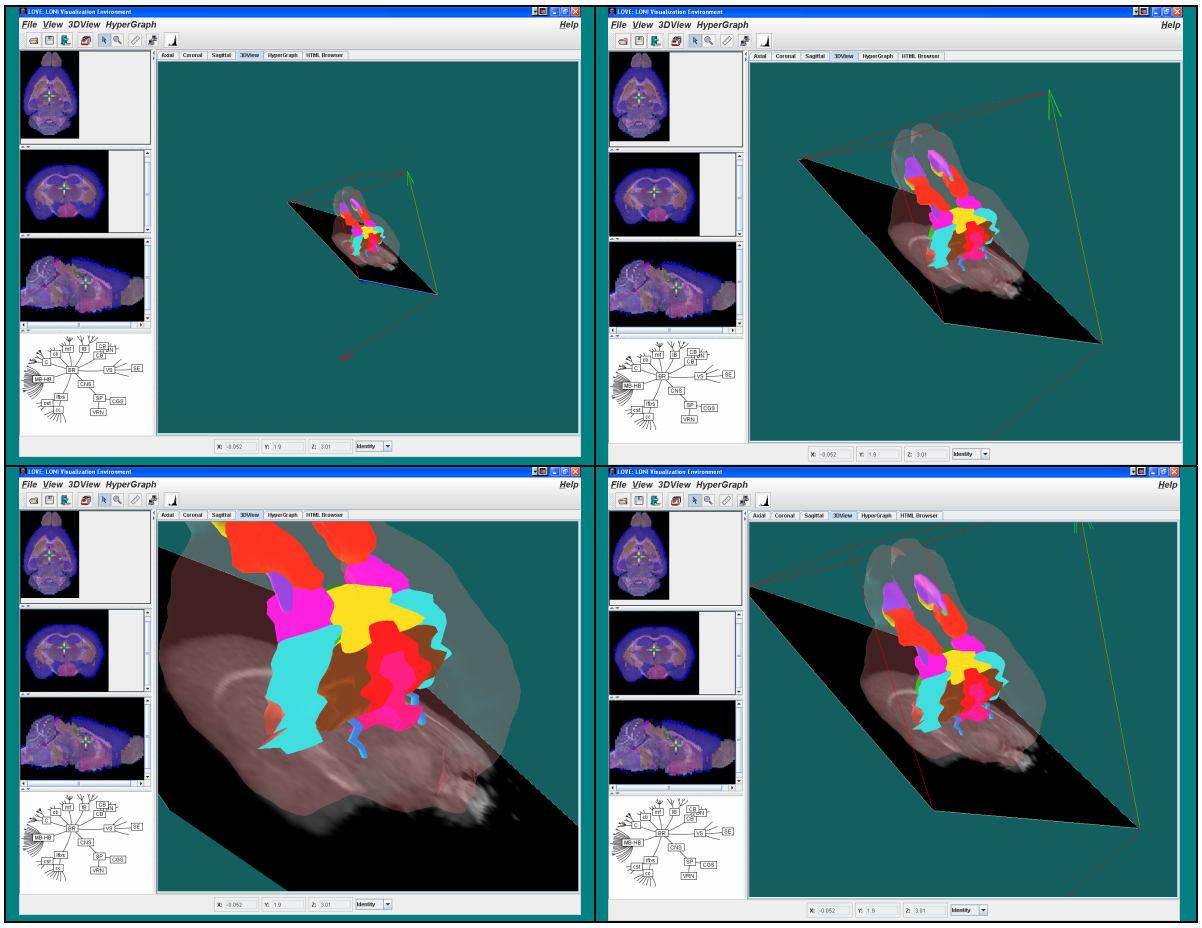
Moving the object in the space

Right-clicks and **drag** the mouse allow paning (moving) the objects in space.

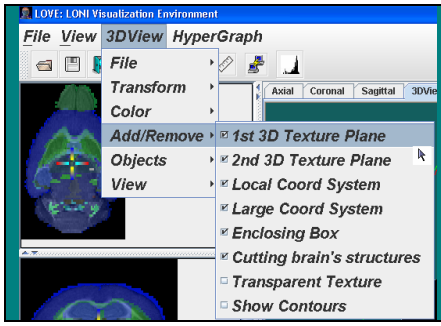


Zooming

While pressing down **ALT** key and **left-click** and **drag** the mouse.
Drag mouse up to zoom in and drag mouse down zoom out.

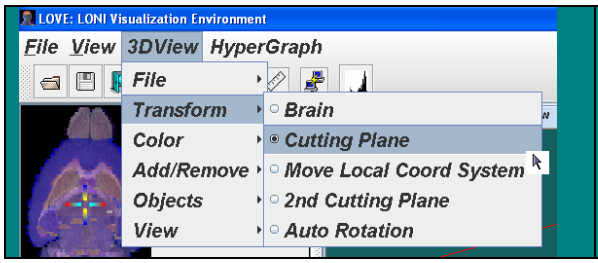


b) Cutting Plane



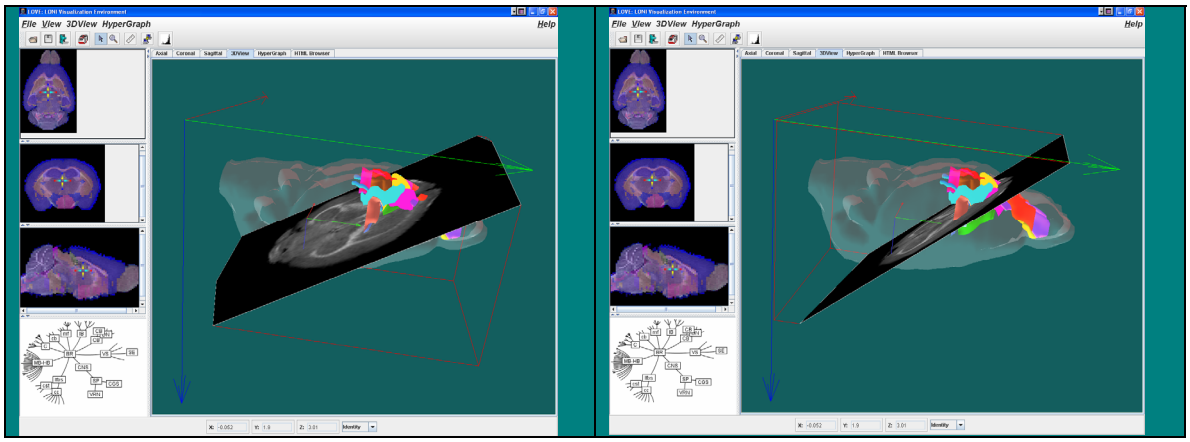
First of all, make sure 1st 3D Texture Plane has been already selected.

3DView > Add/Remove > 1st 3D Texture Plane

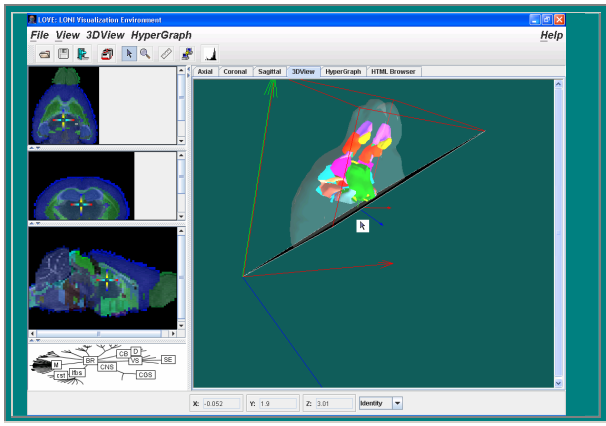


Next select Cutting Plane option
3D View > Transform > Cutting Plane

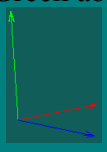
Usage:
Left-Click and **drag** the mouse
Release the mouse where you want to obtain a cut

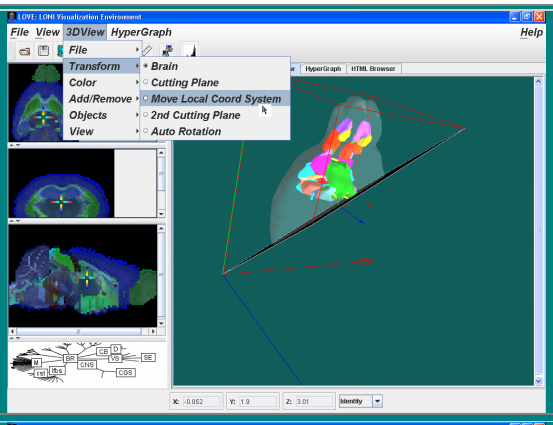


c) Moving Local Coord System

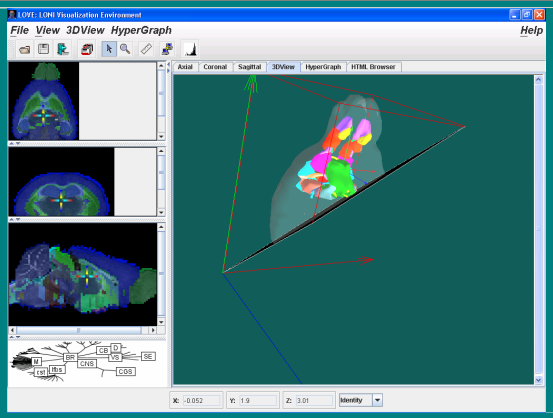


- Local coordinates are shown as a system of 3 orthogonal unitary vectors (Red, Green abd Blue) as depicted below





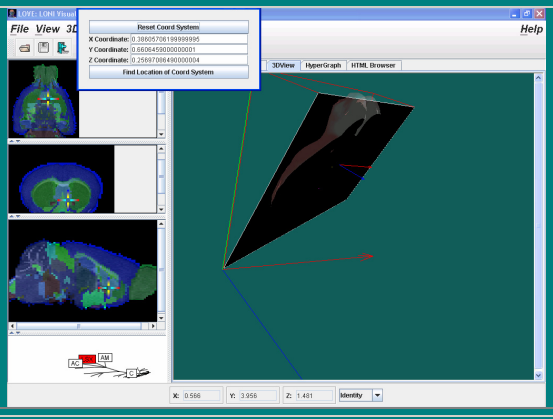
- File>Transform> Move Local Coord System



Displaced local coordinate system – you can always reset the local coordinate system to the center of the volume by: Locate the local coordinate system at the desired location

You can move the local coordinate system in 3D by:

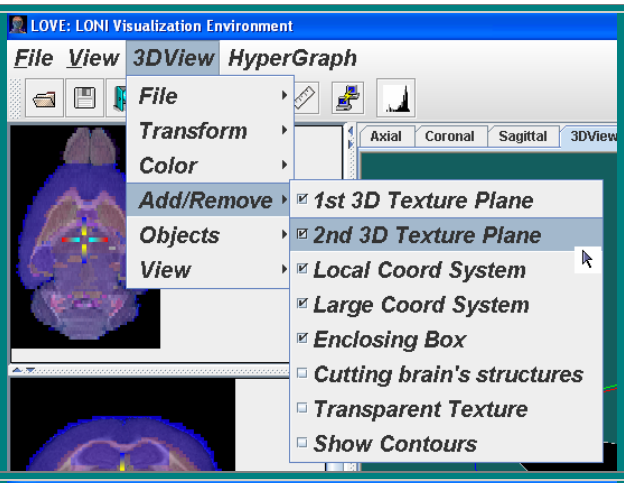
- within plane by right clicking and dragging the mouse and
- depth perspetive by ALT + left click and dragging the mouse.



