HST.583 Functional Magnetic Resonance Imaging: Data Acquisition and Analysis
Fall 2008

# The life cycle of Medical Imaging Data

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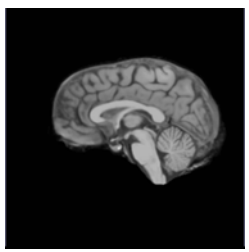
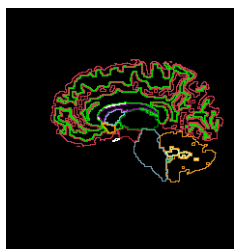
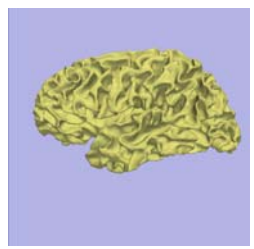
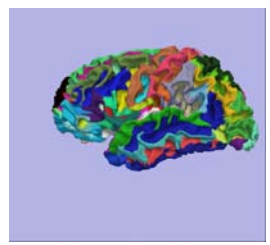
Instructor of Radiology
Surgical Planning Laboratory
Harvard Medical School
http://www.spl.harvard.edu/

# The Life Cycle of Medical Imaging Data

Image: NIH

Acquisition

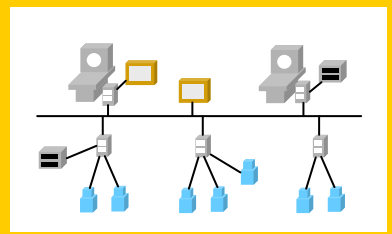
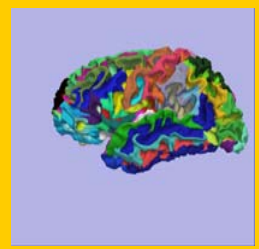


Image by MIT OpenCourseWare.

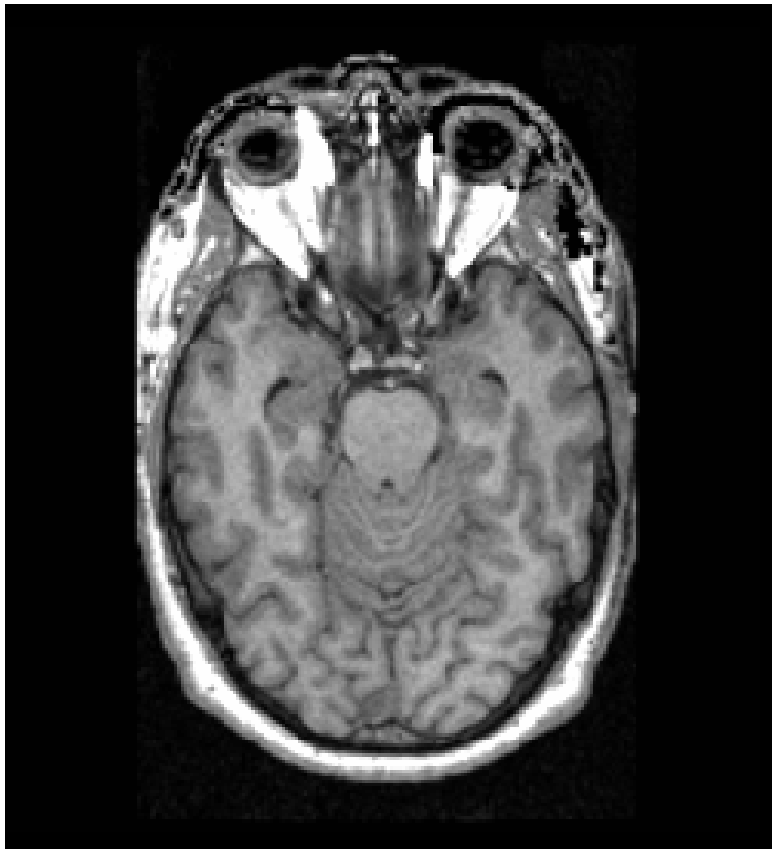
Storage

Display

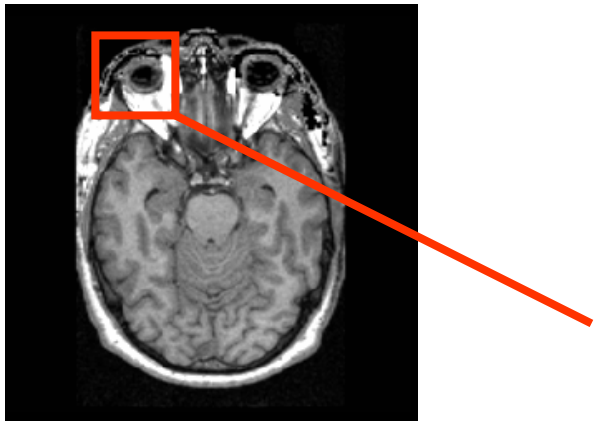


Analysis

# What is an image ?



# What is an image ?



2D array of pixels

# The Life Cycle of Medical Imaging Data

Image: NIH

Acquisition

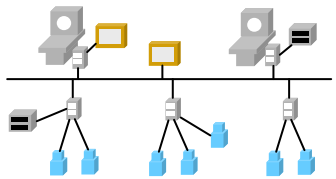
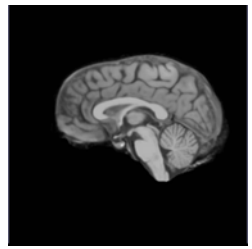
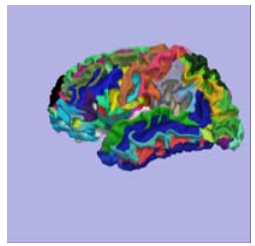


Image by MIT OpenCourseWare.

Storage



Display



Analysis

# Imaging Modalities

Image: National Cancer Institute

X-Ray Fluoroscopy

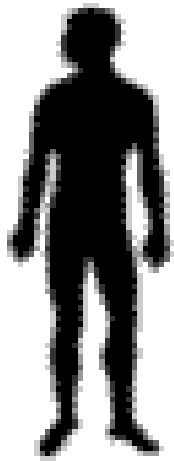


Image: NIH

Computed Tomography

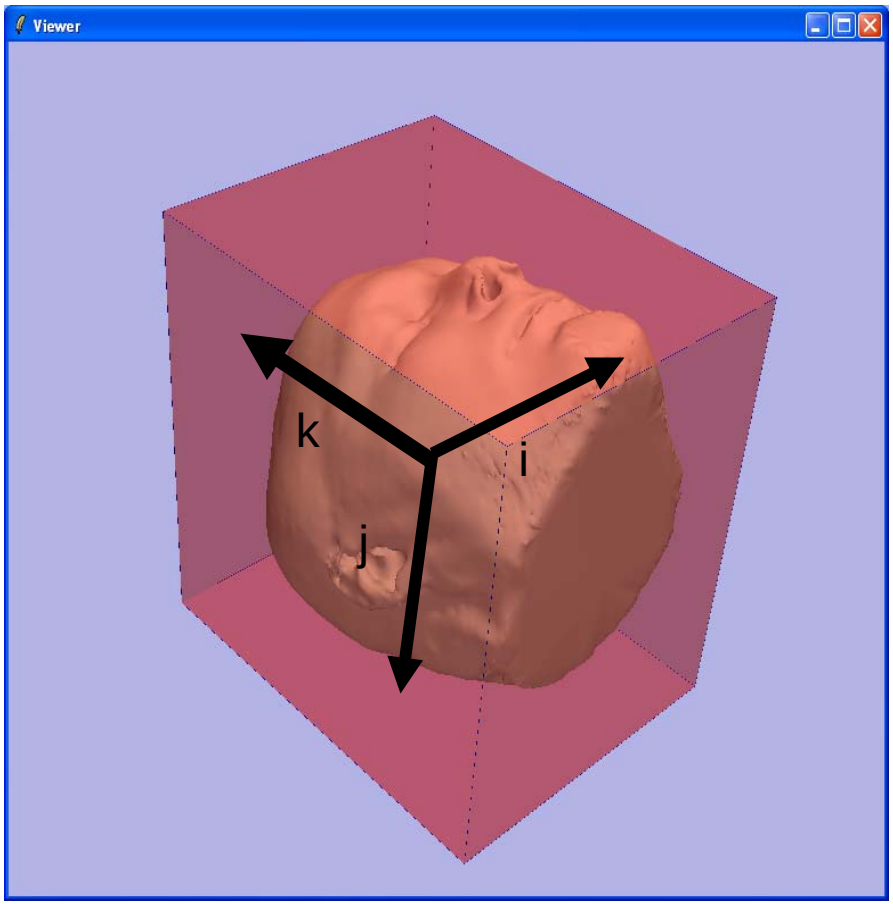
Image: NIH

Magnetic Resonance Imaging

Image: NASA

Ultrasound Imaging

# Data Representation




The result of the acquisition is a 3D Volume of data related to the patient.

The 3D volume is sampled on a 3D grid in the coordinate system (I,J,K).

# The Life Cycle of Medical Imaging Data

Image: NIH

Acquisition

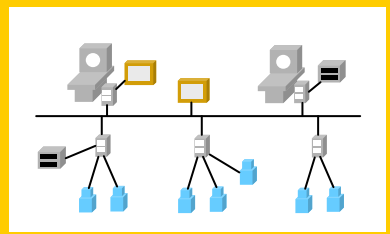
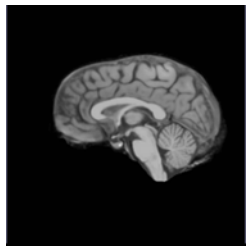
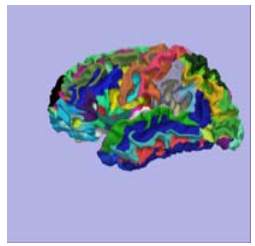


Image by MIT OpenCourseWare.

Storage

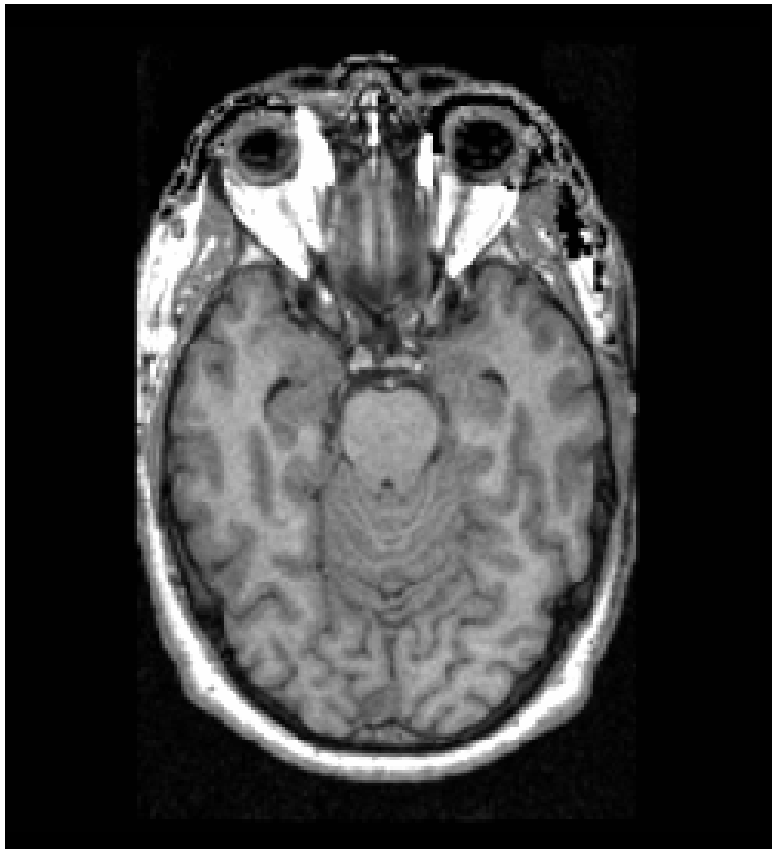


Display



Analysis

# Data Representation



# Data Representation

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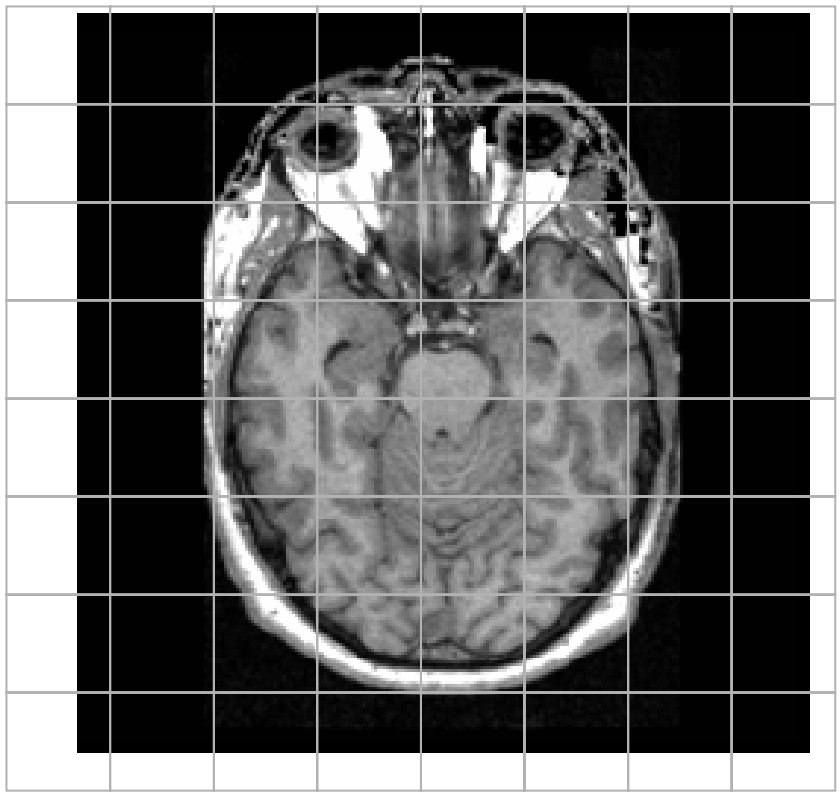
...

- Patient information
- Acquisition information
- Image Information



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0028,0103,Pixel Representation=1
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7FE0,0010,Pixel Data=131072

# Data Representation

header | data

0002,0000,File Meta Elements Group Len=148
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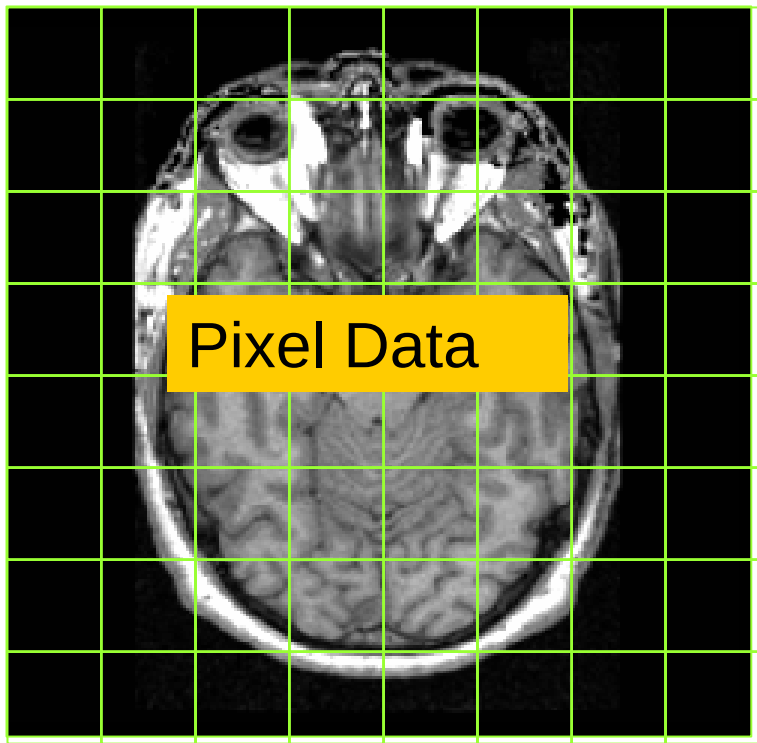
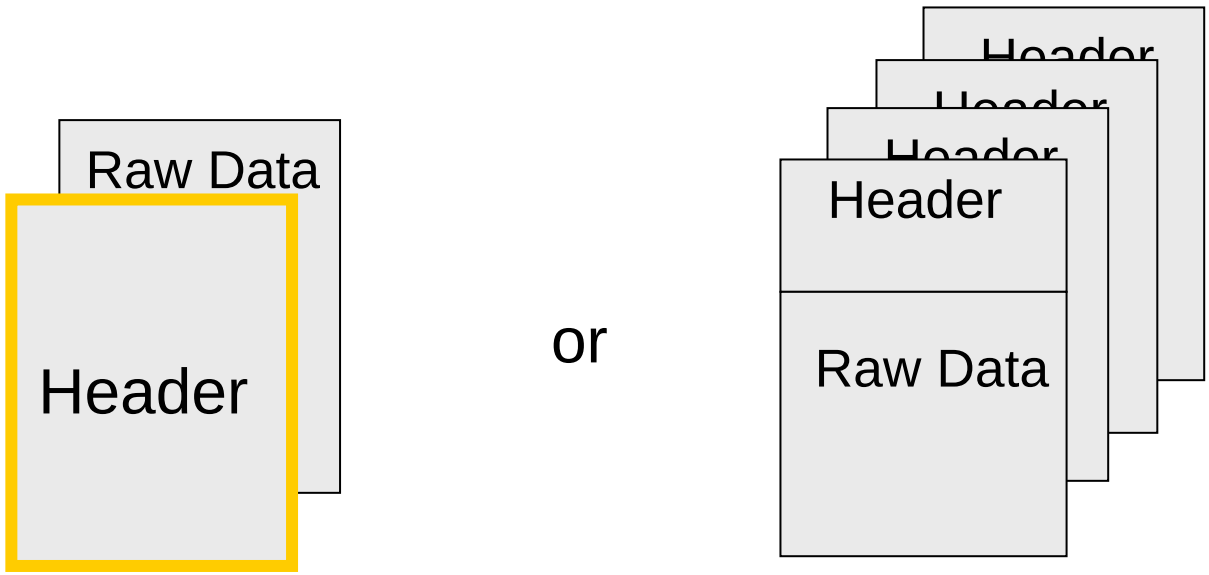


# File Formats



# Vendor Specific Radiological File Format

- GE Advantage: GE format for CT and MRI
- GE Advance PET: GE Advance PET scanner format
- GE StarcamOlder: GE nuclear medicine image file format
- Siemens MAGVIS: Siemens Magnetom Vision MRI format)
- SMISA: small-bore MRI Image file format (Bruker)
- ….

# Standard Radiological File Format

American College of Radiologists (ACR)

& National Electrical Manufacturers Association (NEMA)

- ACR/NEMA 1.0 (1985)
- ACR/NEMA 2.0 (1988)

Digital Imaging and Communications in Medicine

- DICOM 3.0 (1993)

# Example 1: DICOM 3.0

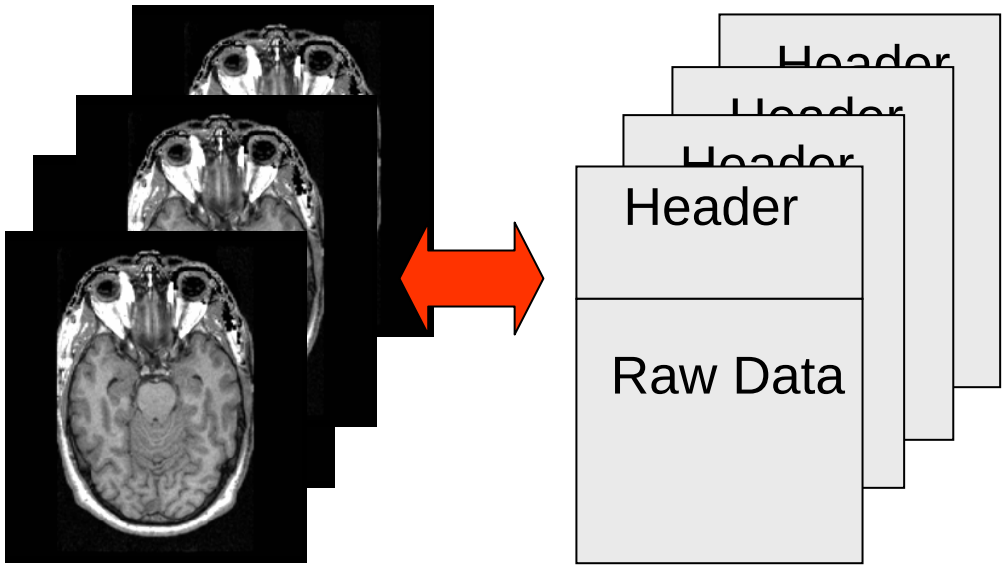


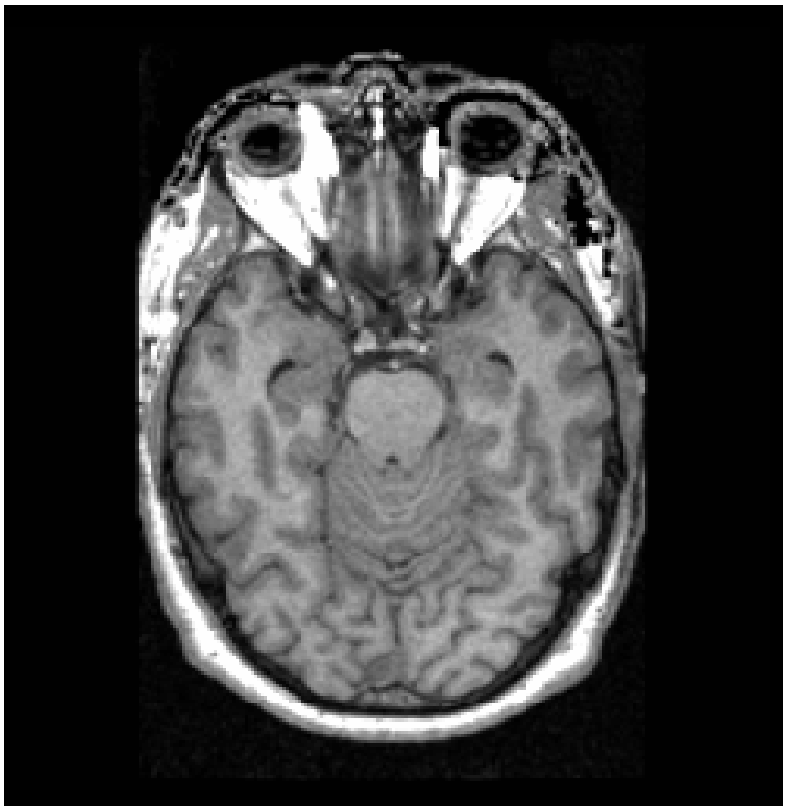

Image001.dcm

Image002.dcm

Image003.dcm

….

# Example 1: DICOM 3.0



Example of DICOM header content

Physician and Study information

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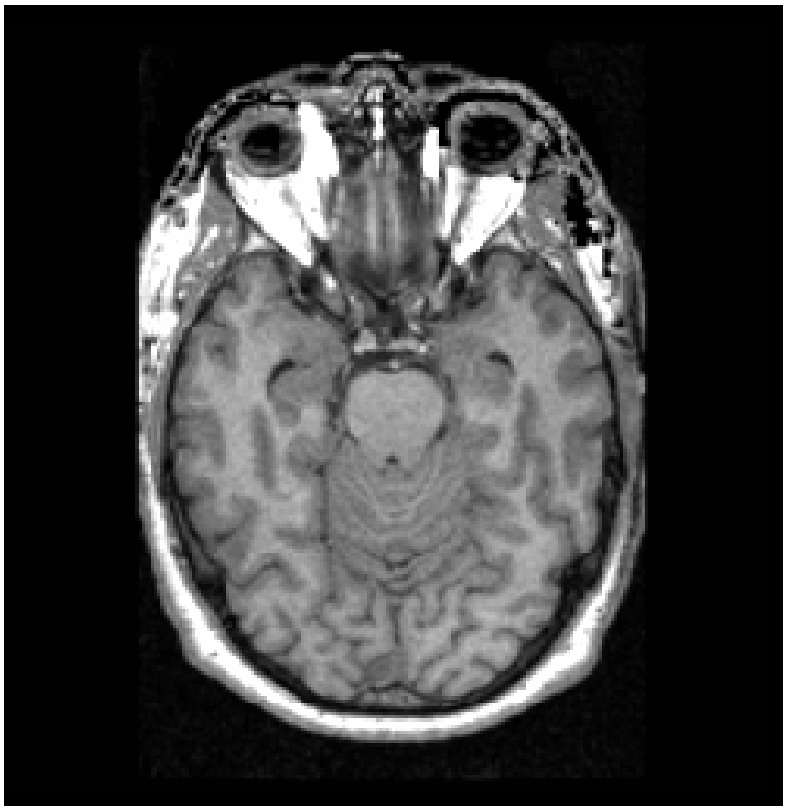

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Patient information

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7FE0,0010,Pixel Data=131072

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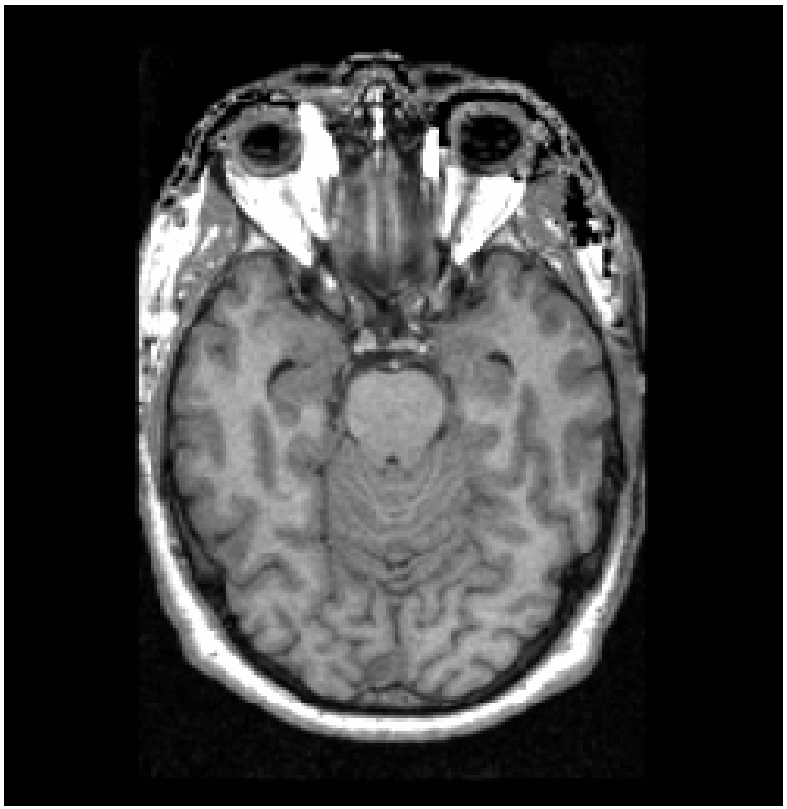

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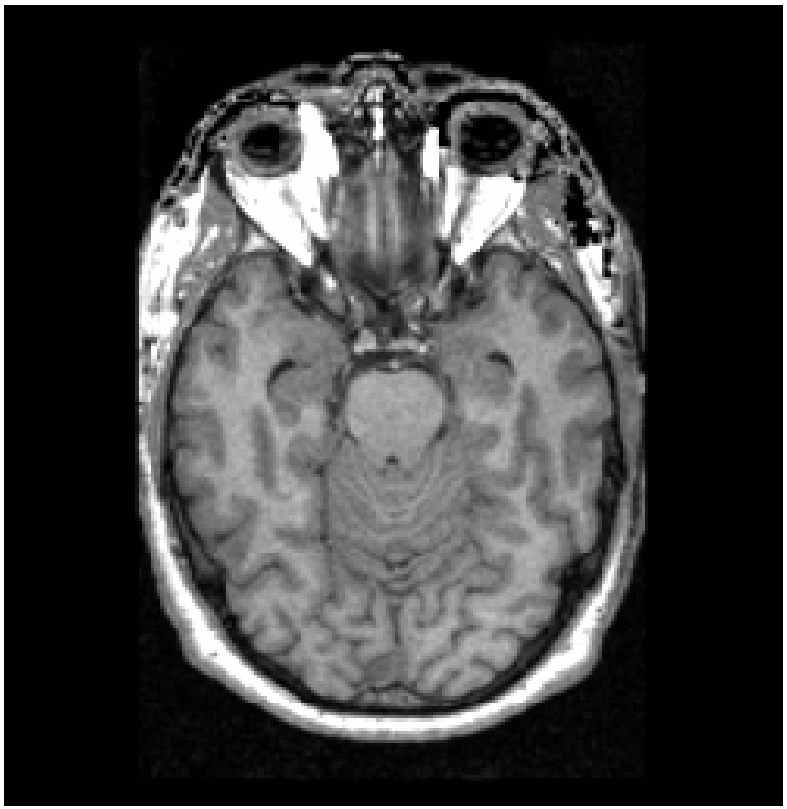
7FE0,0010,Pixel Data=131072

Image information

# Example 1: DICOM 3.0



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0028,0102,High Bit=15
0028,0103,Pixel Representation=1

The data

7FE0,0010,Pixel Data=131072

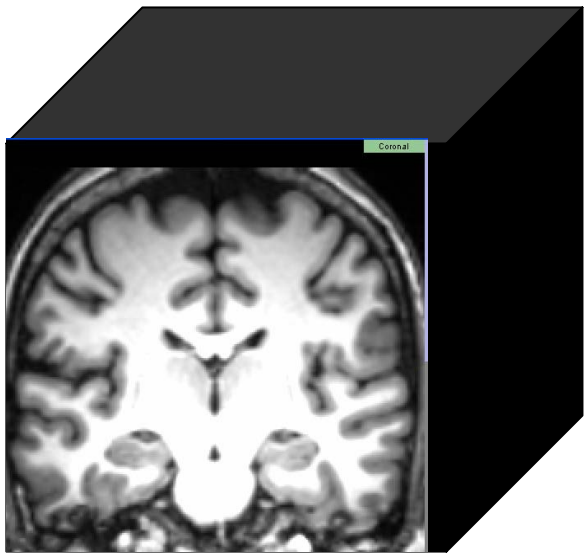
# Image Processing File Format

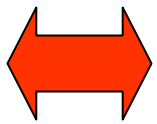
- Analyze 7.5 Mayo Clinic
- Minc (Medical Image NetCDF )

Montreal Neurological Institute

- SPM (Statistical Parametric Mapping)
- NifTI (Neuroimaging Informatics Initiative)

# Example 2: ANALYZE 7.5



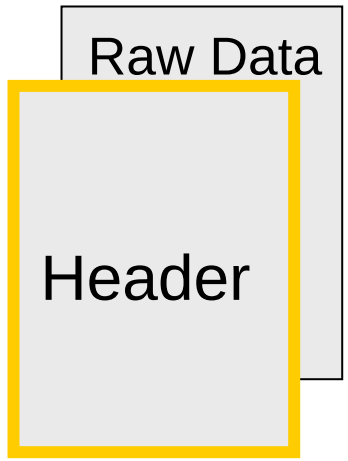



Image.hdr

Image.img

# Example 2: ANALYZE 7.5

Image.img

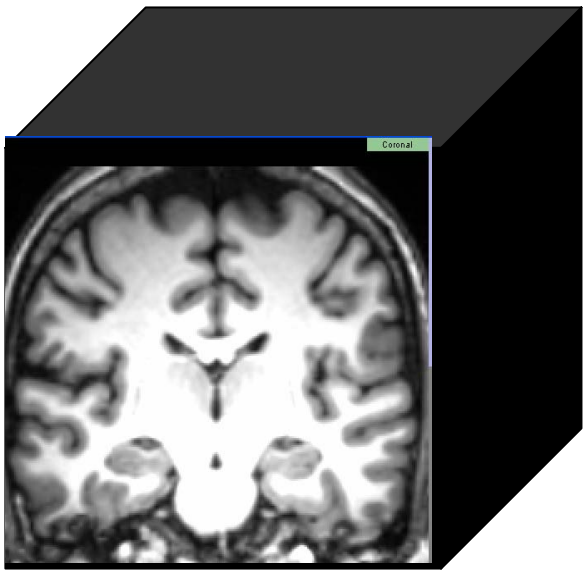



Image.hdr

GW Analyze Header

Clear | Drag .hdr file onto grid | Copy to Clipboard

```
anatomical3T.hdr
Load Status: OK
Memory  Layout: LilEndian
```

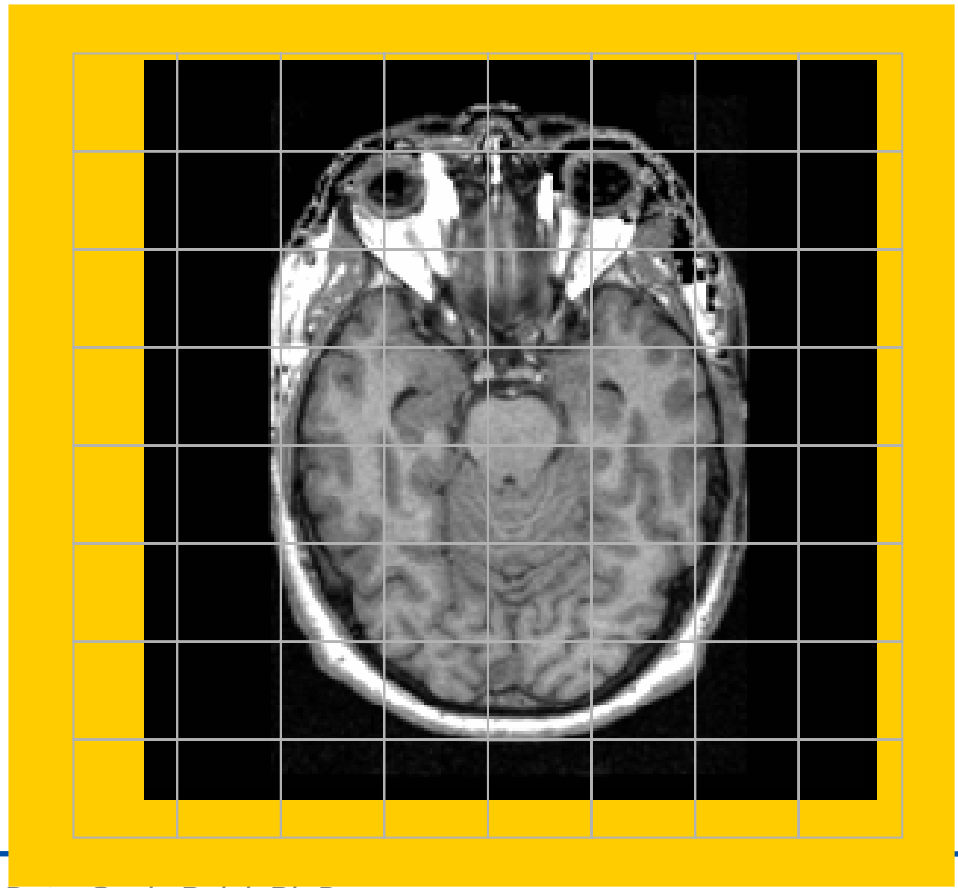
| Num | Field | Offset | Type | Value | Descr |
|---|---|---|---|---|---|
| 0 | key.sizeof_hdr | 0 | int32 | 348 | Should be 348 |
| 1 | key.data_type | 4 | char[10] | | --- |
| 2 | key.db_name | 14 | char[18] | | --- |
| 3 | key.extents | 32 | int32 | 0 | Supposedly should be 16384 |
| 4 | key.session_error | 36 | int16 | 0 | --- |
| 5 | key.regular | 38 | char | r | Should be "r" to indicate all images/volum |
| 6 | key.hkey_un0 | 39 | char | | --- |
| 7 | dim.dim[0] | 40 | int16 | 3 | Number of dimensions in database; usually |
| 8 | dim.dim[1] | 42 | int16 | 157 | Image X dimension; number of pixels in an |
| 9 | dim.dim[2] | 44 | int16 | 189 | Image Y dimension; number of pixel rows i |
| 10 | dim.dim[3] | 46 | int16 | 136 | Volume Z dimension; number of slices in a |
| 11 | dim.dim[4] | 48 | int16 | 1 | Time points; number of volumes in databa |
| 12 | dim.dim[5] | 50 | int16 | | |
| 13 | dim.dim[6] | 52 | int16 | | |
| 14 | dim.dim[7] | 54 | int16 | | |
| 15 | dim.vox_units | 56 | char[4] | | |
| 16 | dim.cal_units | 60 | char[8] | | |
| 17 | dim.unused1 | 68 | int16 | 0 | --- |
| 18 | dim.datatype | 70 | int16 | 4 = Int-16 | Voxel data type |
| 20 | dim.dim_un0 | 74 | int16 | 0 | --- |
| 21 | dim.pixdim[0] | 76 | single | -1.00000 | Pixel dimensions? |
| 22 | dim.pixdim[1] | 80 | single | 1.00000 | Voxel width in mm. |
| 23 | dim.pixdim[2] | 84 | single | 1.00000 | Voxel height in mm. |
| 24 | dim.pixdim[3] | 88 | single | 1.00000 | Slice thickness in mm. |
| 25 | dim.pixdim[4] | 92 | single | 0.00000 | timeslice in ms. |
| 26 | dim.pixdim[5] | 96 | single | 0.00000 | Undocumented. |
| 28 | dim.pixdim[7] | 104 | single | 0.00000 | Undocumented. |
| 29 | dim.vox_offset | 108 | single | 0.00000 | Byte offset in the .img file at which voxels |
| 30 | dim.funused1 | 112 | single | 4.64103 | (SPM99: scale factor) |
| 31 | dim.funused2 | 116 | single | 0.00000 | (SPM2: image intensity zero intercept |
| 32 | dim.funused3 | 120 | single | 0.00000 | --- |
| 33 | dim.cal_max | 124 | single | 0.00000 | Calibration value max |
| 34 | dim.cal_min | 128 | single | 0.00000 | Calibration value min |
| 35 | dim.compressed | 132 | int32 | 0 | --- |
| 36 | dim.verified | 136 | int32 | 0 | --- |
| 37 | dim.glmax | 140 | int32 | 0 | Max pixel value for entire database |
| 38 | dim.glmin | 144 | int32 | 0 | Min pixel value for entire database |
| 39 | hist.descrip | 148 | char[80] | spm - 3D normalized | --- |
| 40 | hist.aux_file | 228 | char[24] | | --- |
| 41 | hist.orient | 252 | int8 | 2 = Sagittal unflipped | Volume Orientation for movie (usually ignor |
| 42 | hist.originator[0] | 253 | int16 | 512 | SPM99: X near Anterior Commissure |
| 43 | hist.originator[1] | 255 | int16 | 0 | SPM99: Y near Anterior Commissure |
| 44 | hist.originator[2] | 257 | int16 | 0 | SPM99: Z near Anterior Commissure |
| 45 | hist.originator[3] | 259 | int16 | 0 | --- |
| 46 | hist.originator[4] | 261 | int16 | -32768 | --- |

