

Brain Mask

User's Guide



Segmentation of the brain from three-dimensional MR images is a crucial pre-processing step in morphological and volumetric brain studies. *BrainMask* software implements a fully automatic brain segmentation from T1-weighted MRI. The algorithm exploits the notion that after thresholding, regions corresponding to the brain and non-brain structures are either “weakly” connected or are separated by strong edges. Due to its sub-voxel morphological erosion and constrained growth operators, *BrainMask* demonstrates high segmentation accuracy. In a recent study of 29 representative datasets, the segmentation error averaged $3.4\% \pm 1.3\%$ [1]. This User's Guide will help you understand the features of *BrainMask* and its user interface. A Quick Start step-by-step tutorial is also available.

[1] Artem Mikheev et al. Fully automatic segmentation of the brain from T1-weighted MRI using Bridge Burner algorithm. *J Magn Reson Imag.* 2008 Jun;27(6):1235-41.

Installation

Follow instructions listed in the file BrainMask_ReadMe.txt to install the program. Briefly:

- Extract files to a new folder
- Run vcredist_x86.exe
- Launch BrainMask.exe
- Paste your computer ID to the email addressed to hr18@nyu.edu
- The reply will include FireVoxel.key to be saved in your folder

When you start the BrainMask application (Fig.1) you will see its main window, the toolbar on the right margin and only two menu items: *File* and *Help*. The gray document area is initially empty. Make sure that the vertical resolution of your screen is fine enough to view the entire toolbar (9 icons).

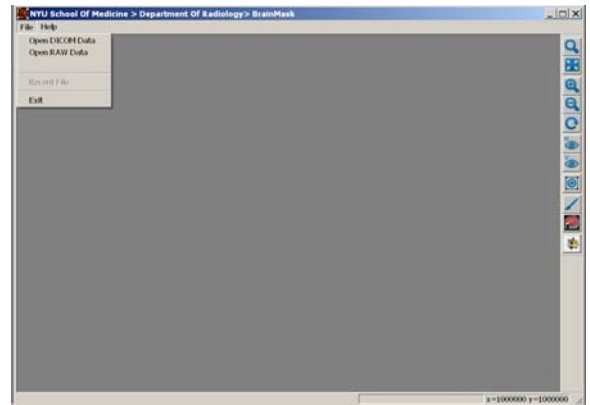


Figure 1. Opening window.

Loading and saving volumetric data

BrainMask is designed to work with several image formats:

- a. DICOM file format (*.DCM, *.DIC, *.). There are typically hundreds of dicom files for one brain MRI.
- b. Two types of RAW image files: Analyze (*.img,*.hdr) and Midas (*.im,*.hd). Midas format is similar to Analyze but with a text header. These formats save a 3D raster volume as pairs of files with the same name and different extensions. Raw image data reside in *.img or *.im file. The header files *.hdr or *.hd describes image resolution and voxel size information.

The current version will not save volumes in Analyze format. Save your images in either DICOM or Midas format.

To open a RAW (Analyze or Midas) image, select *FILE>Open RAW data*. Then choose the File type in the Open dialog box and browse to the desired folder.

DICOMDIR Dialog Box -- loading DICOM images

To load a volume from DICOM files, make sure all files are in the same folder. It is ok to have several subfolders in the DICOM folder. Select *Open DICOM Data* option from the *File* menu and specify (browse) the disk folder that holds the files. The folder should not contain any other files, with one exception of a “master” file named DICOMDIR. DICOMDIR records the structure of files for a more efficient access to images. If DICOMDIR file is present, the program will offer to use it. However, if some files were added or deleted, it is safer to decline the offer. The program will then regenerate the DICOMDIR file.

DICOM organizes files as a tree PATIENT>STUDY>SERIES>IMAGE (Figure 2). An IMAGE is a single 2D slice. A SERIES correspond to the acquisition of a protocol, which usually results in a 3D volume of data. A STUDY corresponds to a set of SERIES acquired in one examination. To help you choose, on the upper right of the dialog box you will see its middle slice preview (Figure 2). Under the preview you will see a summary of the dataset.

DICOM tags are used to describe various elements of the DICOM tree. You can inspect these tags by placing the mouse cursor over the corresponding tag and viewing the “Element Value” field.