Left click will allow you to see coordinate

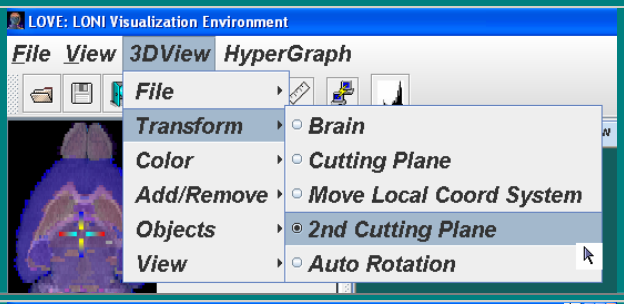
You can also restore orginal setting by clicking on “Restore Coord System” button

d) 2nd Cutting Plane

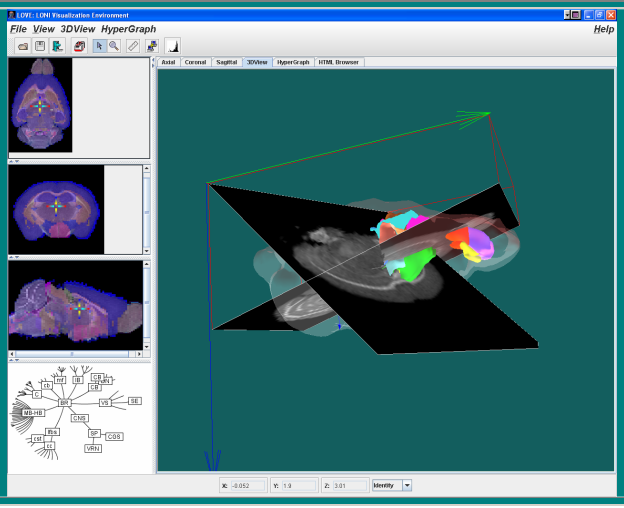


First of all, make sure both 1st 3D Texture Plane and 2nd 3D Texture Plane have been already slected

3DView > Add/Remove / 1st 3D Texture Plane and 2nd #d Texture Plane



Next choose 2nd Cutting Plane option 3DView > Transform > 2nd Cutting Plane

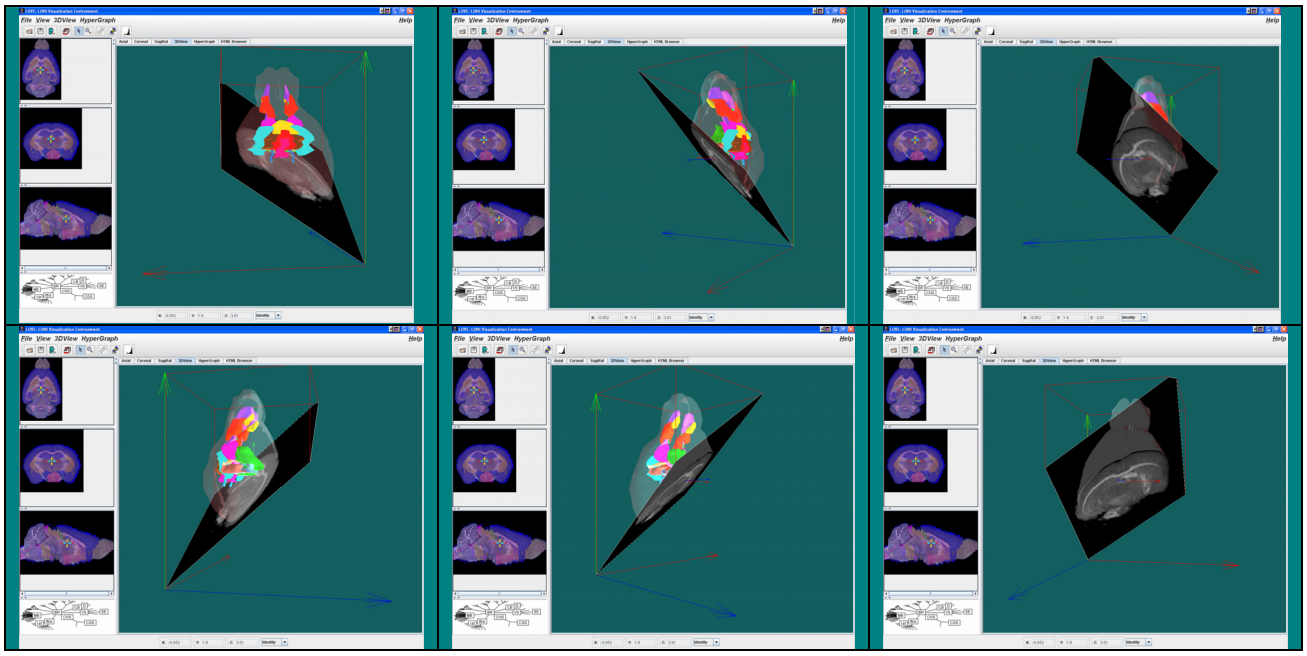


Left-Click and drag the mouse
Release the mouse where you want to make the second cut

e) Auto Rotation

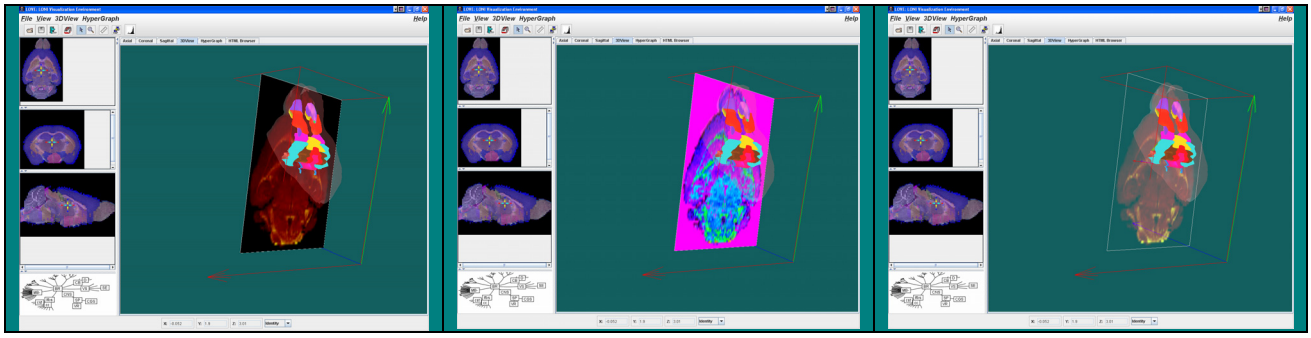
If you want to make a movie of a rotating scene, once your complete your scene design, you can use the auto-rotation function and export (via S-Video) to a recording/projetion device.

3DView > Transform > Auto Rotation

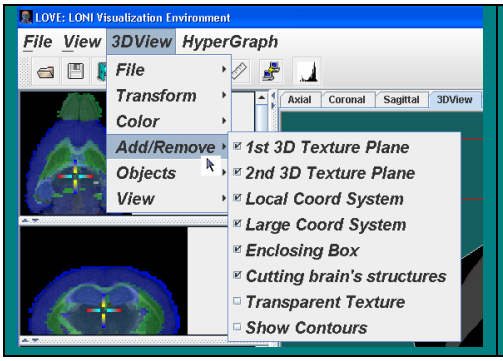


1. Color
    a) Intensity
    b) HotMetal Cmap
    c) Spectral Cmap
    d) Intensity – No Mask
    e) HotMetal – No Mask
    f) Spectral – No Mask

    Color Example:
    The first image is the HotMetal Color Map, the scond image is the Spectral Color Map, and the last image is the HotMetal Color Map with transparency.

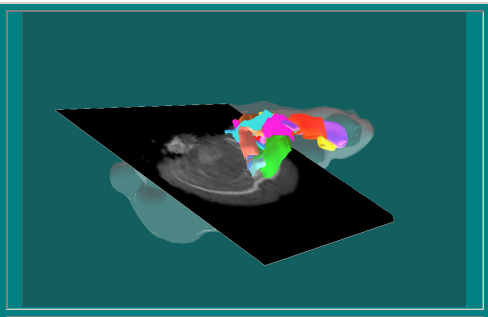
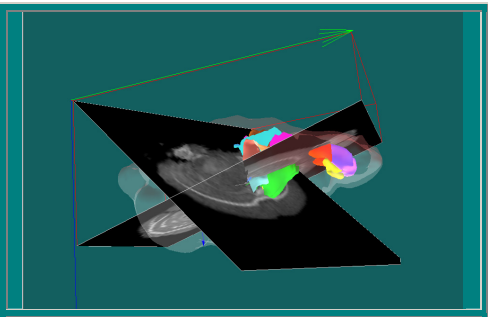
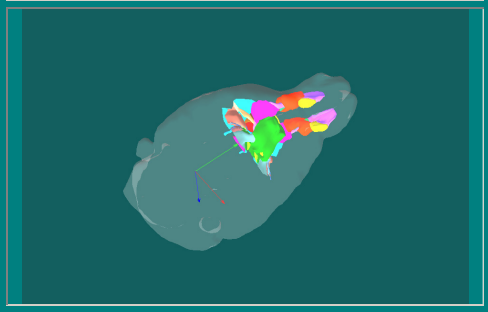
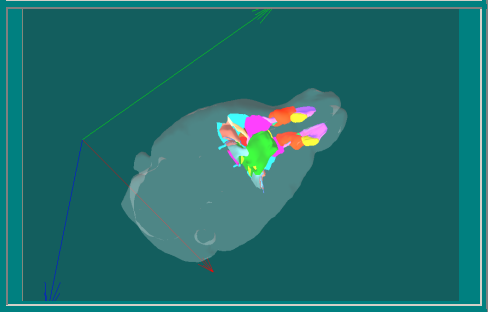
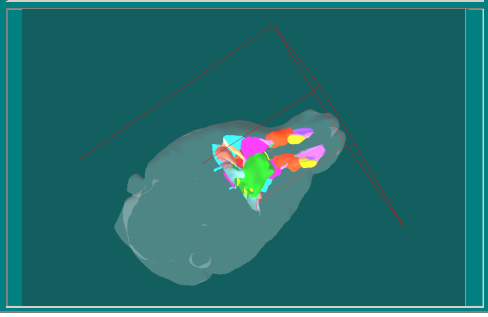
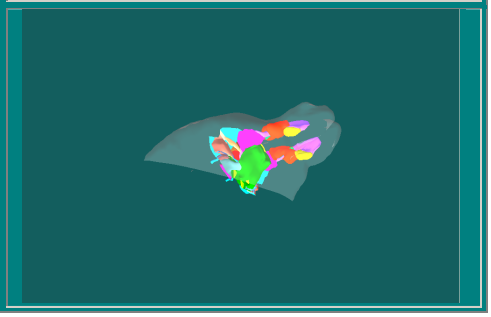


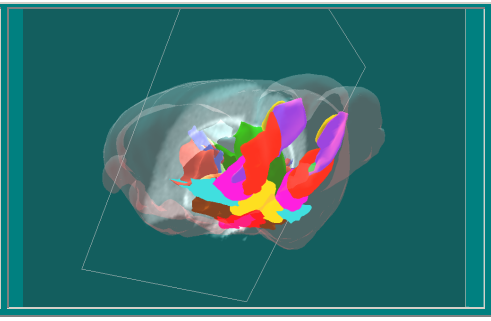
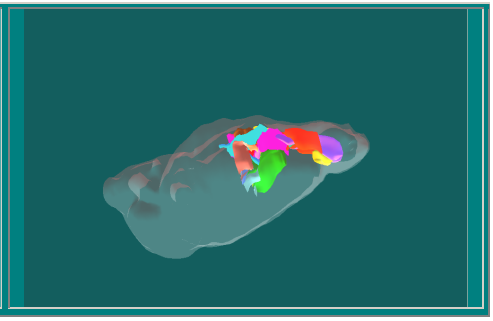
2. Add/Remove



3DView>Add/Remove

Example Views

1st 3D Texture Plane		2nd 3D Texture Plane	
Local Coord System		Large Coord System	
Enclosing Box		Cutting Brain's Structures	

Transparent Texture		Show Contours	

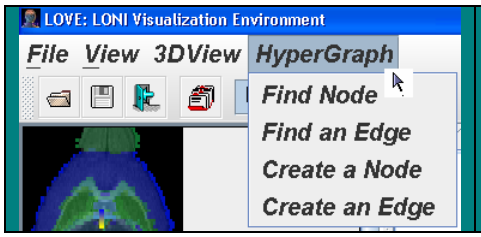
3. Objects
   Need to work

4. View
   Need to work

   a) Restore Axial View
   b) Resore Coronal View
   c) Restore Sagittal View

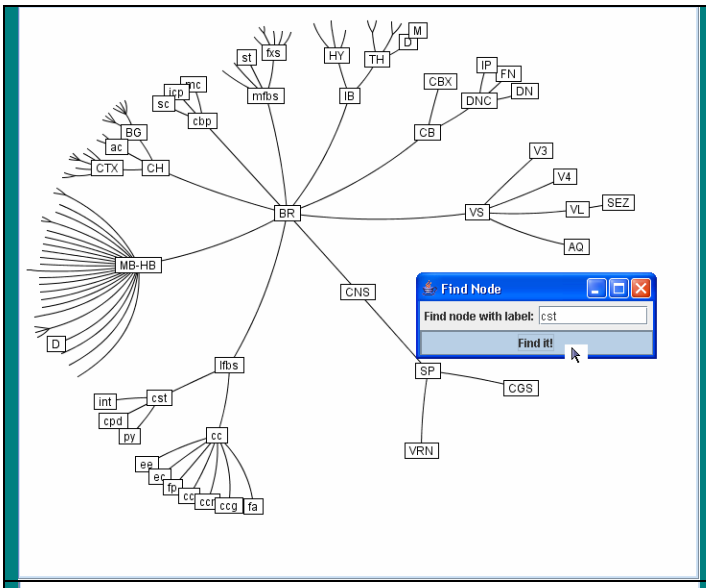
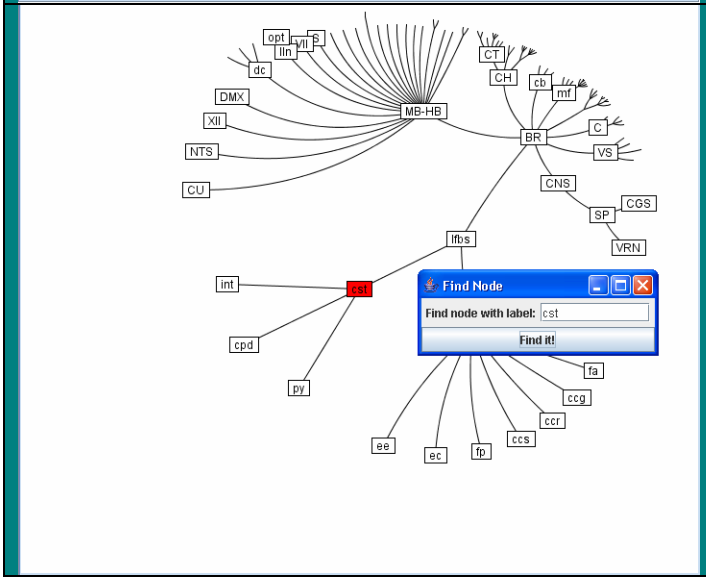
E. Hypergraph