Image information

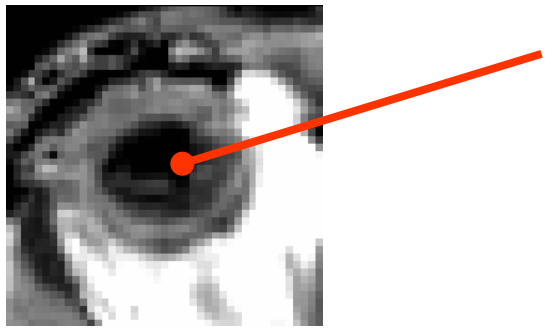
# Pixel Data

| header | data |
| --- | --- |

0002,0000,File Meta Elements Group Len=148
0002,0001,File Meta Info Version=256
0002,0002,Media Storage SOP Class
UID=1.2.840.10008.5.1.4.1.1.4.
…
0008,0060,Modality=MR
0008,0070,Manufacturer=GE MEDICAL SYSTEMS
0008,0080,Institution Name=1852796513
0008,0081,City Name=1852796513
0008,0090,Referring Physician's Name=1852796513
0008,0092,?=1852796513
0008,0201,?=-0500
0008,1010,Station Name=1852796513
0010,0010,Patient's Name=anon
0010,0020,Patient ID=anon
0010,0030,Patient Date of Birth=00000000
0010,0032,Patient Birth Time=000000
0010,0040,Patient Sex=O
0010,1010,Patient Age=000Y
……..
0028,0010,Rows=256
0028,0011,Columns=256
0028,0030,Pixel Spacing=0.937500 0.937500
0028,0100,Bits Allocated=16
0028,0101,Bits Stored=16
0028,0102,High Bit=15
0028,0103,Pixel Representation=1
…….
7FE0,0010,Pixel Data=131072



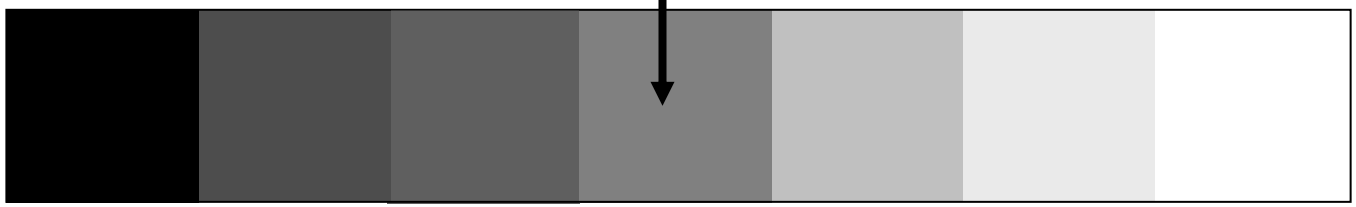
# Pixel Data



pixel (a,b)

Intensity (a,b)

Grey levels scale

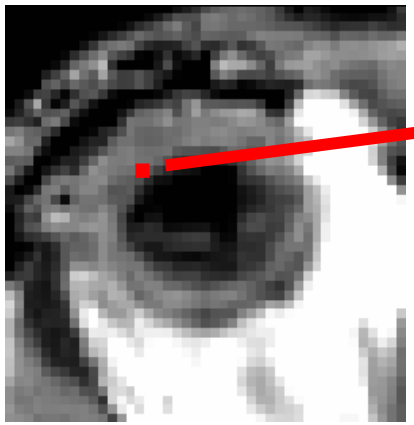


I min → I max

8 bits /pixel → 256 grey levels

16 bits /pixel → 65,356 grey levels

# Pixel Encoding

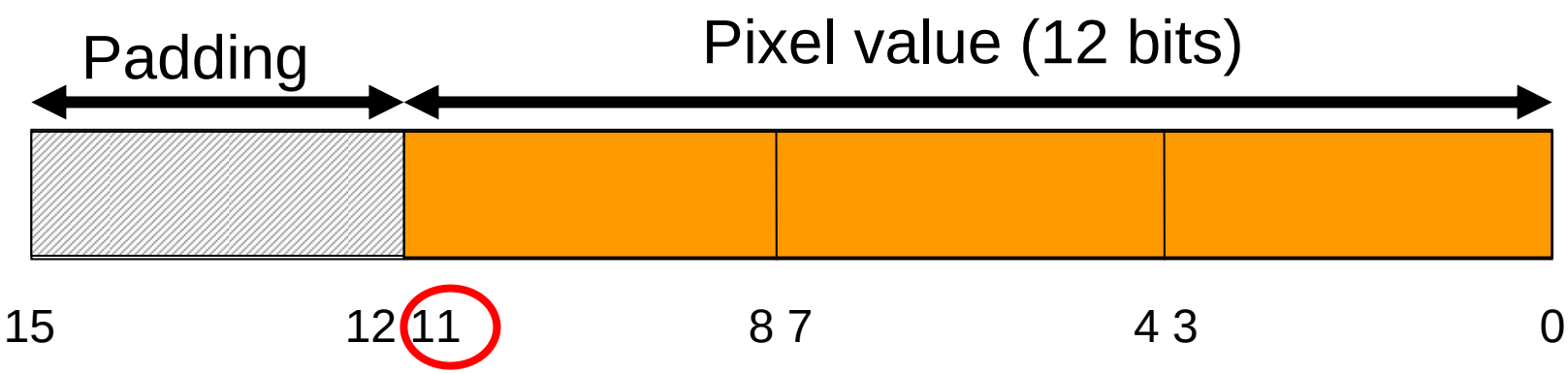


1 pixel = 2 bytes

Bits allocated = 16

Bits stored = 12

High Bit = 11



# Data Compression

2 types of algorithms

The lossless compression techniques allow the exact original data to be reconstructed from the compressed data.

Ex: JPEG-LS

The lossy compression techniques deliberately discard information that is not diagnostically important

Ex: JPEG

# The Life Cycle of Medical Imaging Data

Image: NIH

Acquisition

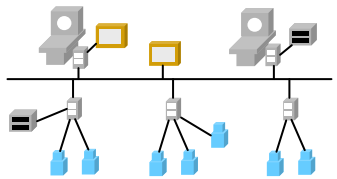
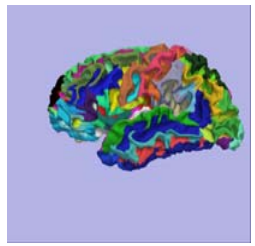


Image by MIT OpenCourseWare.

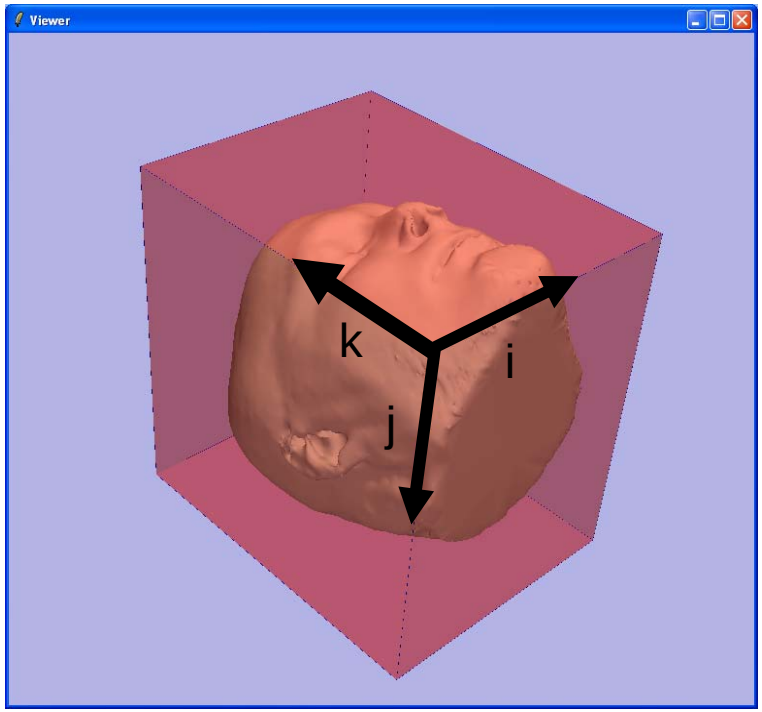
Storage

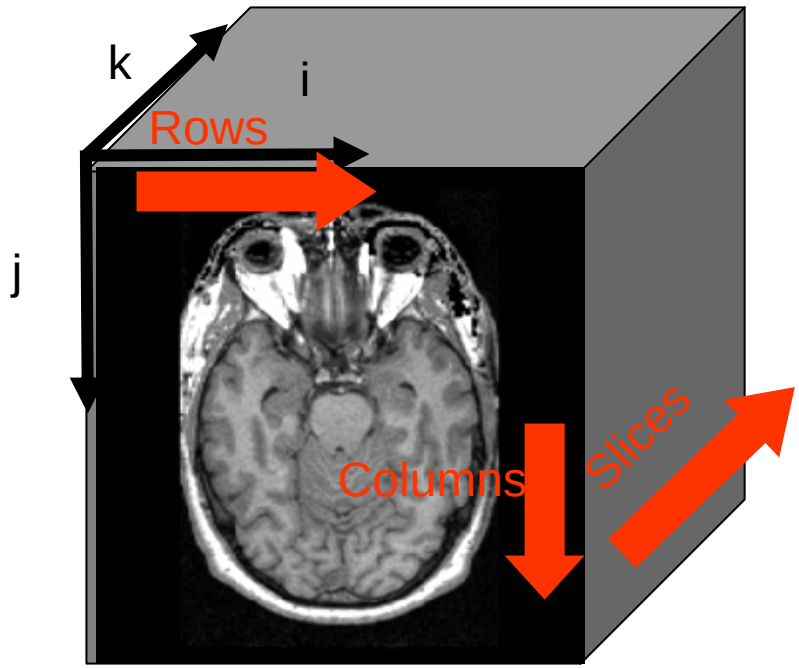
Display



Analysis

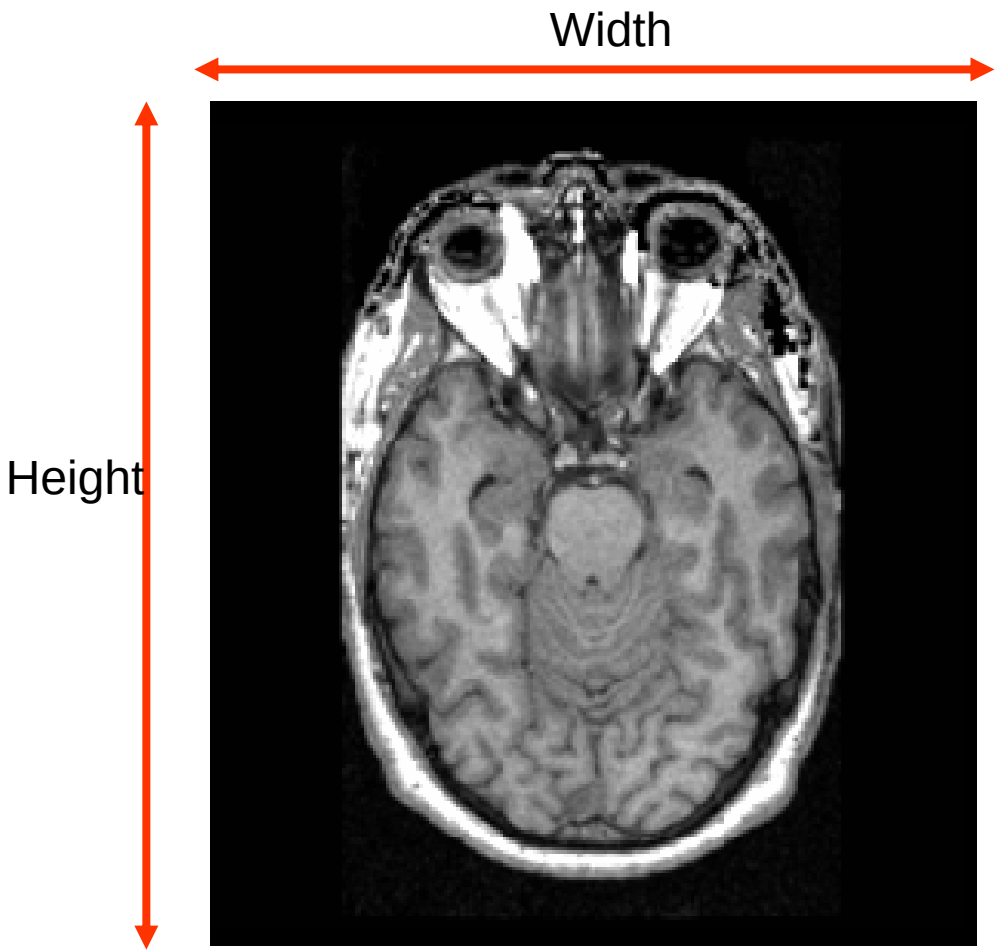
# Data Representation




The 3D volume is sampled on a 3D grid in the coordinate system (I,J,K).

# Image Dimensions



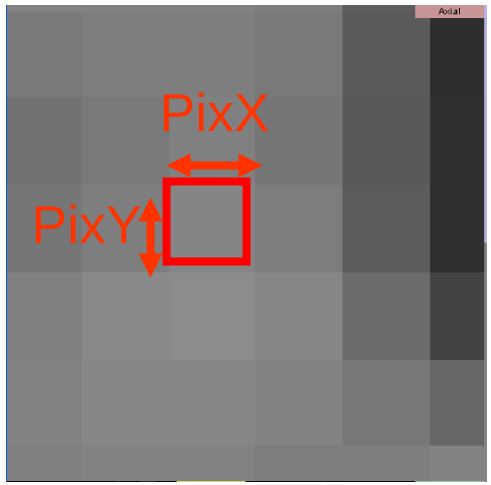

Standard Image Sizes

256 x 256

512 x 512

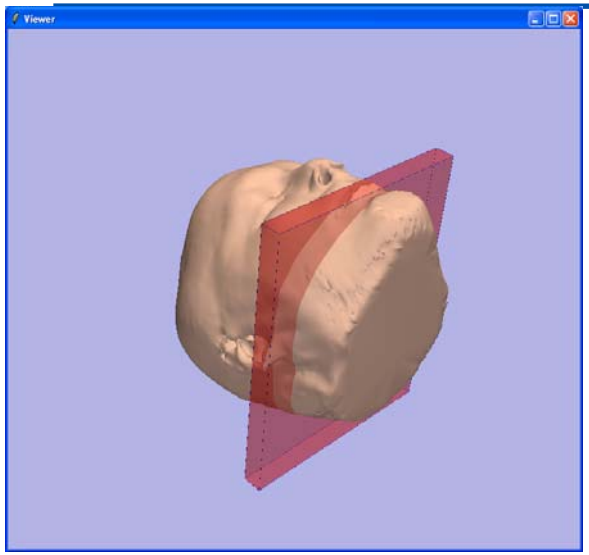
1024 x 1024

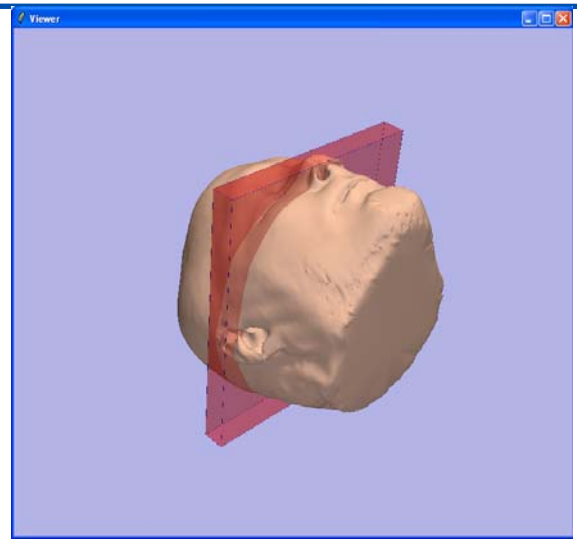
# Pixel Dimensions




The pixel size is the dimension in millimeters of the pixels.

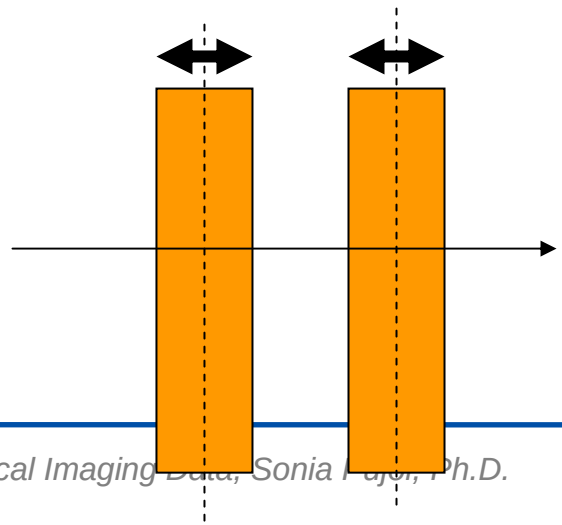
# Slice Thickness





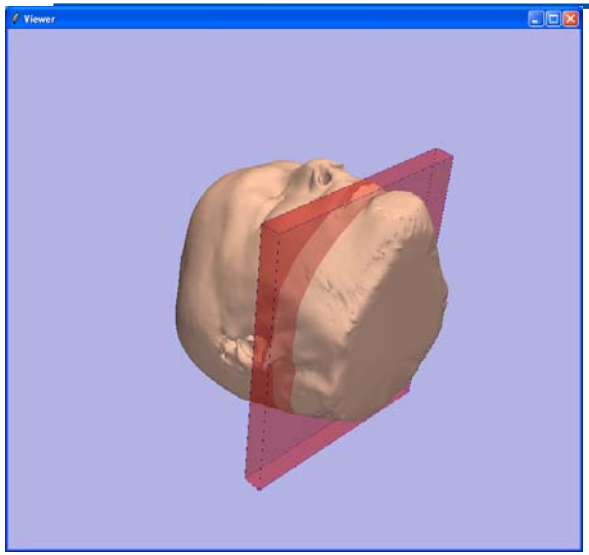
Slice n

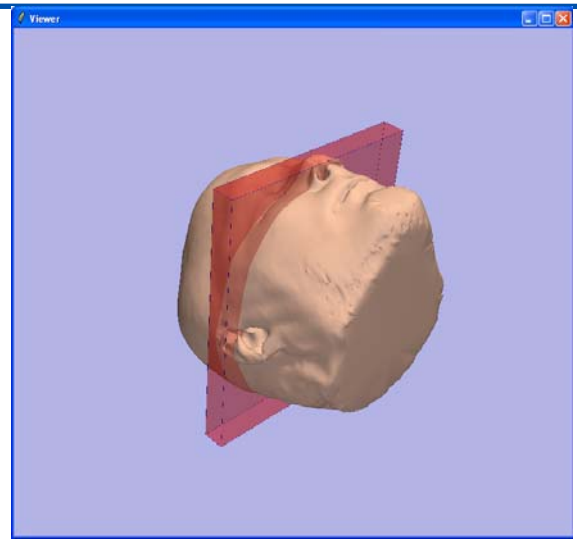
Slice n+1

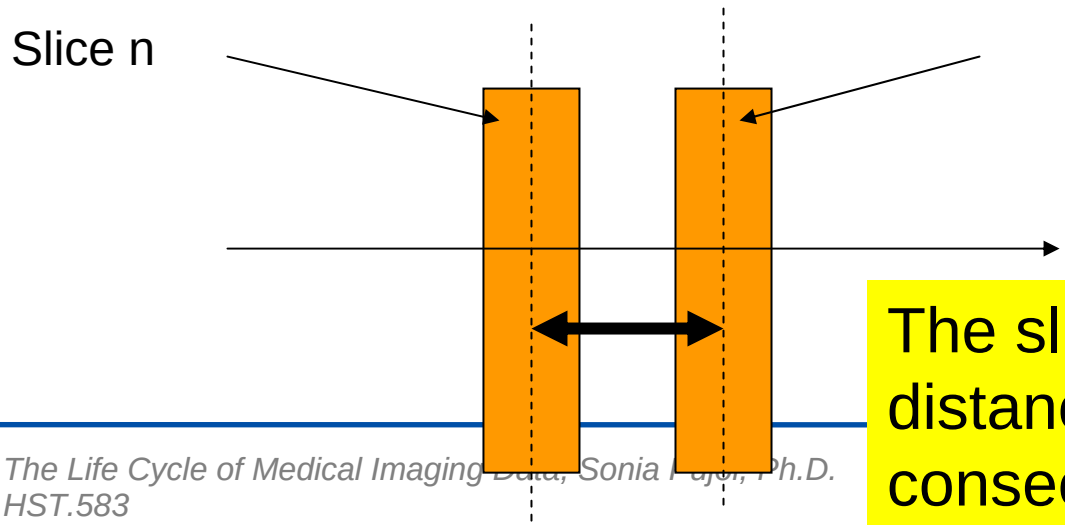


The slice thickness corresponds to the section of the patient being scanned.

# Slice Spacing








The slice spacing is the distance between consecutive slices

# Visualization

Image: National Cancer Institute

Image removed due to copyright restrictions.

X-Ray Fluoroscopy

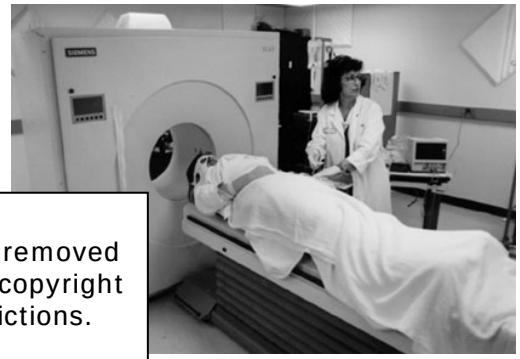
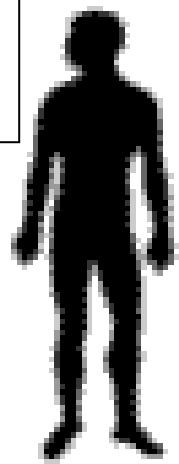


Image removed due to copyright restrictions.

Image: NIH

Computed Tomography



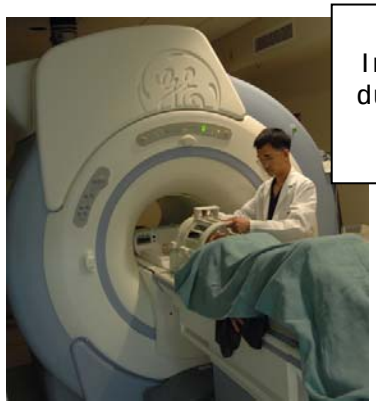


Image removed due to copyright restrictions.

Image: NIH

Magnetic Resonance Imaging

Image removed due to copyright restrictions.

Image: NASA

Ultrasound Imaging

# 3D Slicer platform

Launch the executable

slicer2-linux-x86

located in the directory

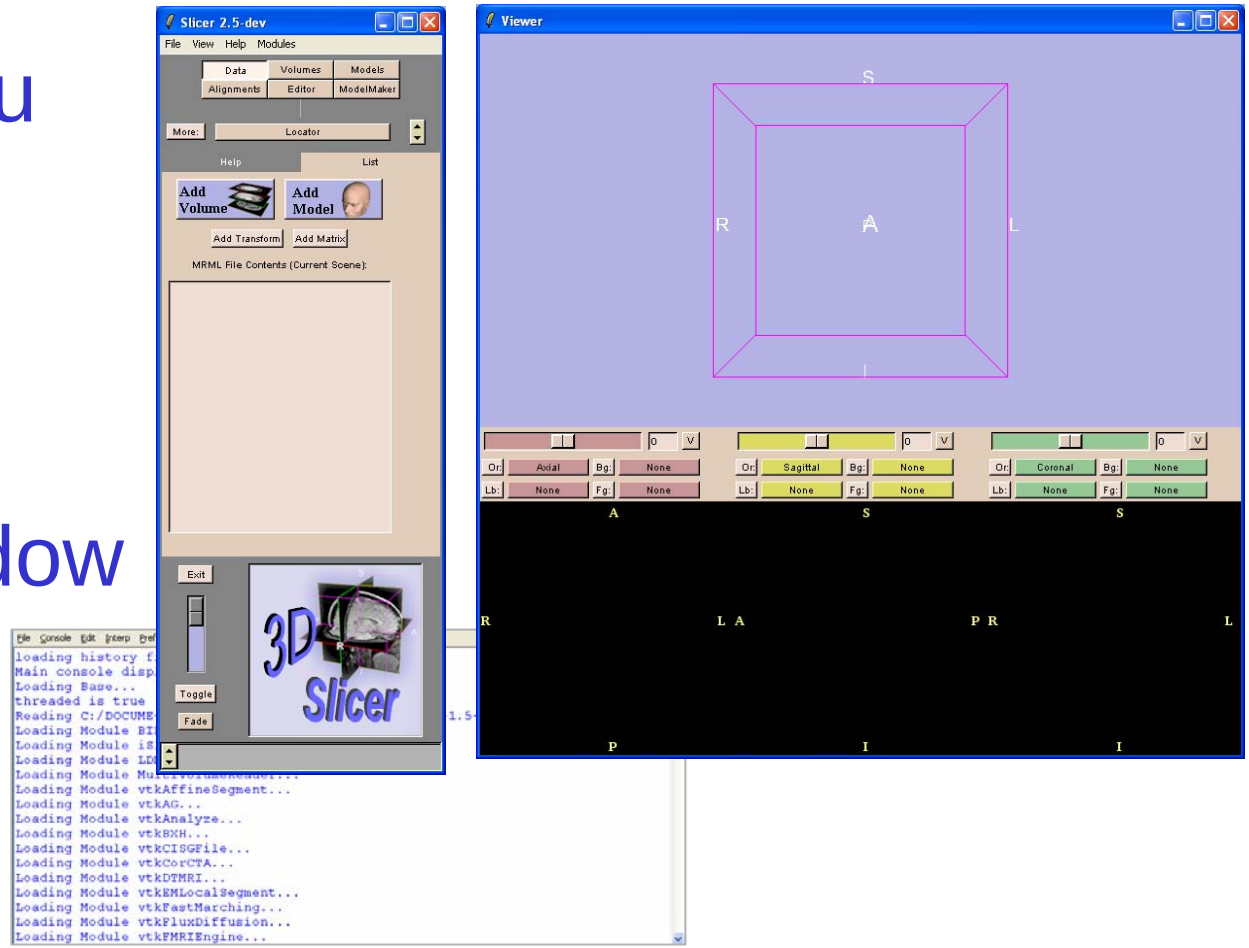
slicer2.6-opt-linux-x86-2006-09-08/

# 3DSlicer Platform

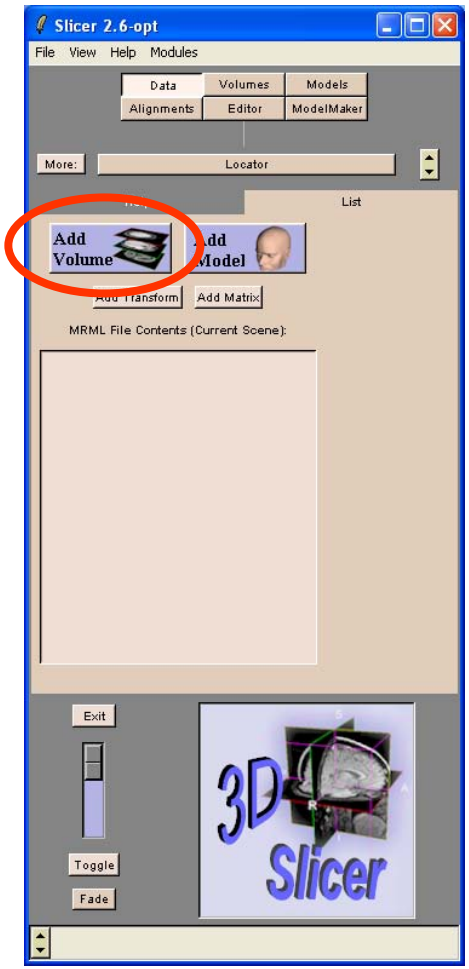
Menu

Tk window

Viewer

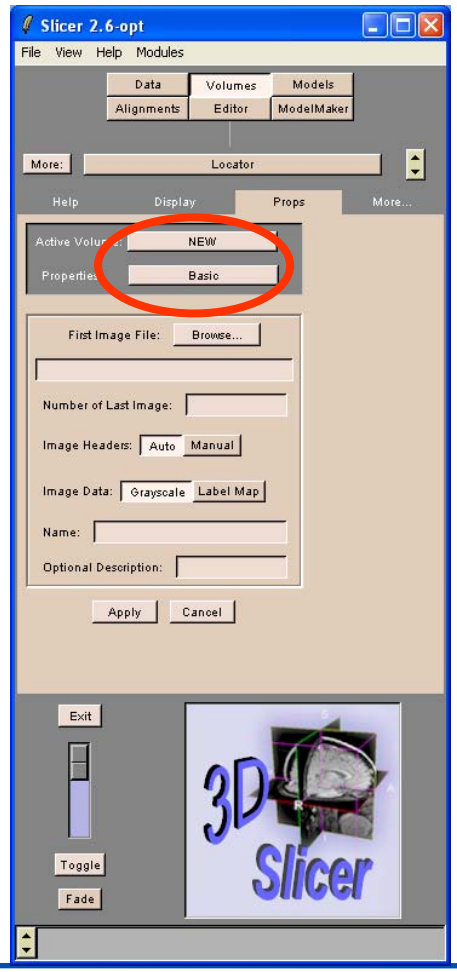


# Image Header




Click Add Volume in the left panel.

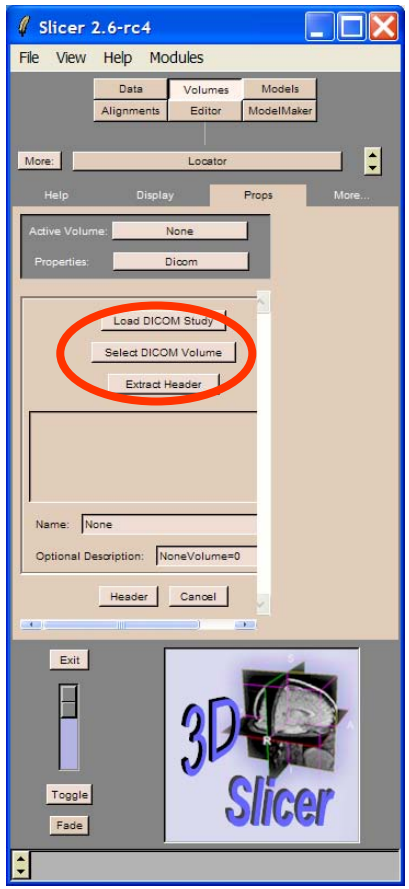
# Image Header




The panel Props of the module Volumes appears.

Left-Click on Properties Basics, and select the format DICOM.

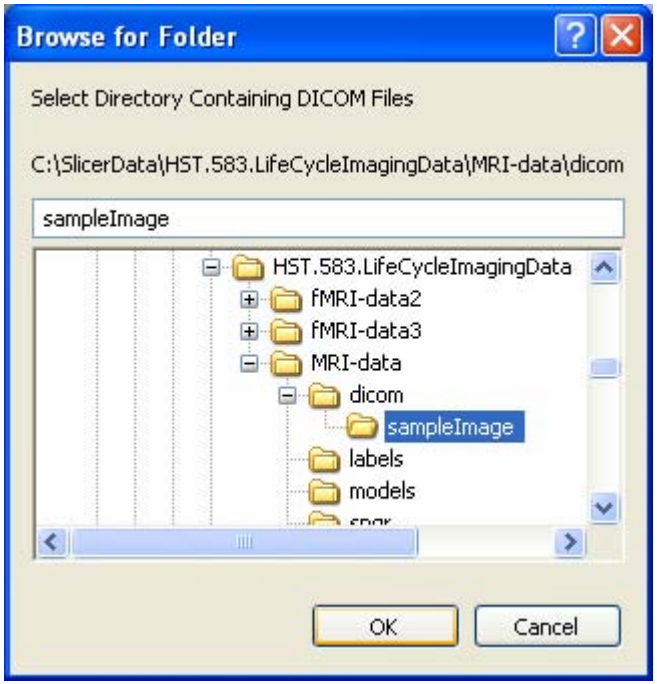
# Image Header




The DICOM reader panel appears.