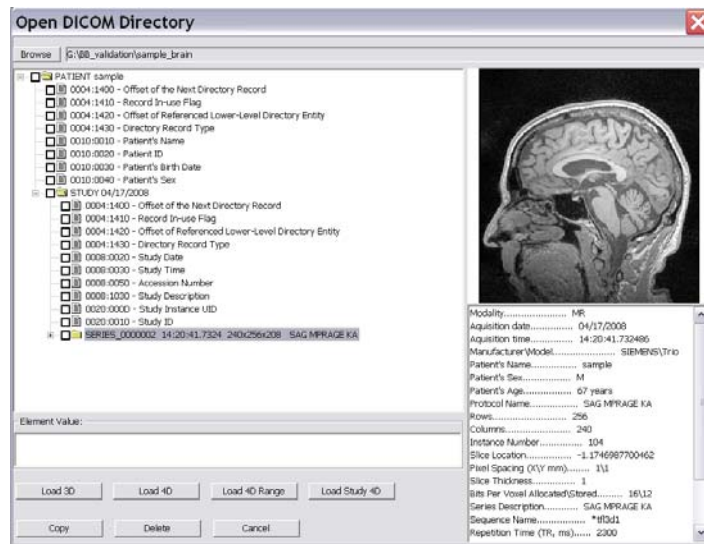


Figure 2. DICOM dialog box.

To load a 3D dataset, you highlight with the mouse the corresponding SERIES (there is no ability to load an individual 2D slice) and press the *Load 3D* button.

Occasionally a series will consist of several subvolumes. A typical example is a multi-echo MRI acquisition. It might make more sense to load each subvolume separately. This is done by clicking on the small box with a plus sign, located to the left of the series name. This will expose the series into subvolumes and let you load them individually.

Copying and Deleting DICOM series

Sometimes you may want to copy or delete individual series of the DICOMDIR tree structure. To accomplish this, you should first check the bold square boxes (initially empty) located on the left of the desired elements. Then press the “Copy” or “Delete” button (Figure 2). When copying, you will be prompted for the destination folder. You can copy/delete individual images, series, studies, or patients.

Film View and Slice View

After loading a volume, its images are displayed in either *Film View* or *Slice View* mode. The *Film View* (Fig. 3) gives you the overview of the entire volume, with individual slices arranged as tiles. This helps us to understand the dataset and to quickly get to the desired slice. In the *Slice View* mode you are presented with a single slice. To navigate through the stack of slices you can use the mouse wheel or the keyboard arrow keys. To switch to the ***Slice View***, point to any slice and right-double-click.

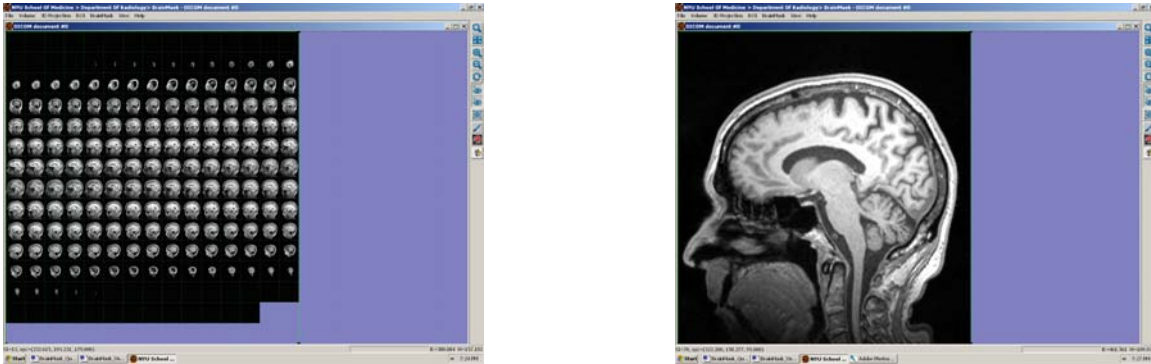


Figure 3. Film view and Slice view.


Press *Orthogonal Projections* icon  (the lowest icon on the toolbar, right margin) to generate additional windows with orthogonal view of the volume (Figure 4).



Figure 4. Three orthogonal views, each set to single slice mode.

Navigating through the dataset


You can load multiple volumes in separate resizable windows. Independently you can resize the volume relative to the document window using the four zooming

icons. In the *Slice View*, the mouse wheel lets you scroll through slices. You can also press up-arrow and down-arrow keyboard keys to increase/decrease the z-coordinate of the currently displayed slice.