Interactive Brain Ontology Viewer –
Brief introduction is reqiured

	Click on "HyperGraph" menu

1. Find a Node

	Select " Find Node" from a drop-down list ander the HyperGraph menu looks like left will pop up

	• Type in a name for the node to search for • Click on “Find it!” button
	If the node is found in the graph, it will be highlighted and located in the center of the screen. If the node is not found, “BR” (brain) is hightlighted and located in the center of the screen. This is a hyperbolic graph display

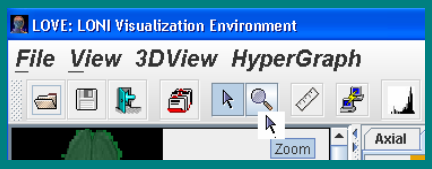
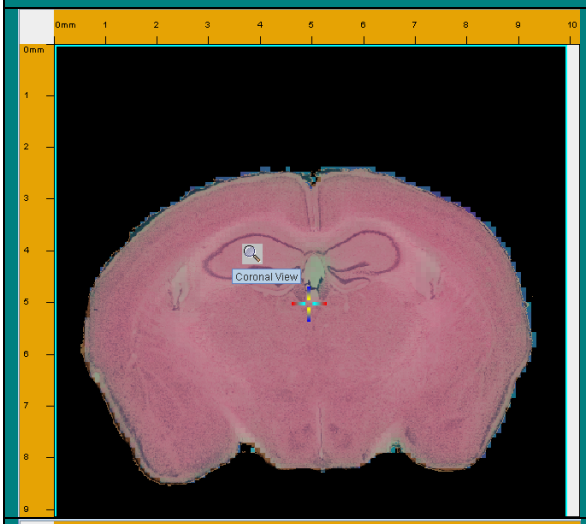
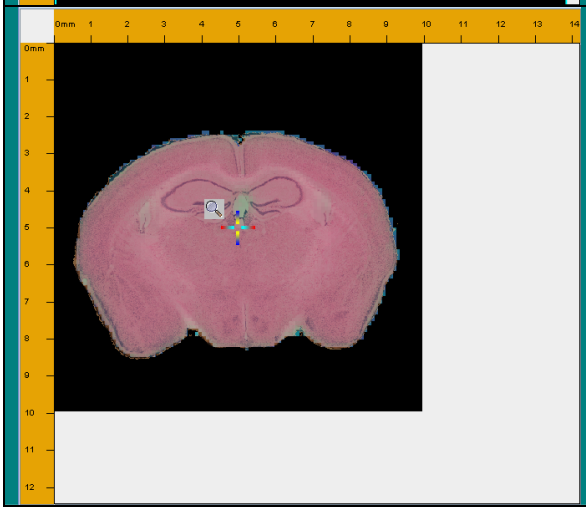
2. Find an Edge
   Need more information

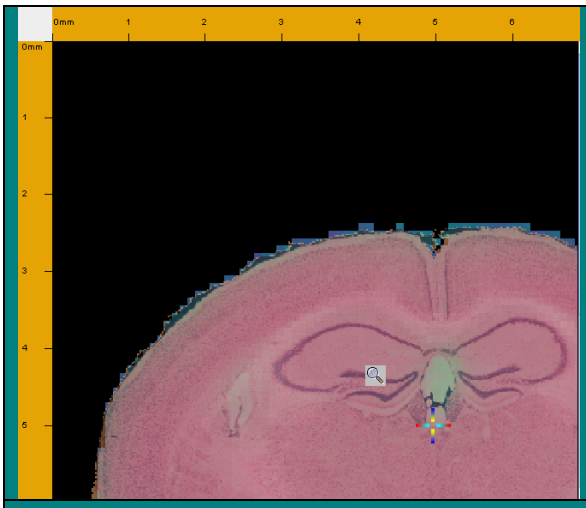
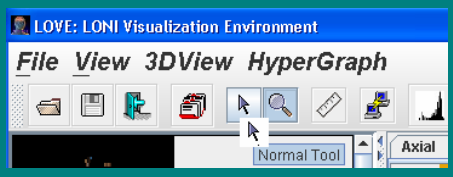
3. Create a Node
   Need more information

4. Create an Edge
   Need more information

F. Zoom

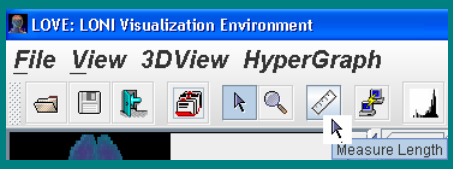
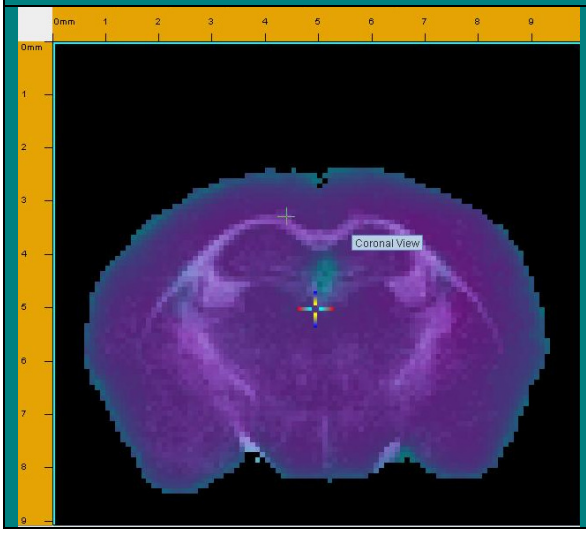
Tool for pixel-based image magnification

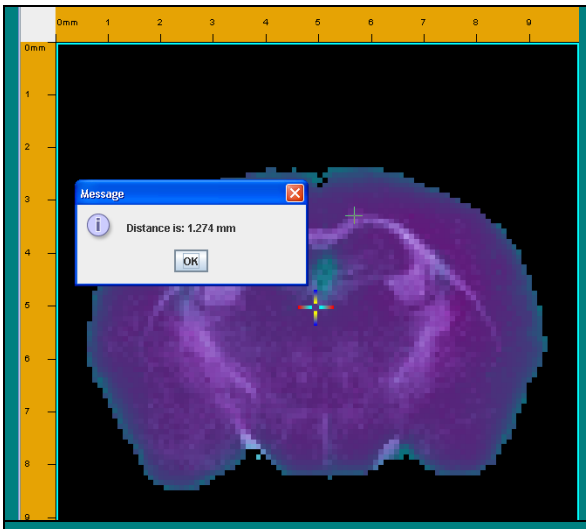
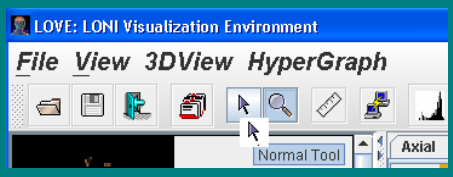
	Click on “Zoom” tool button Cursor will change to
	Place where you want to zoom in or out
	Drag mouse up to zoom in

	Drag mouse down to zoom out
	Click on “Normal Tool” tool button deactivate zoom mode.

G. Measure Length

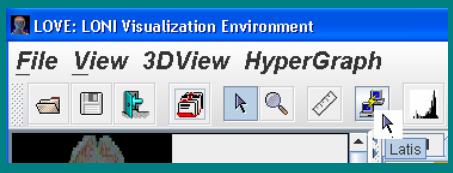
Eucleadian measure of (shortest) distance between two selected co-planar voxels

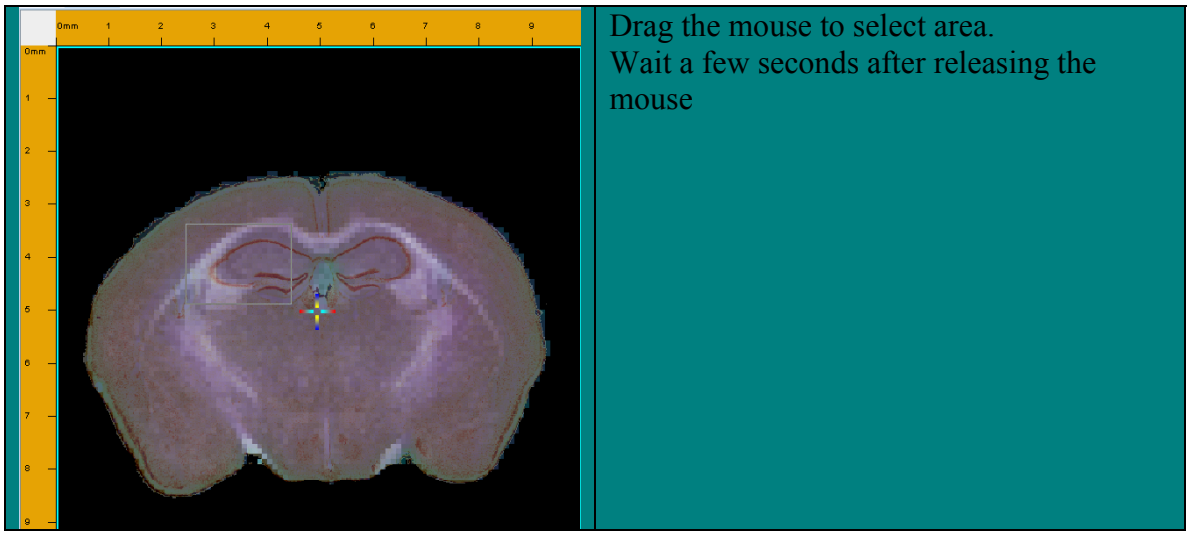
	Click on “Measure Length” Cursor will change to +
	Place and left click where you want to measure a distance from

	Place and left click on the destination Click on “OK”
	Click on “Normal Tool” to to deactivate measure diatance mode

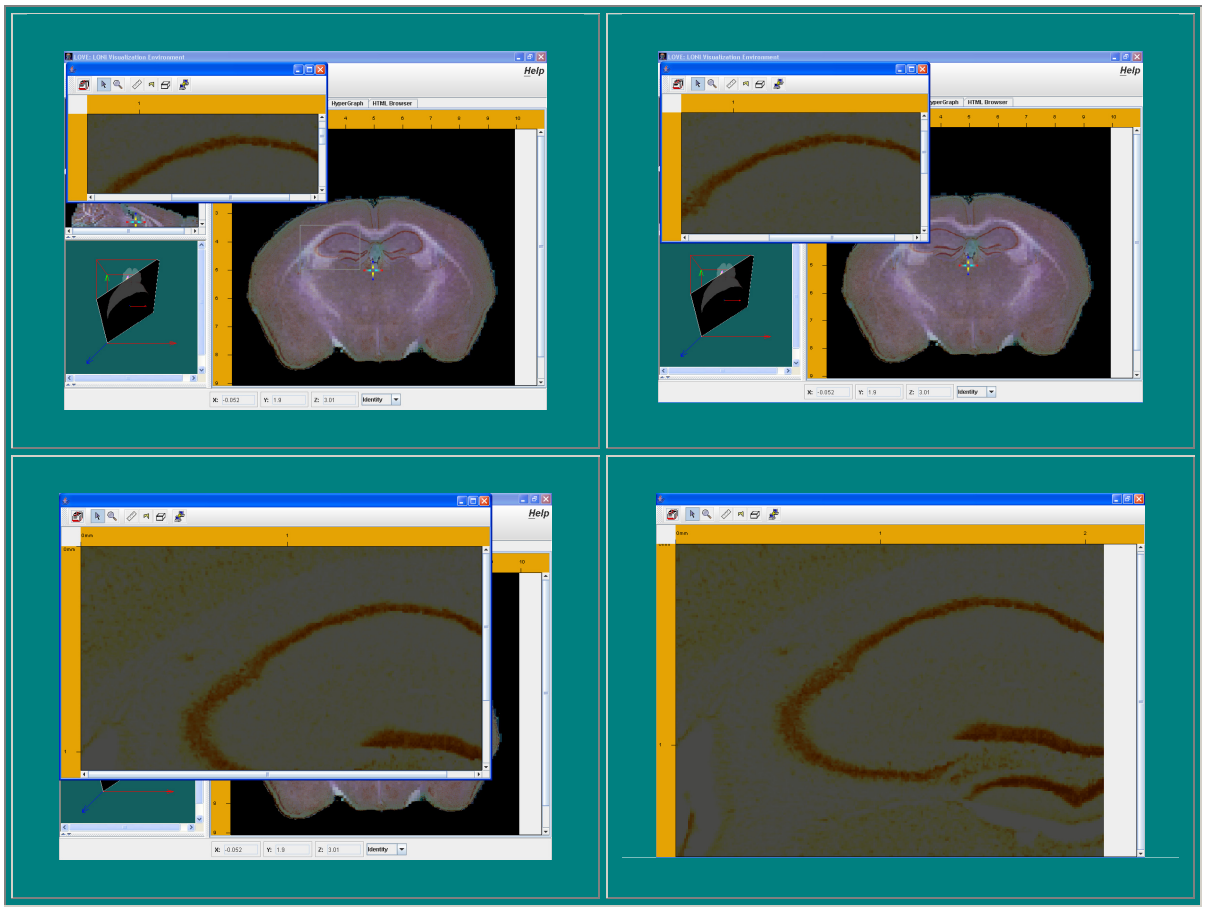
H. LONI atlas transfrmation & Information Server (LATIS)