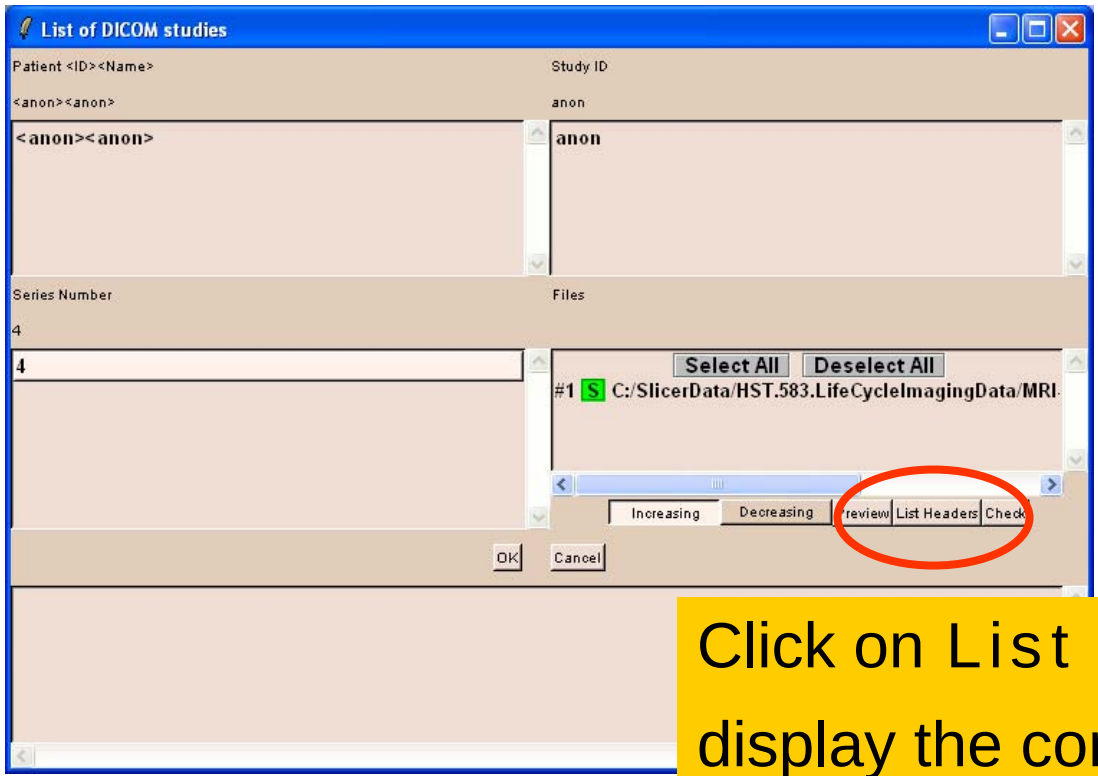
Click on Select DICOM Volume

# Image Header



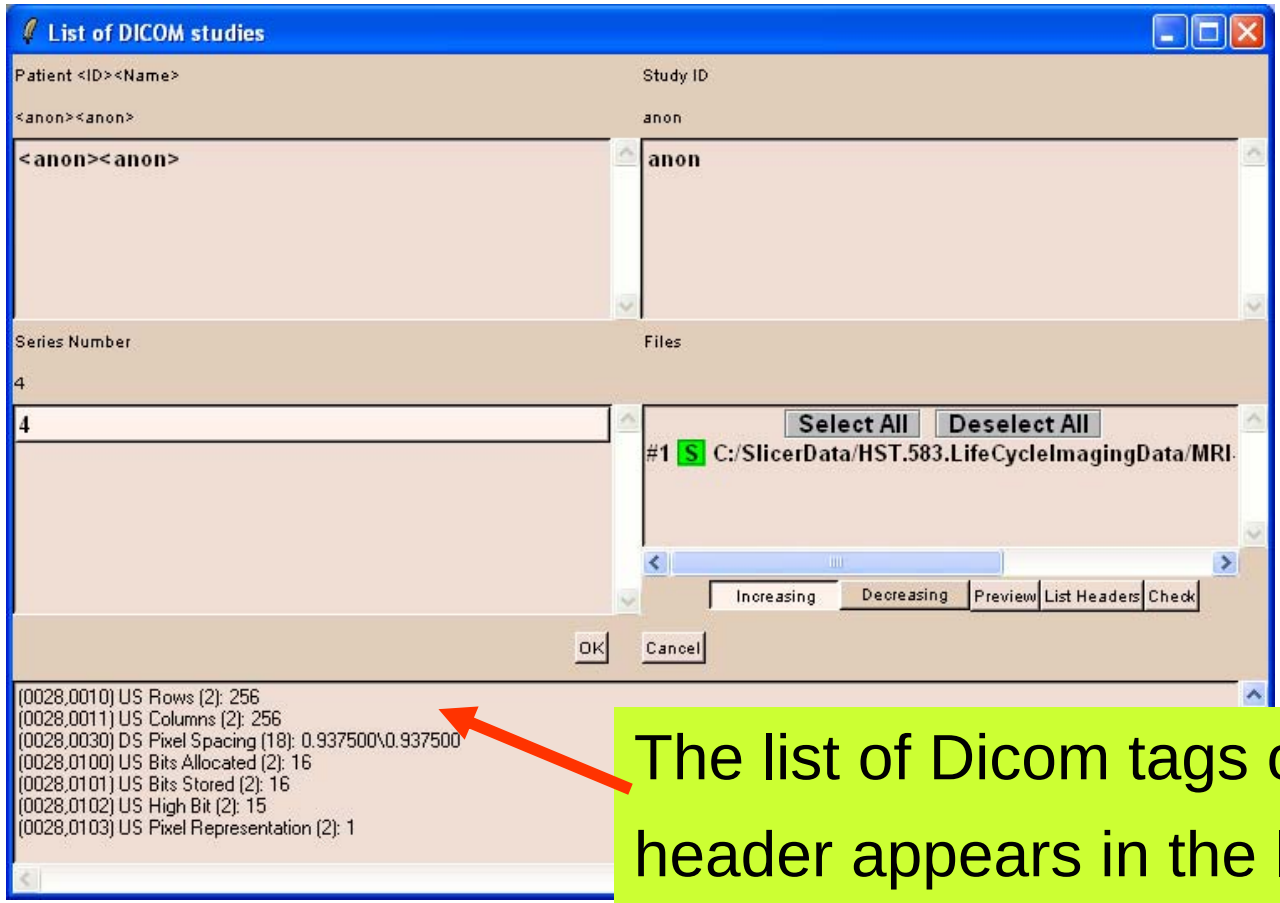

Select the sub-directory sampleImage in the directory /MRI-data/dicom/ and click on OK

# Image Header



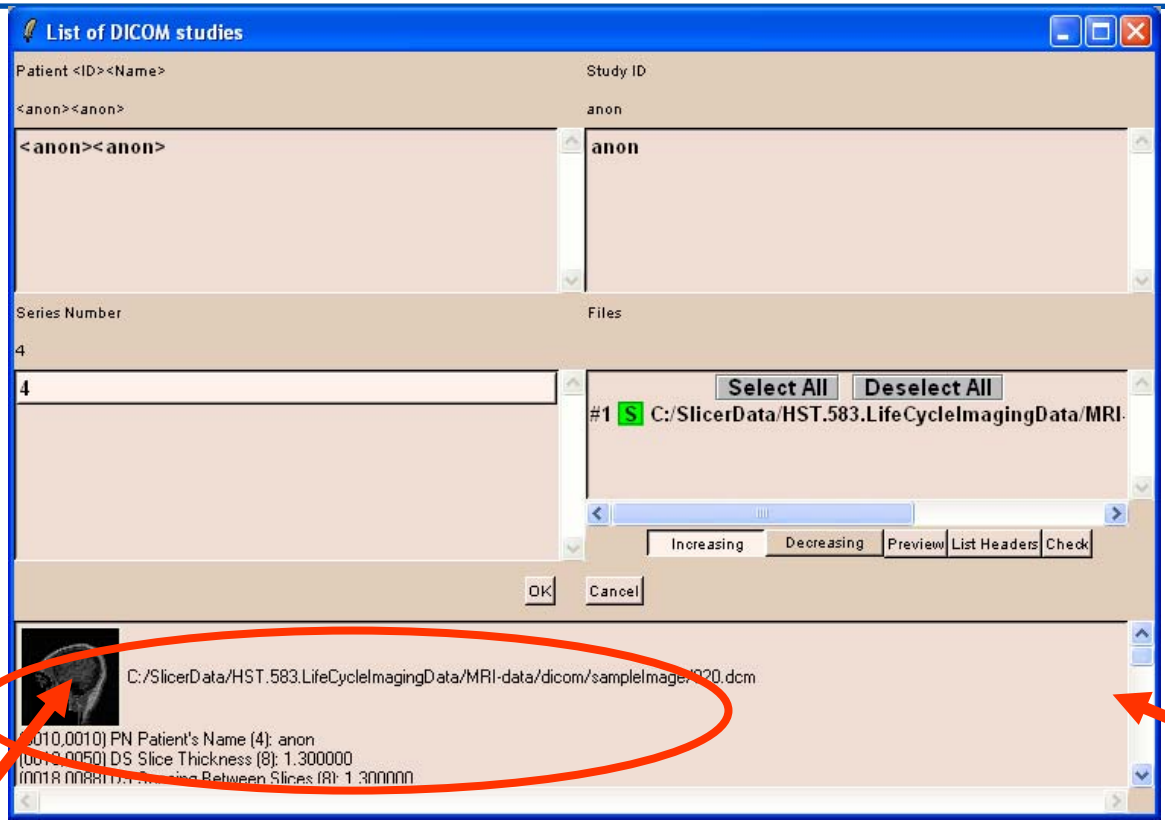

Click on List Headers to display the content of the header of the first image.

# Image Header



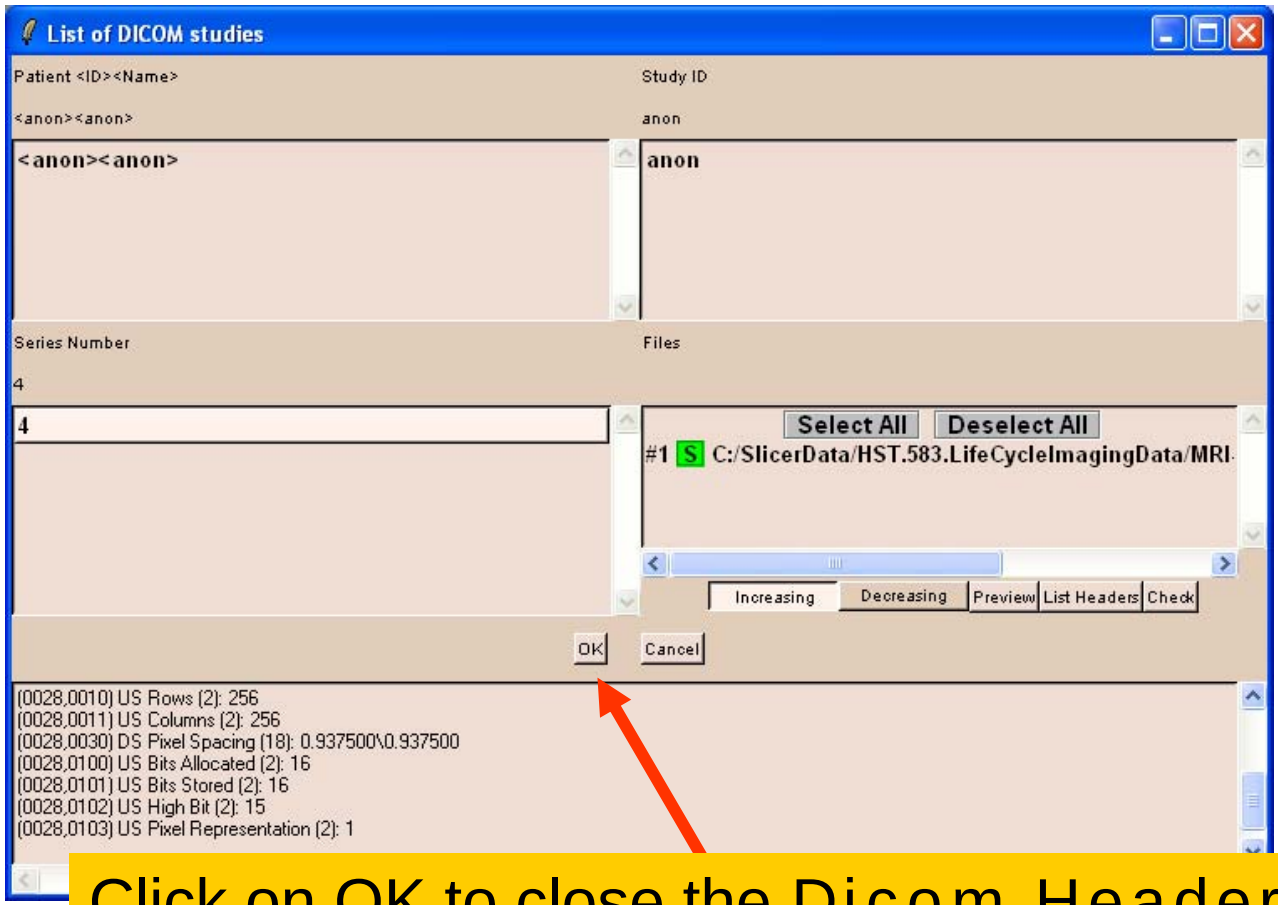

The list of Dicom tags of the header appears in the lower part in the lower part of the window.

# Image Header




Scroll up and down to display the values of the different tags

# Image Header



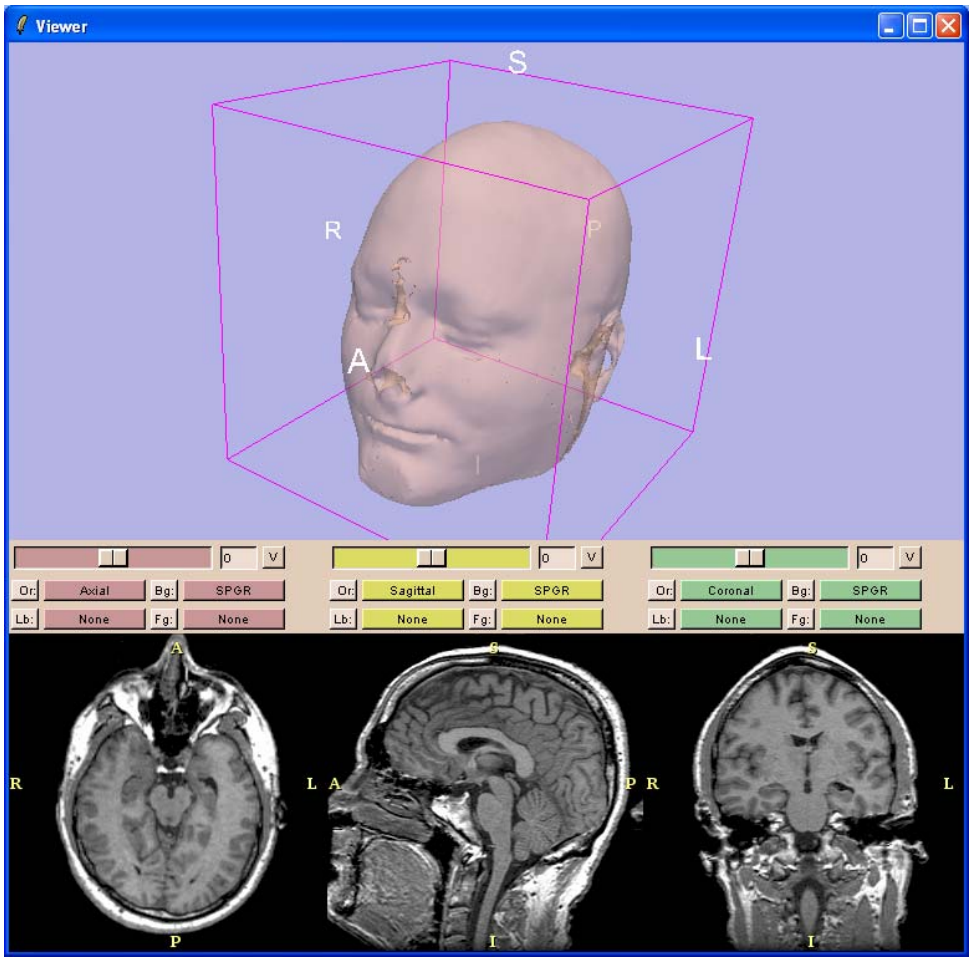

Click on OK to close the Dicom Header Window

# Anatomical Planes


Select File→OpenScene in the Main menu

Select the scene AnatomicalPlanes.xml in the directory MRI-data/

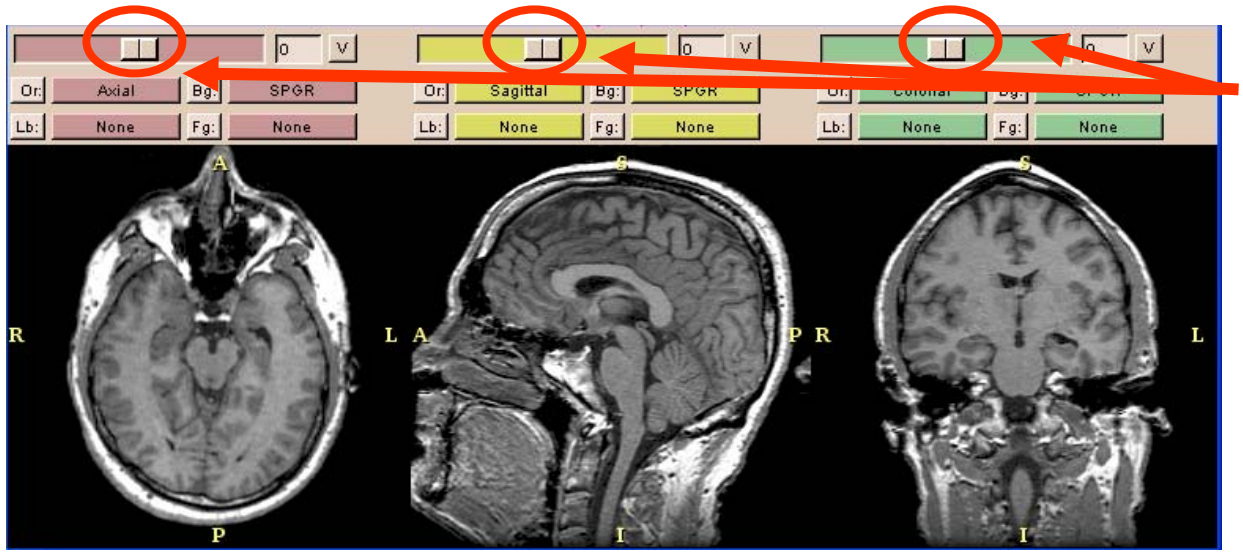
# Anatomical Planes




The 3DViewer displays a model of the head.

The 2DViewer displays the three anatomical planes.

# 2D Viewer



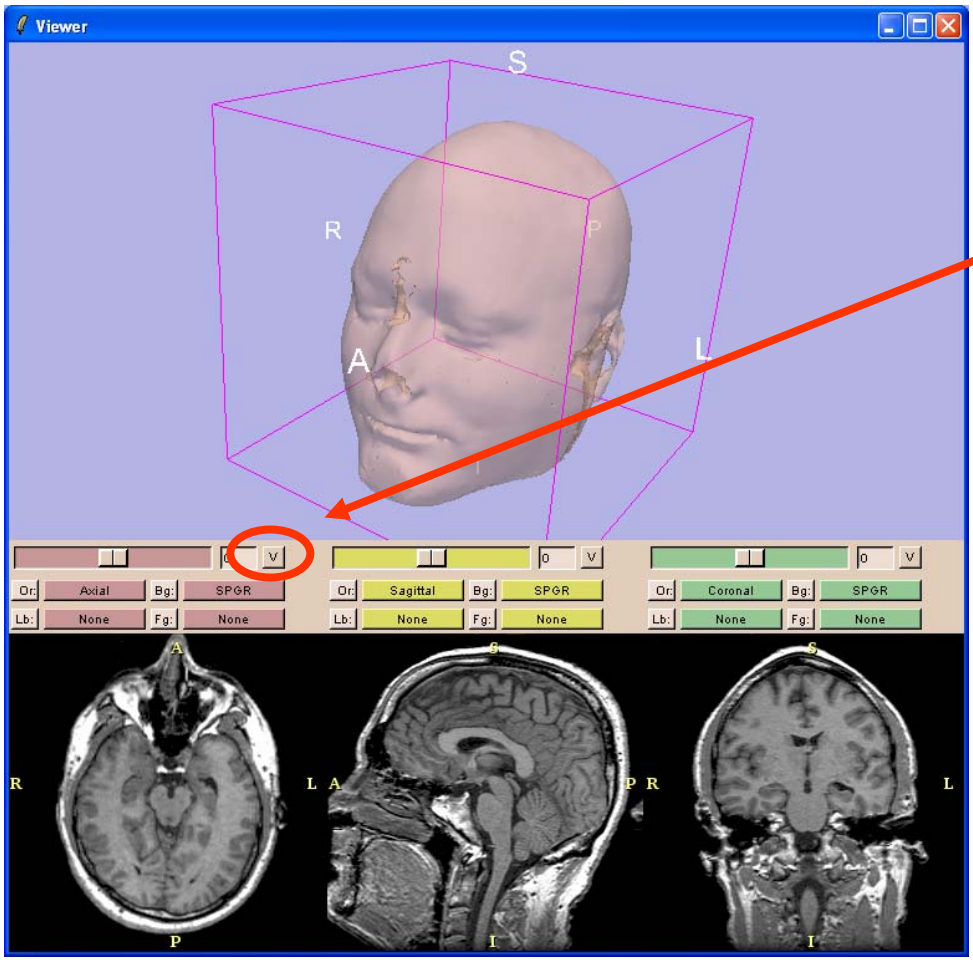

Sliders

Axial View

Sagittal View

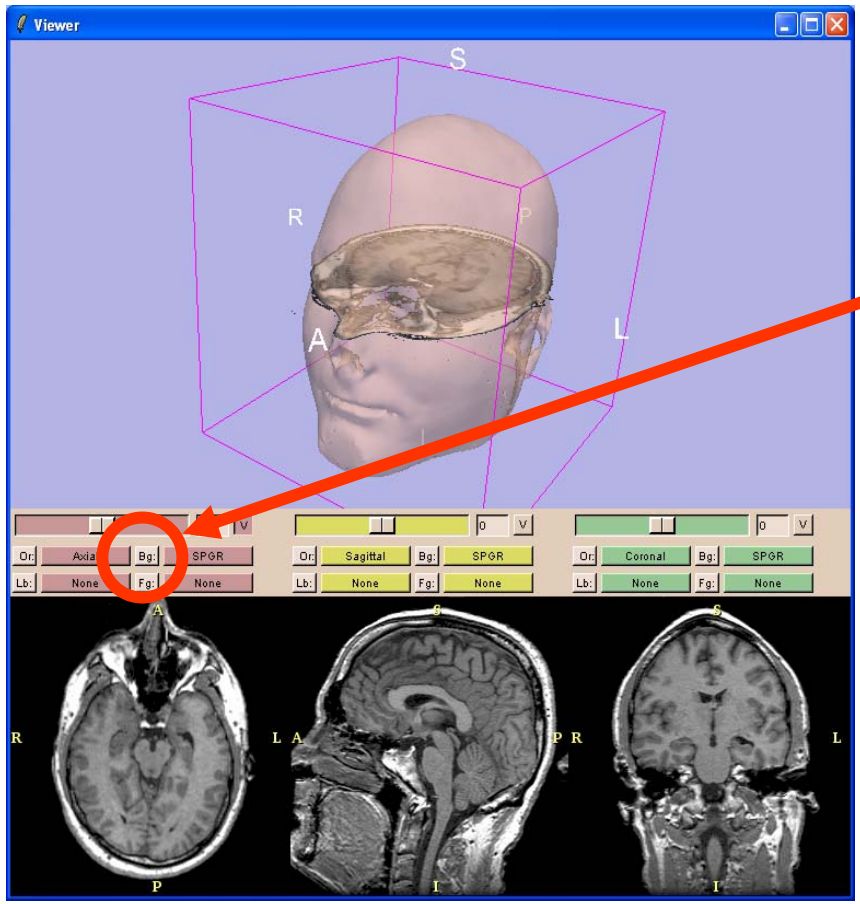
Coronal View

# Anatomical Planes



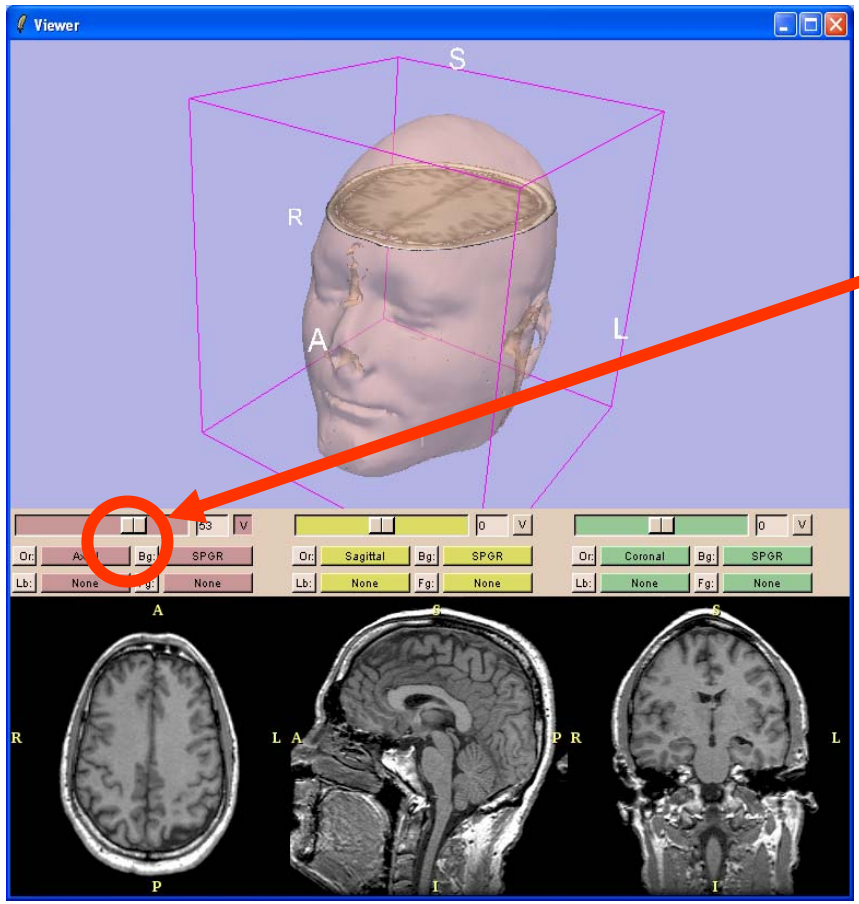

Click on the button V (Visualization) to display the axial slice in the 3DViewer.

# Axial View



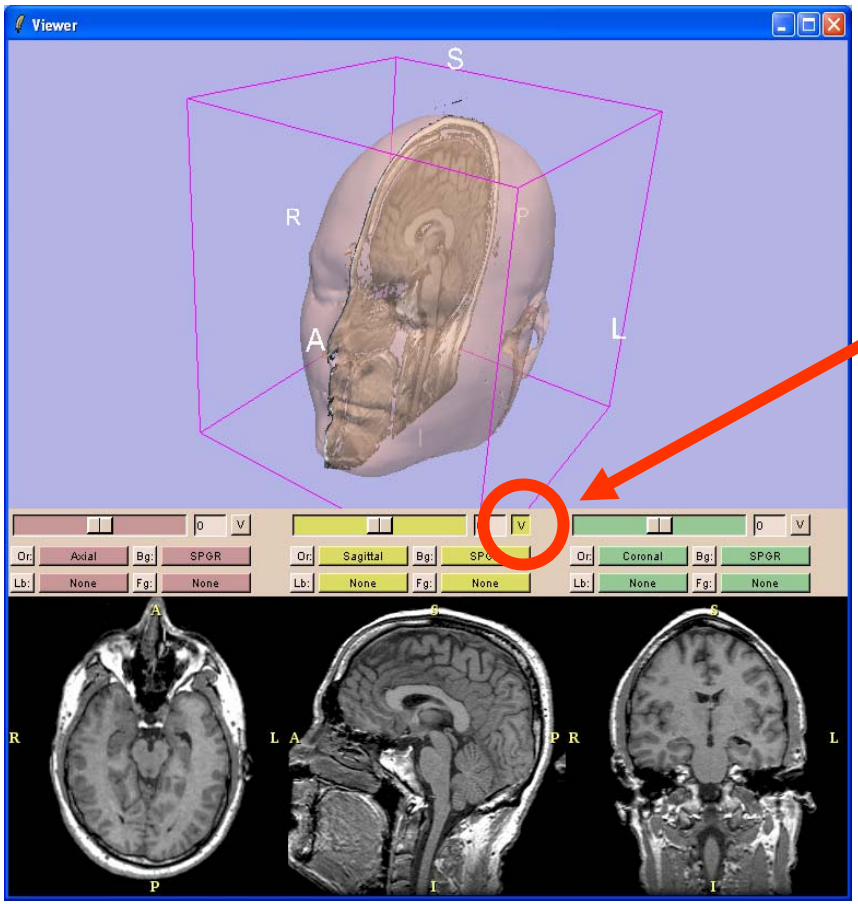

Slicer displays the axial slice in the 3DViewer

# Axial View



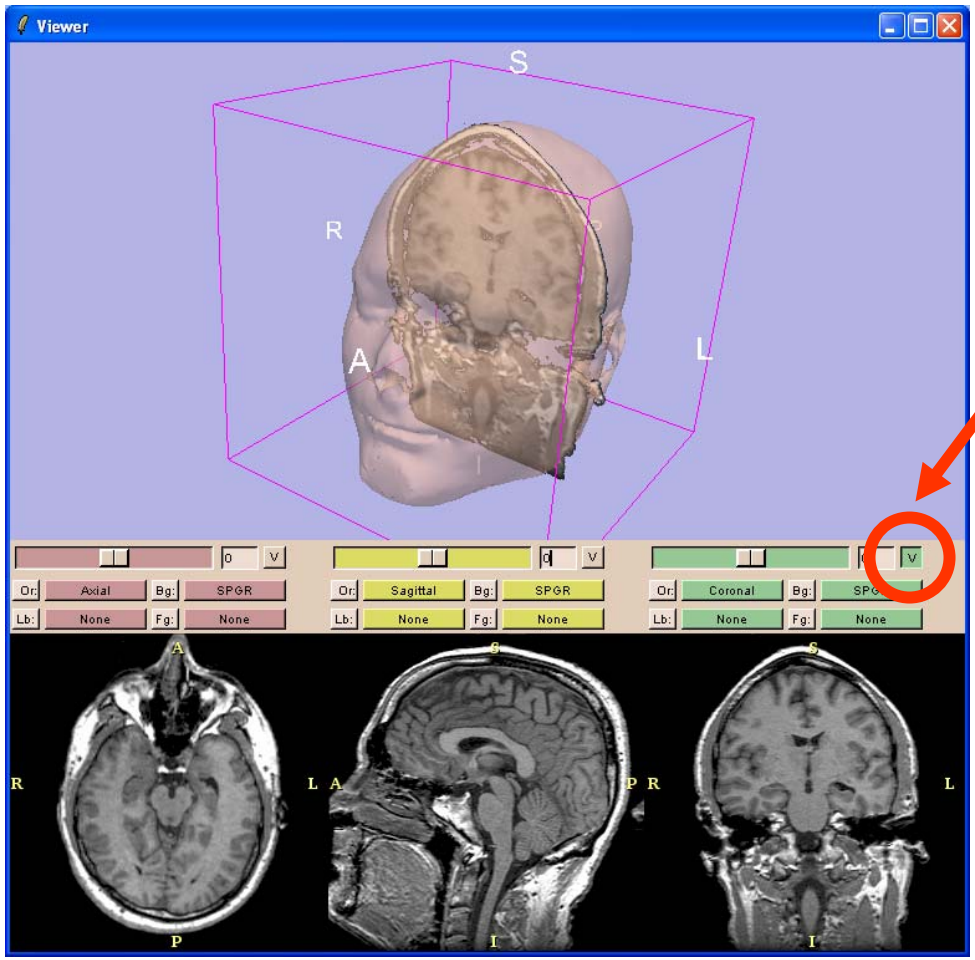

Use the slider to scroll inside the MRI volume

# Sagittal View



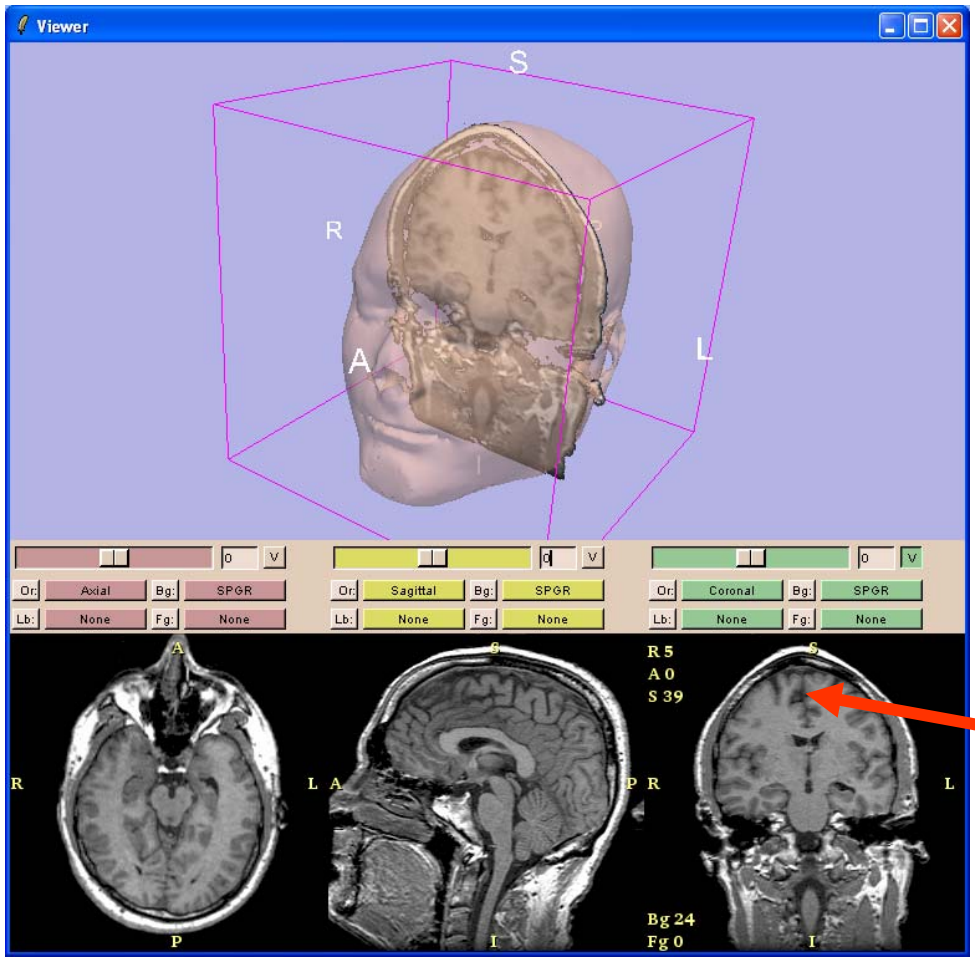

Deselect the axial view and click on V to display the sagittal slice in the 3DViewer.

# Coronal View




Deselect the sagittal view and click on V to display the coronal slice in the 3DViewer.

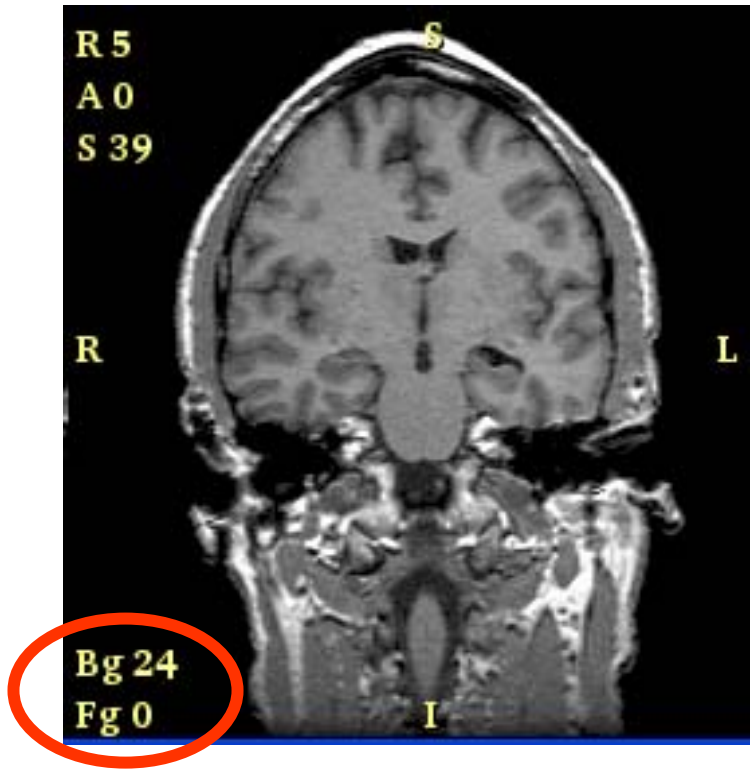
# Coronal View




Move the mouse over the coronal image in the 2DViewer.

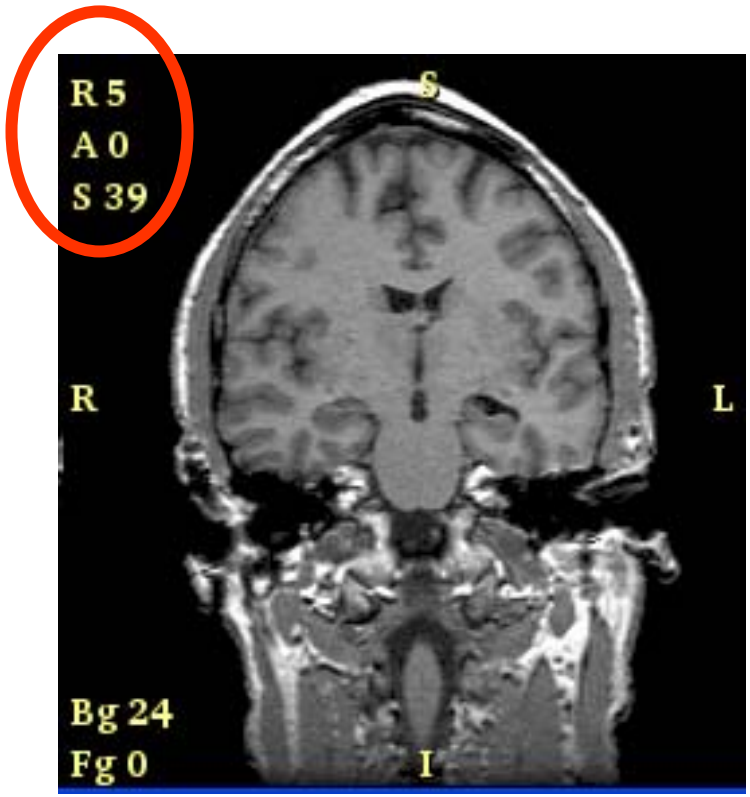
# Image Intensity

The value of the pixel intensity of the volume loaded in Background (Bg) is displayed on the image.

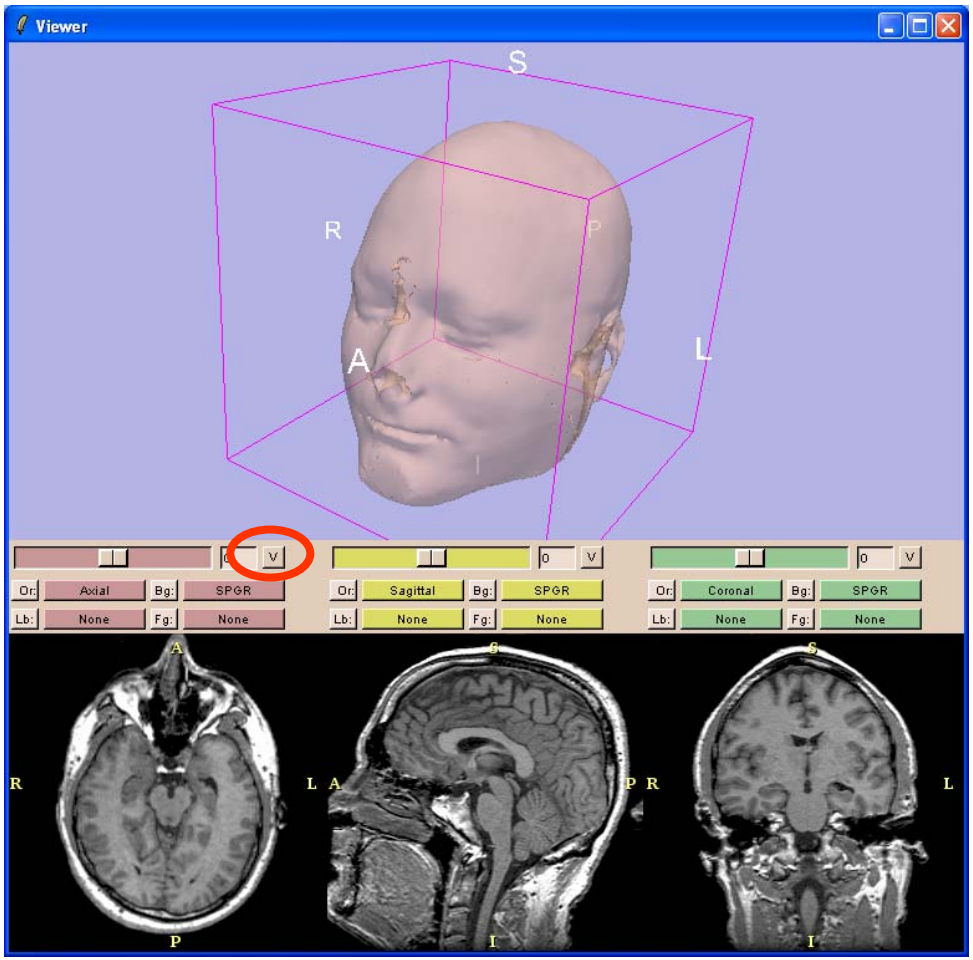


# RAS coordinates

The coordinates of the pixel pointed by the mouse appear in the left corner of the image.