The position of the voxel pointed to by the mouse cursor is displayed at the bottom left corner of the *BrainMask* window, inside the status bar. The signal intensity (SI) is also shown.

Zooming tools

To modify magnification, use one of the zooming tools located in the toolbar on the right (Figure 5).

a) zoom by window selection: click on the magnifying glass icon , then hold on the left mouse button and make a rectangular selection with the cursor over the volume. The selection will fill the entire window when the mouse button is released.

b) zoom all : fills the window with the entire image.

c) zoom in  and zoom out .

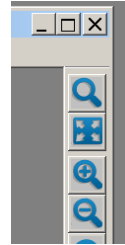


Figure 5. Zooming tools.

Layers and ROIs

Each raster entity lets you superimpose volumetric raster images, all sharing the same resolution and dimensions. Each volume resides in a layer, indexed by an integer, beginning with the base layer (Fig.6). What you see in a multi-layered window is determined by the reverse order of layers (from top to base) and layer transparency α . Layer transparency value ranges from 0% to 100%, with $\alpha=0\%$ defined as fully transparent (invisible) and $\alpha=100\%$ defined as fully opaque. Currently up to 10 layers can be displayed.

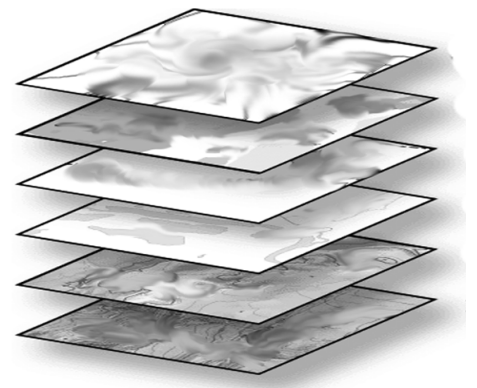


Figure 6. Volumetric raster entity containing six layers.

A very common type of a raster image is a mask (Fig.7), also referred to as a binary volume, region of interest (ROI), or volume of interest (VOI).

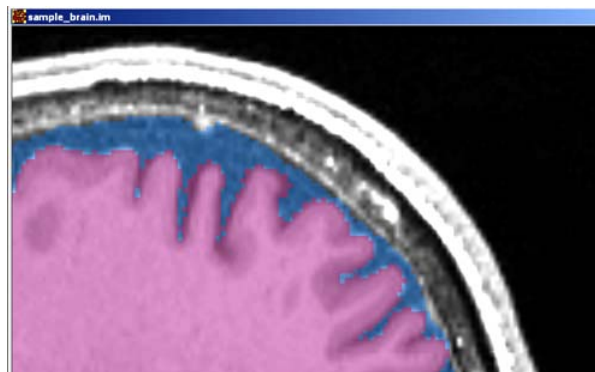


Figure 7. T1-weighted MRI loaded as the base layer at $\alpha=100\%$, followed by a blue ROI at $\alpha=30\%$, and a red ROI at $\alpha=50\%$.

Position the mouse cursor over the image and left double-click to activate the Layer Control dialog box (Figure 8).

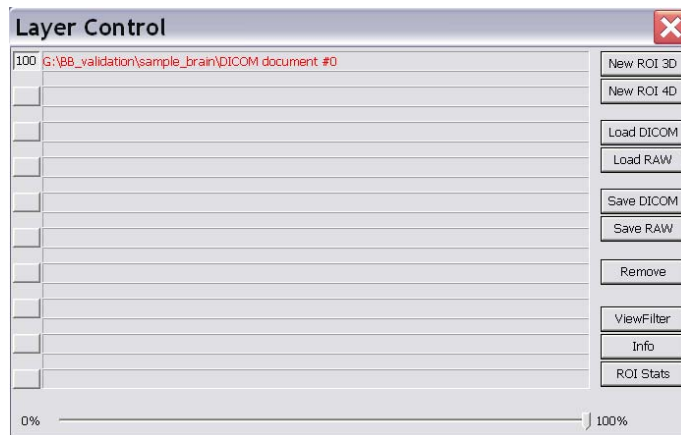


Figure 8. Layer Control.