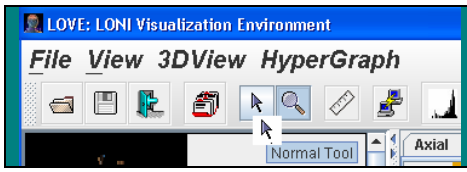
(Internet-connection required) retrieval of high-resolution imaging data via LONI online server

	Click on “LATIS” tool button



Few screen shots



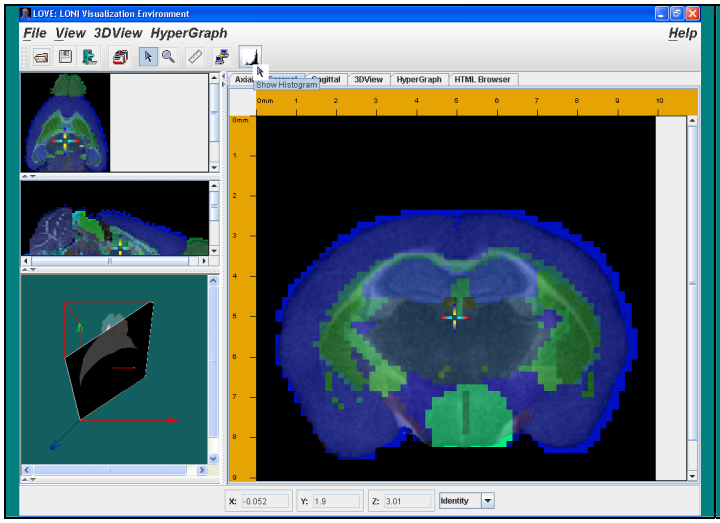


Click on “Normal Tool” tool button to deactivate “LATIS” mode

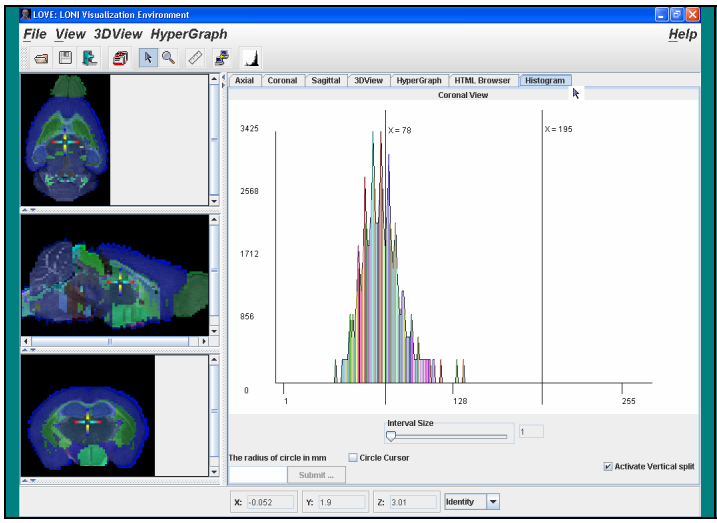
Icon	Name	Description
	Show Layer Control	Allows control of image colormaps, opacities and volume properties (point to Layer-Contrl Section above)
	Normal Tool	Default Tool
	Zoom	Tool for pixel-based image magnification
	Measure Length	Eucleadian measure of (shortest) distance between two selected co-planar voxels
	Measure Area	An estimate of the measure of an arbitrary 2D region
	Measure Volume	An estimate of the volume of an arbirtrary 3D solid
	LATIS	(Internet-connection required) retrieval of high-resolution imaging data via LONI online server

I. Histogram and ThreeColorMap

1. Drawing a histogram.



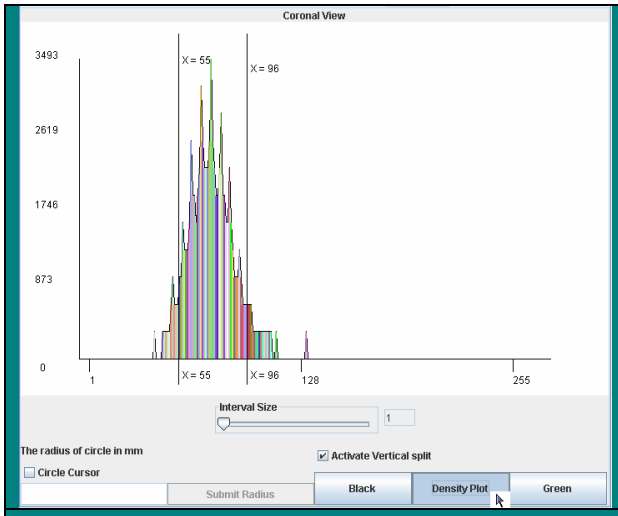
- Select a brain view tab such as “Axial”, “Sagittal”, or “Coronal”
- Click the “Histogram” icon



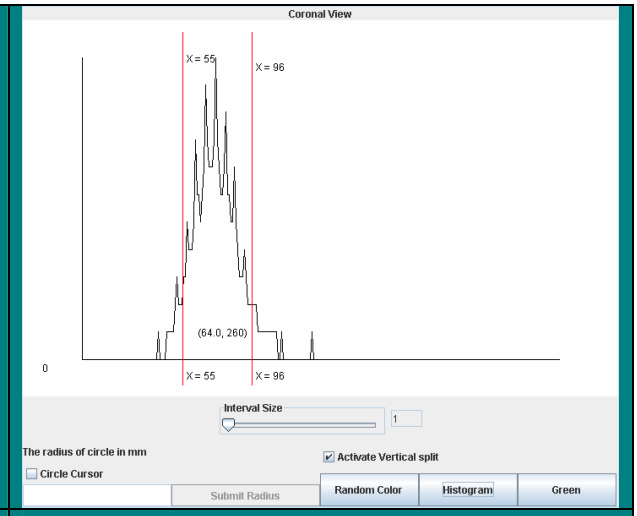
- Click the “Histogram” tab

2. Switching view
   - Select a brain view tab
   - Click the “Histogram” tab

3. Density Plot

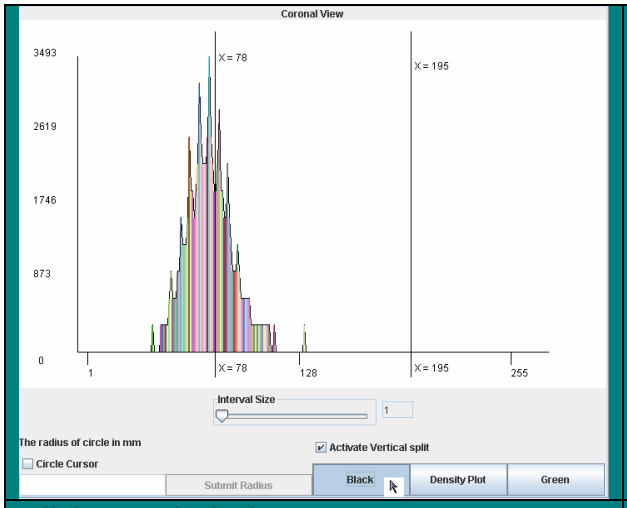


Click on “Density Plot” Button

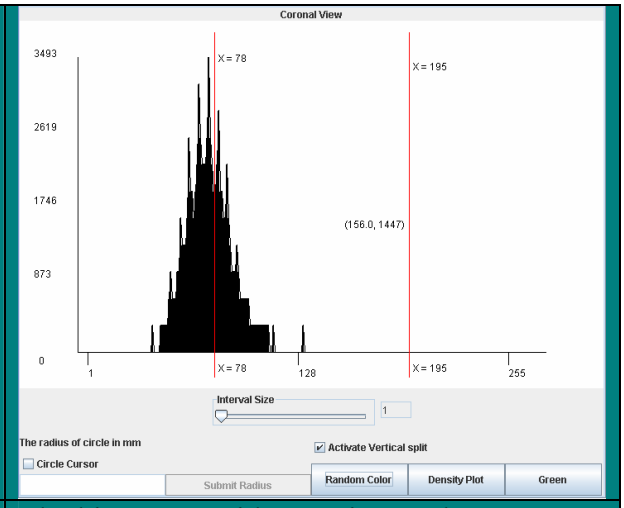


A view of density plot.
If you want to go back to histogram, click on “Histogram” Button

4. Unique Coloring Of The Histogram

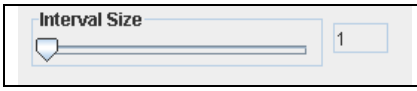


Click on “Black” button



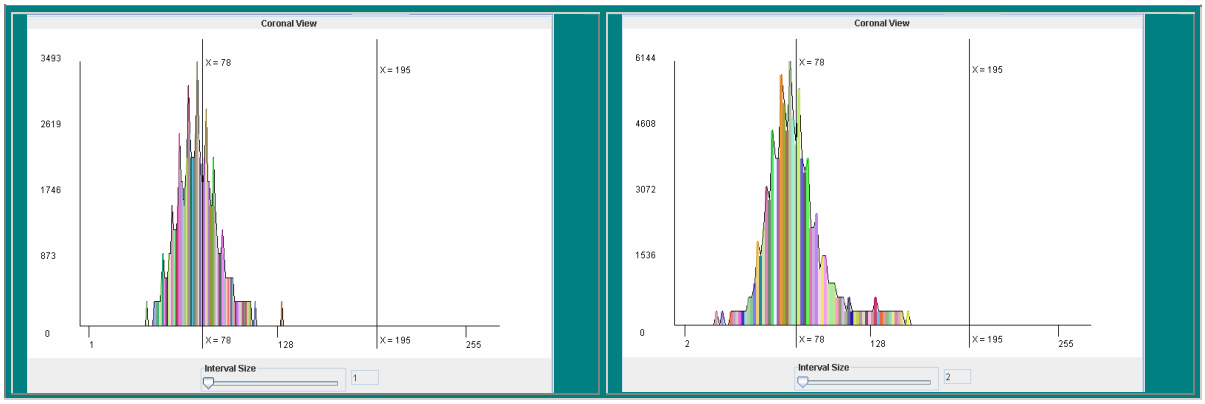
The histogram with an unique color
If you want to go back to histogram with random colors, click on “Random Color” Button

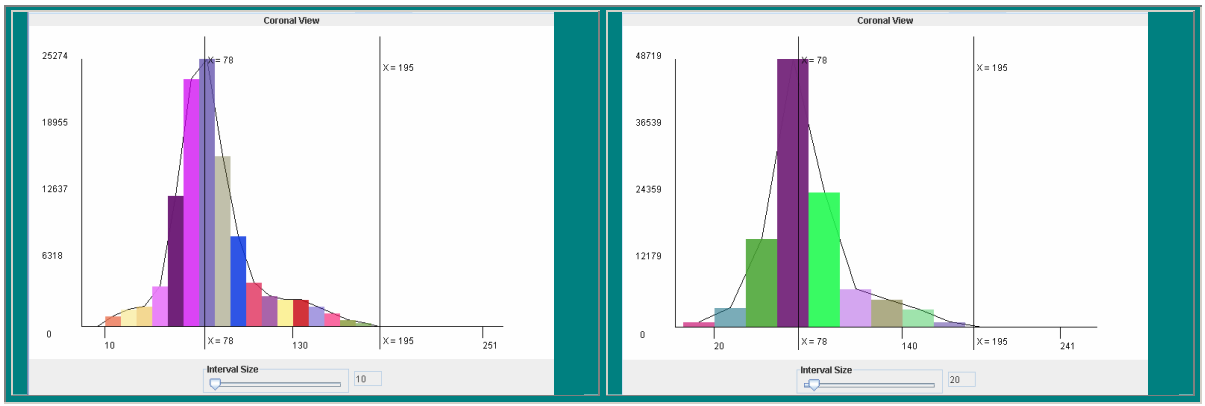
5. Changing Interval Size



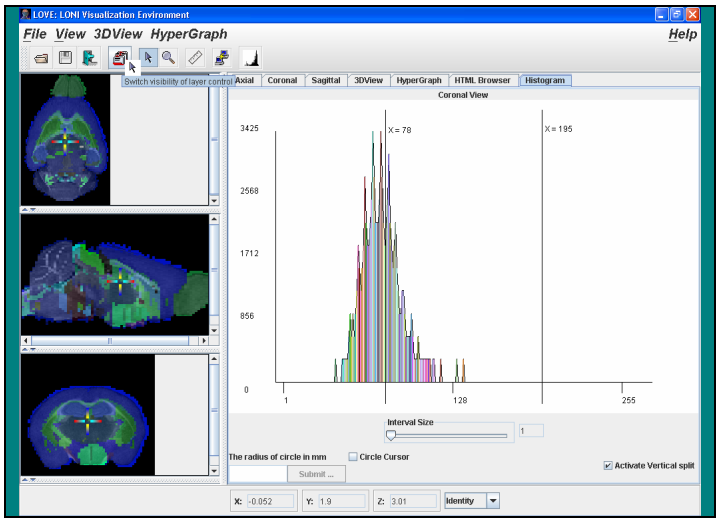
You can change interval size by clicking on “Slider” or by dragging “Slider”