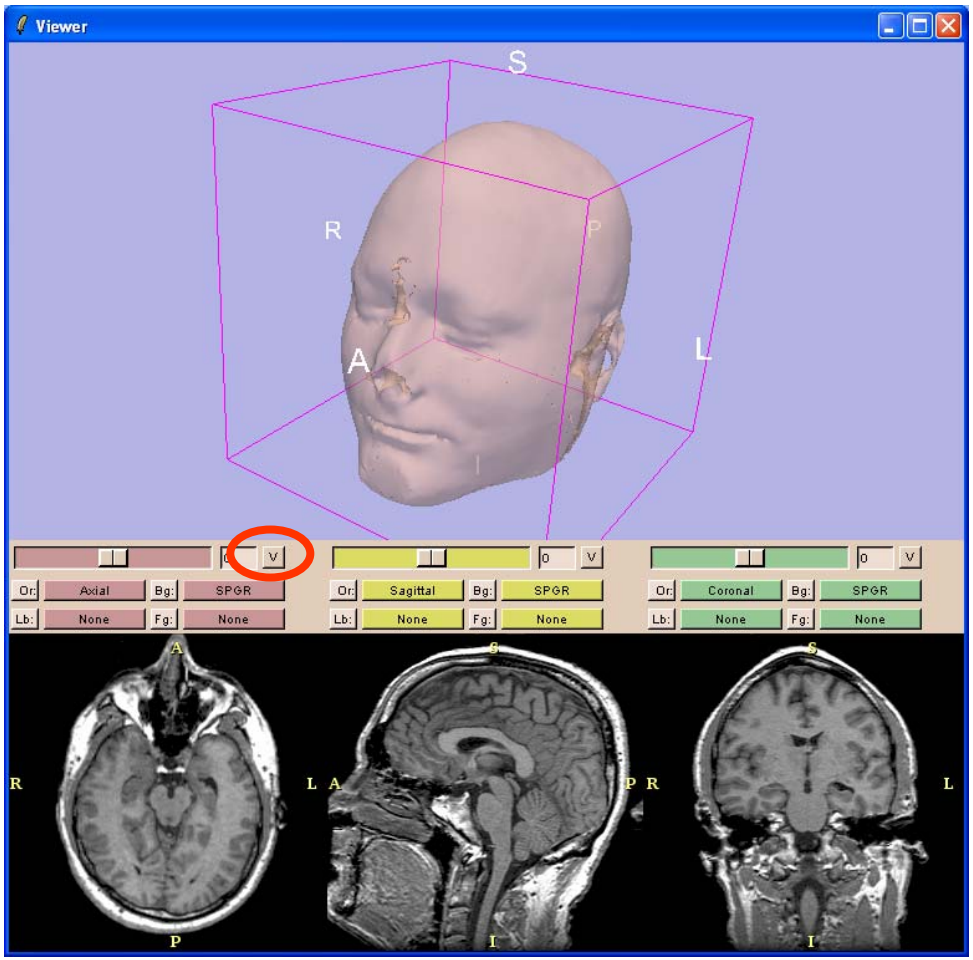
# Anatomical Planes




3D visualization
Position the mouse on the 3D model inside the Viewer
Left-click and move the mouse to the left

The model moves to the left

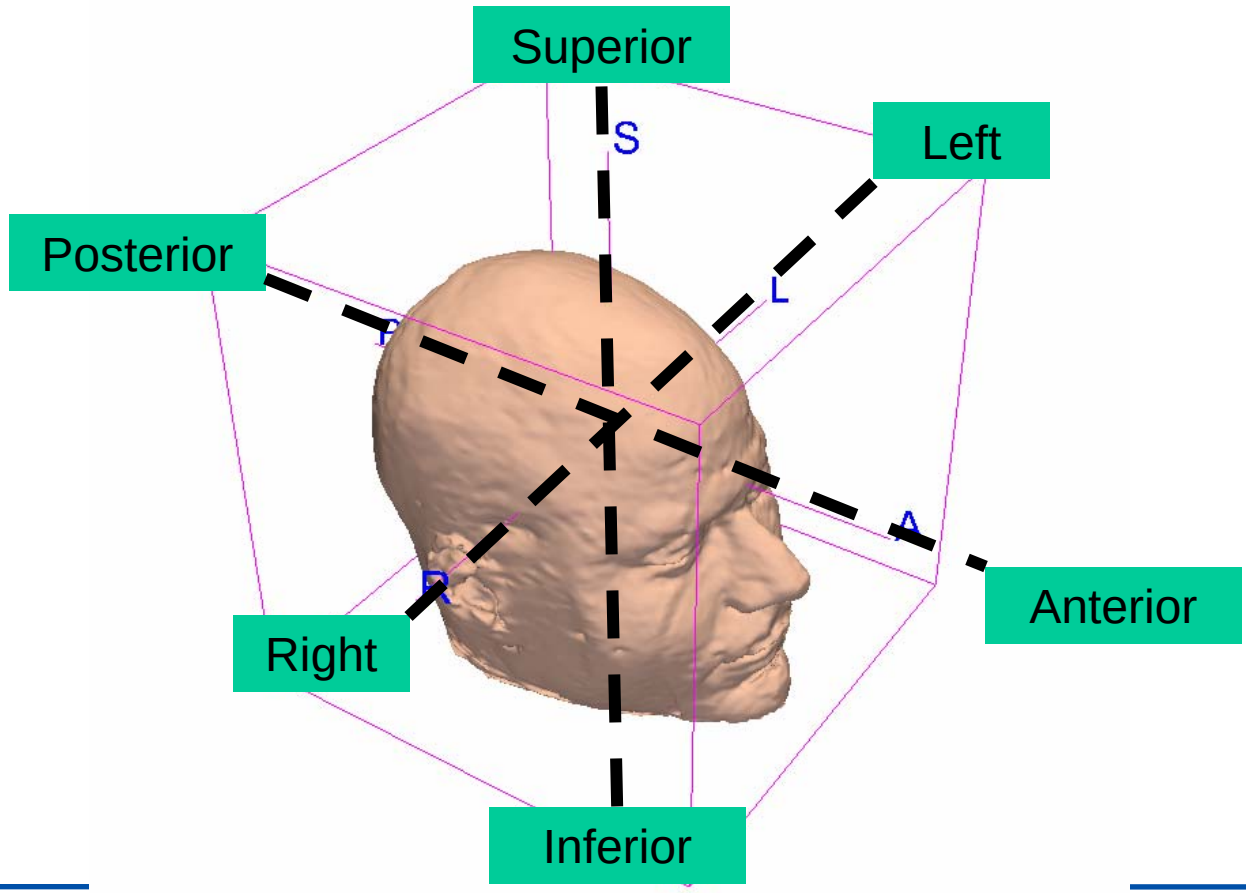
# Anatomical Planes



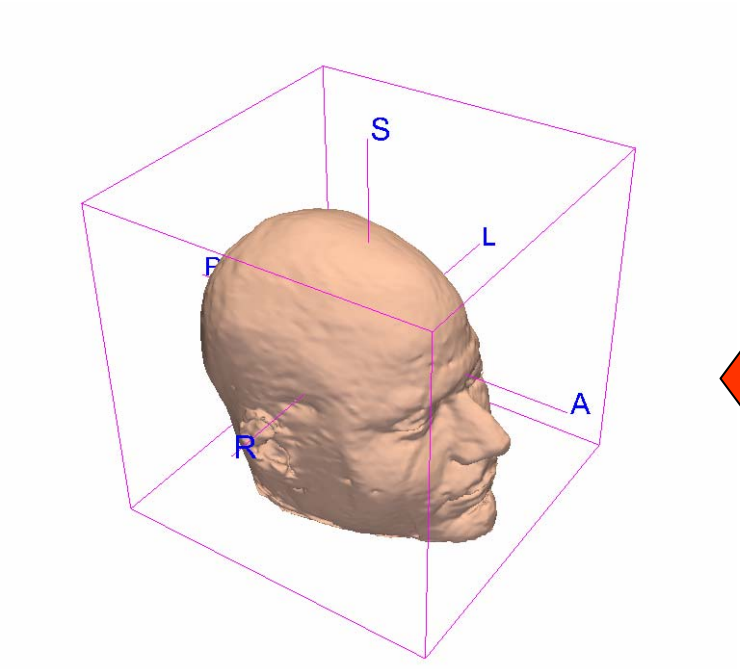

3D visualization
Position the mouse on the 3D model inside the Viewer
Left-click and move the mouse to the right

The model moves to the right

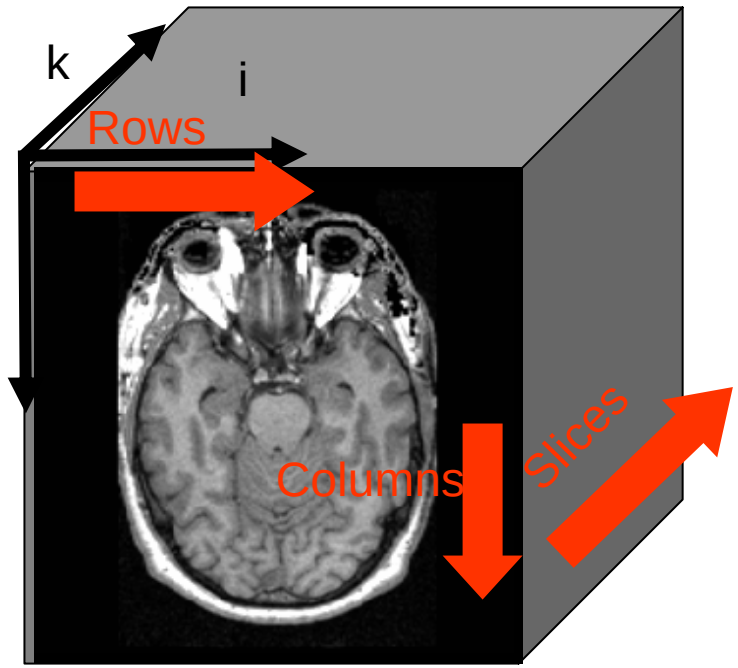
# Space Directions



# Voxel ordering

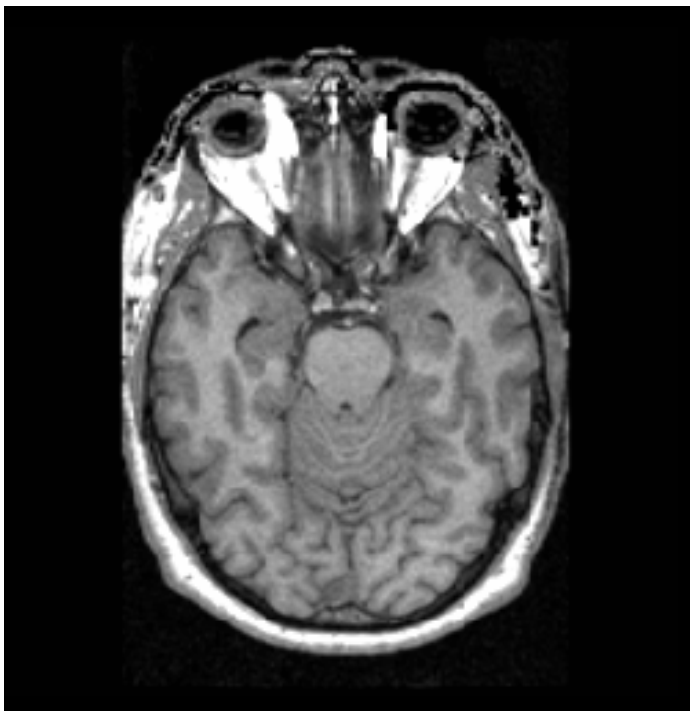


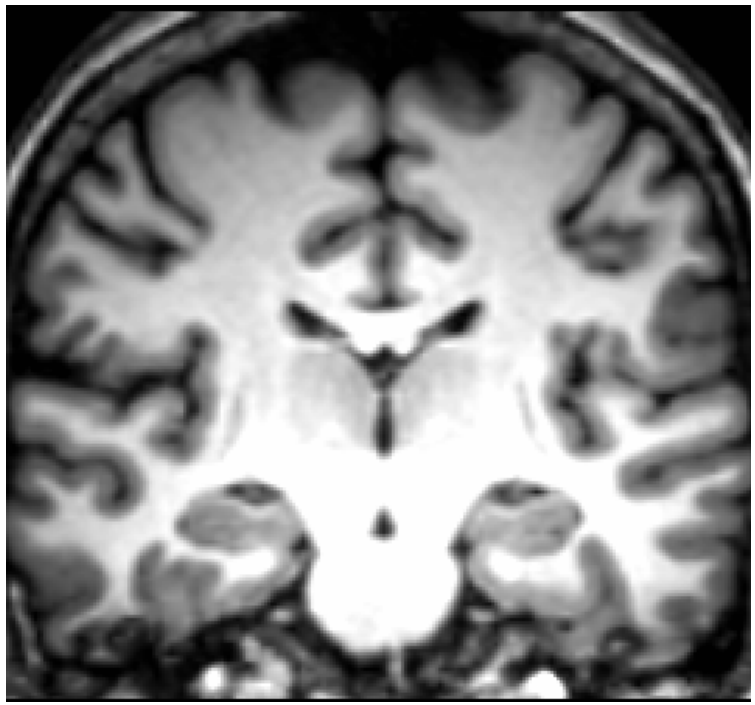

?




Problem: Which directions are the rows and slices ?

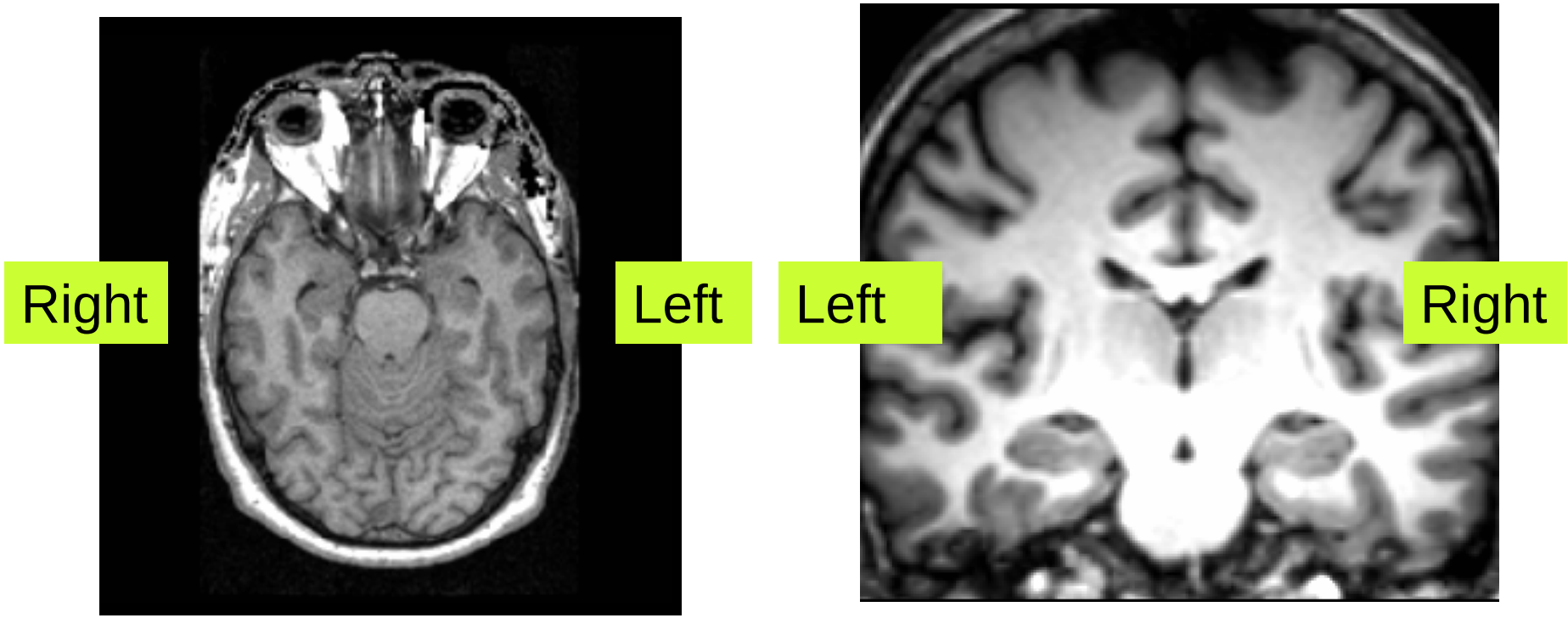
# Space Orientation





Indicate the left and right side of the patient in the images

# Space Orientation



# Example

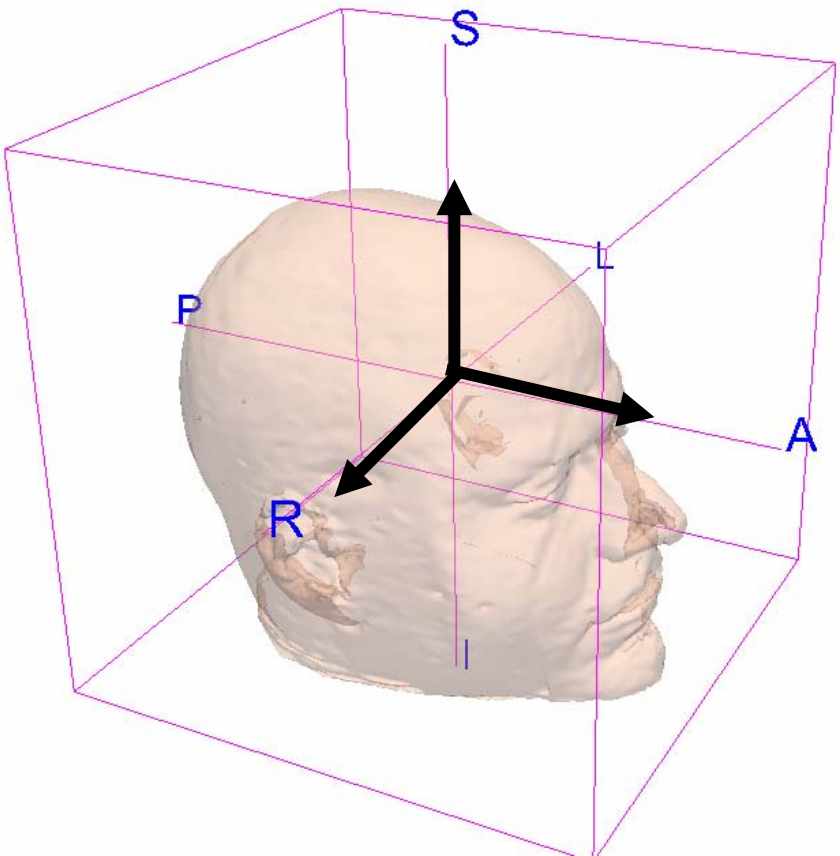
fMRI study:

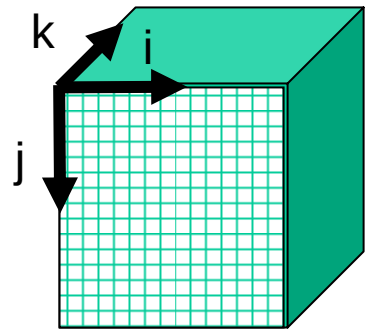
- Finger-tapping task
- Alternating left-hand / right-hand
- Contralateral side vs Ipsilateral side

→Knowledge of left/right side of the patient in the image is crucial for the interpretation of the results.

# Axes for Spatial Coordinates

RAS: Right-Anterior-Superior



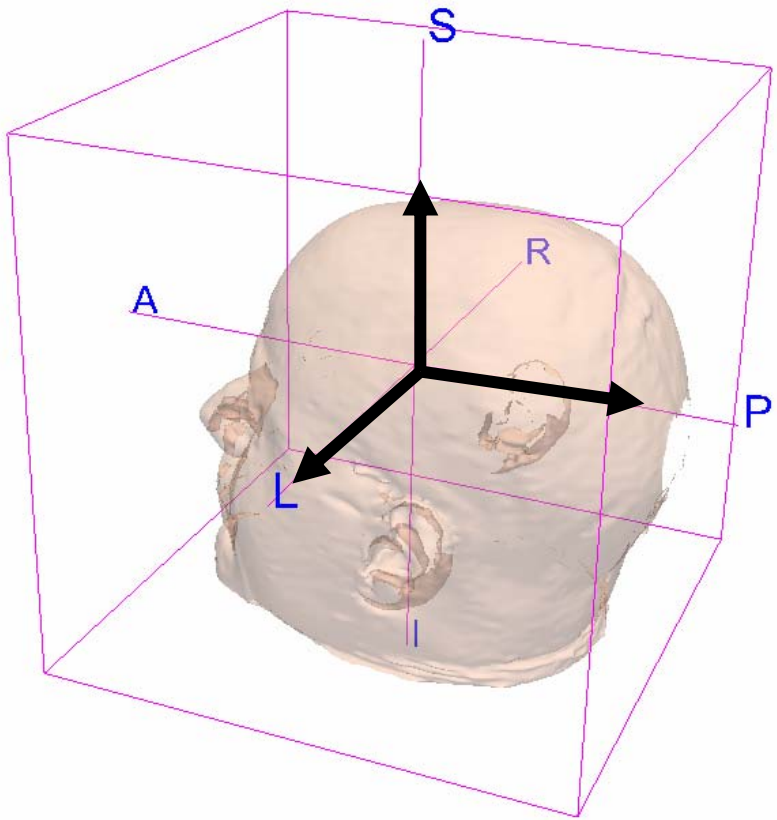

The index i in the file increases from the Left to the Right side of the Patient.

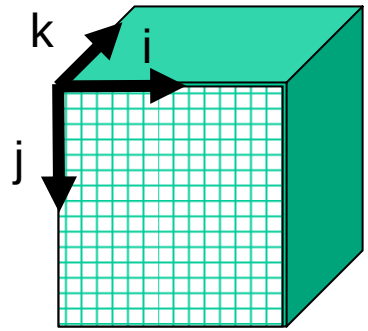
The index j in the file increases from Posterior to Anterior.

The index k in the file increases from Inferior to Superior.

# Axes for Spatial Coordinates

LPS: Left-Posterior-Superior




The index i in the file increases from the Right to the Left side of the Patient.

The index j in the file increases from Anterior to Posterior.

The index k in the file increases from Inferior to Superior.

# Real Clinical Situation

- …is not straightforward: the image volume is not aligned to some exact orthogonal directions

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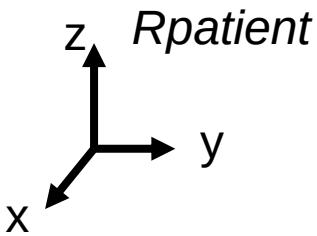
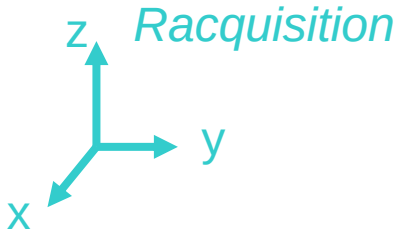
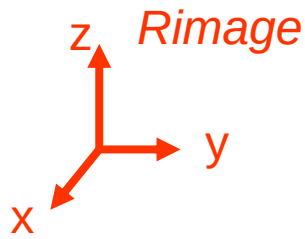
- However, the acquisition parameters determine which set of axes the voxel indices correspond to most closely.
- Spatial transforms are used to align a volume to a specific space.

# Reference Frames



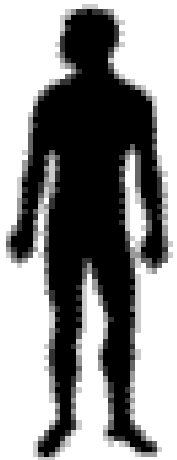
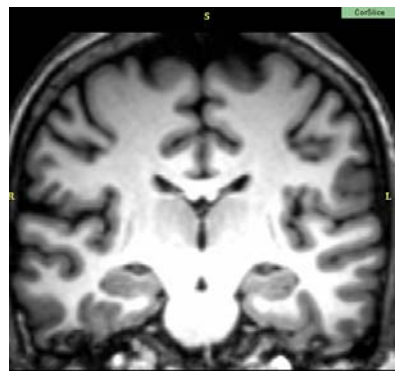
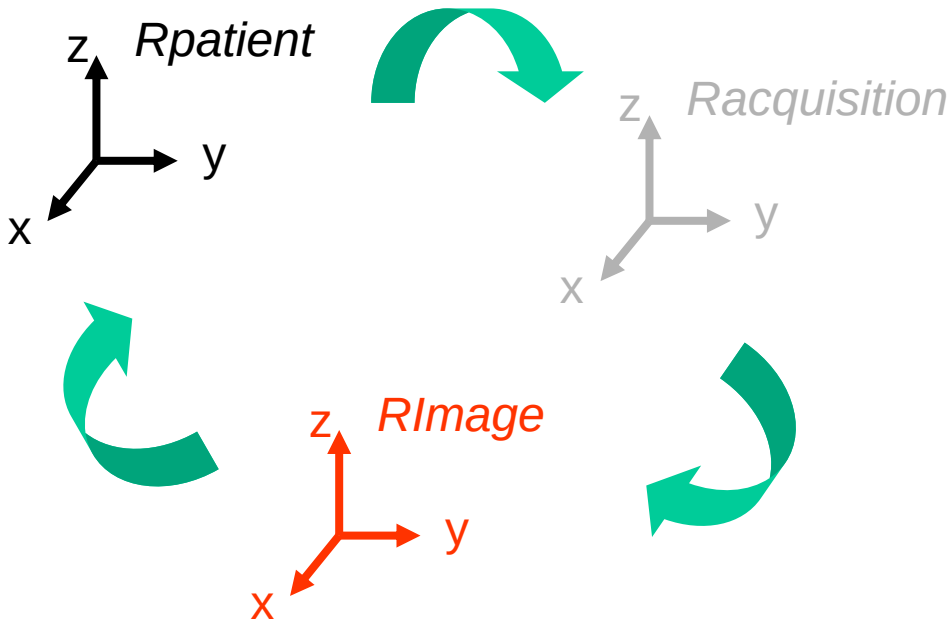



Image: NIH



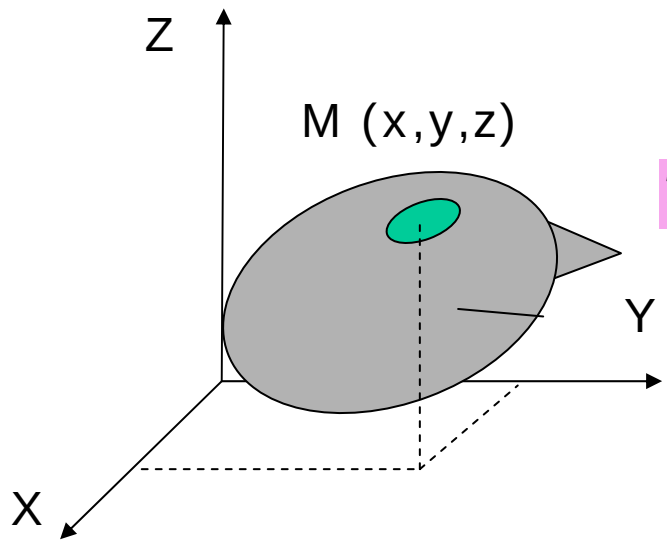
# Registration

Registration is the process of transforming these three different spaces into a common reference frame



# Patient → Image Transform

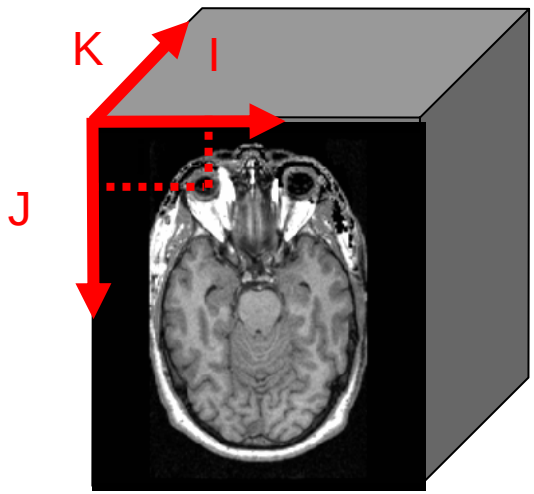
Patient Space




M (x,y,z)

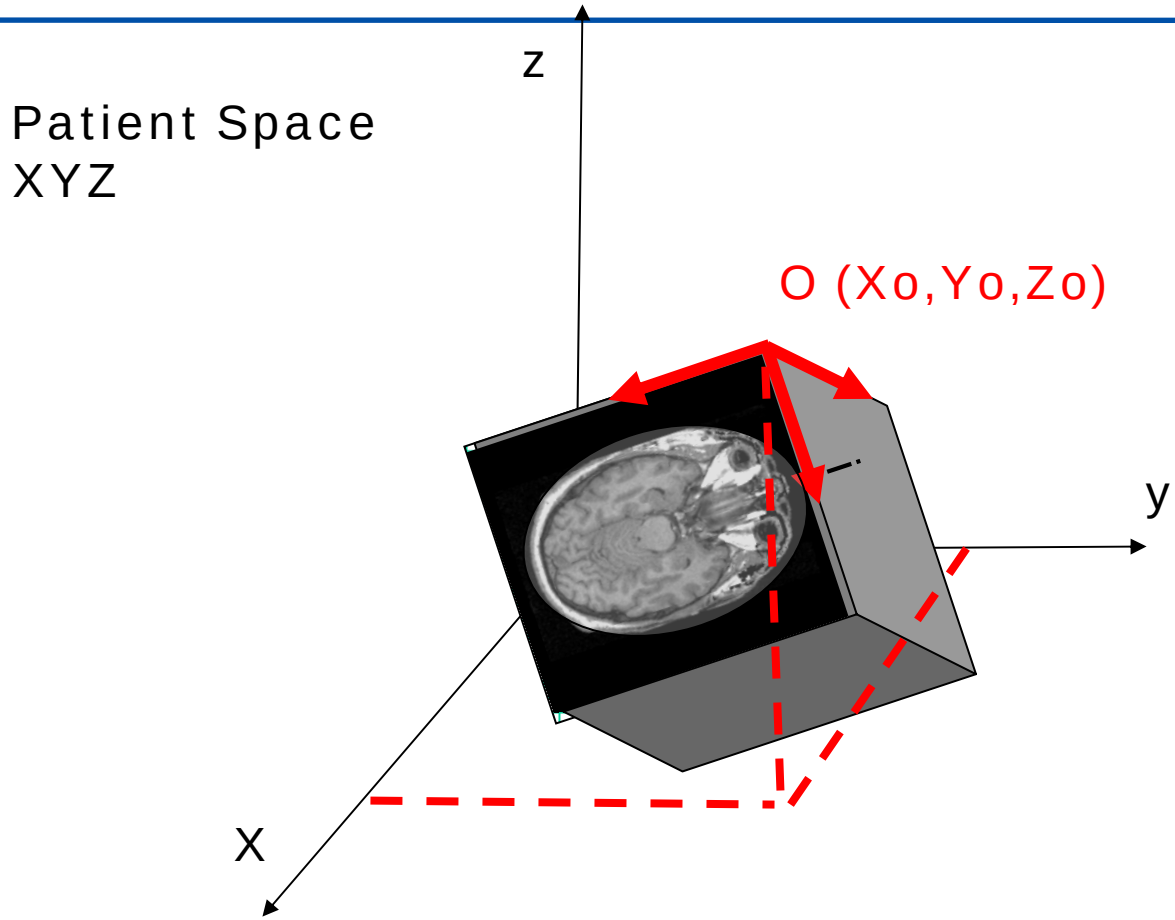
$T_{patient \rightarrow \mathrm{Im}\, age}$

Image Space




M(a,b,c)

# Patient → Image Transform



# Homogenous Coordinate Transform matrix

$$M(x,y,z,1) = T_{image \rightarrow patient} * M(a,b,c,1)$$

$$T_{Image \rightarrow Patient} = \begin{pmatrix} m_{01} & m_{01} & m_{02} & Tx \\ m_{10} & m_{11} & m_{12} & Ty \\ m_{20} & m_{21} & m_{22} & Tz \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Spatial transformation of homogenous voxel coordinates between the image space and the patient space

# Homogenous Coordinate Transform matrix

$$M(x,y,z,1) = T_{image \rightarrow patient} * M(a,b,c,1)$$

$$T_{Image \rightarrow Patient} = \begin{pmatrix} m_{01} & m_{01} & m_{02} & Tx \\ m_{10} & m_{11} & m_{12} & Ty \\ m_{20} & m_{21} & m_{22} & Tz \\ 0 & 0 & 0 & \end{pmatrix}$$

Coordinate of the first voxel in patient space

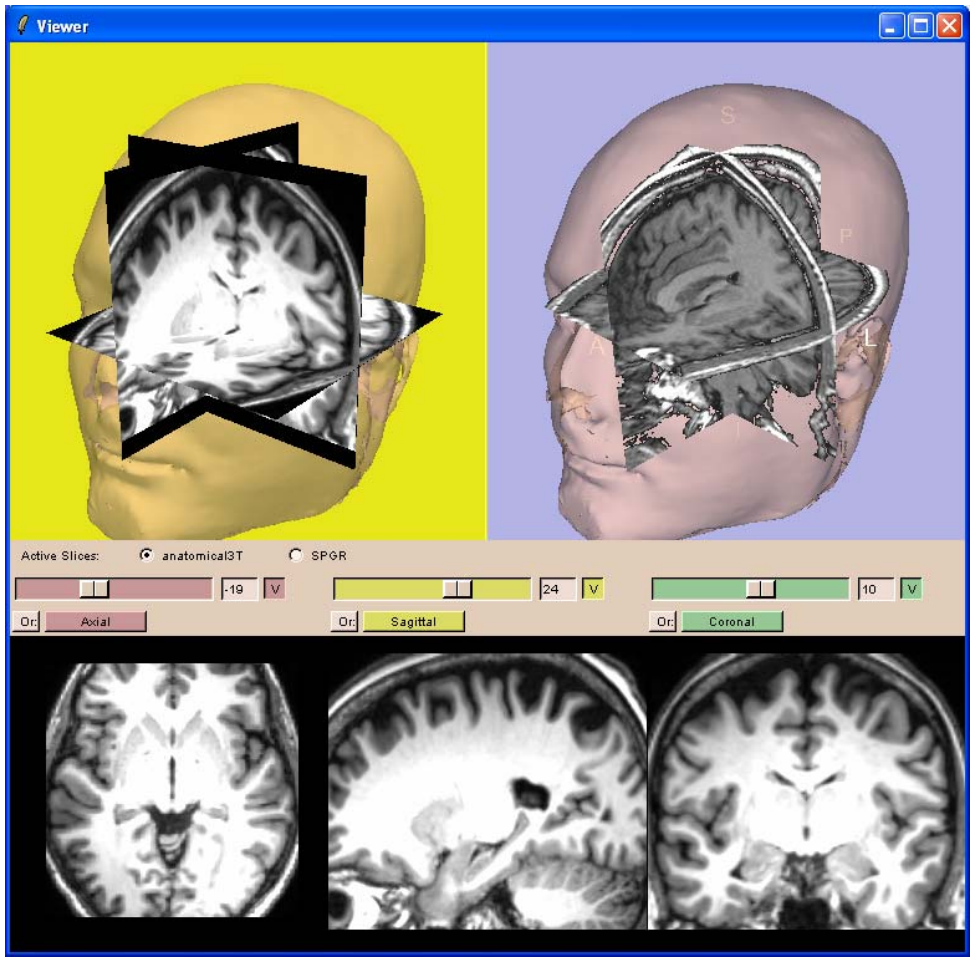
# Homogenous Coordinate Transform matrix

$$M(x,y,z,1) = T_{image \rightarrow patient} * M(a,b,c,1)$$

$$T_{Image \rightarrow Patient} = \begin{pmatrix} m_{01} & m_{01} & m_{02} & Tx \\ m_{10} & m_{11} & m_{12} & Ty \\ m_{20} & m_{21} & m_{22} & Tz \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

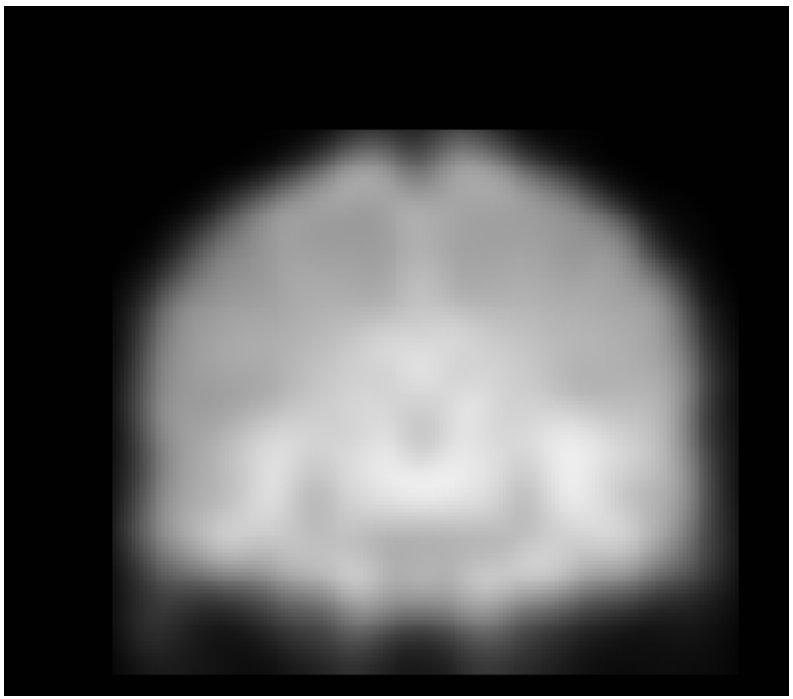
Rotation matrix

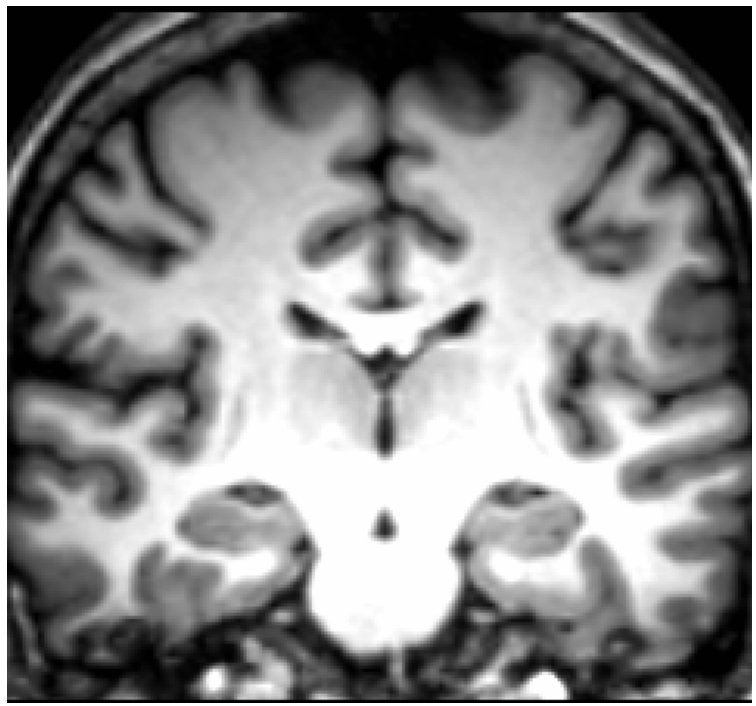
# Data Fusion




Registering all the images in a common reference frame allows a quantitative analysis of multi-modality datasets.