This dialog box shows layers and their properties:

- Layer Name. If the layer was loaded from a file, this is the file name.
- The active layer is shown in red.
- α setting for each layer is shown inside the show\hide box, to the left of the name.
- The slide bar (0%-100%) at the bottom will change α setting of the active layer.
- Show\Hide checkbox is used to show or hide the layer (this overrides α).

Base Layer – is the first layer in the list. It is used as a default operand for several tasks.

Active Layer – is the layer displayed in red. The results of image processing are usually placed as the last layer and it becomes an active layer. You can select any layer as *Active* by pointing the mouse cursor and left clicking on its title. The layer will be displayed in red.

The order of two consecutive layers in the list can be swapped by left double-clicking on the space between two layer titles in the list.

Gray level window control – View Filter

To visualize the active dataset in color or to set the gray level window select *View Filter* button in the *Layer Control* box (Fig. 8). Before changing the display, make sure the desired image is active (red layer). Also, slide away to the left the *Layer Control* box to make sure the relevant part of the image is visible.

With *View Filter* dialog box you can (Fig. 9):

- a) Change the *Intensity Window Center/Width* settings. These settings could be either typed-in or adjusted through the scroll buttons.
- b) Select desired *Color Mapping* scheme. Currently there are 8 schemes.
- c) Invert the scale.

To undo alteration made to *View Filter*, click on *Default*.

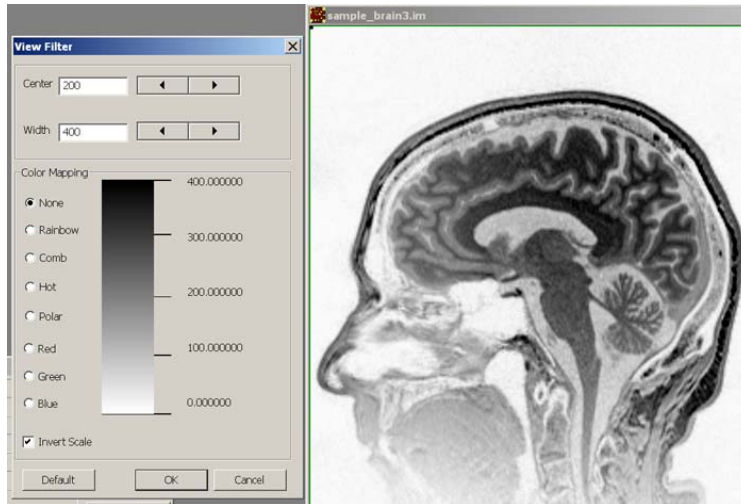


Figure 9. View Filter controls color maps. MRI is shown in inverted scale.

Layer Information

You can display information about the data in the *Active Layer* by pressing the *Info* button in the *Layer Control* box. If the volume was loaded from a DICOM dataset, all DICOM tags should be available for the viewing. In the image loaded from RAW format file, minimal information is known.

Saving Volumes

In a common scenario, a 3D dataset is loaded, processed, and the new volume is formed. To save the result, select the desired layer as active and click on the *Save DICOM* or *Save RAW* button. This will save the active layer to either DICOM or MIDAS file formats. (Saving in Analyze format is not yet implemented). With *Save DICOM*, the standard *SaveFile* dialog box will prompt you for (a) the folder and, (b) the base name (prefix) for the files. Images will be saved as *.dcm files, with each file corresponding to a 2D slice and having a unique name formed from the base name.

By default DICOM files are compressed using lossless JPEG compression. If you don't want compression, go to *Main Menu>Volume>Processing Options>Special Processing* and uncheck the box *Compress DICOM files*.

Manual ROI editing

When you press *New ROI* button in the *Layer Control* box, a new (empty) layer is generated and given a name of form *ROI_n*. All voxels that belong to the ROI are displayed with an initially arbitrary Foreground color. All voxels not in ROI are completely transparent, regardless of α . To change ROI Foreground color:

- a) Press *View Filter* button in the *Layer Control* dialog.
- b) Select the desired color in *Color* dialog box.

ROI editing is done with the combination of Paintbrush and Eraser tools. To paint, hold down the keyboard CTRL key in combination with the left mouse button. To erase, hold down CTRL key and the right mouse button. Editing is typically done in the *Slice View*.

You can control the paintbrush and eraser radius. The default paintbrush radius is 3 voxels, which is equivalent to the diameter of 7 voxels. To change the paintbrush size, select the *Paintbrush* icon from the toolbar at the right margin.