A histogram view with different interval size

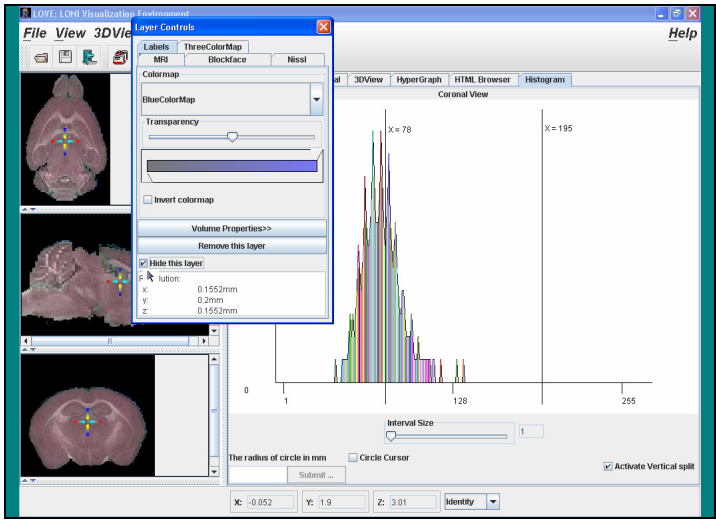




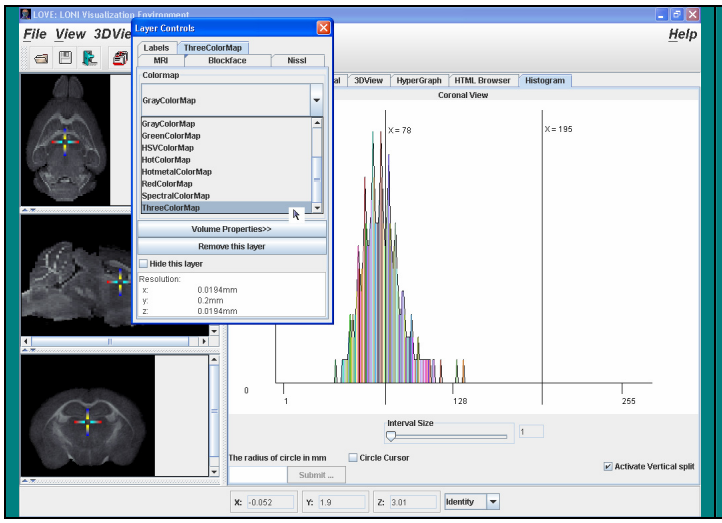
6. ThreeColorMap
   a) To View "ThreeColorMap"



- Click on "Historgram" icon
- Click on "Histogram" tab
- Click on "Switch Visibility Layer Controls" icon

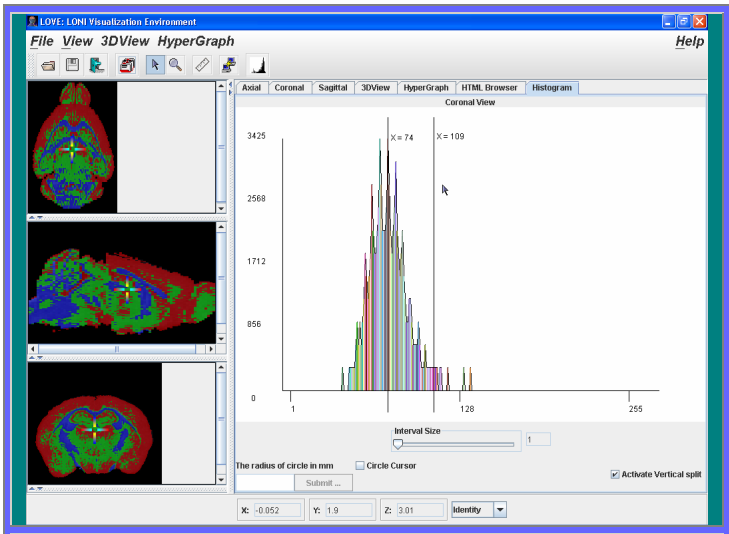


- Hide all layers except for ThreeColorMap and MRI (See "Layers Controls" for more detail)

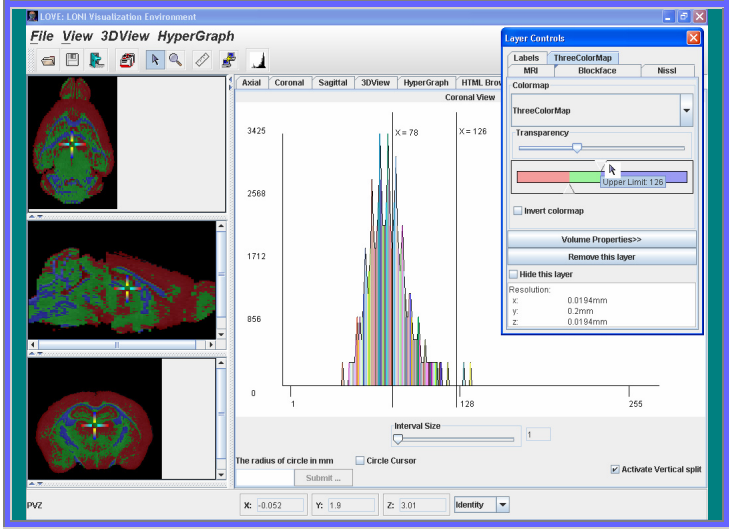


- Click on “ThreeColorMap” tab
- Under “Colormap” menu, select “ThreeColorMap”

b) Three-Color Controls

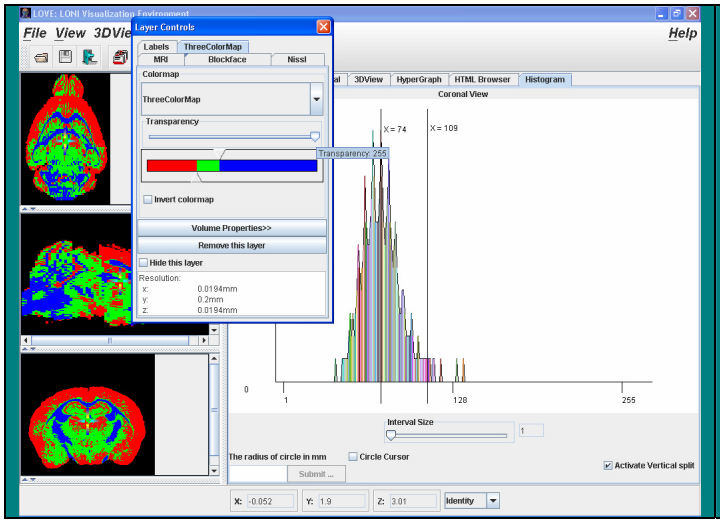


1) Using “Histogram” Mode
   - Clikck on “Histogram” tab
   - Adjust vertical bars to distribute amount of each color (e.g. green, blue, or red) to obtain desired view



2) Using “Layer Controls” Mode
   - Click on “Layer Controls” icon
   - Adjust upper and/or lower limit to distribute amount of each color (e.g. green, blue, or red) to obtain desired view

c) Transparency Controls



- Click on “Layer Contorls” icon
- Select “ThreeColorMap” or “MRI” tab
- Adjust “Transparency” slider to obtain desired view
- (See “Layers Controls” for more detail)

d) Circle Cursor

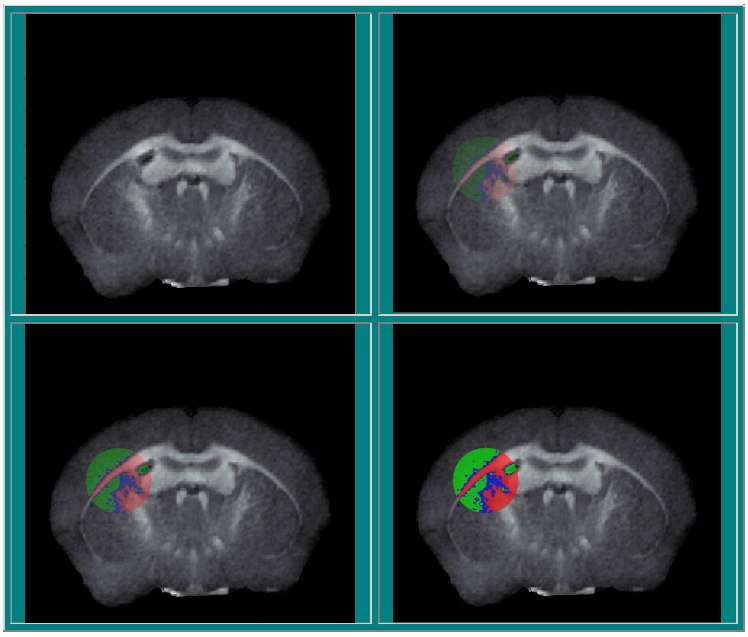
1) Selecting “Circle” cursor
   - Change cursor style to “Circle Cursor” using either steps: View>Cursor Style>Cirlce or Select “Histogram” tab and check “Circle Cursor” check box

2) Changing radius of the “Circle” cursor
   - Select “Histogram” tab
   - Type a radius in text field using integers (e.g. 3 or 4)
   - Either press enter key or click on “Submit Radius” button

3) Viewing ThreeColorMap
   - Select a brain view tab such as “Axial”, “Sagittal”, or “Coronal”
   - Move curosor to a desired location to see “ThreeColorMap”

4) Transparency With The Circle Cursor
   - Press and hold shift key
   - Move mouse in and out of the circle area
   - Release shift key when you find desired view

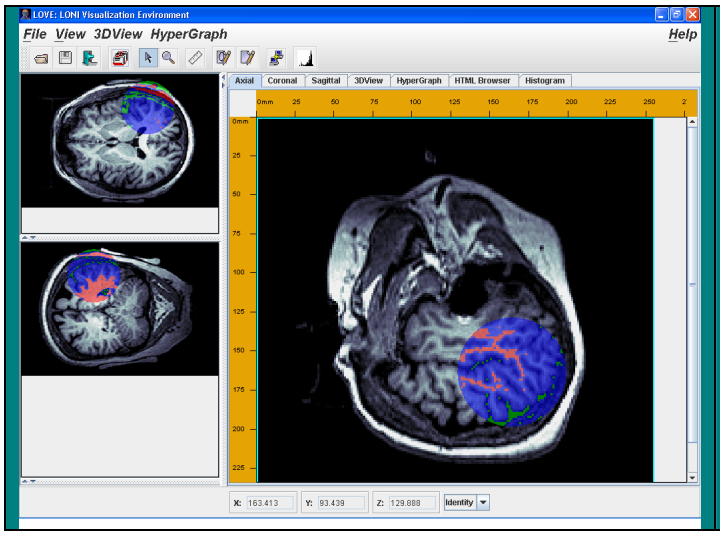
Circle cursor with different transparency



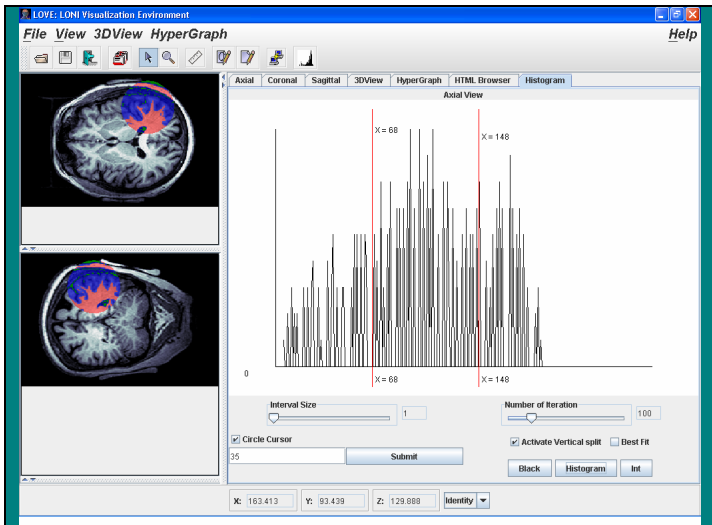
e) Finding the best locations of the vertical bars