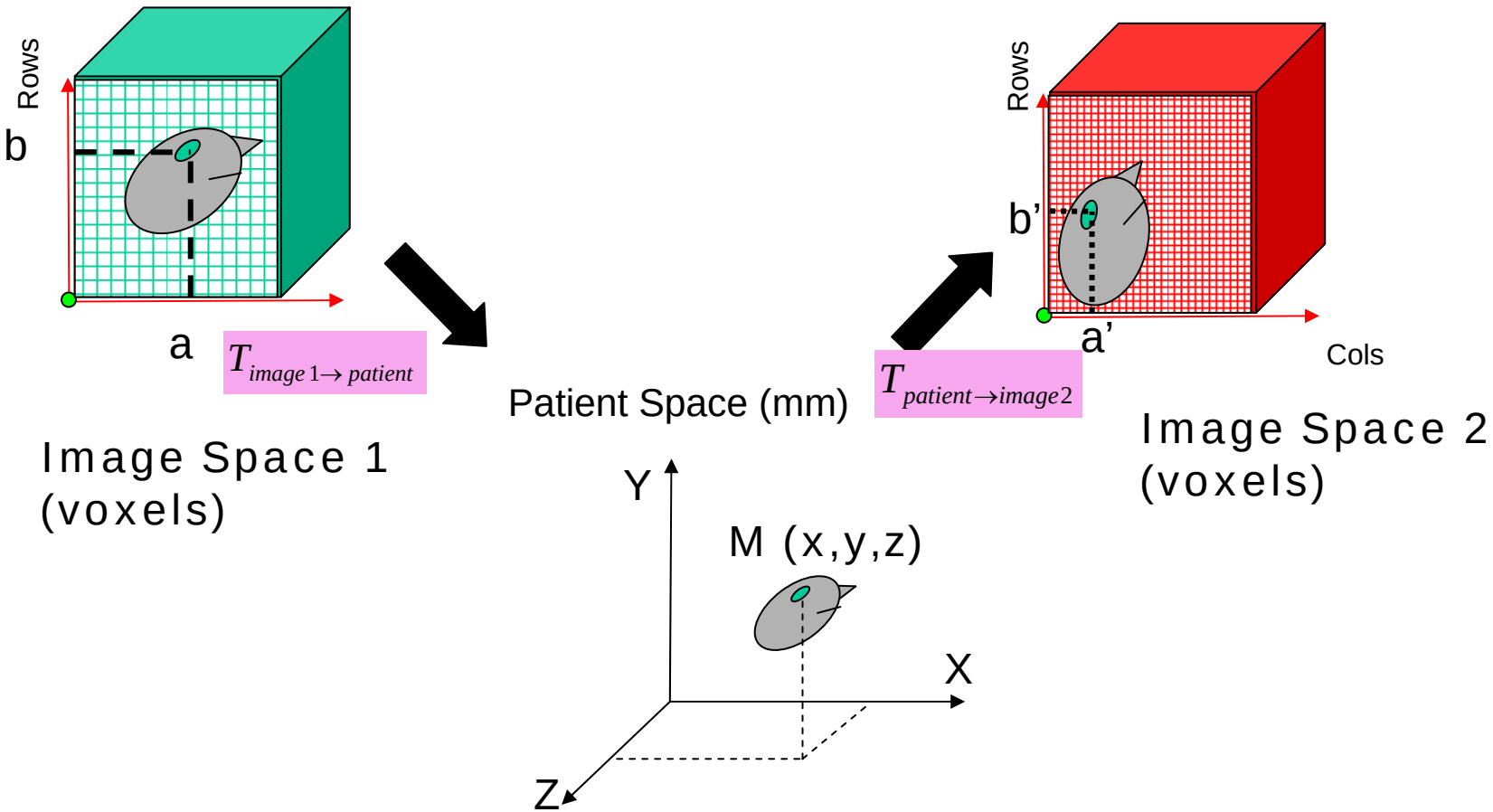
# Data Fusion





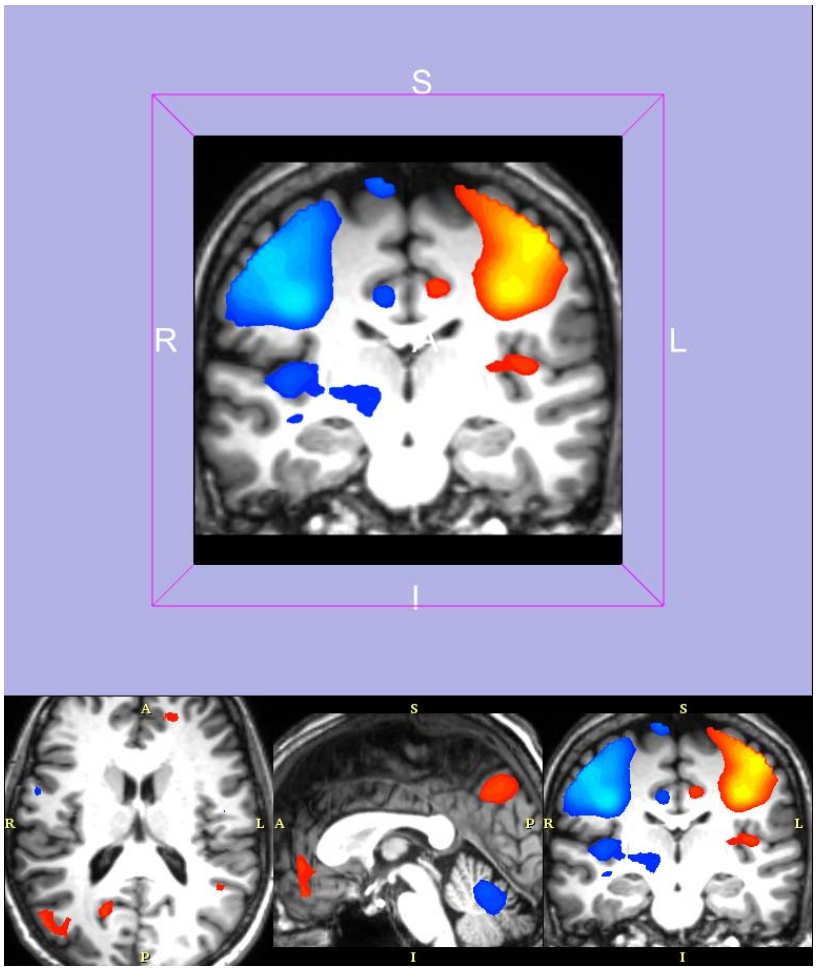
Example: Registration of high-resolution anatomical and functional datasets to improve localization of findings for fMRI analysis

# Homogenous Coordinate Transform matrices




$$M(a',b',c',1) = T_{patient \rightarrow image2} * T_{image1 \rightarrow patient} * M(a,b,c,1)$$

# Data Fusion Example




fMRI activation map superimposed on the anatomical images

# The Life Cycle of Medical Imaging Data

Image: NIH

Acquisition

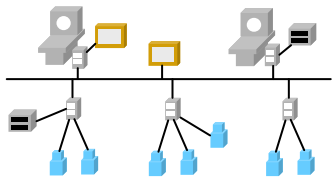
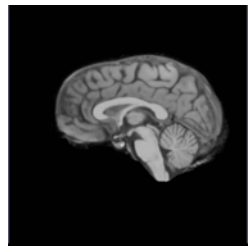
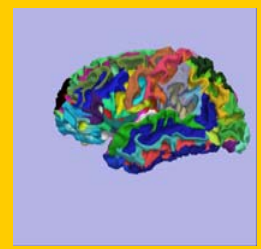


Image by MIT OpenCourseWare.

Storage



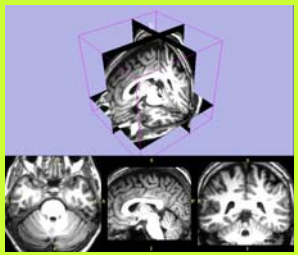
Display



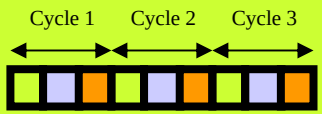
Analysis

Analysis

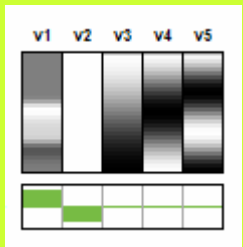
# fMRI Analysis Workflow



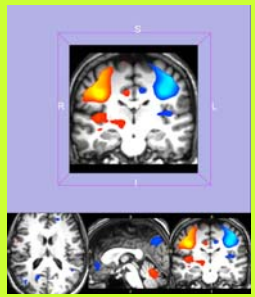
Data Loading



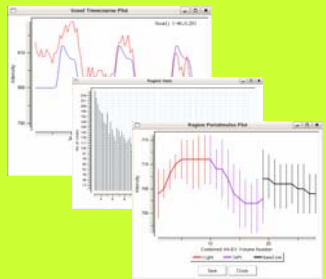

Paradigm Description




Signal Modelling

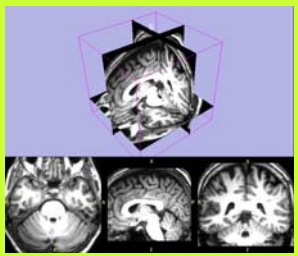


Activation Detection

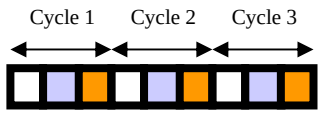


Statistical Analysis

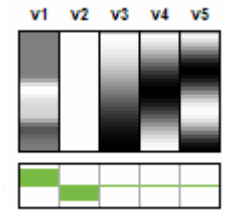
# fMRI Analysis Workflow



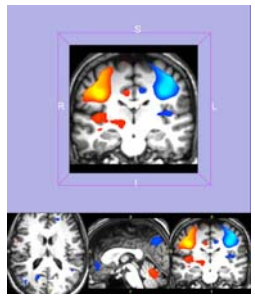
Data Loading



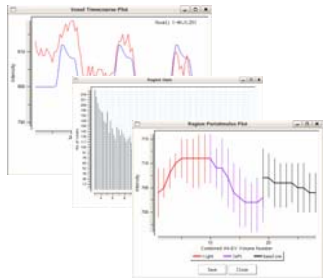

Paradigm Description




Signal Modeling

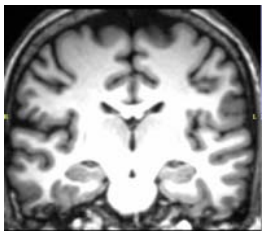


Activation Detection



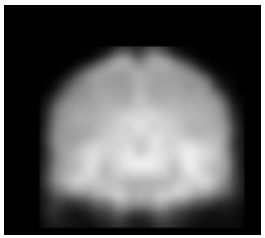
Statistical Analysis

# Data description



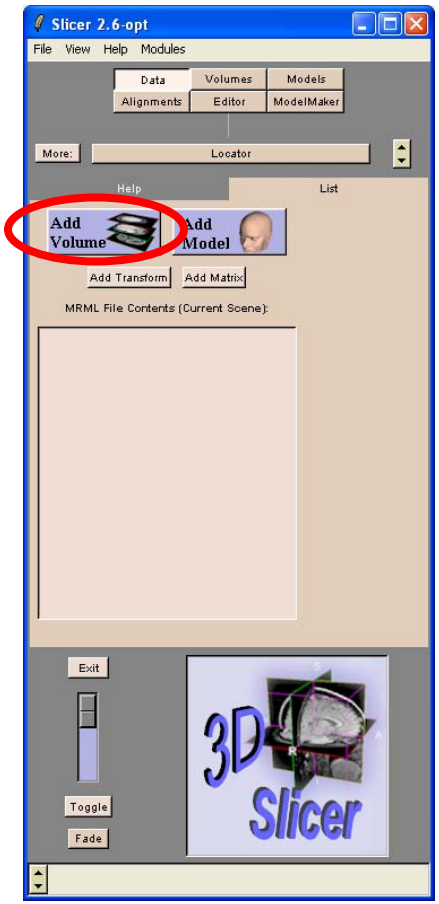
Structural (MPRAGE):  ANALYZE format
135 slices

Normalized to MNI



Pre-processed Functional (EPI): NIFTI format
68 slices

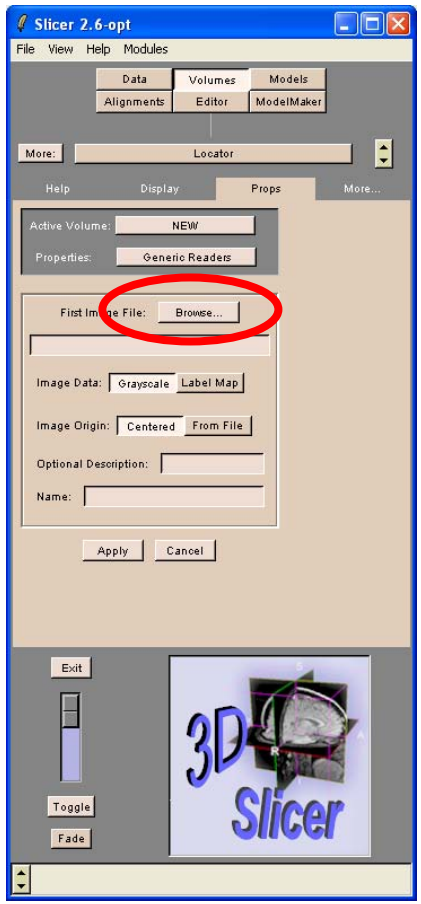
# Loading the structural dataset




Click on File→Close Scene to close the scene containing the first MRI-dataset.

Click on Add Volume in the main menu

# Loading the structural dataset



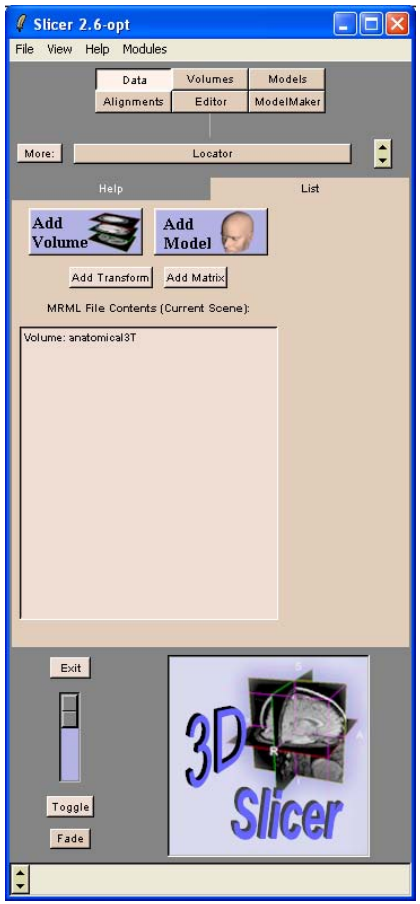

Select the reader Generic Reader in the Props Panel of the module Volumes.

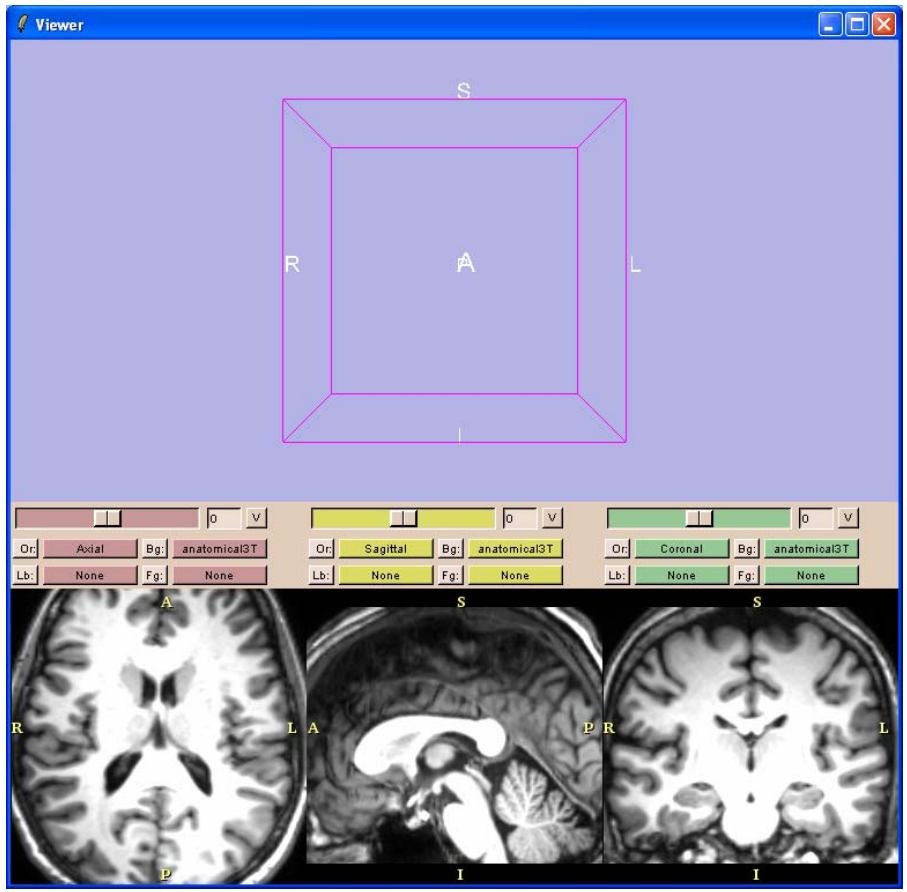
Click on Browse, select the file Anatomical3T.hdr in the directory

/fMRI-data1/structural/

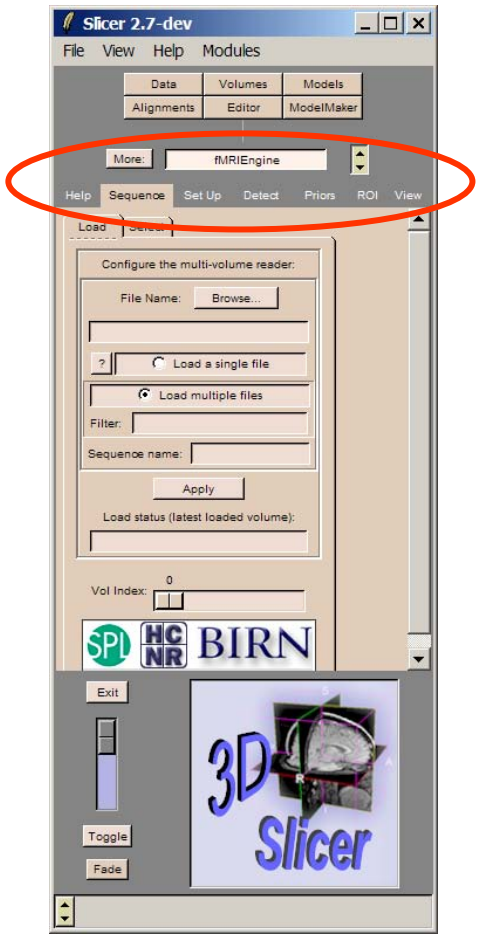
Click on Apply to load the dataset.

# Loading the structural dataset



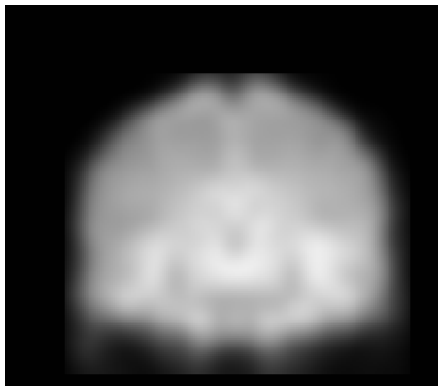
# Loading the fMRI dataset




Select Modules in the main menu

Select Application→fMRIEngine

# fMRI Data pre-processing (SPM)



Realignment

↓

Motion Correction

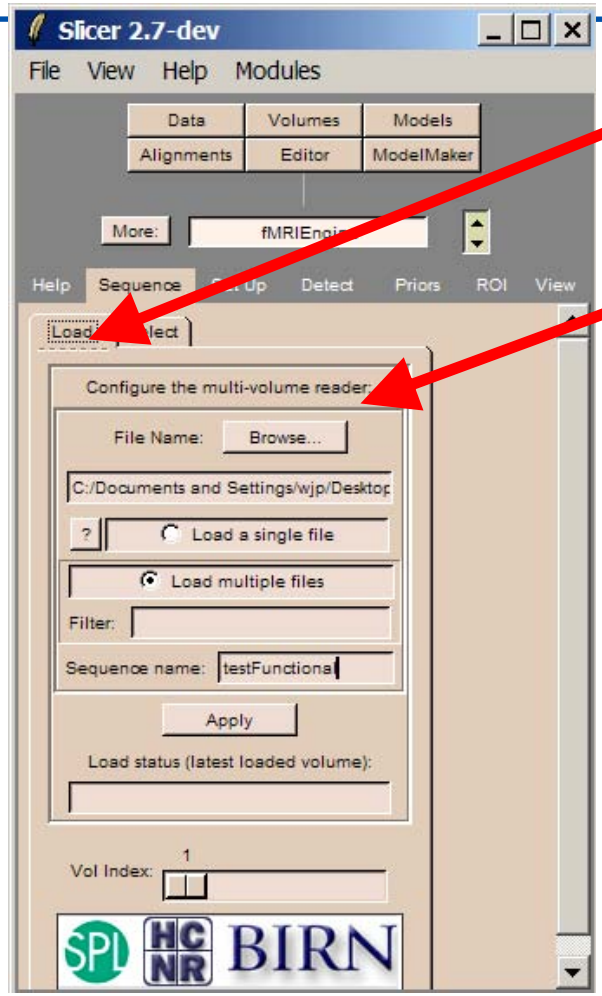
↓

Normalization to MNI

↓

Smoothing

# Load Image Sequence




Pick Sequence → Load tab

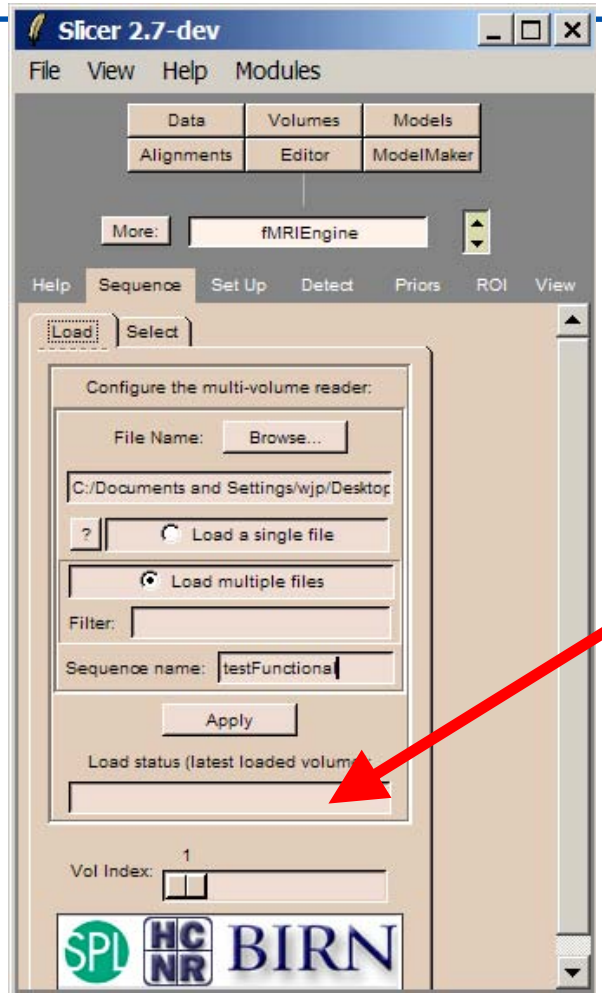
Click on Browse and select the file functional01.hdr in the directory

/fMRI-data1/structural/

Select Load Multiple Files

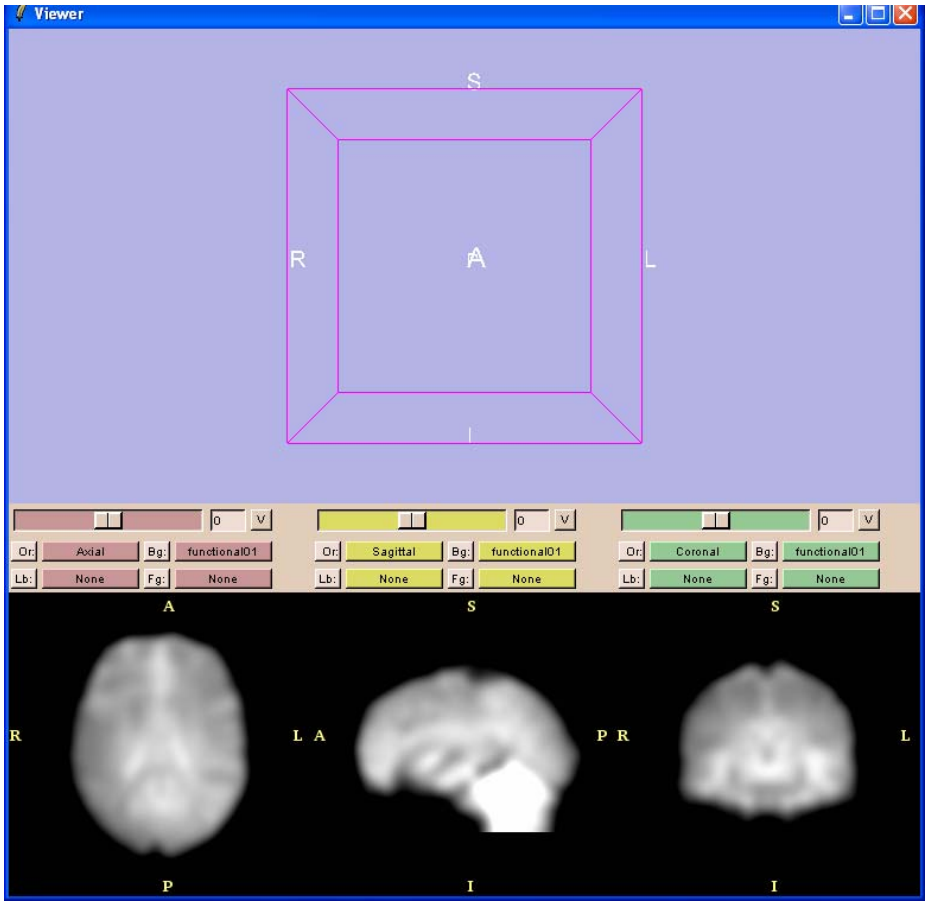
Enter the sequence name testFunctional and click on Apply.

# Load Image Sequence



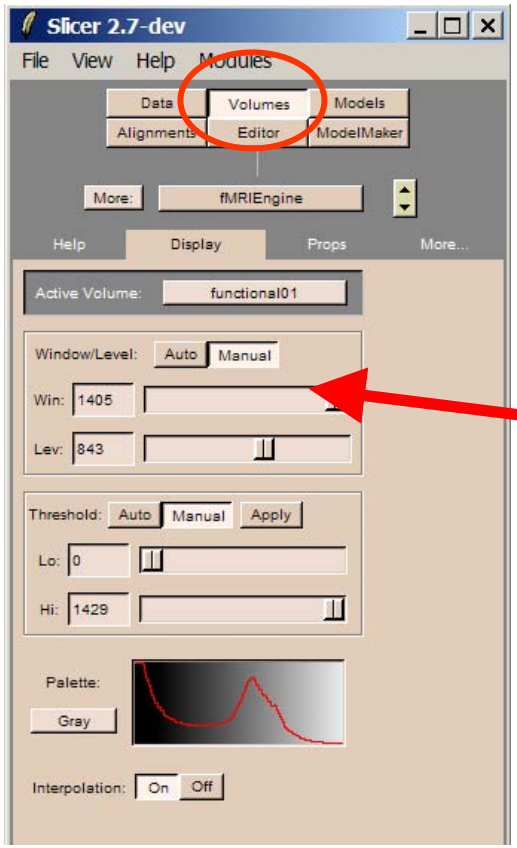

Slicer displays the load status of the 30 functional volumes.

# Load Image Sequence




The functional volumes appear in the Viewer.

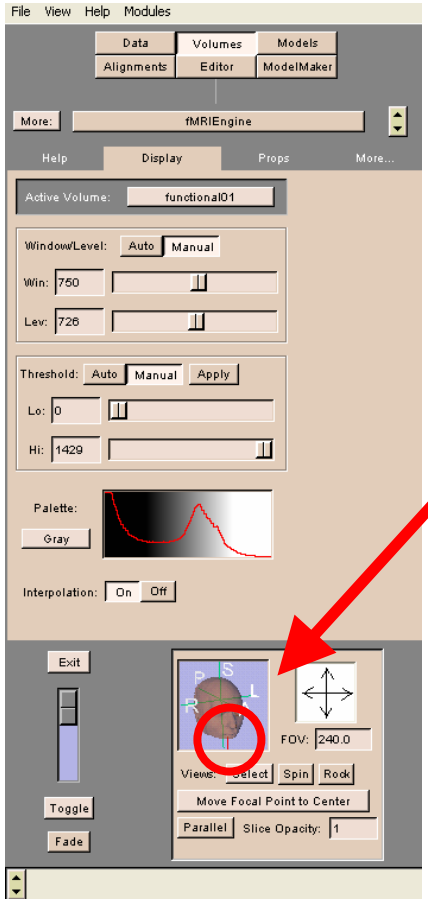
# Set Image Display




Click on the module Volumes, and select the panel Display

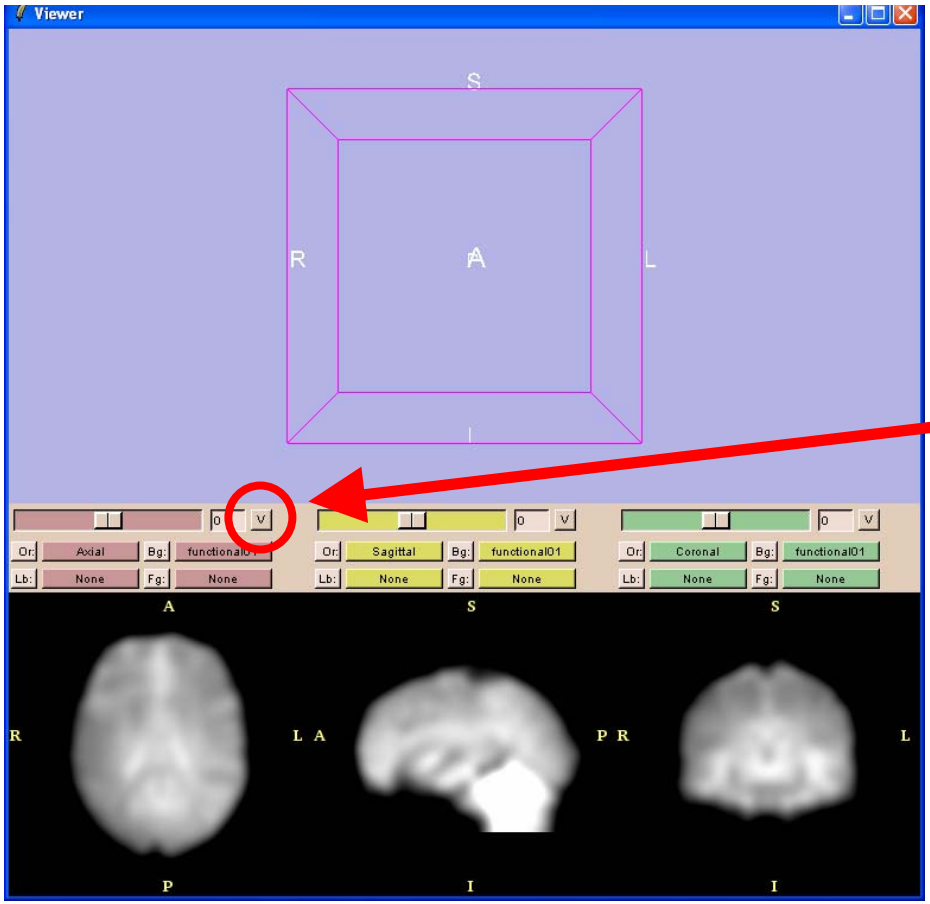
Adjust Win and Lev to get best display of image data

# Set Image Display



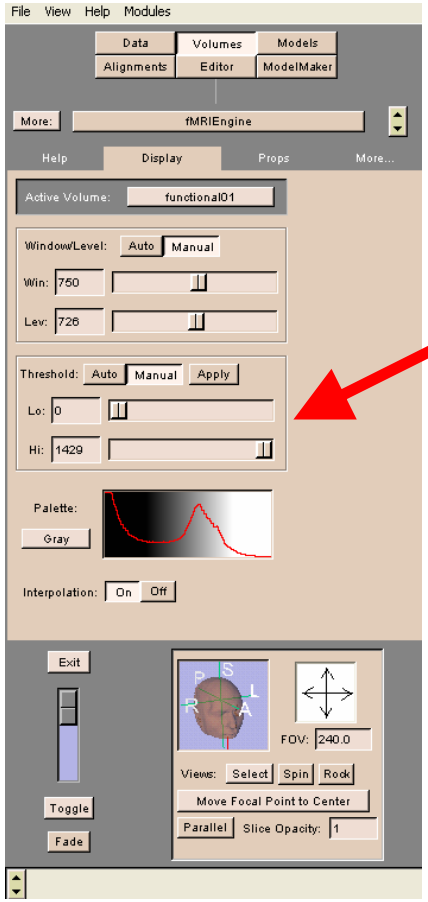

Click on the letter I (Inferior) in the control window to display the Inferior view.

# Set Image Display



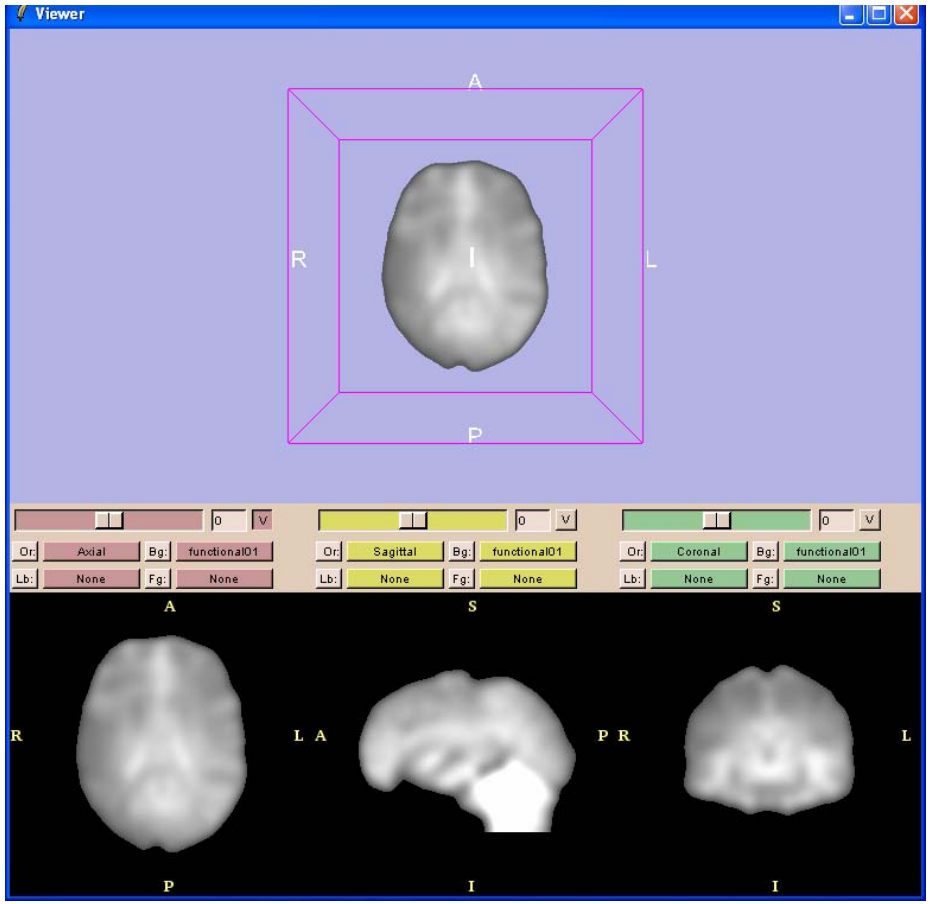

Click on the V button to display the axial slice in the Viewer.