BrainMask multi-layer visualization facilitates ROI drawing. Orthogonal views show reformatted image data together with a reformatted view of existing ROIs. As ROIs are modified on the main view, changes are reflected on the orthogonal views.

Sometimes a quickly drawn ROI, when viewed in single slice mode, has a donut shape with holes inside. To fill the holes, select *ROI>Fill 2D Contours* from the main menu.

ROI tools

Unlike manual tracing, the threshold tool generates ROIs quantitatively in a reproducible manner. With this tool your ROI consists of voxels in the base image whose signal intensity lies within a given range specified by its lower and upper bounds. Choose *BridgeBurner >Run BridgeBurner* from the main menu or click on the *BridgeBurner* icon in the toolbar (red arrow, Fig. 15 below). In the dialog box set *SI_Low*, *SI_High* to the minimum and maximum threshold, specify “absolute SI” (rather than “relative to seed average”), set *Peel=0*, *Grow=0*, and click OK.

Morphological transformations are invoked from the main menu, *ROI>Inflate\deflate raster ROI*. The “deflate” operator removes the boundary pixels from an ROI. The “grow” or inflate operator is the reverse of deflate. It adds one layer of boundary pixels to an ROI. Layer thickness is specified in mm (default) or in voxels. The positive value of the “radius” entry results in ROI growth, the negative value is used to deflate the active ROI.

Since an ROI is a set of voxels, it is natural to apply basic *Boolean operations*. *ROI>Layer operations* tool performs union, intersection, or difference of any two ROIs selected using check marks in *Volume Layer Operations* dialog box.

ROI statistics

To obtain the regional signal intensity measurements of the image located in Base layer. Make the desired ROI layer active by using the Layer Control box, then press the *ROI Stats* button.

ROI Stats panel (Fig. 10) displays the signal intensity histogram; the minimum, maximum, average and standard deviation of Base Layer image within the ROI. The total number of voxels and their volume (in voxels and cm^3) is displayed below the signal intensity statistics. It should be noted that all values refer the entire 3D ROI, not just the currently displayed slice.

As a shortcut, you can access statistics for the active ROI by pressing the F4 button, without going through Layer Control. The F3 button is another shortcut. It loads the average signal intensity value to the paste buffer to quickly transfer it to another application.

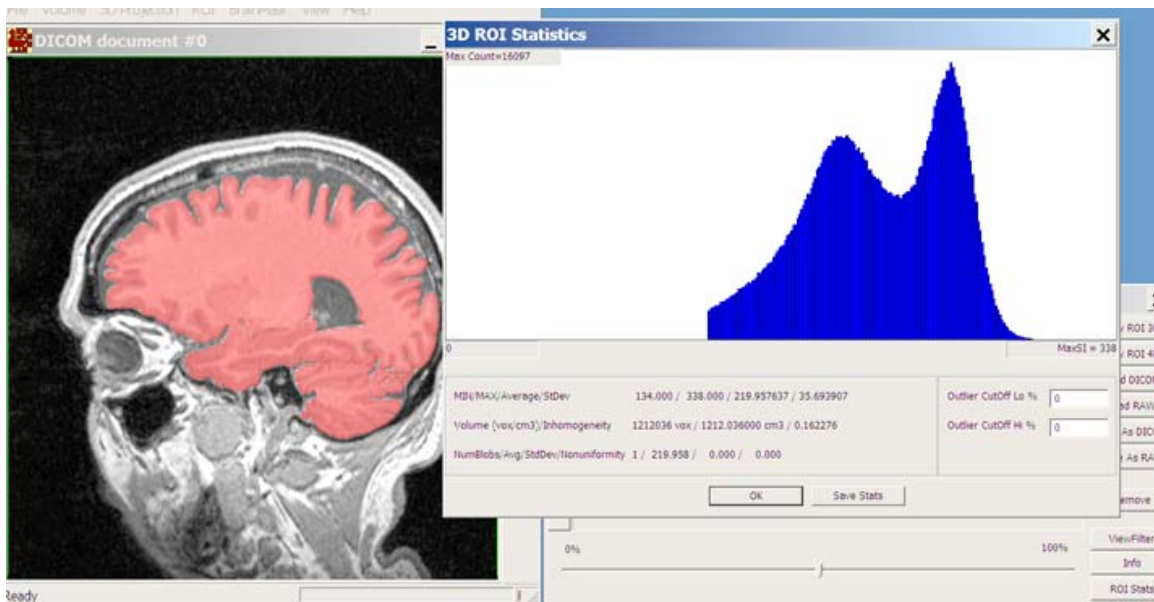


Figure 10. ROI Stats display.