We have implemented an efficient mixture model fit for automatically identifying the white matter, gray matter and cerebro-spinal fluid. The algorithm relies on iterative Expectation-Maximization statistical method to estimate the parameters of the Gaussian-mixtures and the weight coefficients (To learn more about gnerlaized expectation maximization http://www.stat.ucla.edu/~dinov)

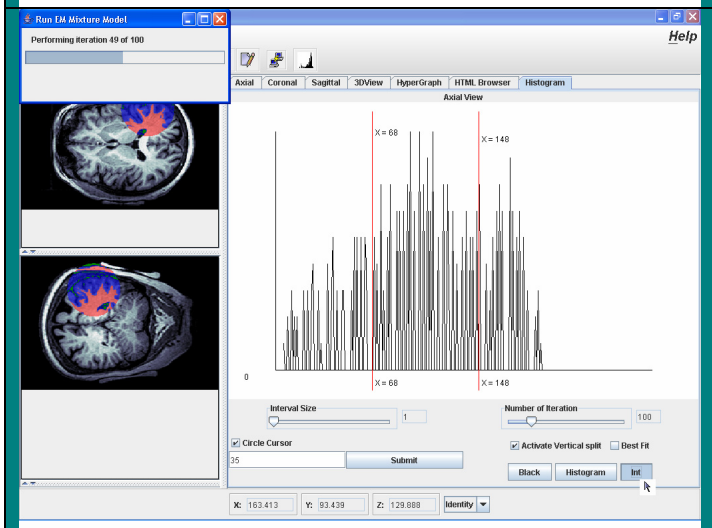
Example:



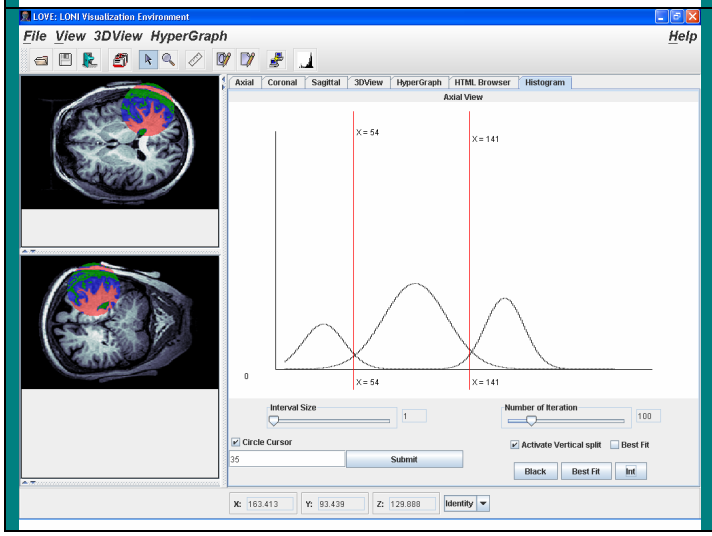
- We want to identify the white matter, gray matter and cerebro-spinal fluid inseide the circle cursor by running Expectation-Maximization Modeling Algorithm(EMM) .
- For more information about how to use circle cursor, refer the section: I. Histogram and Three Color Map – Circle Cursor



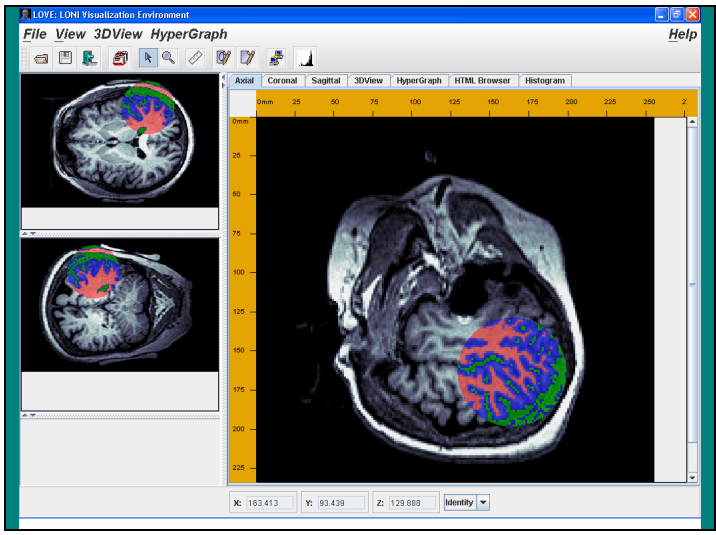
- Select the histogram tabbed pane
- Set initial locations of vertical bars
- Set number of iteration



- Press “Int” button and pop up menu will be showing while running

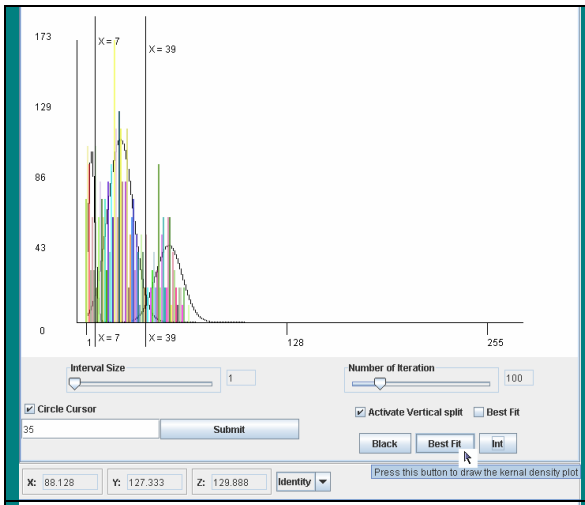


- Result with best fit graph
- Viewing other grahps will be explained below

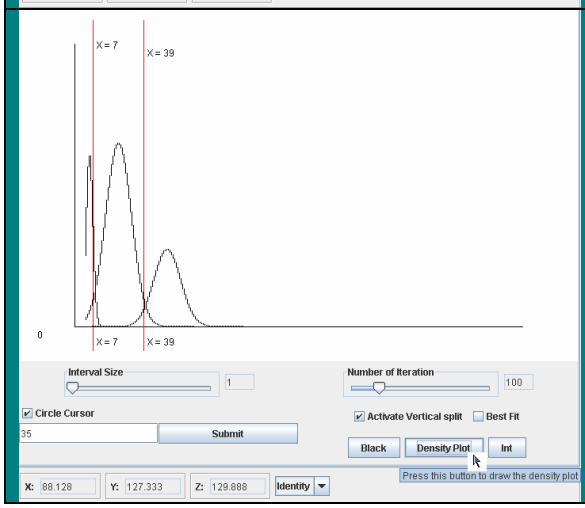


- To view the result, select the brain view which you started with

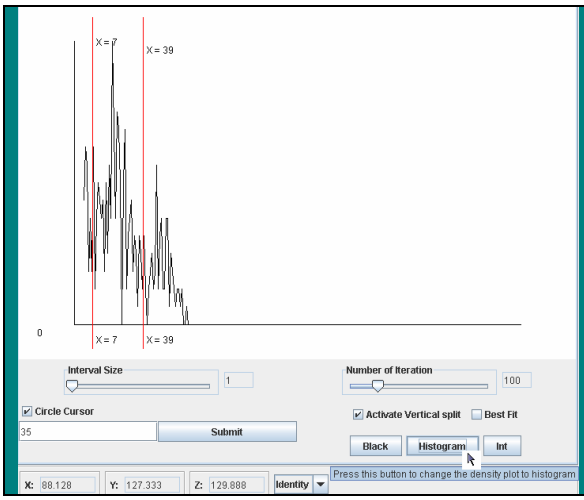
How to view different graphs



- After running EMMixture Model, to view best fit graph, press “Best Fit” button to view
- The graph will change to best fit graph and the button that you just pressed will change to “Density Plot” button

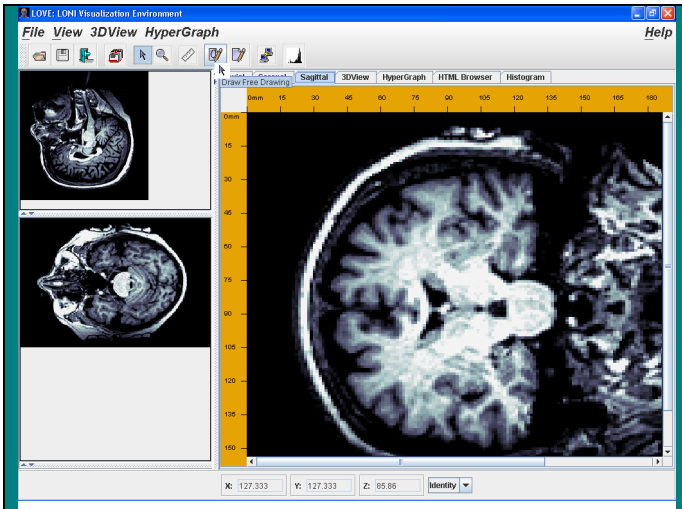


- Press “Density Plot” button to view density plot
- The graph will change to density plot and the button that you just pressed will change to “Histogram” button

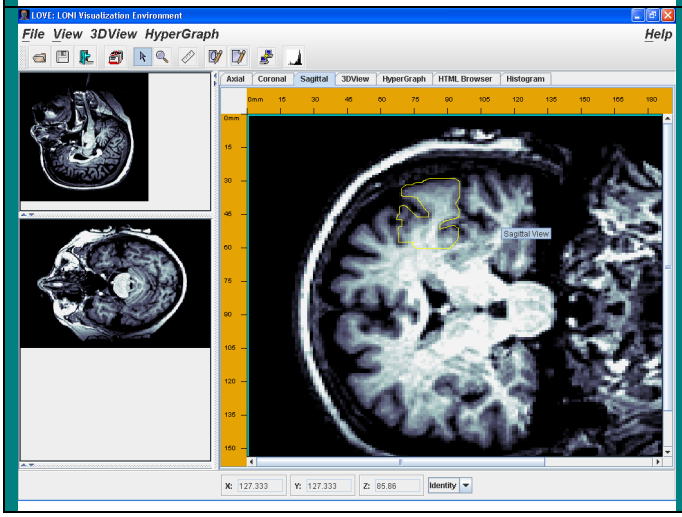


- Press “Histogram” button to go back to original graph

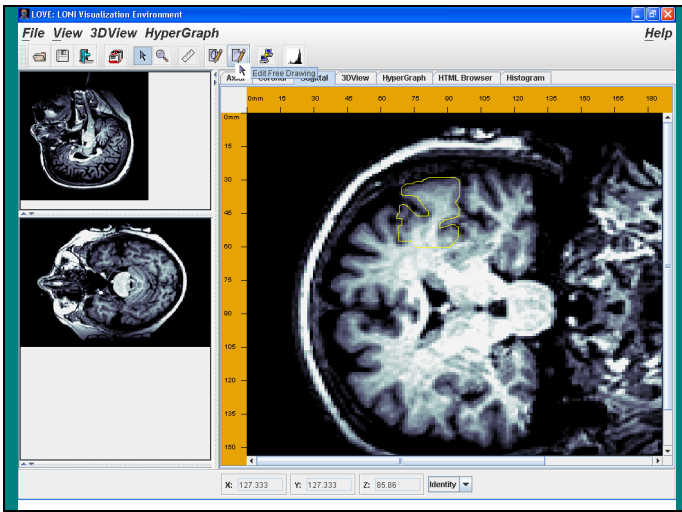
J. Free Style Drawing



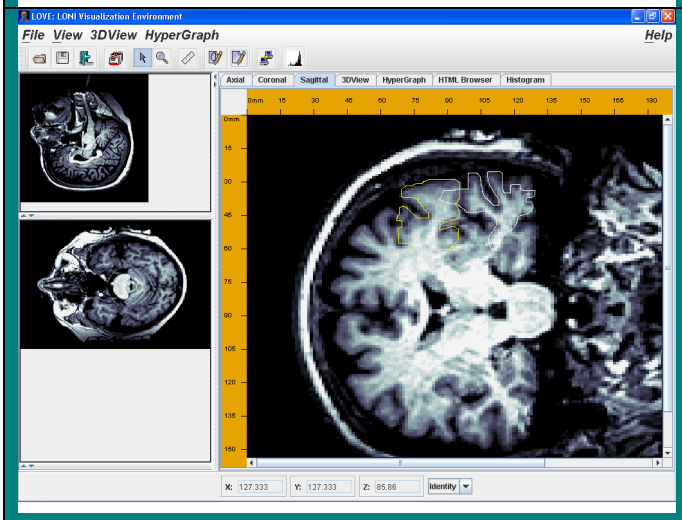
- To draw contour on surface of a brain view, press on a tool button 