# Set Image Display



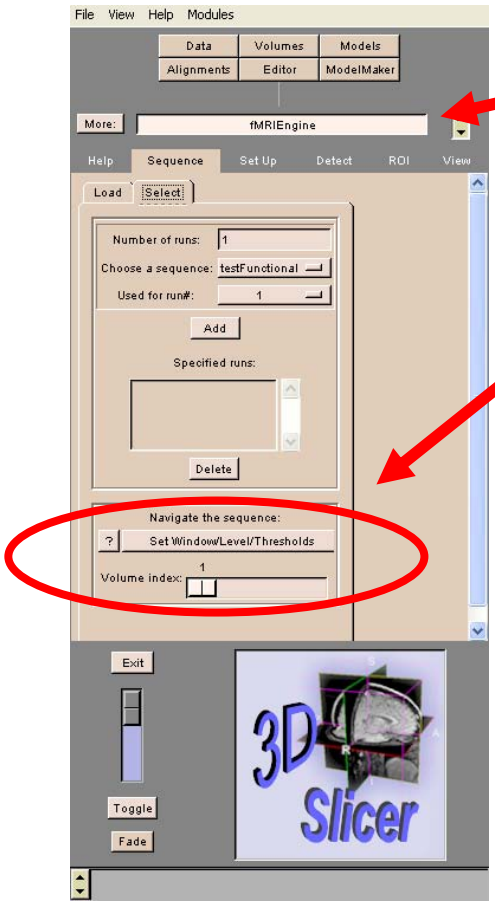

Adjust the low threshold Lo to mask out background

# Set Image Display




The display settings apply to currently viewed image in the sequence only

# Set Sequence Display

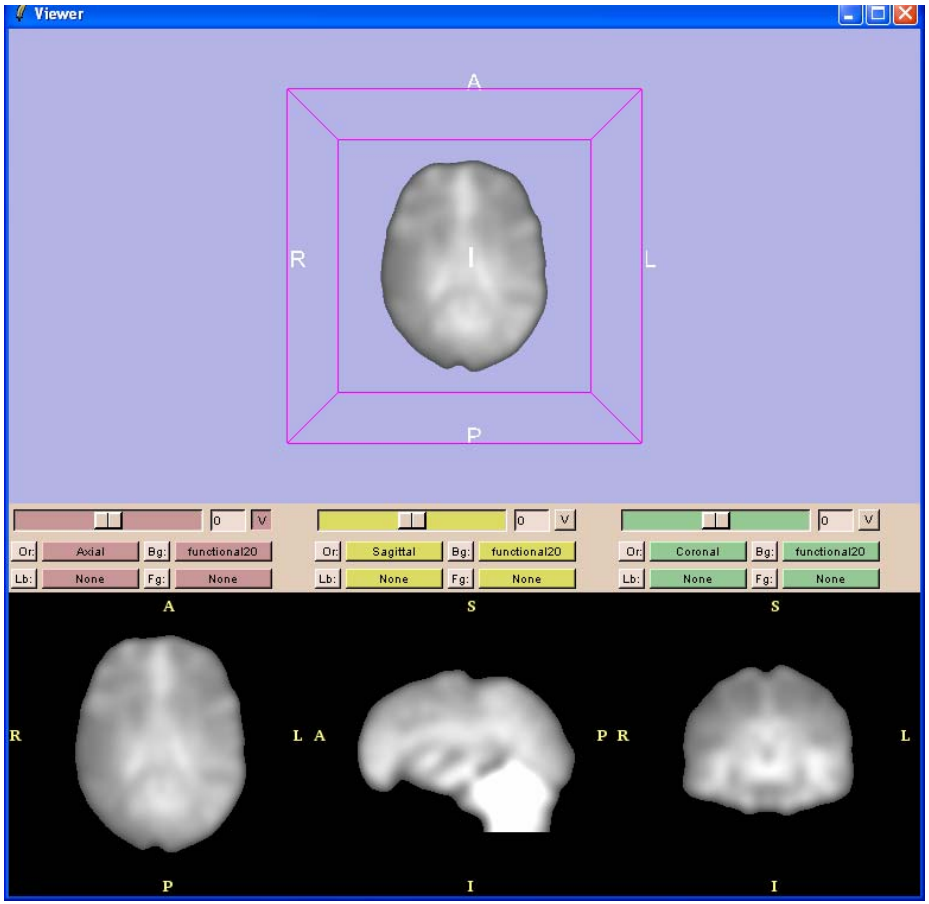



Click on fMRIEngine, select the panel Sequence, and pick the tab Select

Click Set Window/Level/Thresholds to apply to all volumes in the sequence

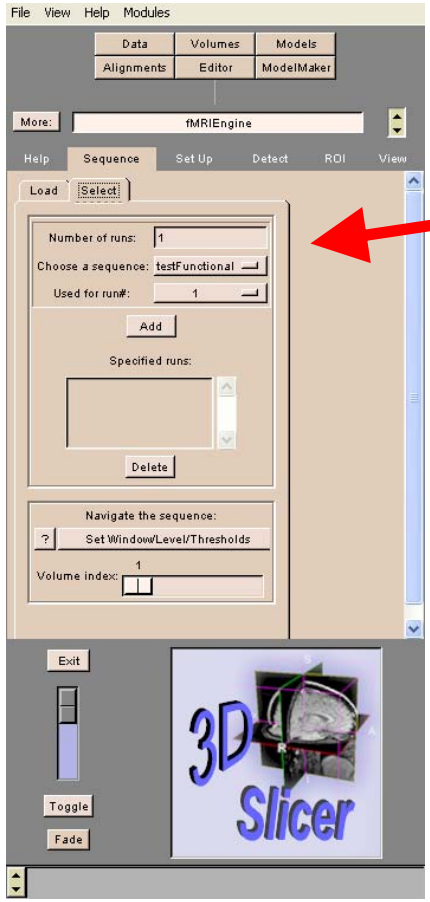
Visually inspect sequence using the Volume index to check for intensities aberrations

# Inspect Image Display




Slicer displays the volumes of the sequence.

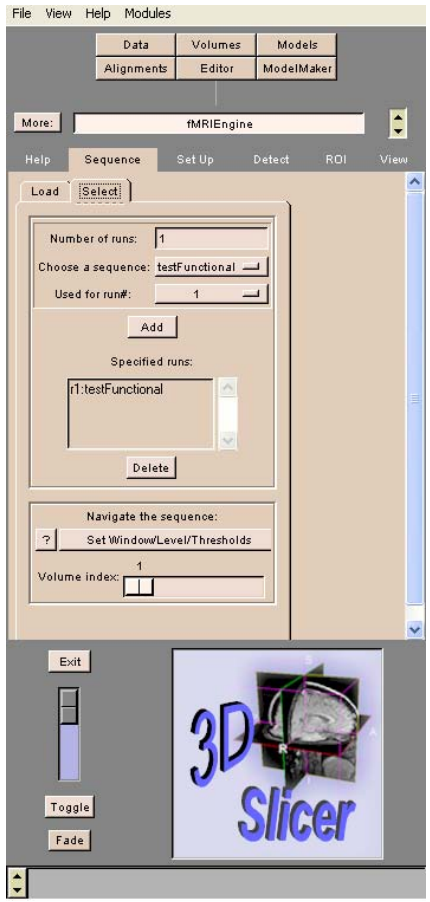
# Select Image Sequence




Specify the number of runs = 1, select the sequence testFunctional

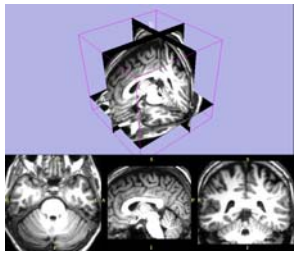
Click **Add** to assign sequence to run 1

# Select Image Sequence

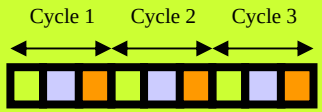



Slicer assigns the sequence to run 1

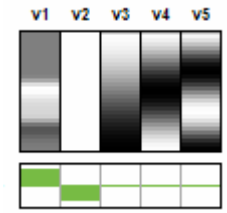
# fMRI Analysis Workflow



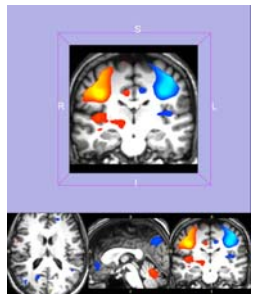
Data Loading



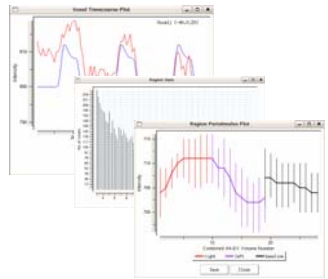

Paradigm Description




Signal Modelling



Activation Detection



Statistical Analysis

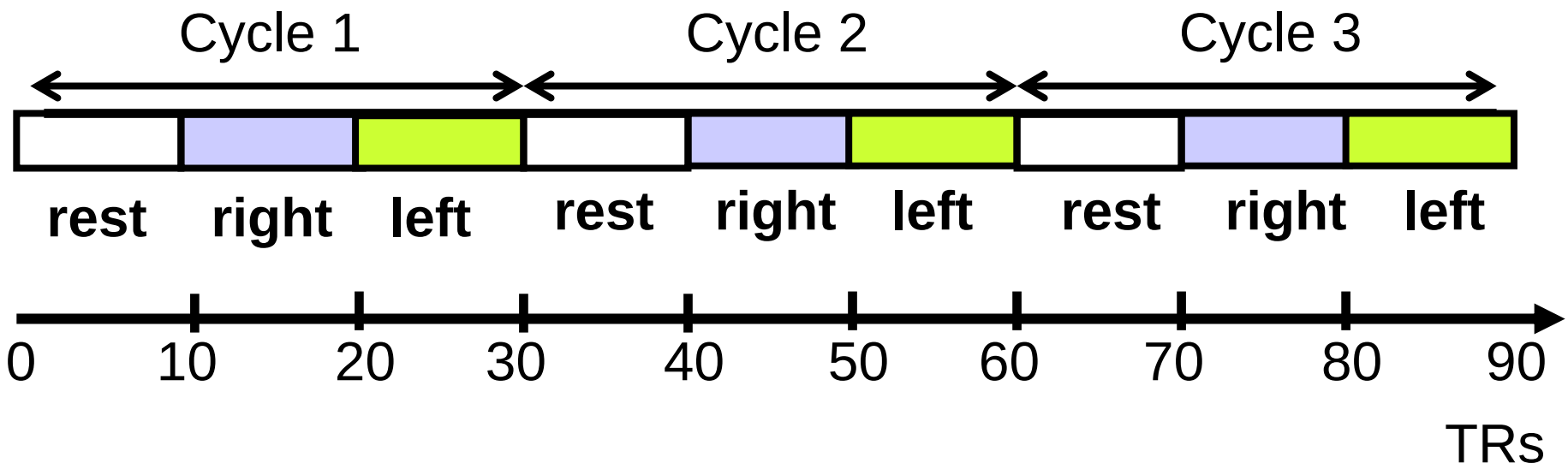
# Paradigm description

- Finger sequencing fMRI task to elicit activation in the hand regions of the primary sensory motor cortex
- Block design motor paradigm
- Subject touches thumb to fingers sequentially within block (thumb touches first through fourth finger)
- Subject alternates left and right hand

# Paradigm design

Three cycles

rest | right hand | left hand



# Paradigm timing parameters

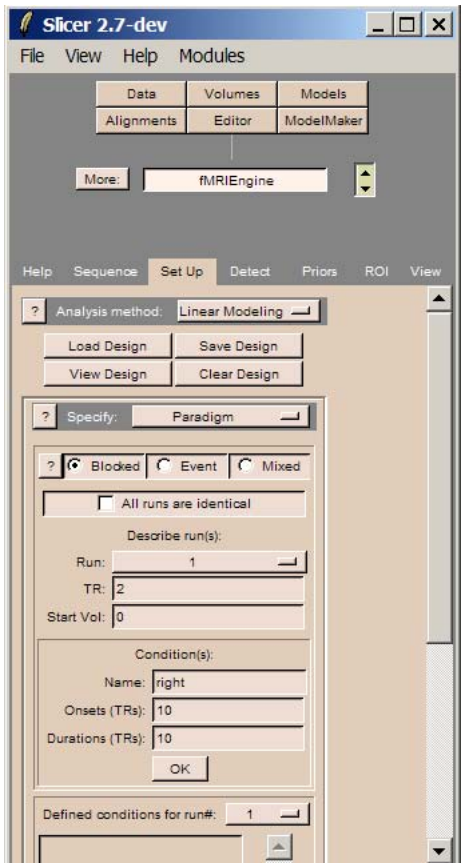
- Repetition Time TR = 2s
- Durations: 10 TRs in all epochs
- Onsets (in TRs):

Rest: 0 30 60

Right: 10 40 70

Left : 20 50 80

# Stimulus schedule




Pick Set Up Tab in the fMRIEngine and choose the Linear Modeling detector

# Linear Modeling

The General Linear Modeling is a class of statistical tests assuming that the experimental data are composed of the linear combination of different model factors, along with uncorrelated noise

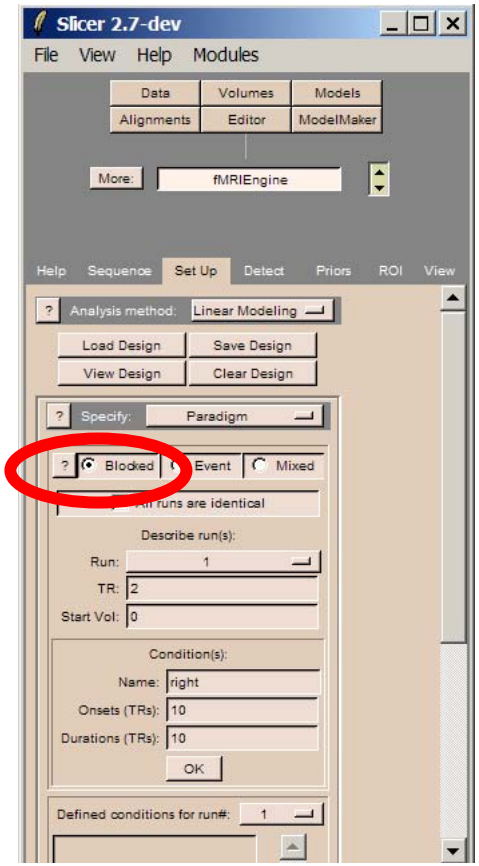
$$Y = BX + e$$

B = set of experimental parameters

Y = Observed data

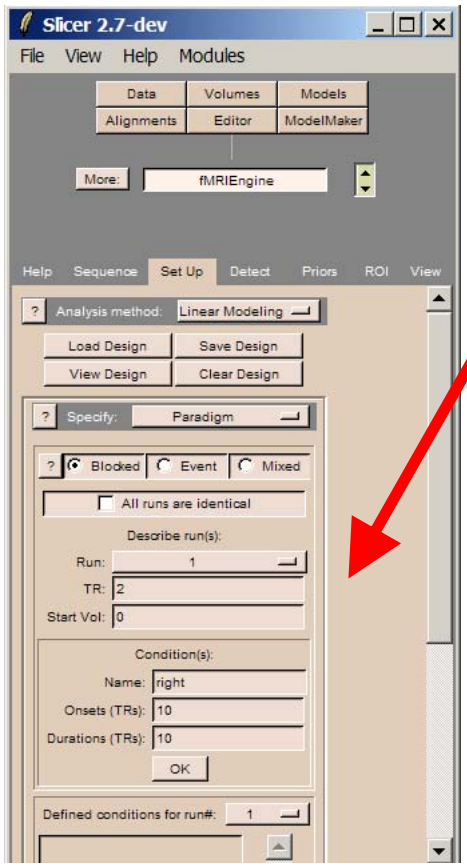
X = Design Matrix e = noise

# Stimulus schedule



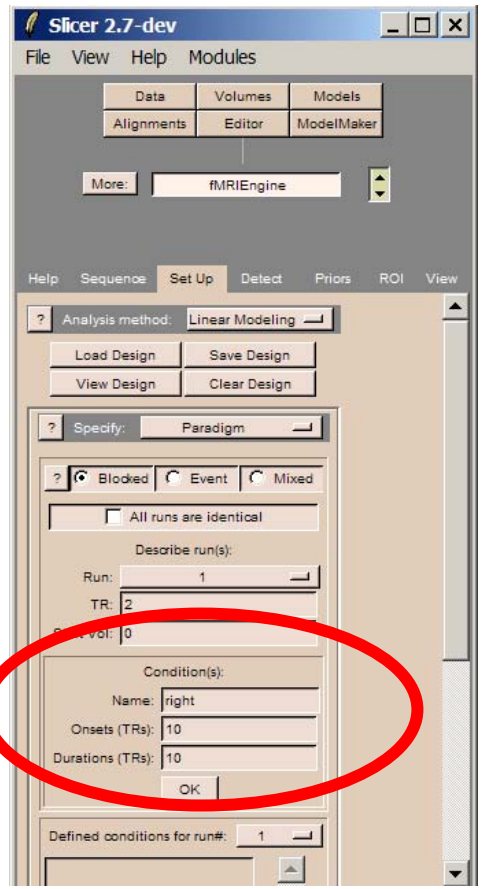

Select the design type
Blocked

# Stimulus schedule




Enter the characteristics of the run
TR = 2 and Start Volume = 0 (ordinal number)

# Stimulus schedule




Enter the schedule for the first condition:

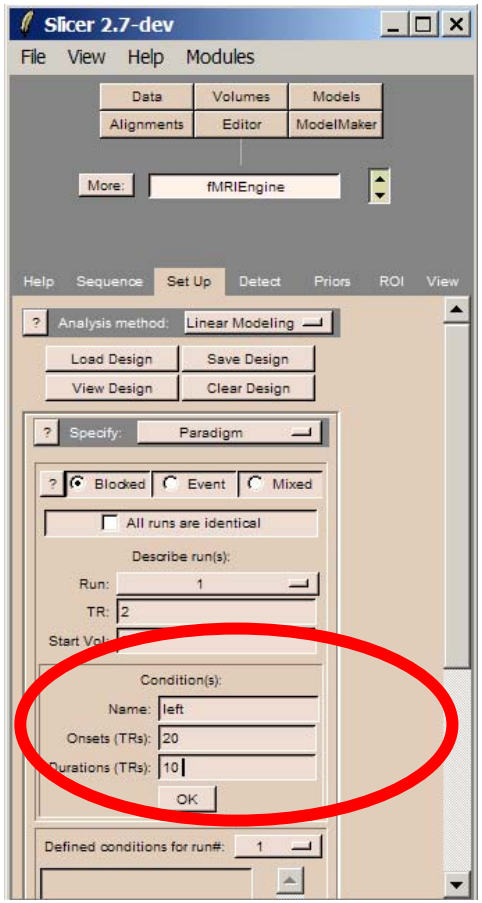
Name = right

Onset = 10

Durations = 10

Click on OK to add this condition to the list of defined conditions

# Stimulus schedule




Enter the schedule for the second condition:

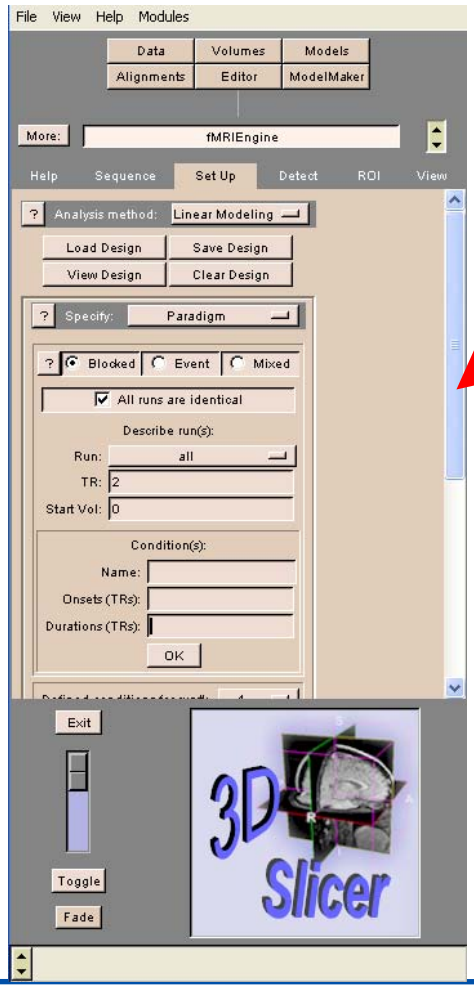
Name = left

Onset = 20

Durations = 10

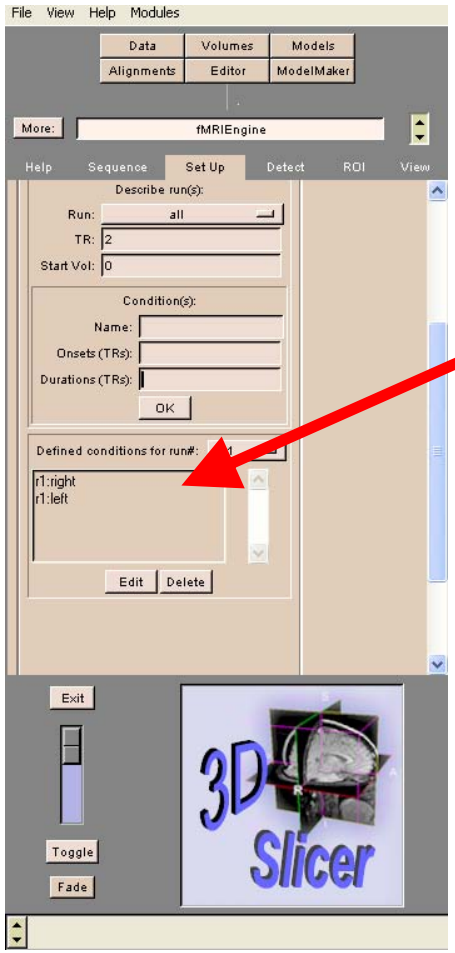
Click on OK to add this condition to the list of defined conditions

# Stimulus schedule



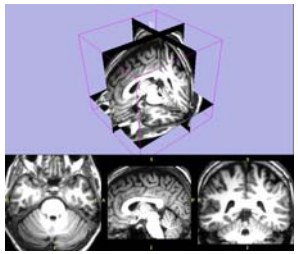

Scroll down in the Set-up panel to see the list of defined conditions

# Editing the Stimulus schedule

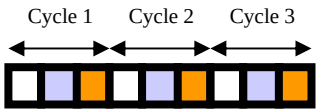



The list of specified conditions appears in the left panel

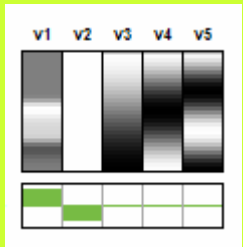
# fMRI Analysis Workflow



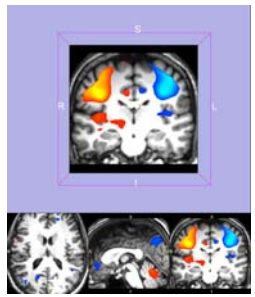
Data Loading



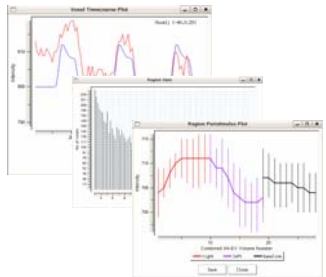

Paradigm Description




Signal Modelling

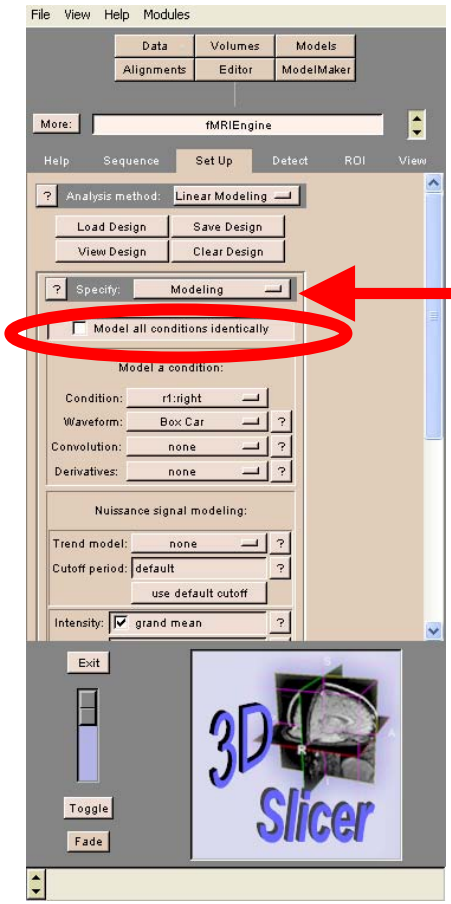


Activation Detection



Statistical Analysis

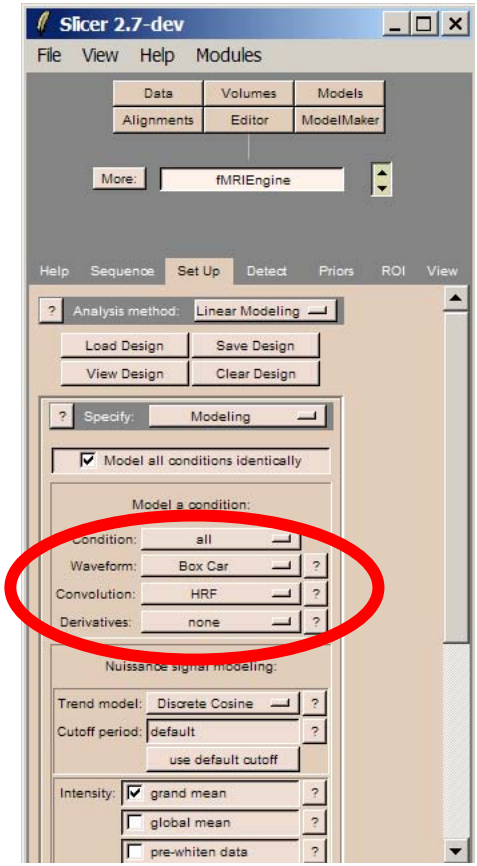
# Model a Condition




Select Specify Modeling

Click on Model all conditions identically

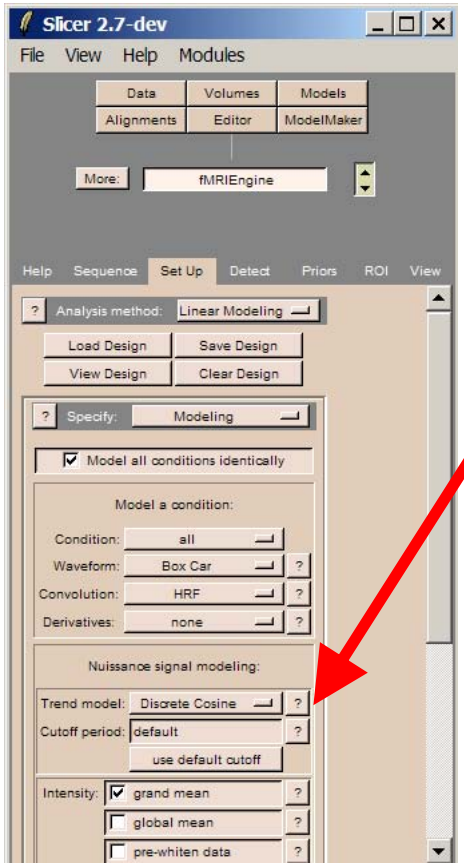
# Model a Condition




Select
- Condition: all
- Waveform: BoxCar
- Convolution: HRF

(Hemodynamic Response Function)
- Derivatives: none

# Nuisance Signal Modelling



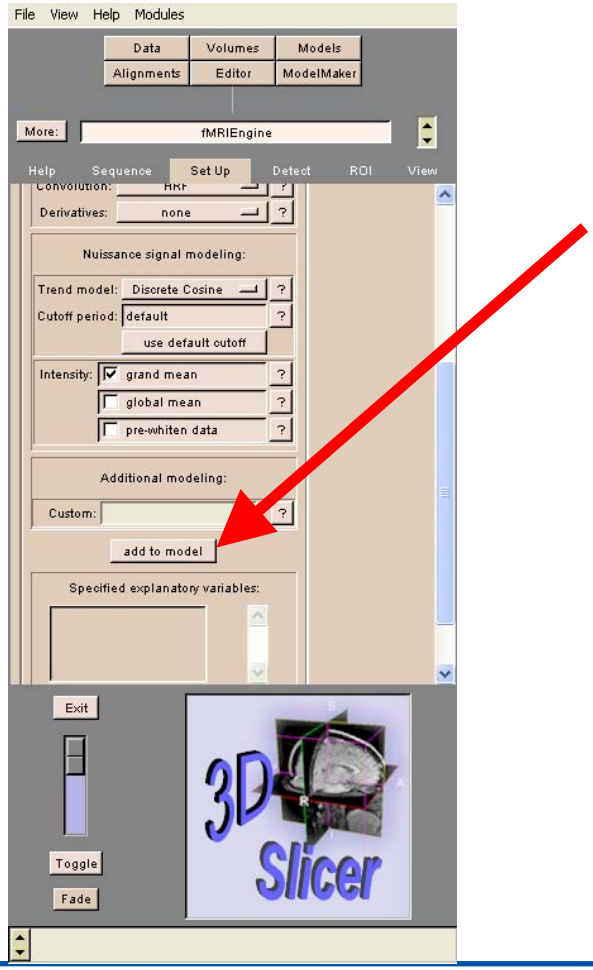

On the subpanel Nuisance signal modeling, select

Trend model: Discrete Cosine

Cutoff period: default

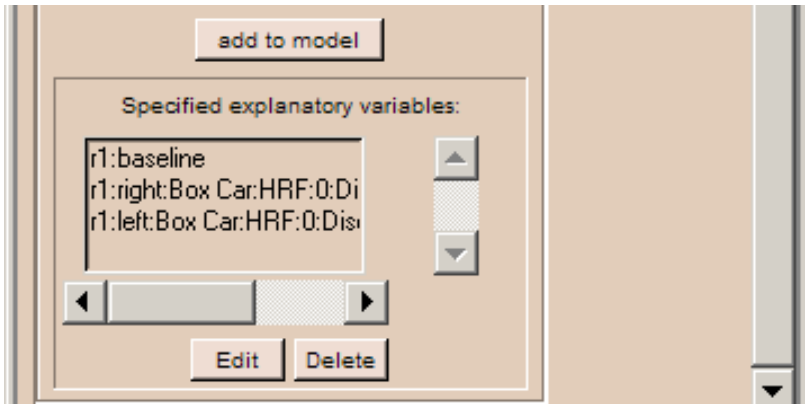
Click on use default cutoff

# Nuisance Signal Modelling



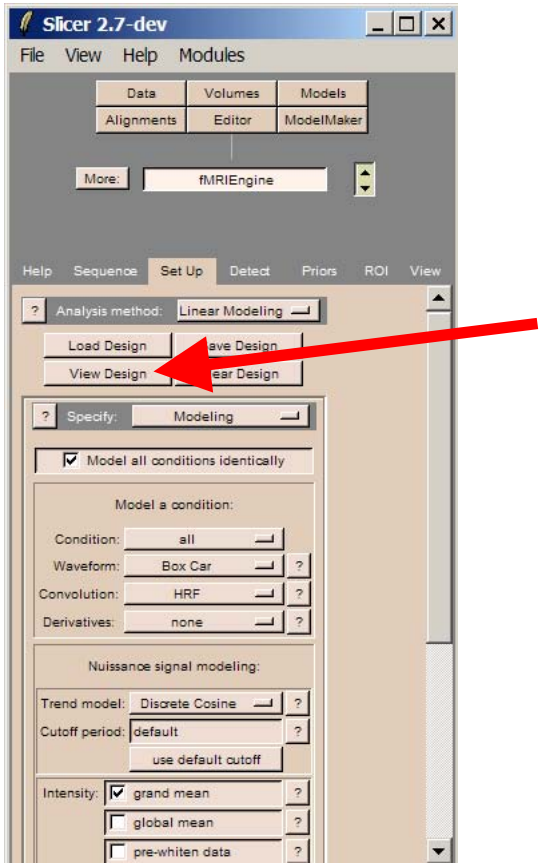

Scroll down in the Set Up panel and click on add to model

# Nuisance Signal Modelling



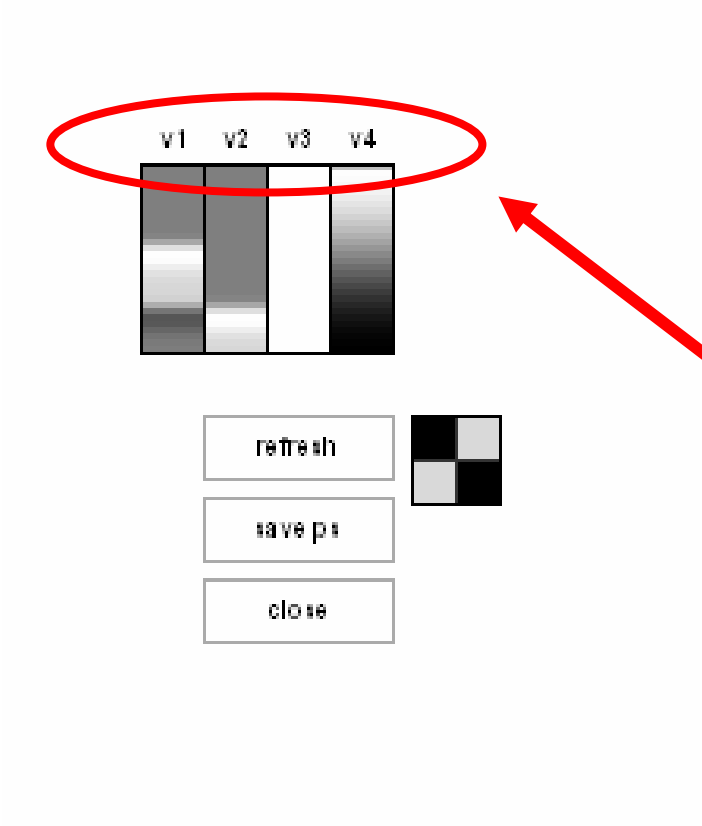

The list of explanatory variables (EV) appears in the left panel, including the baseline that is automatically added. The strings are Slicer specific representations of the model.

# View Design Matrix




Click View Design to display the design matrix

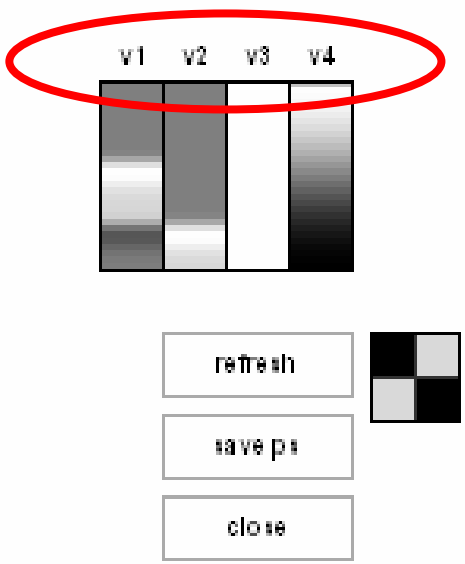
# Design Matrix




A window displaying the model design appears.

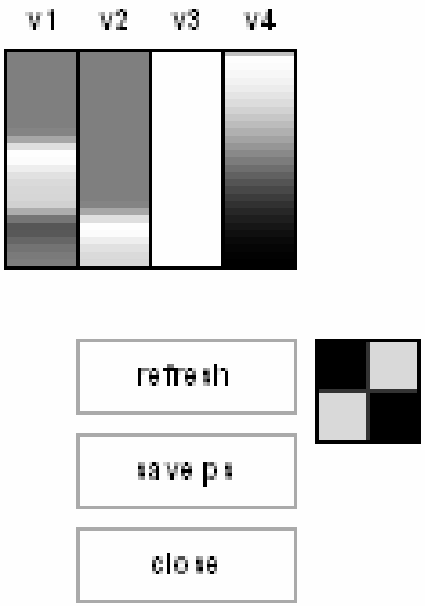
Move the mouse from left to right over the columns of the matrix to display the characteristics of the modelled conditions.