If the ROI consists of several 3D connected components (blobs), their statistics are also computed. The average signal intensity is computed internally for each blob and their average value and standard deviation is shown on the last line of the box.

Vector ROI

The vector ROI tool allows you to define geometric boxes that are useful for annotating, cropping and other tasks. To create a new box, click on the *Construct Vector ROI* button (see red arrow, Fig. 11), then position the mouse on the lower left corner of the box, drag the mouse to the upper right coordinate, and release

the mouse button. You can resize the rectangular box using the lower-left and upper-right corner handles. The box can be repositioned by dragging it with the right mouse button.

The box will initially span a single slice. To extend the box to specified slices, left double-click on the box. This brings up the ROI properties dialog box (Fig.12). You can now specify the starting (Z0) and ending (Z1) slice number and press OK to expand the box in the third dimension. You may now find it convenient to switch to the Film View or Orthogonal views to visualize the box.

Load/save vector ROIs items in the ROI menu can be used to permanently record these values in a file. The vector ROI box includes the following features:

- Name: allows you to assign a name to the given vector ROI
- Coordinates: contains the lowest and the highest coordinates of the box. Each field can be changed by typing in a new value and pressing Tab.
- Dimensions/Center: allows an alternate definition of box coordinates by specifying the center and the box dimensions.
- Units: Coordinates, dimensions and center can be expressed in voxels or in mm.
- Center button: moves the box to align it with the center of the entire volume.
- Full Volume button: extends the box to include the entire volume.
-

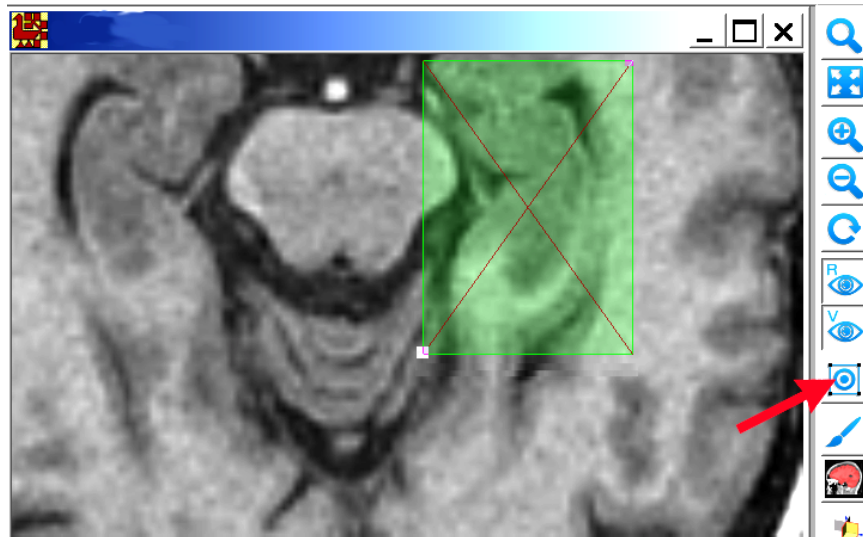


Figure 11. Vector ROI. The red arrow points to the tool *Construct Vector ROI*.

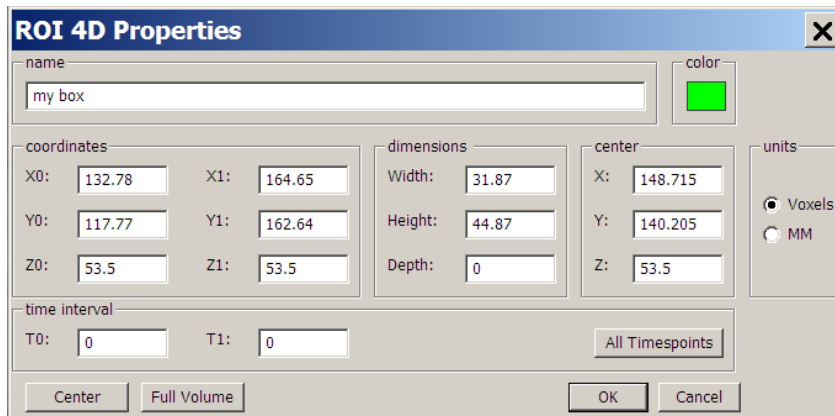


Figure 12. Vector ROI properties.