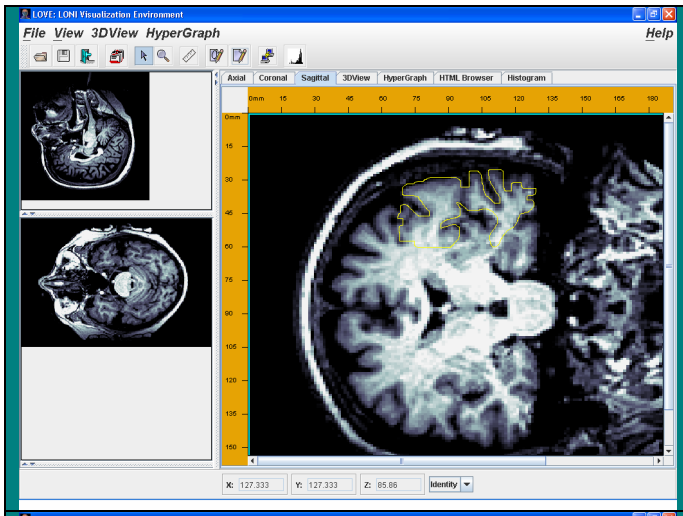
- Draw a contour as you want



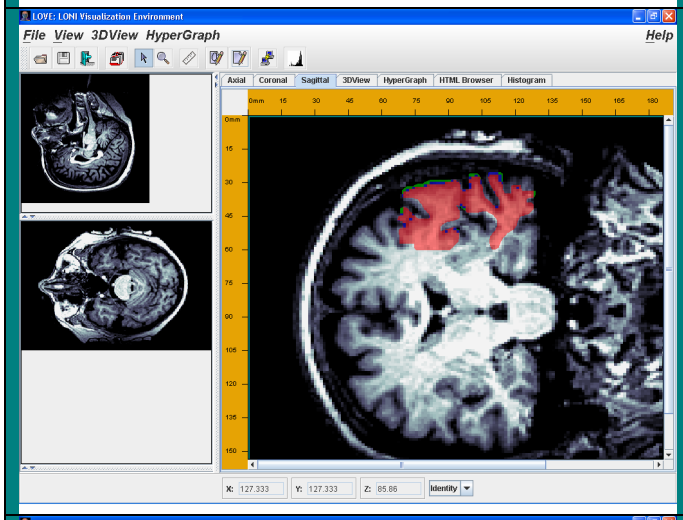
- If you dislike the region, you might edit it
- To edit, press a tool button
- In case you want to start over, “Left-Click” on the mouse while holding down “CTRL” key



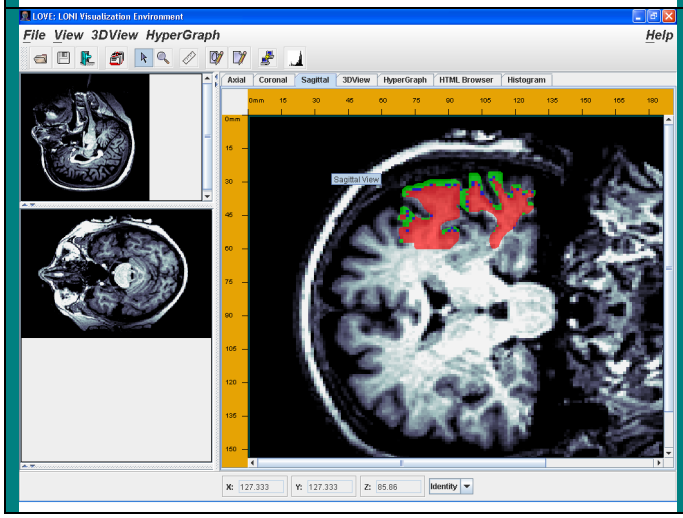
- Draw another contour over the region where you wish to add or substract.
- If you Right-Click on the mouse over the region where the intersection is, then the intersection region will be selected.
- If you Right-Click on the mouse over the region where the original region is, then the original region after the intersection is removed will be selected.
- If you Right-Click on the mouse outside of two regions, then the combined region will be selected.



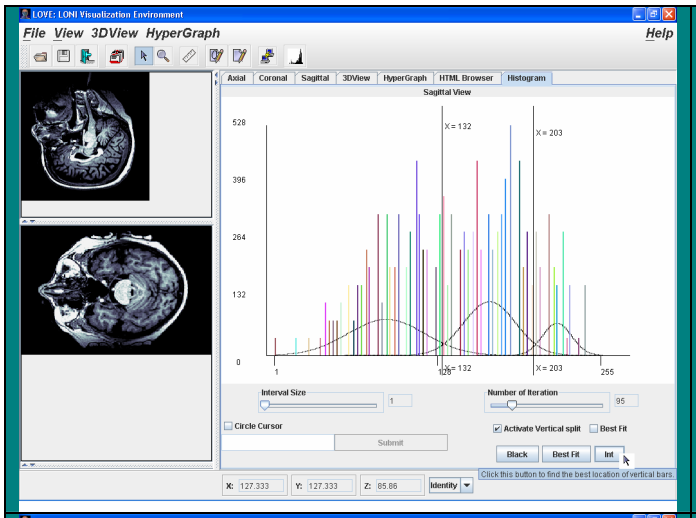
- Example: Combined region is selected



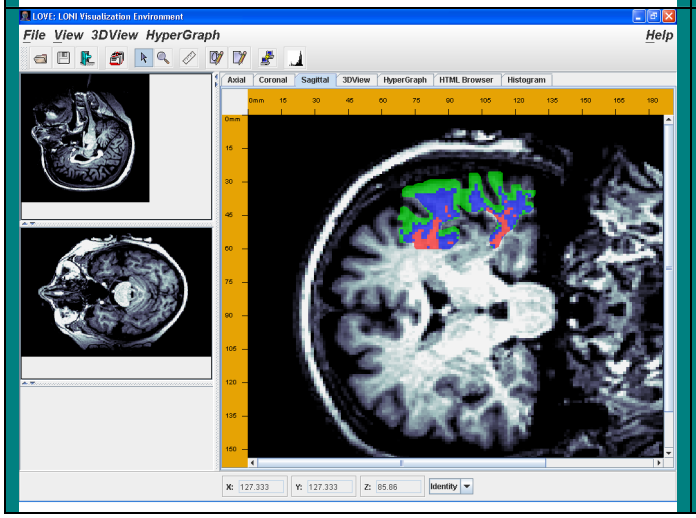
- To draw three color map, “Left-Click” on the mouse while holding down “ALT” key



- You can run EMM by “Left-Click” on the mouse while holding down “Shift” key
- If it doesn’t give a good result after running it 3 or 4 times, you might run EMM at the histogram tabbed pane as described below



- Select histogram tabbed pane
- Set number of iteration size
- Set inititial vertical bar locations
- Press “Int” button
- If you are satisfied with result graph, select the brain view which you start with to see the result



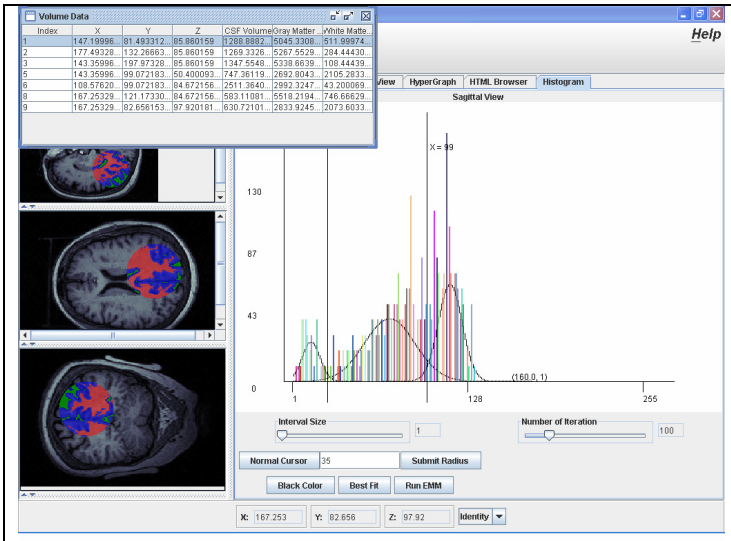
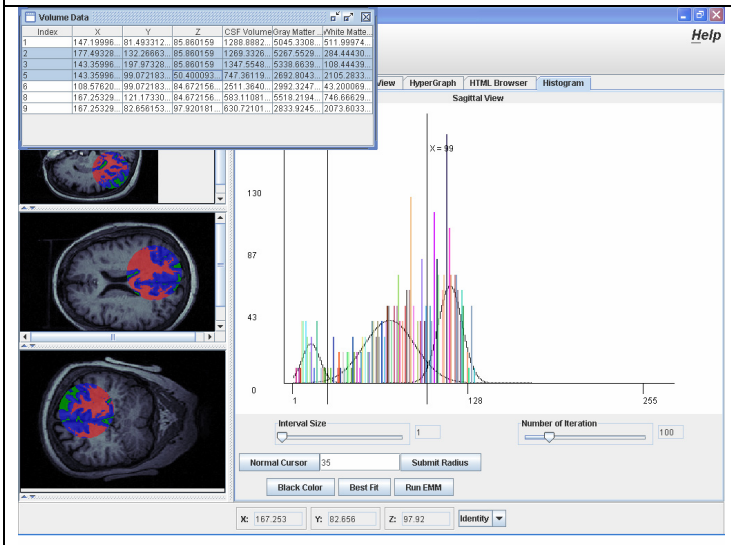
- Result
- To quit the free drawing, press the tool button,  once more

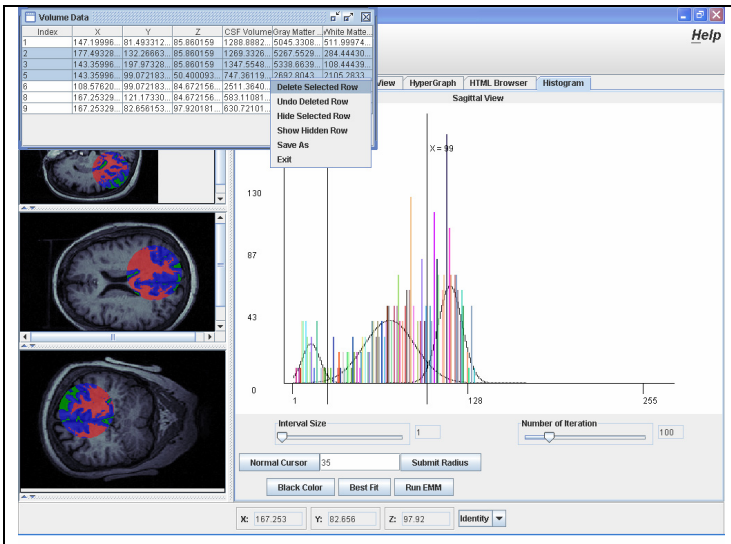
Mouse and Key summary for free drawing

CTRL + Right Click	Clear any contour
ALT + Right Click	Fill the contour with three color
Shift + Right Click	Run EMM
Left Click (after complete editting)	Select the rigion
Shift + Mouse’s Movement (without any click)	Change transparency

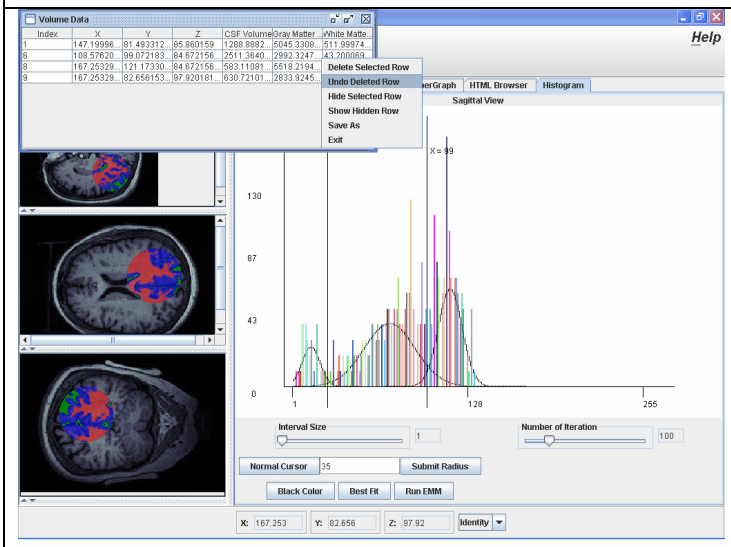
K. Volume Property Table

This table contains the tissue volumes for different 2D areas (disk or free form). Each row includes the center-of-gravity coordinates (x, y, z) that anchor the region. User can edit and save this table accordingly.