# Design Matrix




v1 = right finger tapping
v2 = left finger tapping
v3 = baseline
v4 = low frequency noise

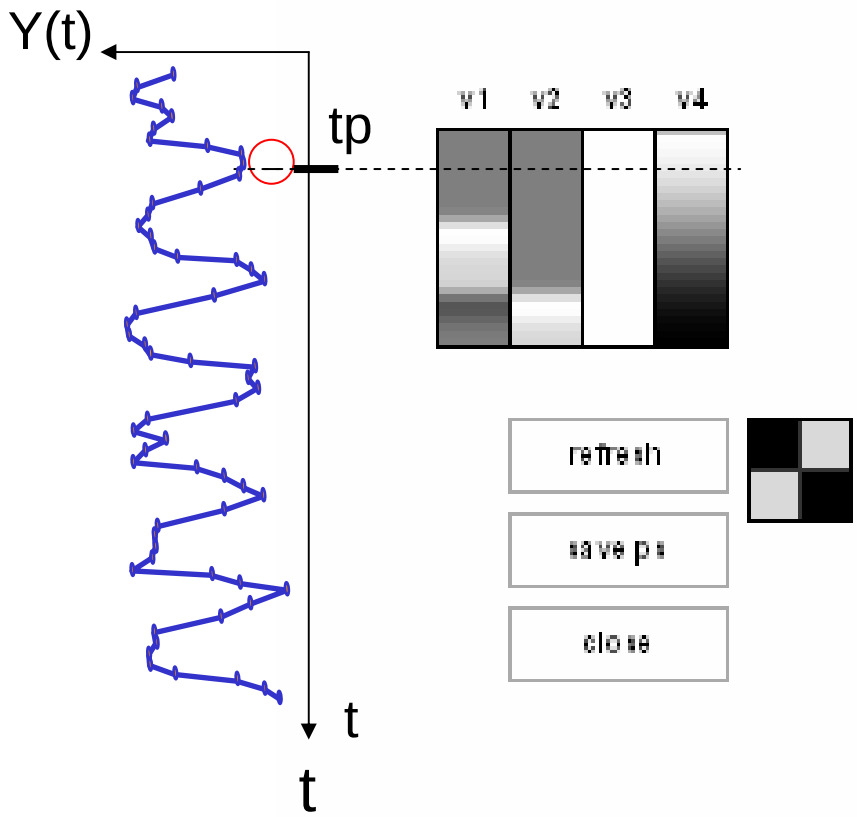
# Design Matrix




Observe the different values of the signal intensity in the matrix.

White → positive signal intensity 1
Mid-Grey → null intensity 0
Black → negative intensity - 1

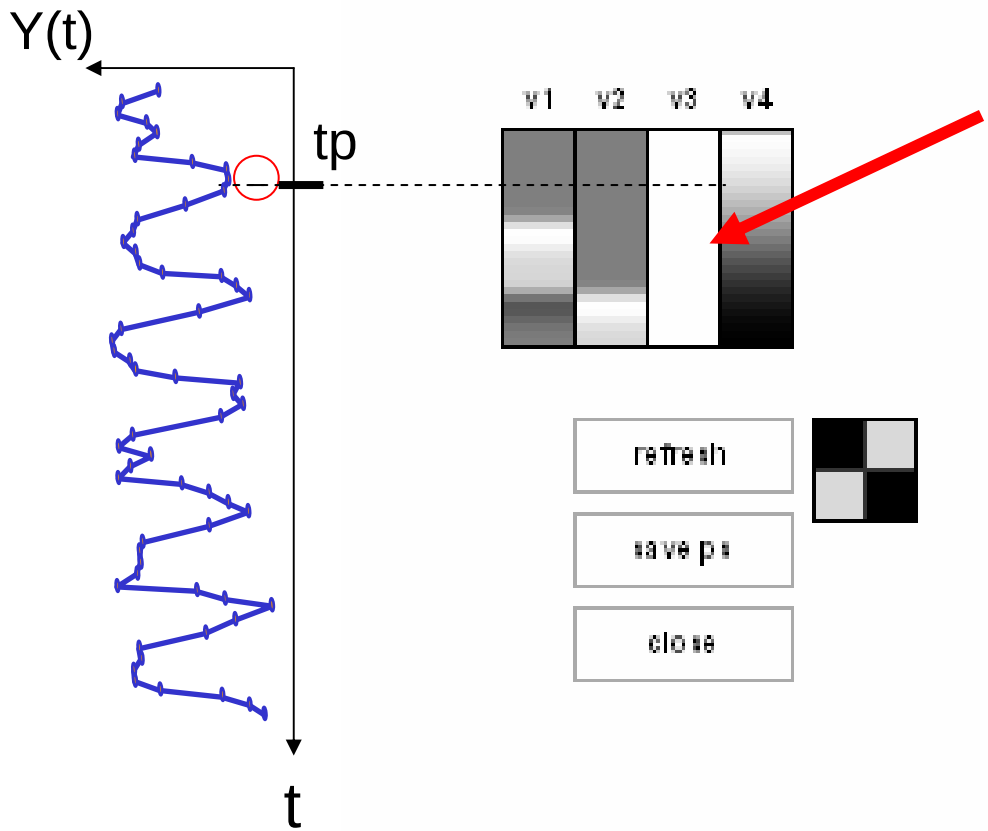
# Design Matrix




Each column represents the contribution from each condition we might see in a voxel time course.

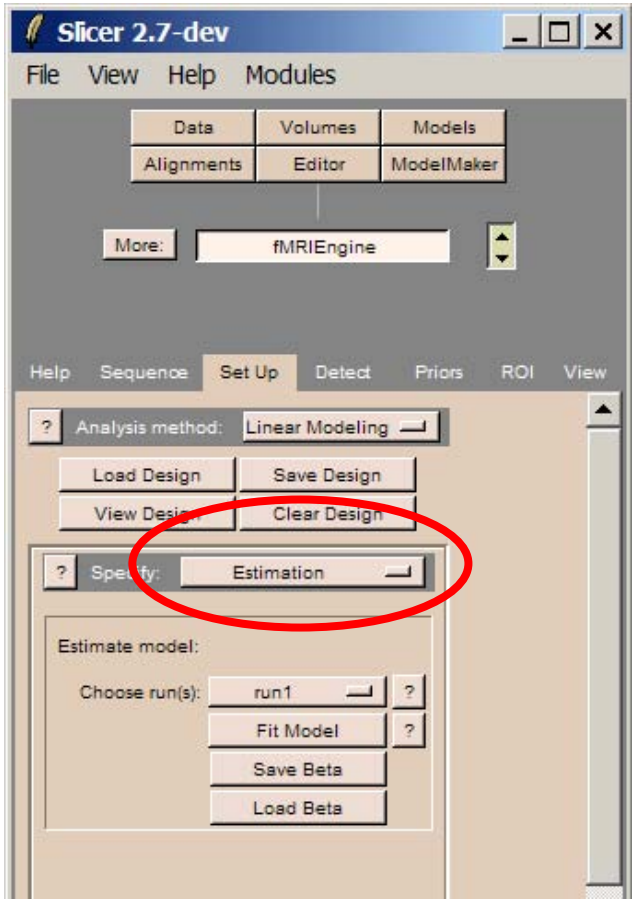
Modelled Signal Y = BX + e

# Design Matrix




Move the mouse up and down to browse the different volumes associated with the time points.

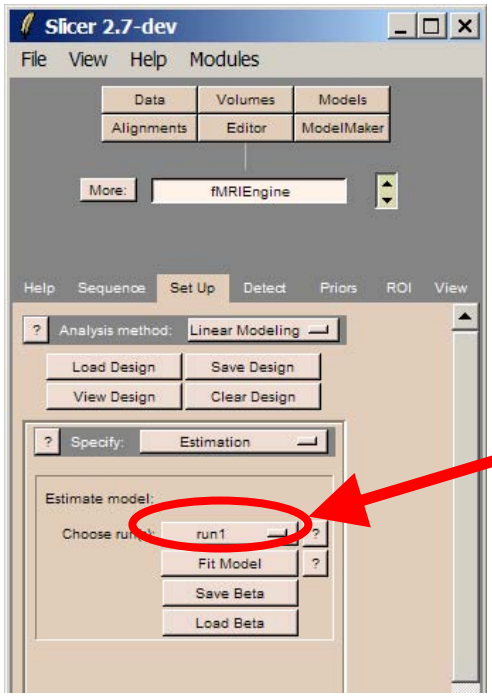
# Estimation




Select Specify Estimation to estimate B and e at every voxel:

$Y = BX + e$

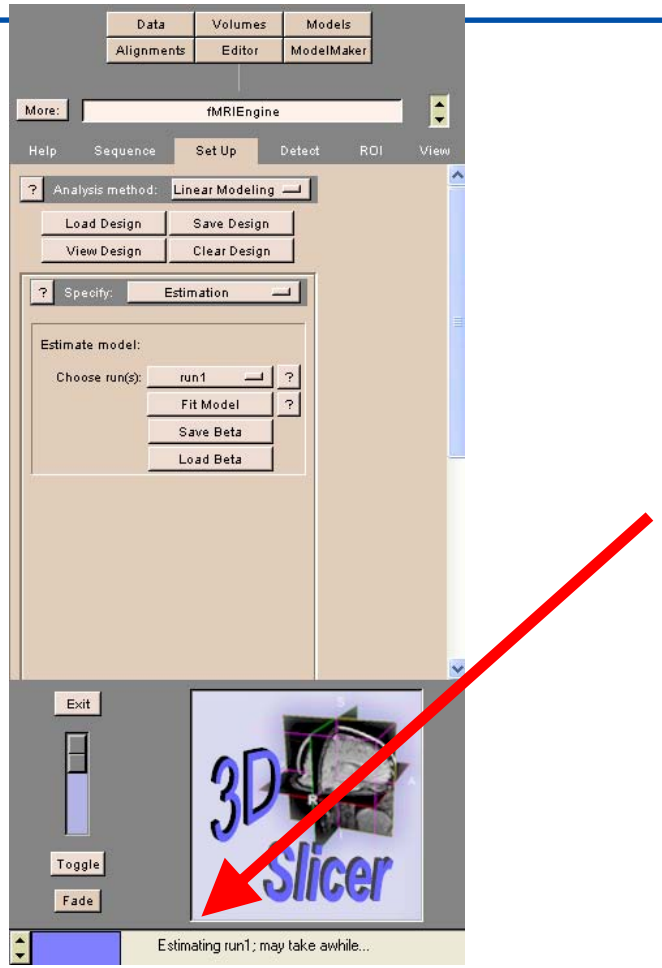
# Estimating model parameters




The Estimation panel appears

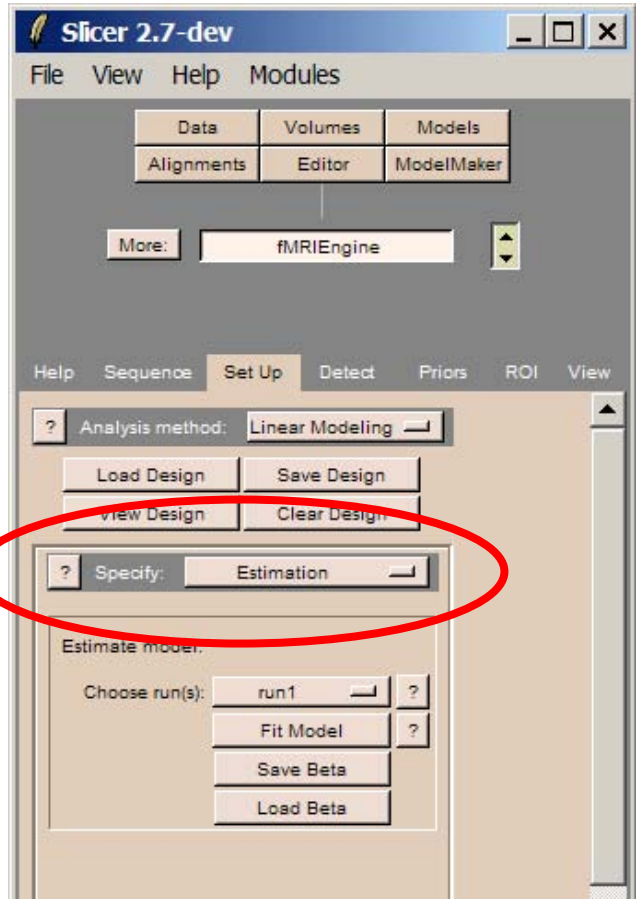
Select run1 and click on Fit Model

# Estimating model parameters



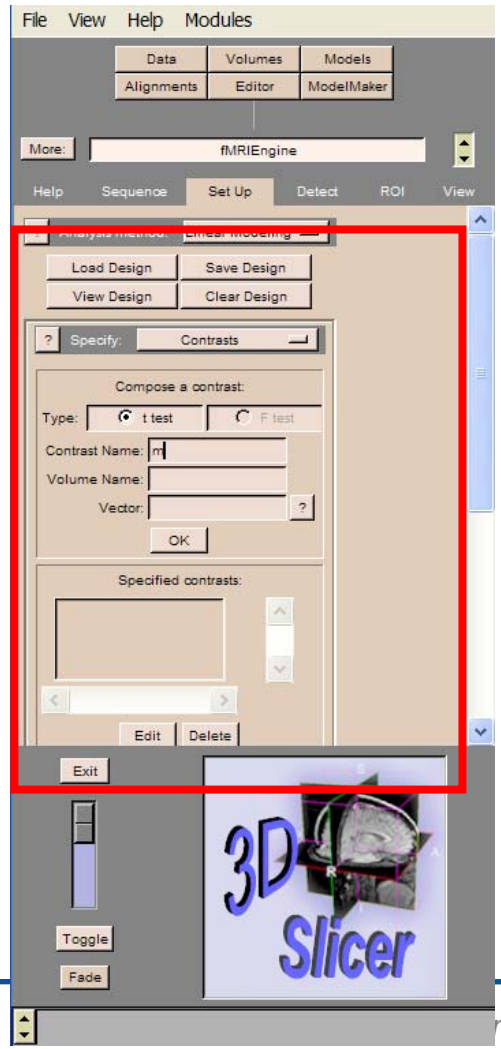

Slicer shows the progress of model estimation

# Specify Contrasts



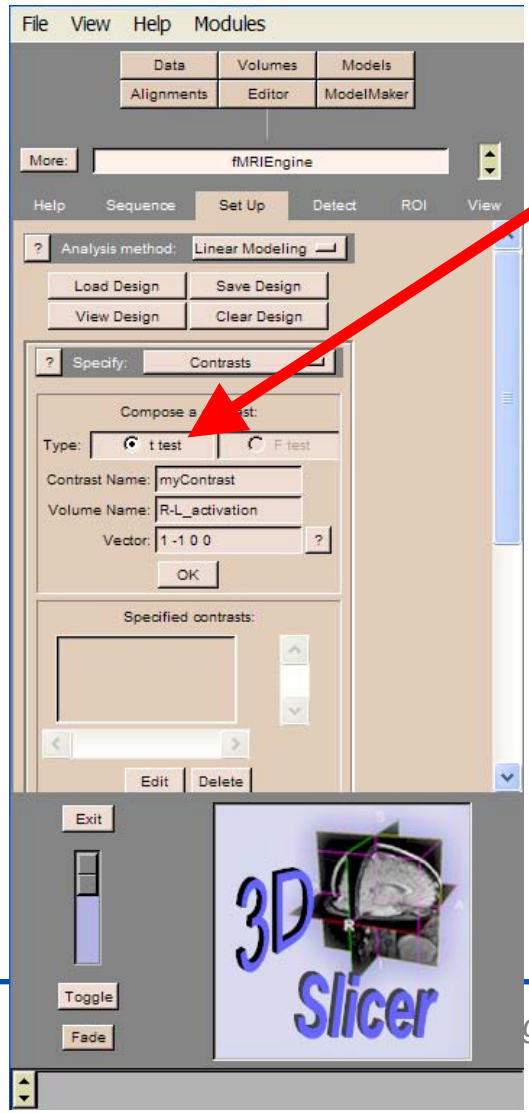

In the SetUp panel, select Specify → Contrasts

# Specify Contrasts




The Panel for the contrasts appears

# Specify Contrasts




Choose the contrast type *t-test*

Enter the contrast name myContrast, and the Volume Name R-L_activation

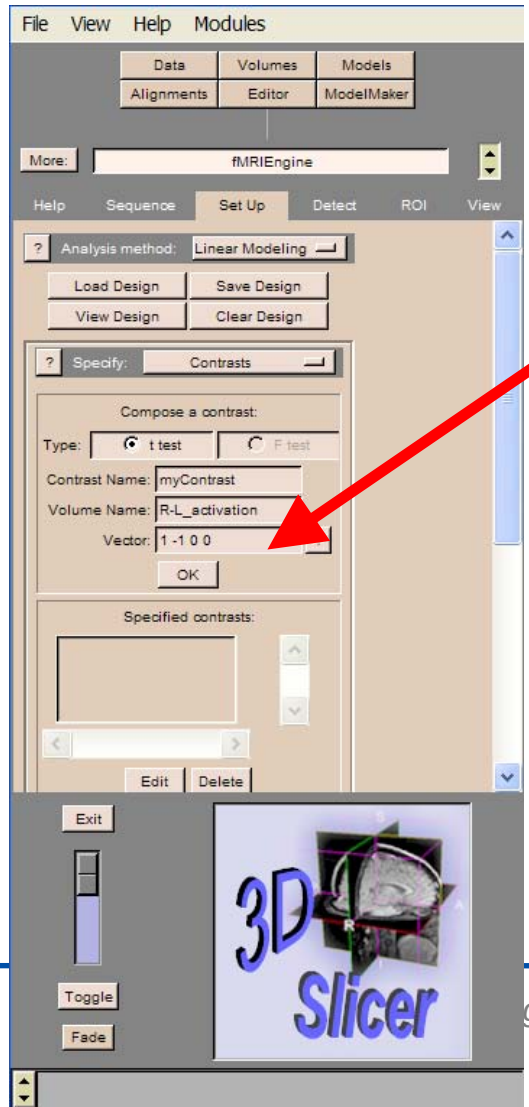
# Contrast Vector

- Encoding of the effect that you want to test
- A contrast component per column in the design matrix ( trailing zeros may be omitted)

  1 0 0 0 → test for whether there is any effect for the right hand

  1 -1 0 0 → statistically contrast the effect for the right and left hand

# Specify Contrasts

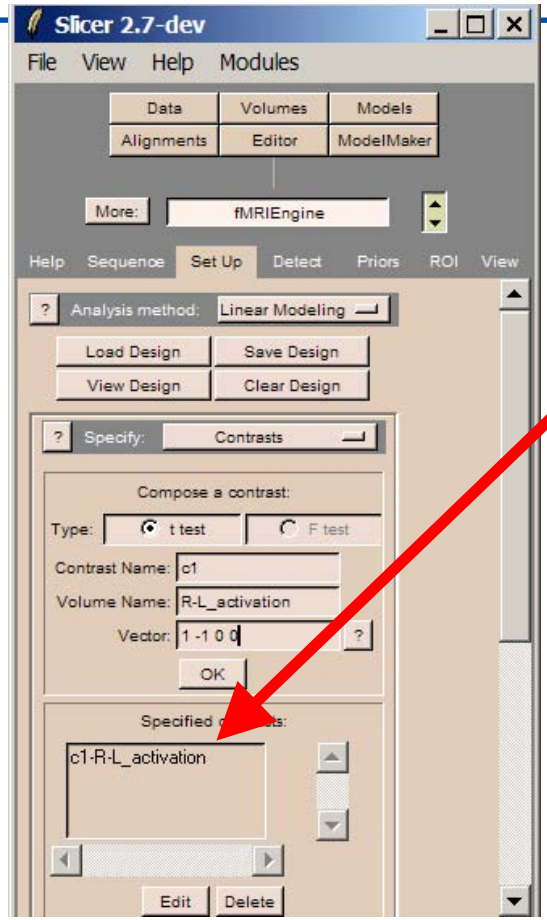



Select the statistical test t-test

Specify the contrast vector 1 –1 0 0 (enter a space between the values)

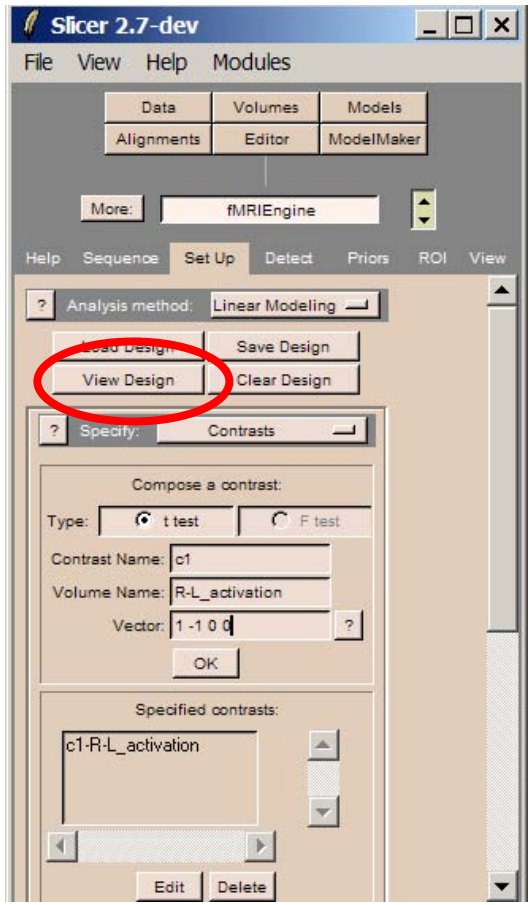
Click OK to add this contrast to a list of defined contrasts

# Specify Contrasts




The resulting contrast named myContrast-R-L_activation appears in the list of specified contrasts.

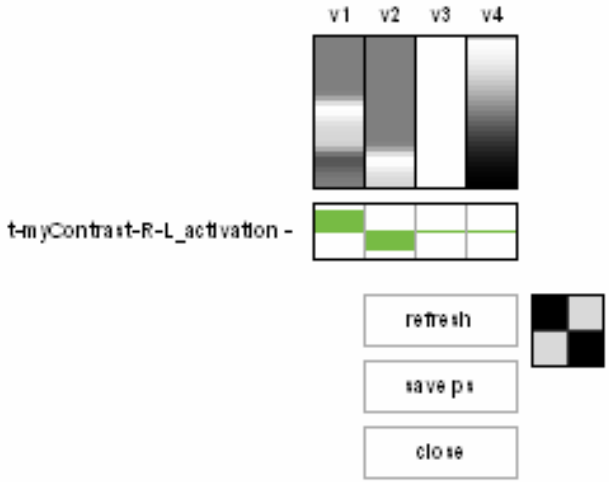
# Check contrasts & model




Click on View Design to display the Design matrix

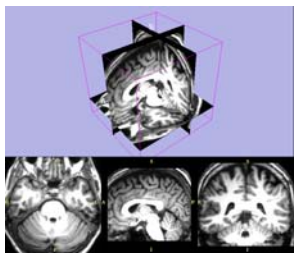
# Design Matrix

A window displaying the design matrix and contrast vector appears.

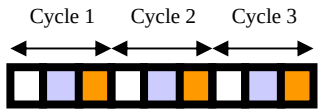



Check that the contrast and model are correct.

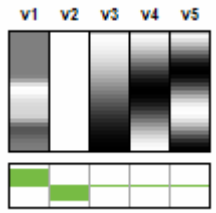
# fMRI Analysis Workflow



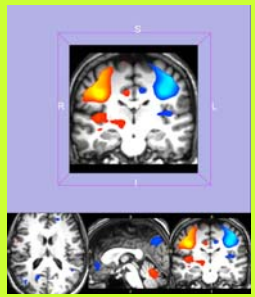
Data Loading



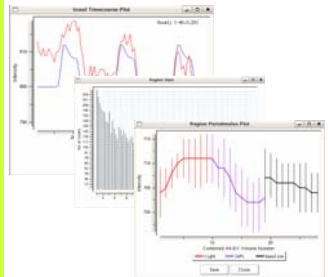

Paradigm Description




Signal Modelling

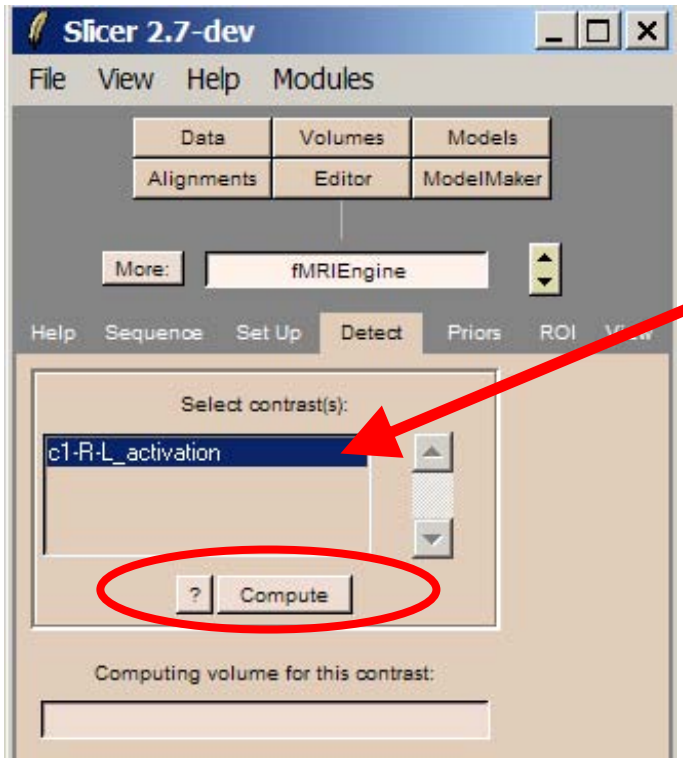


Activation Detection



Statistical Analysis

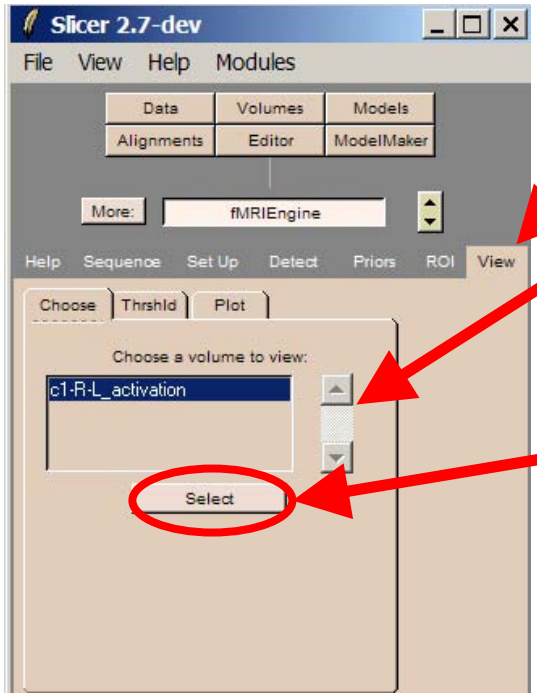
# Perform activation detection




Click on the tab Detect and select the contrast myContrast-R-L_activation

Click on Compute to compute the statistical map of activation (t-test)

# Select the activation volume

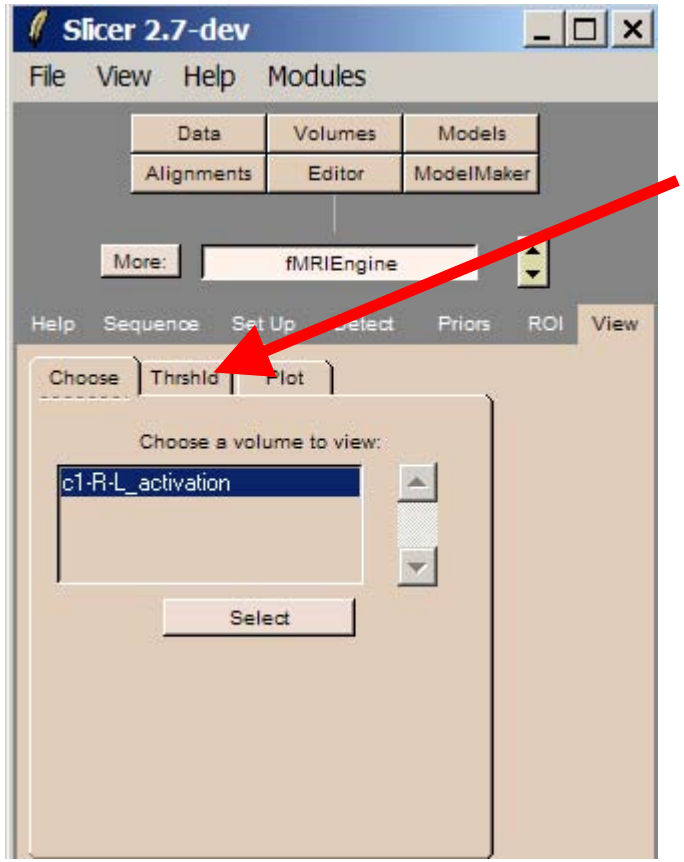



Click on the View Tab

Select the resulting activation volume (t-map) myContrast-R-L_activation

Click on Select

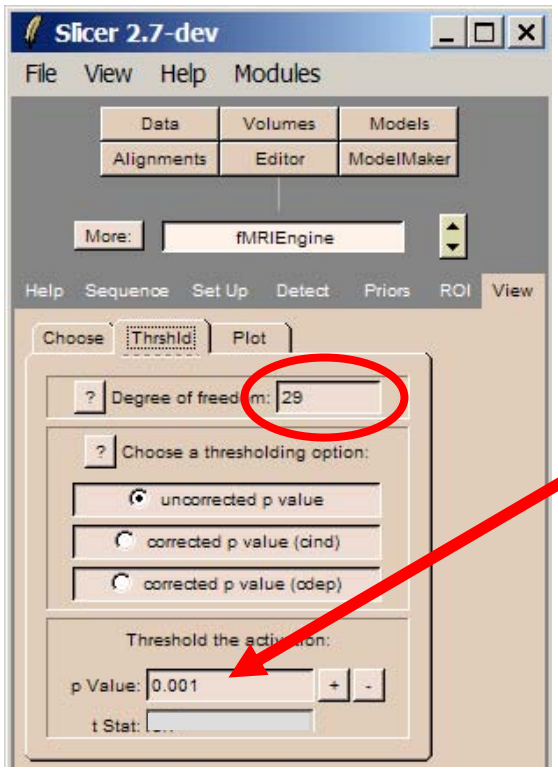
# Threshold




Click on the Thrshold Tab

# Threshold

Slicer indicates the degree of freedom (DoF): Nvol-1=29




Enter the p-Value 0.001

and hit ENTER

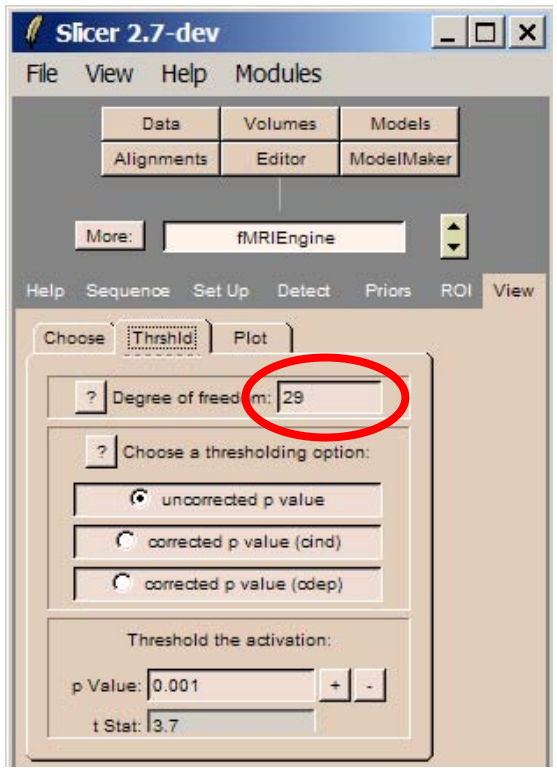
# Null hypothesis

- H0: the difference between the right hand condition and left hand condition has no consequence on the fMRI signal.

- If the resulting probability is lower than the experiment's alpha value ($p < 0.001$), the null hypothesis can be rejected.

# Threshold

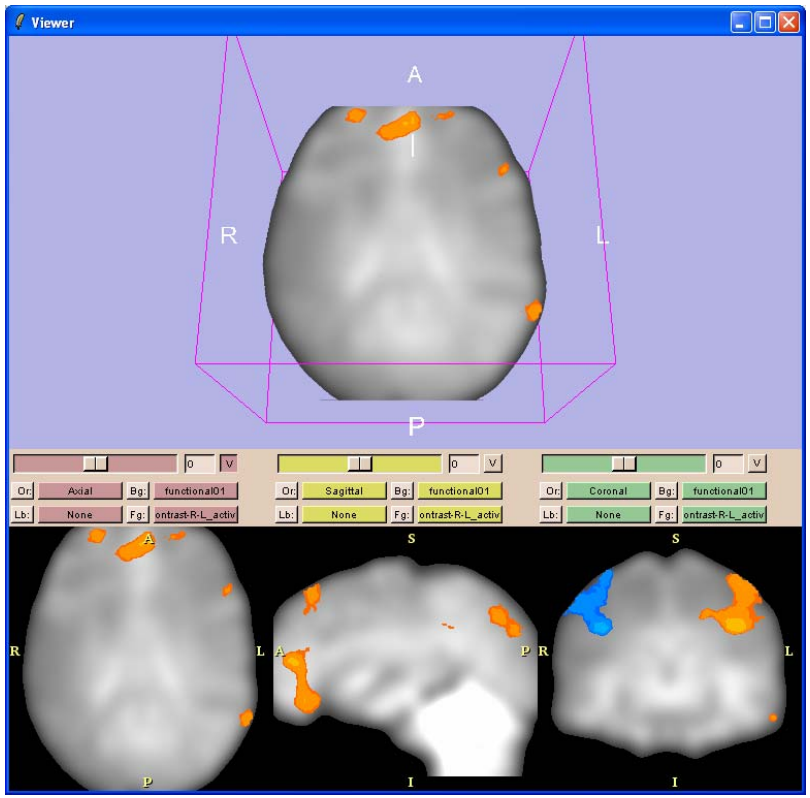
Slicer calculates the corresponding threshold t Stat



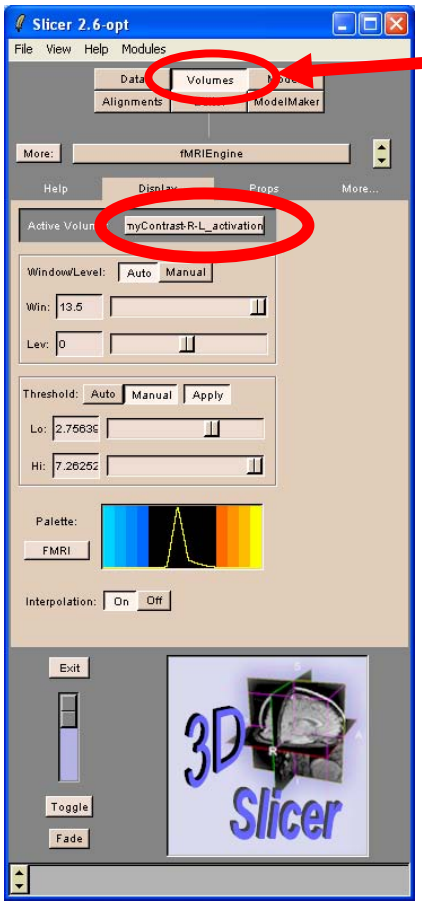

t Stat = 3.7

# Activation map

The activation map is superimposed on the fMRI images.