Volume Cropping

Cropping creates a subset of the base image that is limited to the extent of a given vector ROI. The result of cropping is a new volume. (Since cropped image has different dimensions, it cannot be part of existing multi layer structure). To perform cropping:

- a) Load a 3D image to be cropped (multiple layers are OK).
- b) Specify a vector box ROI as discussed above.
- c) Select the ROI using the left mouse button.
- d) From Main Menu select Volume>Crop4D command.

Selecting *Active Layer* crops the active layer. Selecting *Crop All Layers* will crop all the layers present. The new document appears, while the original document remains intact.

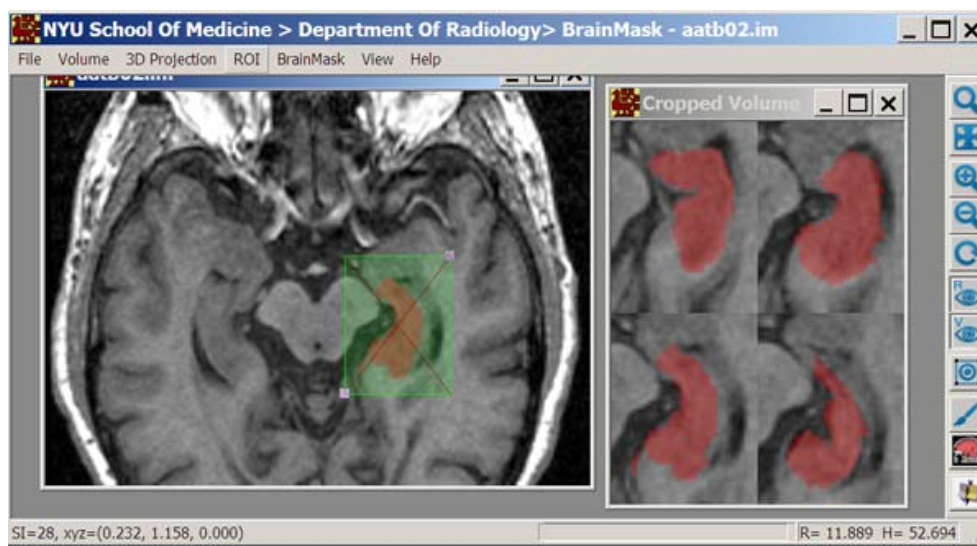


Fig. 13. Cropping an image.

Non-uniformity correction tool – N3

BrainMask includes a powerful tool for correcting the intensity non-uniformity in MR data. The algorithm, developed by John Sled, employs an iterative approach to estimate the multiplicative smooth “bias field”. The method is described in the paper of John G. Sled et al “A Nonparametric Method for Automatic Correction of Intensity Nonuniformity in MRI Data”. *IEEE Transactions on Medical Imaging* 17(1), 87-97, 1998.

The tool is selected from the main menu *BridgeBurner>Bias Field Correction (N3)*. The N3 dialog box is shown in Fig. 14.

- *Subsample* performs initial sub-sampling of the volume by the specified factor. This reduces number of voxels to process and therefore reduces the computation time.
- *Number of iterations* specifies the maximum number of iterations.
- Checking *Output Bias Field* box specifies that you want to output the multiplicative Bias Field image, instead of the corrected volume.

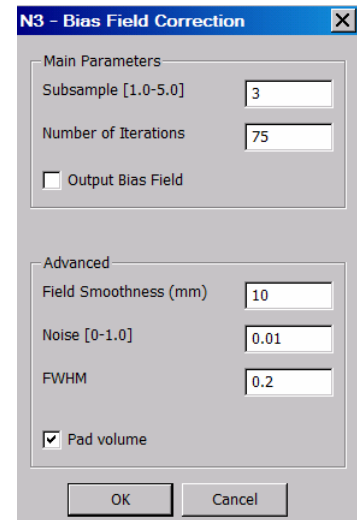


Figure 14. N3 dialog

Bridge Burner segmentation

This segmentation algorithm is fully described in the paper by Artem Mikheev et al “Fully automatic segmentation of the brain from T1-weighted MRI” *JMRI* 27, 1235-41, 2008. To perform the segmentation:

- a) Load a T1-weighted MRI of a brain.
- b) Specify a vector ROI that contains pure white matter. This can be done automatically using the command: *BrainMask>FindWhite Matter Seed-ORIENTATION*, with appropriate orientation (either sagittal, coronal, or axial). You could also select the white matter vector ROI manually. The average signal intensity within the box is referred to as “seed average”.
- c) Choose *BridgeBurner >>Run BridgeBurner* from the main menu or click on the BridgeBurner icon in the toolbar (red arrow, Fig. 15). The BridgeBurner dialog box will appear. The four key parameters are SI_Low, SI_High, Peel, and Grow.

SI Low, SI High: These parameters specify the range of signal intensity values that cover all the voxels in the tissue of interest. These values can be absolute, or relative to “seed average”. In the latter case, they will be calculated by multiplying “seed average” by the SI Low and SI High. In the initial step, the program generates a “Core” VOI by selecting all MRI voxels within the specified range.

Peel Distance: Specifies the size of the “bridges” to be eliminated from the “Core”. Bridges have signal intensity of the target tissue (i.e. the brain) and connect the target tissue to a different tissue in the “Core”. The purpose of the Peel is to eliminate such connections and to separate the tissue of interest from other tissues.

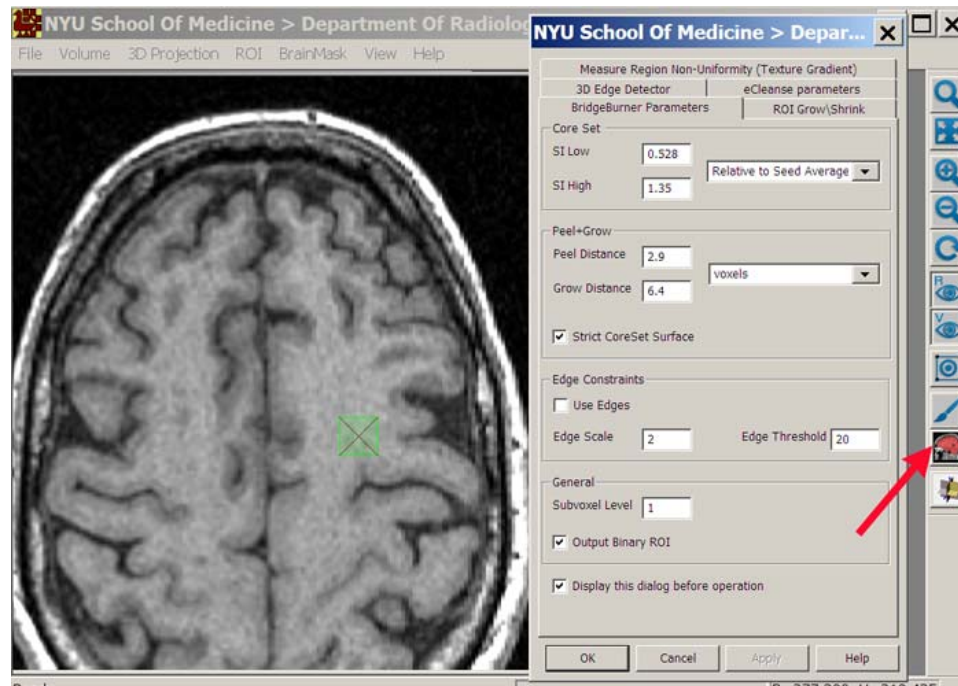


Figure 15. Bridge Burner dialog box.

Grow Distance: This describes the extent to which we want to re-grow the core set to compensate for the elimination of valid voxels during the Peeling stage. It should be equal to or larger than the *Peel distance*. Both Peel and Grow values could be expressed in voxels or in mm. For improved accuracy the algorithm implements a fractional peel/grow algorithm.

3D Edge Constraints: This parameter specifies if the edge detection should be used to assist the Bridge Burner algorithm. The default setting will not use the edge detector. When used, the edge detector is of 3D Canny type.

Output Binary ROI: This places the resulting mask as a new binary layer. With this box cleared, the algorithm instead sets to zero all voxels of the base layer that fall outside the mask.