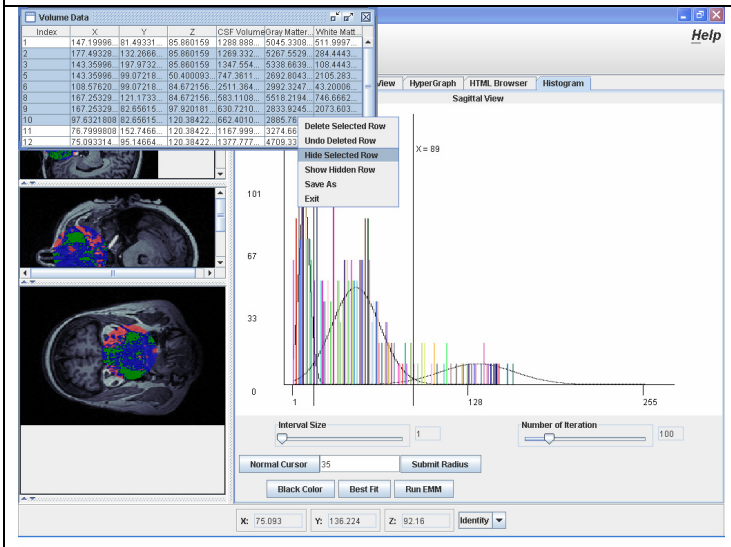
	• Right click on histogram pane will triger volume a proprty table with location of the cursor
	•



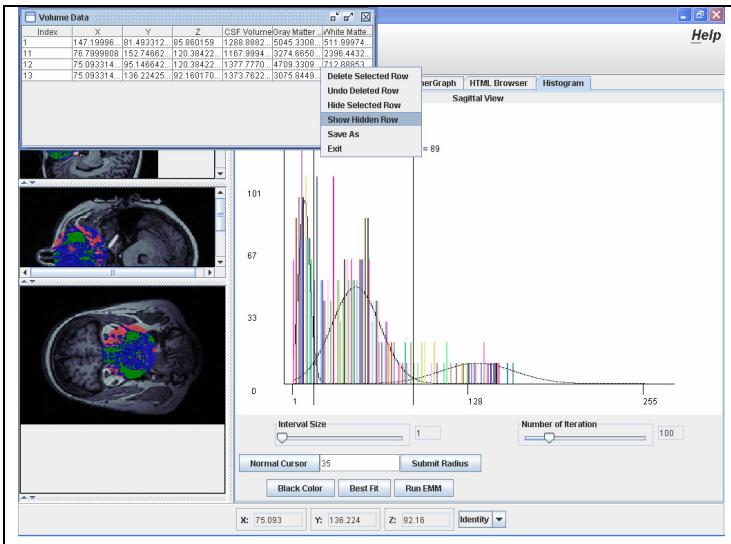
- Deleting Row
- Highlight a row or rows which you want to delete
- Right Mouse Click and select “Delete Seleted Row”



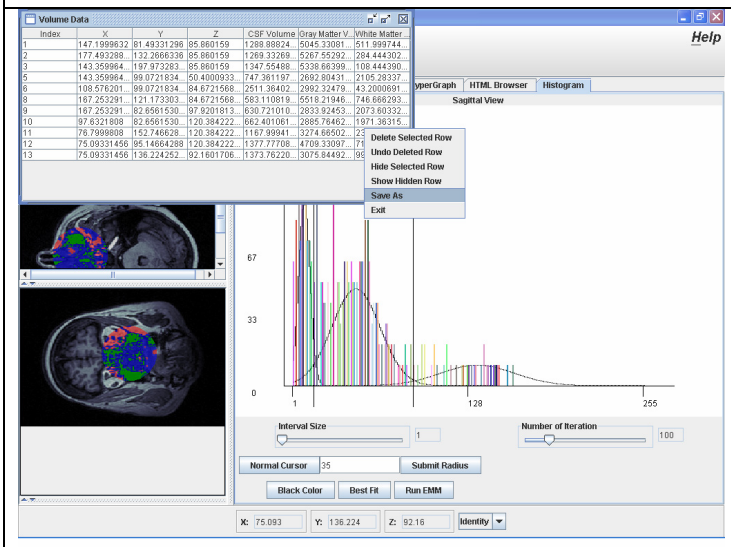
- You can undo a row or rows that you just deleted



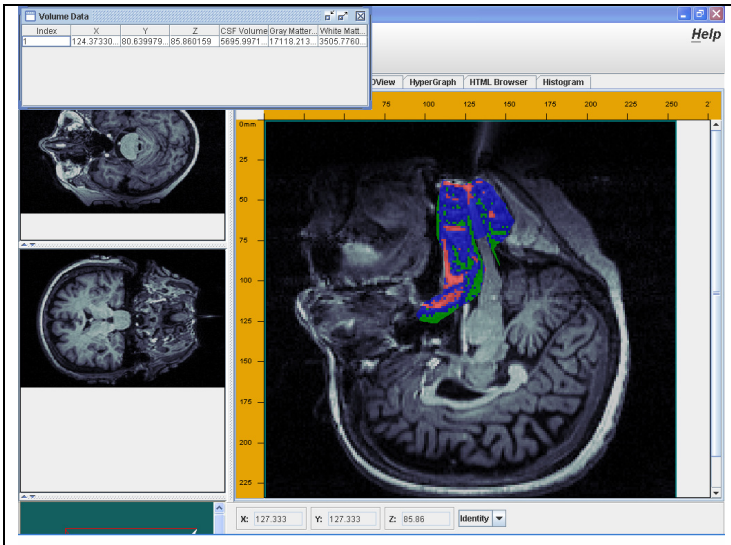
- Hiding a row or rows
- Highlight rows which you want to hide Right mouse click
- Choose “Hide Selected Row” from the menu



- Reveling rows that you hid
- Right Mouse Click
- Choose “Show Hidden Row” from the menu



- Save
- Right Mouse Click
- Choose Save As from the menu



- You also construct a table from the big brain view panel; however, you have to choose “Free Style Drawing” first
- See the section, “Free Style Drawing” to learn about how to use the free style drawin
- When you are satisfied with three color map you have, ALT + Right Mouse Click to see the table

L. Save

Need more information

M. Exit

- File > Exit or Click on “Exit LOVE” button
- “Confirm Exit” pop up menu will appear, then click on “Yes” button

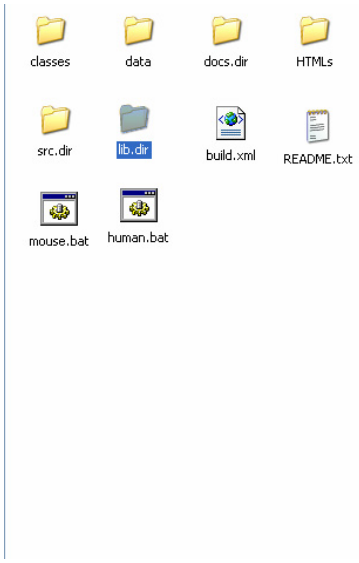
VIII. JAVA CLASS DOCUMENTATION FOR LOVE

Java Class Documentation for LOVE

IX. DEVELOPER’S REFERENCE

In order to use Statistics Online Computational Resources (SOCR), a developer has to follow steps.

1. Create a folder where the build file is located.

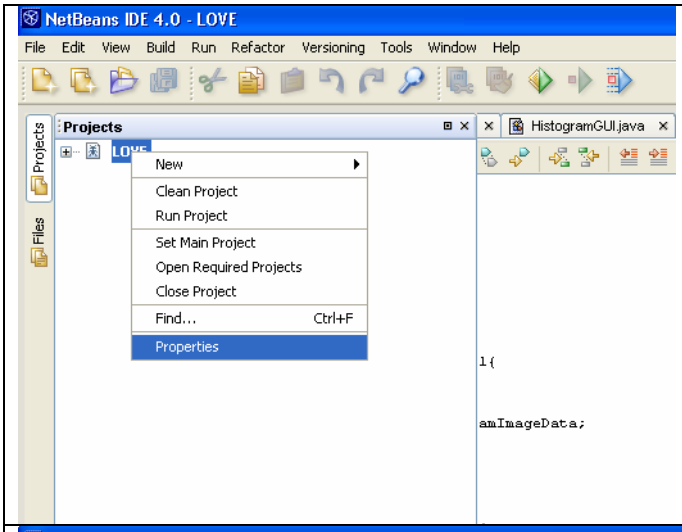
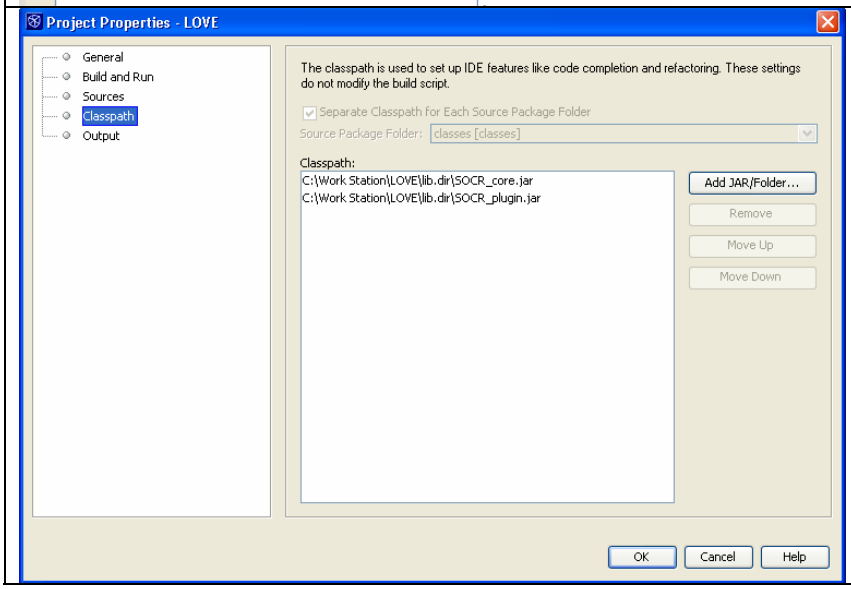


2. Download SOCR
[Downloading SOCR]

3. Unzip and put two jar files SOCR_core.jar and SOCR_plugin.jar inside the folder.

4. Set class path

   a. Build file: add <property name="classpath" value=":lib.dir/SOCR_core.jar:lib.dir/SOCR_plugin.jar"/>
   b. Net Beans: it depends on which version of Net Beans is being used
   For Net Bean IDE 4.0

	Right click on your project and select Properties from submenu
	Choose Class path from popup screen and Add two jar files.

   c. .bat file:
echo off
cd classes

```
rem          HUMAN DATA TEST
java -cp .;..\lib.dir\SOCR_core.jar;..\lib.dir\SOCR_plugin.jar
```

5. Local import

Import any package where it is needed, for example,
import edu.ucla.stat.SOCR.util.*;

X. RESULTS and ANALYSIS

XI. CONCLUSIONS and RECOMMENDATIONS

XII. APPENDIX

Data Descriptor (HADER) Files
Input Data & File Formats
Multi-Contour Files (MCF)
Running LOVE

Data Descriptor (HADER) Files

- **LOVE** is a diverse viewer which reads GZIPed or uncompressed Net CDF, MINC Net CDF, DICOM and RAW (ANALYZE) data files. For the latter, raw, files we allow various formats for the header files describing the data. e.g., **ANALYZE** and **ASCII** header files describing the data. It expects, however, that any such header file descriptor has a name like **myFile.hdr**, **myFile.LHD**, **myFile.lhd** or **myFile.header** (Loni HeaDer). Moreover, for the **ASCII** header files the content of this file needs to contain, anywhere inside the file, lines with the following delimiters:

volume	myFile.img
bits/pixel	8
x_dim	181
y_dim	217
z_dim	181
x_step	1.000000e+00
y_step	1.000000e+00
z_step	1.000000e+00
x_start	-90
y_start	-126
z_start	-72

- The **volume=** delimiter is not necessary and **bits/pixel=** can be replaced by **data_type=**.

Input Data & File Formats

- LOVE reads in 1, 2 or 3D (dimensional) (GZIPed or uncompressed) data sets of the following types:
  - RAW BINARY (ANALYZE) data files having the following name convention:

    myFile.img

  - And auxiliary **ANALYZE** or **ASCII** header files RAW-HEADER with data types as follows:
    a. 8 bit (byte), range [0 : 255], code: 8;
    b. 8 bit (byte), range [-128 : 127], code: 9;
    c. 16 bit (unsigned) short integer data, range [0 : 65535], code: 16;
    d. 16 bit (signed) short integer data, range [-32768 : 32767], code: 17;
    e. 32 bit (unsigned-integer), code: 32
    f. 32 bit (signed-integer), code: 33
    g. 32 bit (float), code: 34
    h. 64 bit (double), code: 64

    Note: "code" refers to the data-type listed in the auxiliary header file, where for example a line like "data_type=16" is equivalent to "bits/pix=16" and both mean 16 bit (2 byte) unsigned data (short integer).

- Network Common Data File format - Net CDF (NC), and its specialization Montreal Net CDF - Minc (MNC)
- DICOM DICOM files could be visualized as 2D series of images (default), or if renamed to **file###.dicom** and saved in a single directory the series could be used to reconstruct a Montreal Net CDF file (mnc) and visualized in 3D. To do this DICOM --> MNC conversion you need to have all dicom files into a new directory. Select the **directory** from the File-->Load menu (not any one file) and it will grab all dicom files and reconstruct the 3D stereotactic data representation in a MNCDF file, which you can finally load in.
- Various rasterized image formats (e.g., TIFF, GIF, etc.)
- Starting LOVE is done by either of:
  - WINDOWS: click on the "LOVE_driver.bat" icon
  - UNIX%> **LOVE_driver**
  - UNIX%> **LOVE_driver myFile**
  - UNIX%> **java LOVE2**
  - UNIX%> **java LOVE2 myFile**
  - other%> **java -jar LOVE.jar [file]**

Running LOVE

- Create a batch file(windows)
- Create an executable shell file(unix/linux)

Multi-Contour Files (MCF):