# fMRI color palette

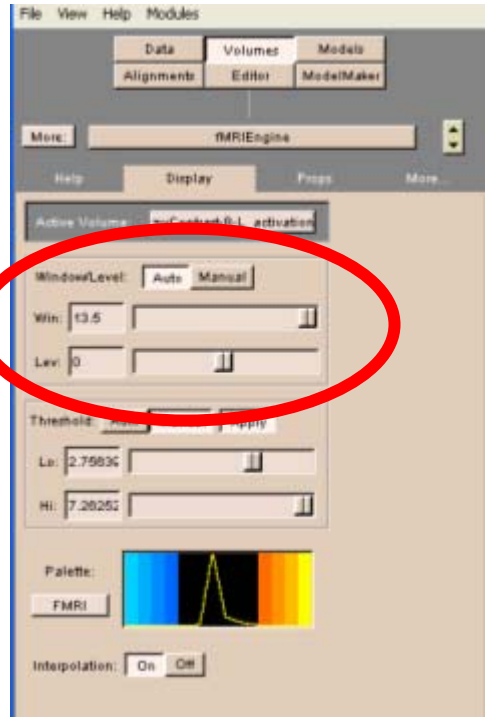



Click on the module Volumes

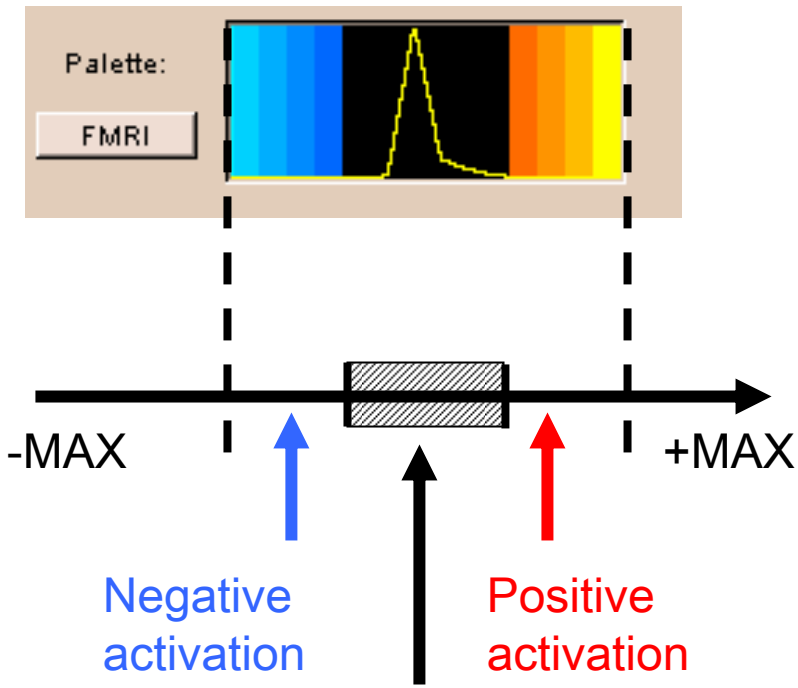
Select the panel Display
and set the Active Volume to be
the activation volume
myContrast-R-L_activationMap

# fMRI color palette

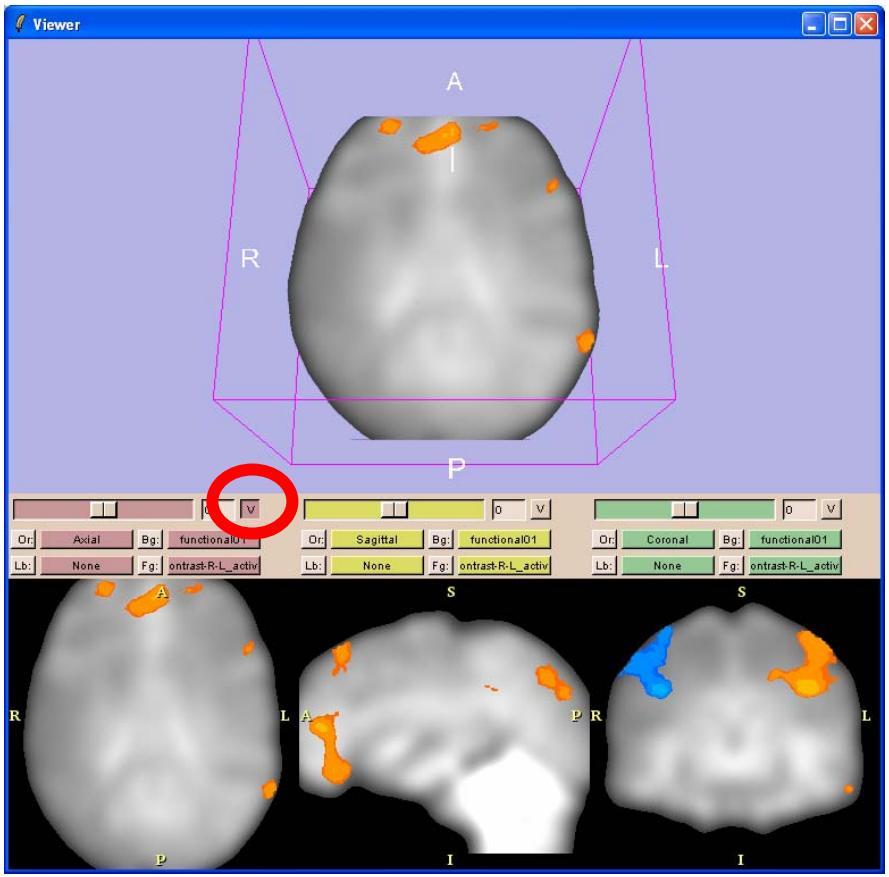
Adjust the Window and Level of the color palette for the volume myContrast-R-L_activationMap



# fMRI color palette



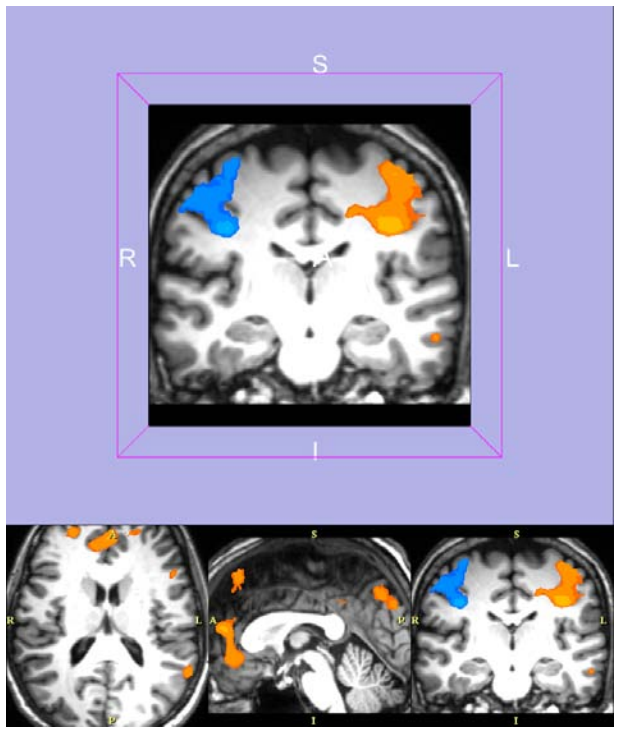
# Visualize



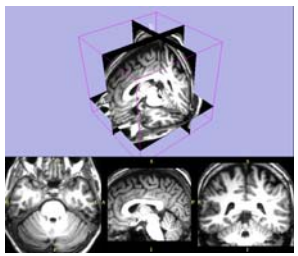

Left click on Bg in the 2D anatomical viewers to display the volume anatomical 3T in background

# Visualize

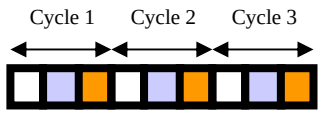
The activation map is superimposed on the anatomical images.



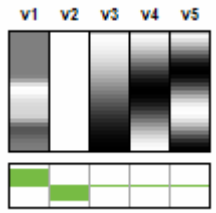
# fMRI Analysis Workflow



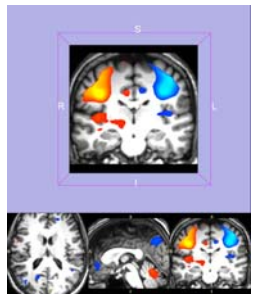
Loading



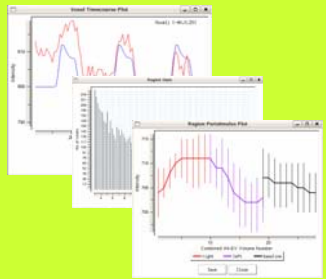

Paradigm Description




Signal Modelling

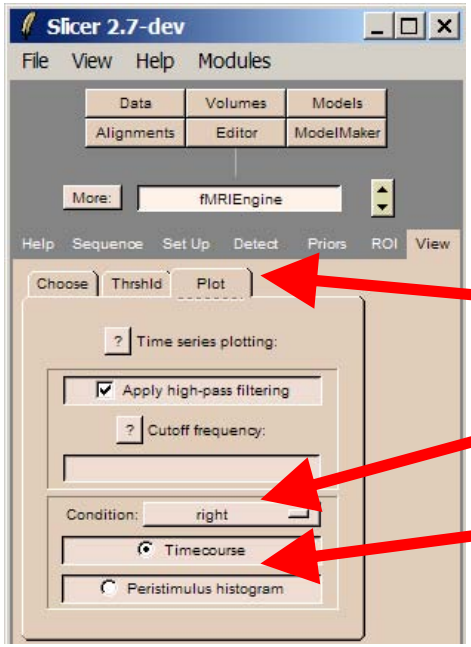


Activation Detection



Statistical Analysis

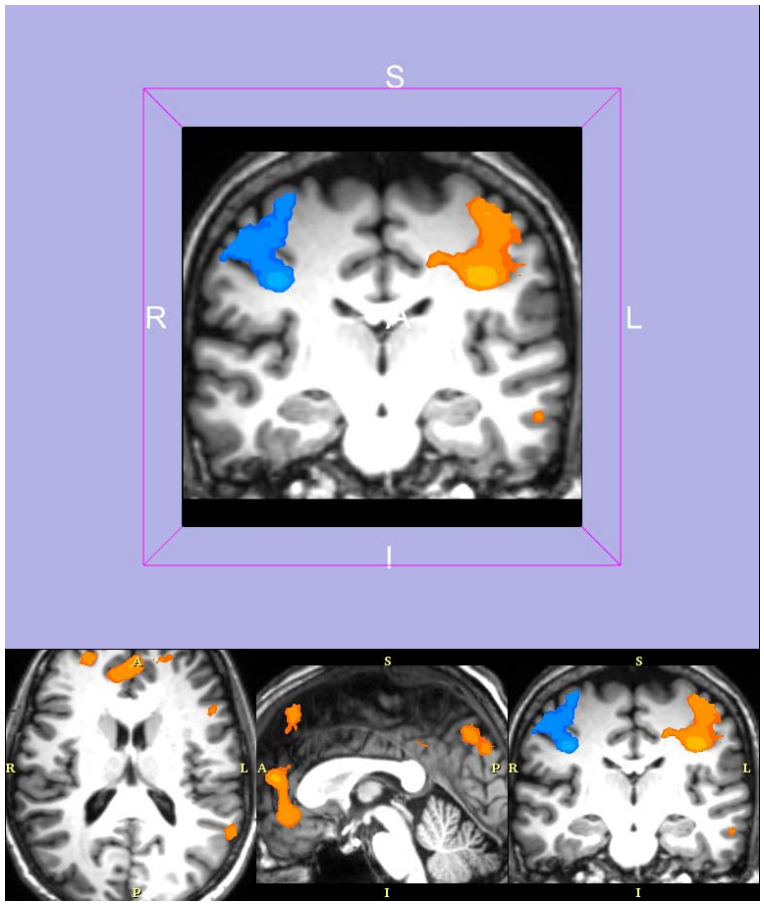
# Threshold, visualize, inspect




Pick the tab Plot and select the condition = right

Select the plot option Timecourse

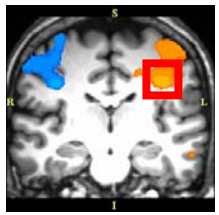
# Voxel Timecourse

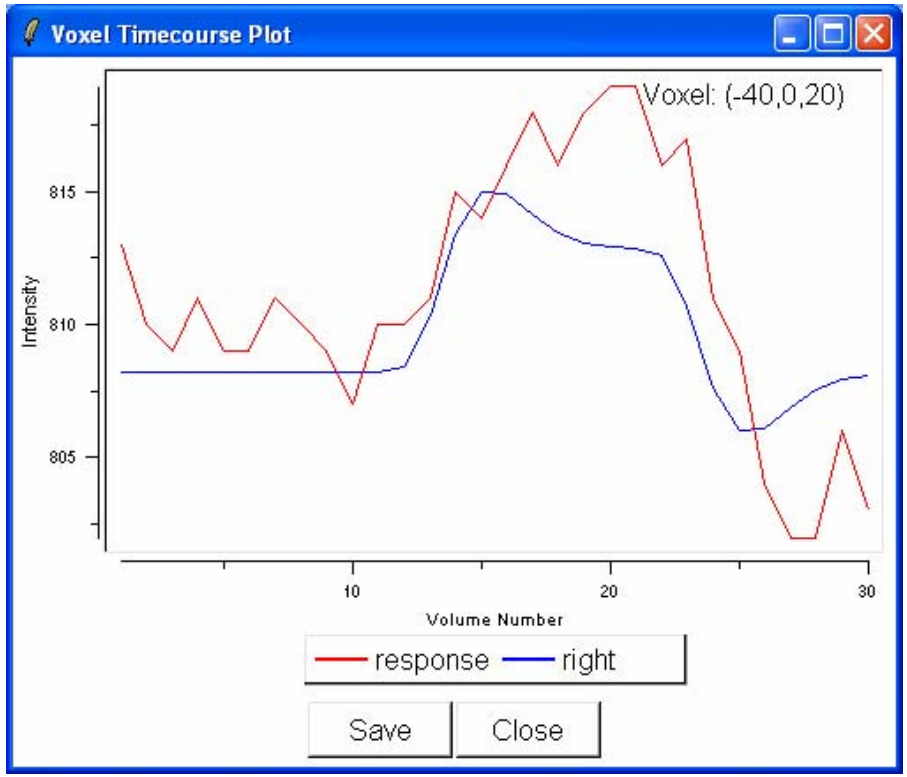



Position the mouse on a pixel located in the activation map in the 2D anatomical views.

# Voxel Timecourse

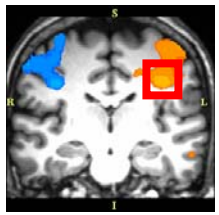
The voxel's timecourse plotted with the modelled condition for the selected voxel appears.

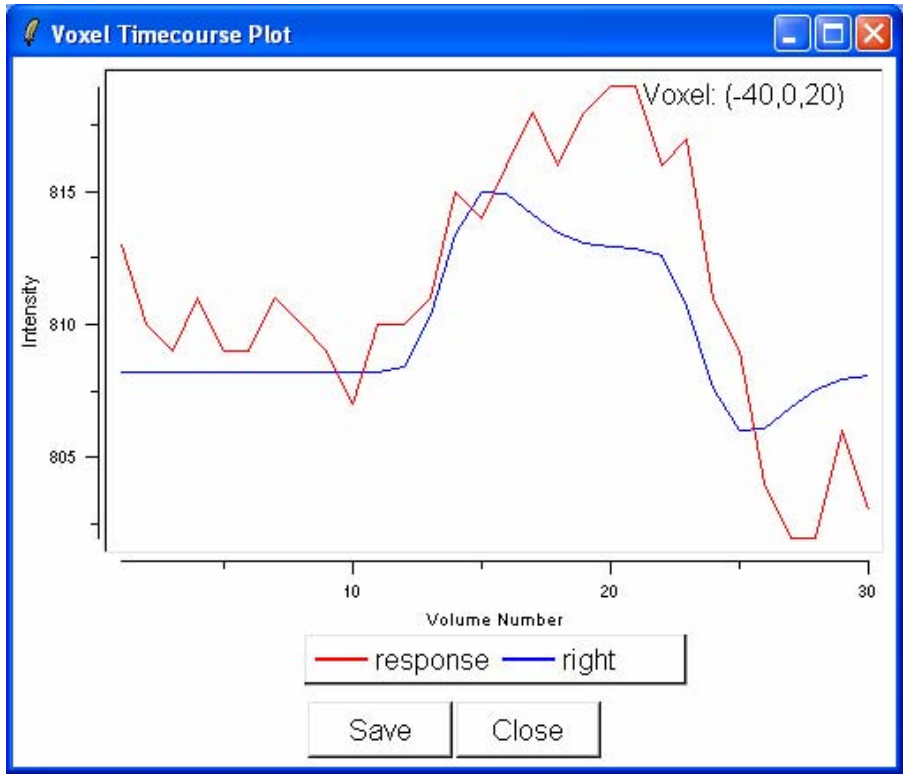




# Voxel Timecourse

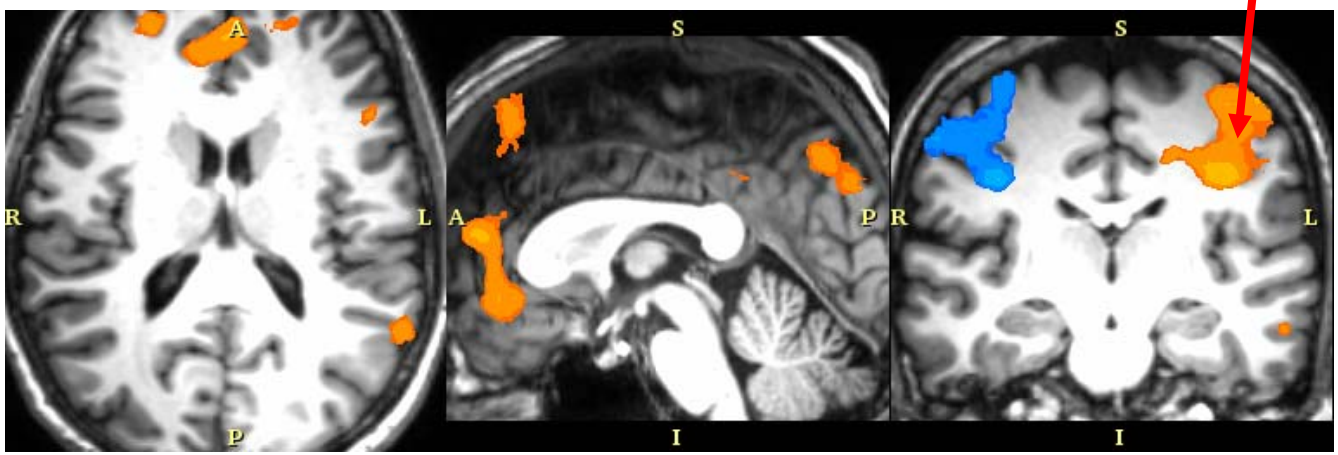
The graphs show a good correlation between the observed BOLD signal Y(t) and the model.



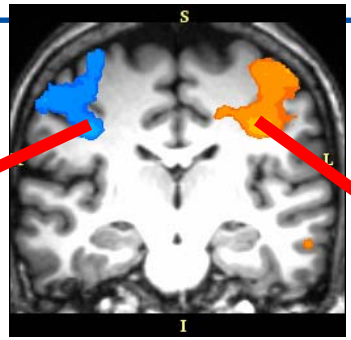


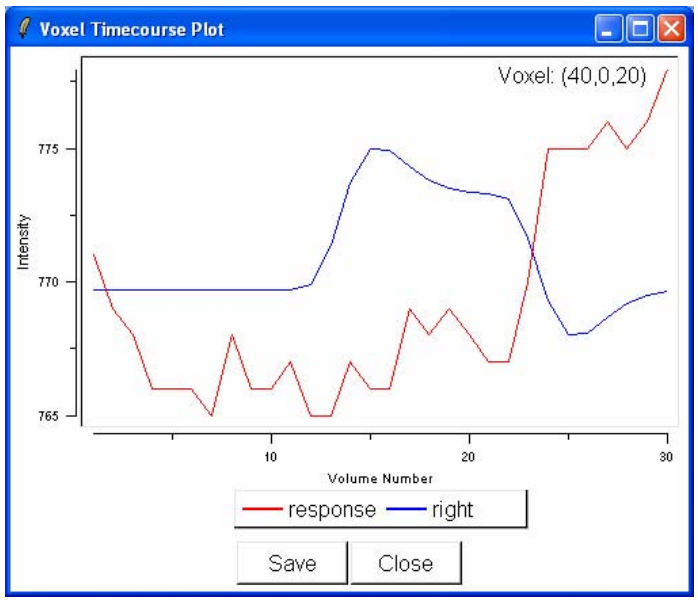
# Threshold, visualize, inspect

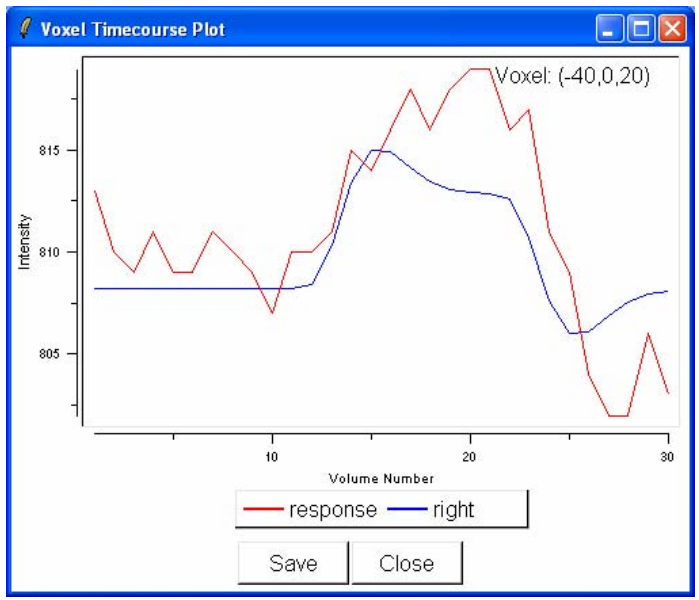
Mouse over labelled area in Slice Window and left click on the pixel R = 40 A = 0 S = 20, which is low responder in the activation map



# Contralateral side vs Ipsilateral side

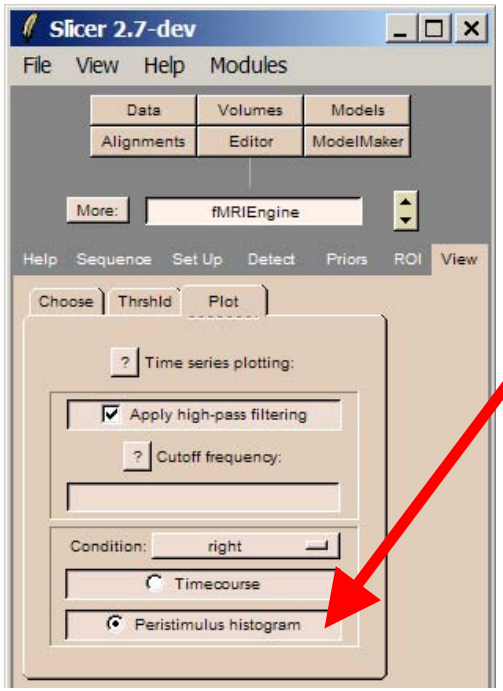


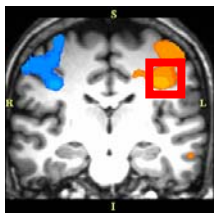

During the right condition, the observed signal decreases in the ipsilateral side and increases on the contralateral side.

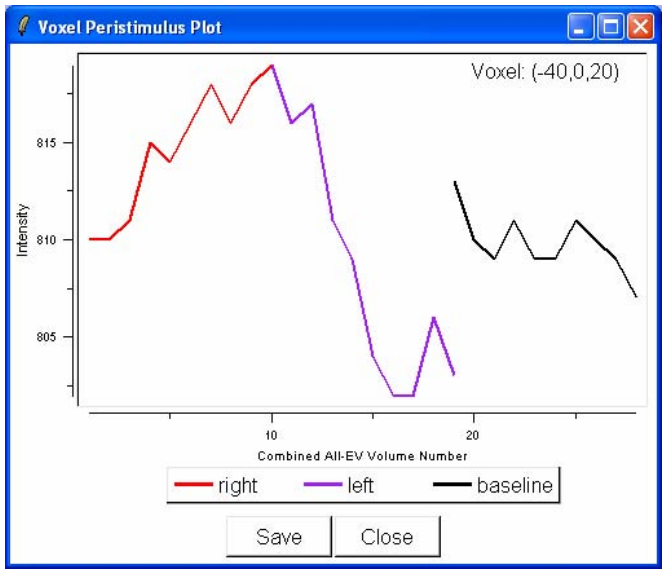
# Threshold, visualize, inspect




Select Peristimulus histogram option and click on the voxel (-40,0,20) in the positive activation region

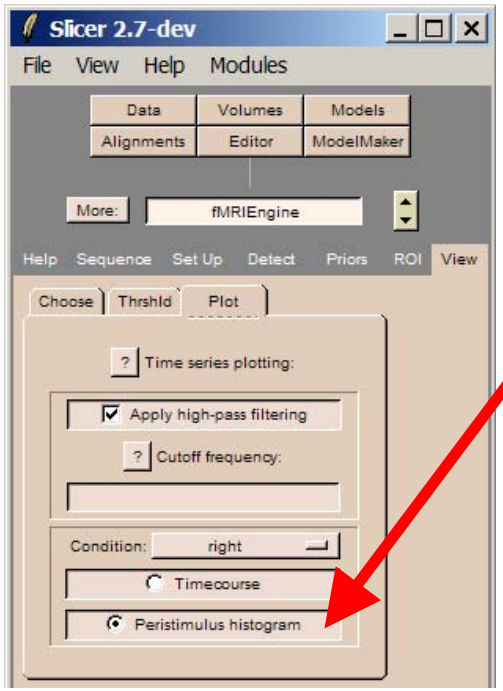
# Voxel Peristimulus Plot





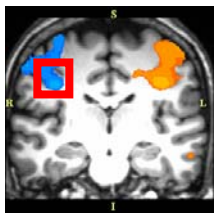

Slicer displays a plot of the mean time course values of the selected voxel in the positive activation region during different blocks

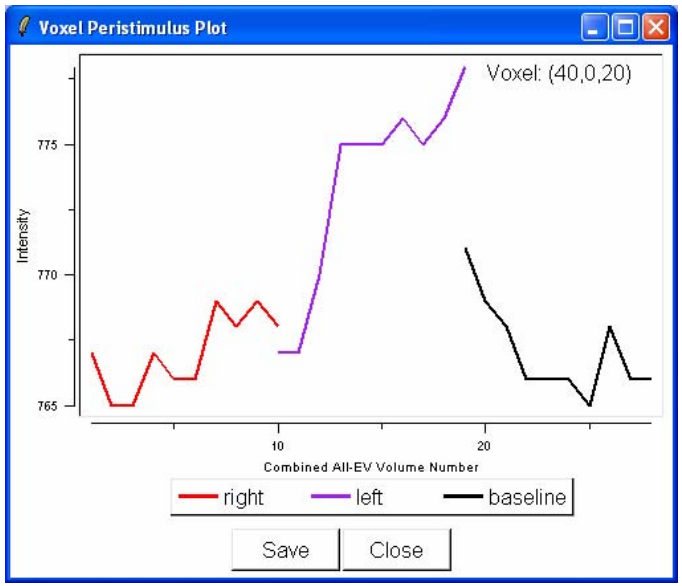
# Threshold, visualize, inspect




Select Peristimulus histogram option and click on the voxel in the negative activation region (40,0,20)

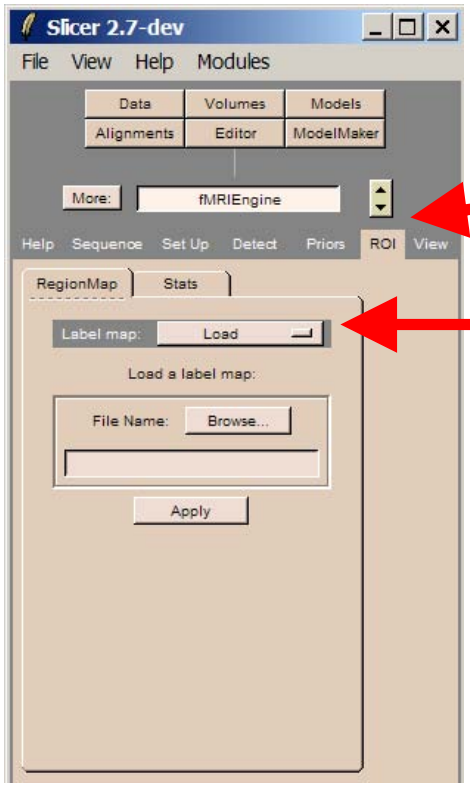
# Voxel Peristimulus Plot






Slicer displays a plot of the mean time course values of the selected voxel in the negative activation region during different blocks

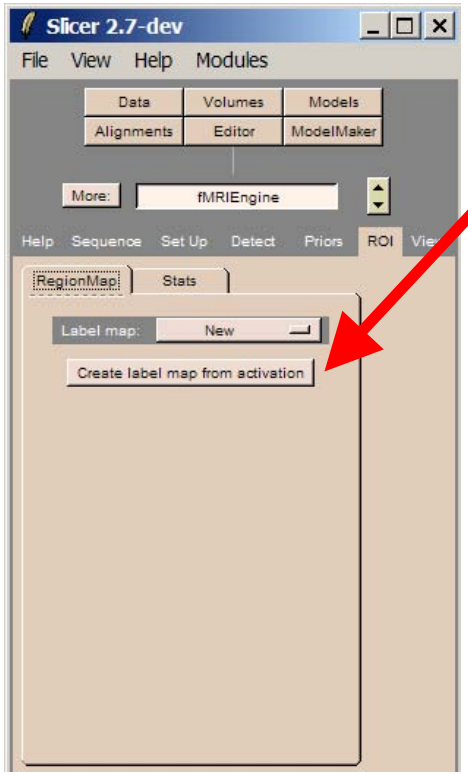
# Activation-based region of interest




Select the ROI panel and RegionMap tab

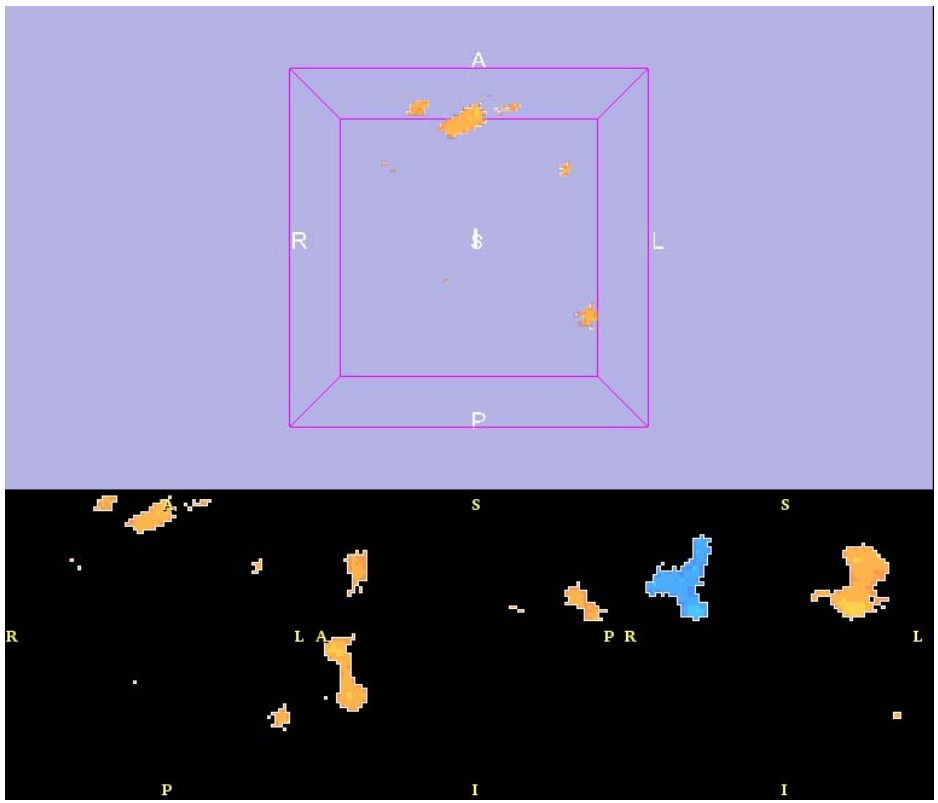
Choose New Activation

# Threshold, visualize, inspect



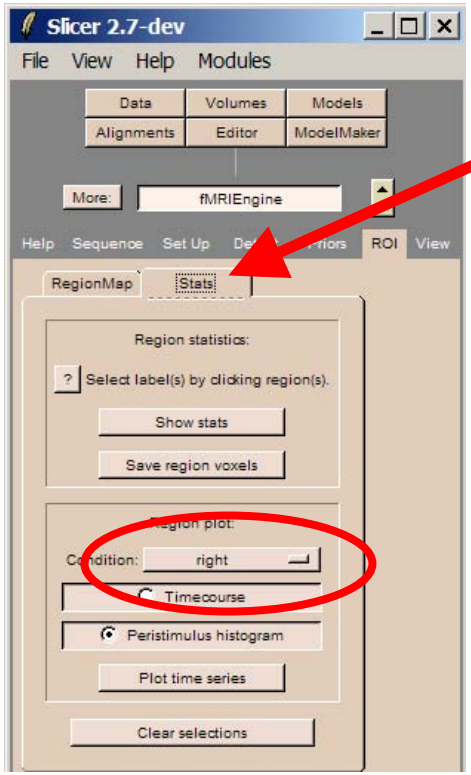

Click Create label map from activation, and wait while activation “blobs” are labelled

# Threshold, visualize, inspect




The label map is shown in Foreground, and the activation map is shown in Background.

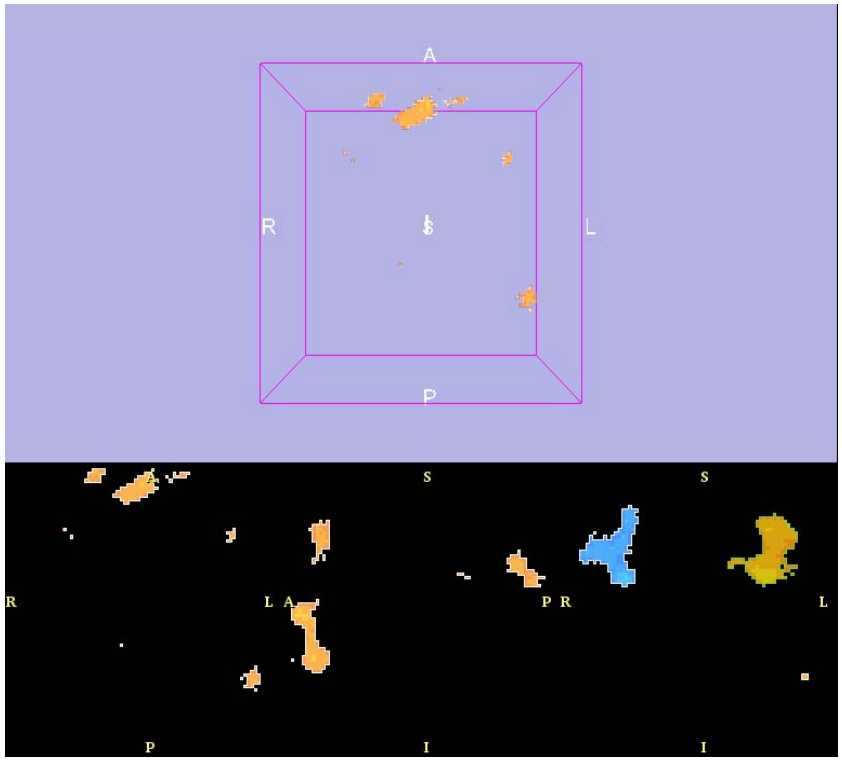
# Regions Statistics




Select the subtab `Stats`
Select one or multiple regions in the left hemisphere to include in analysis by clicking in Slice Window.

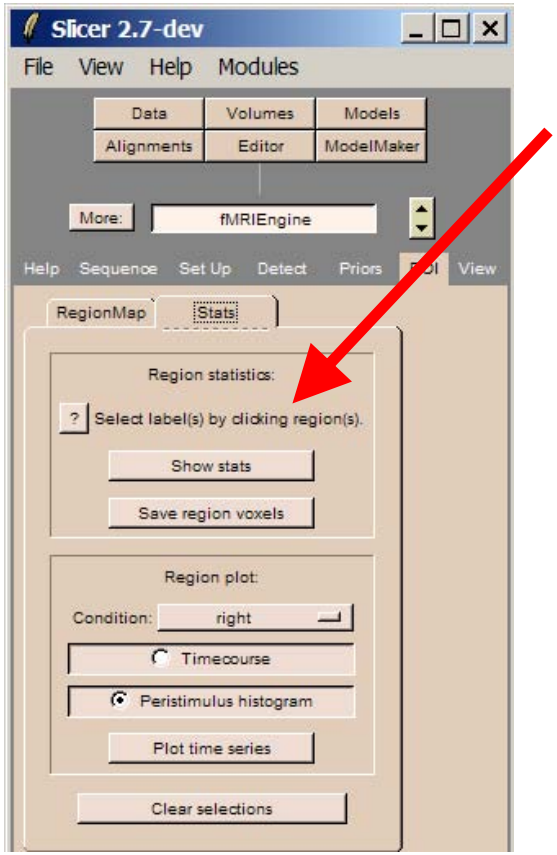
Select the condition `right`.

# Region Statistics



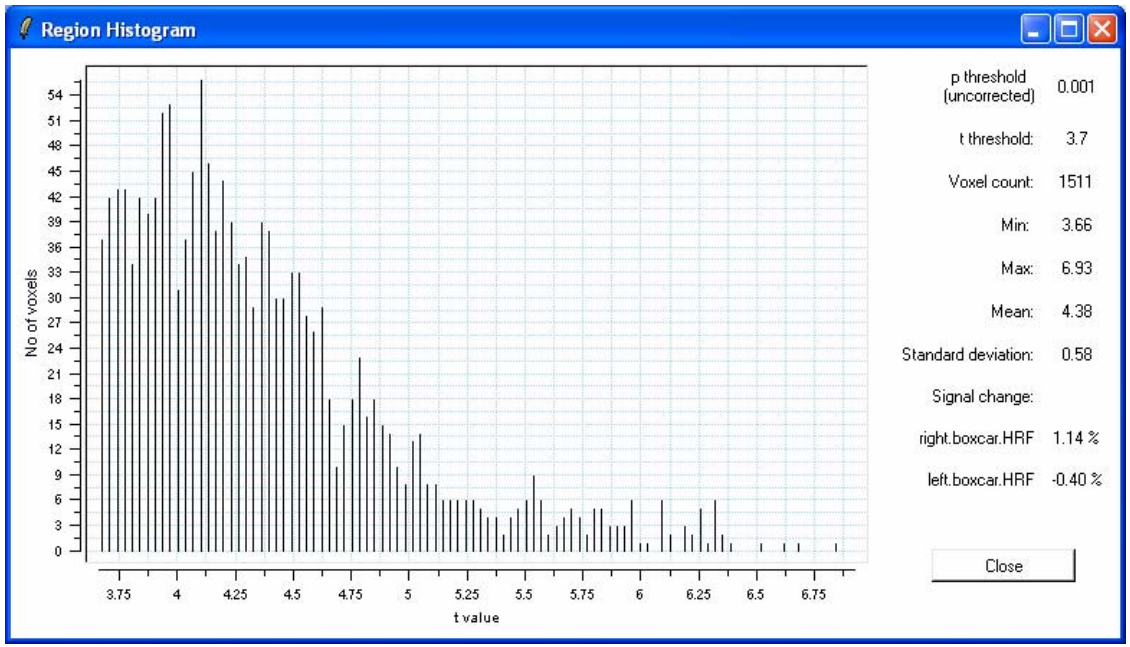

The selected regions appear in green.

# Region Statistics



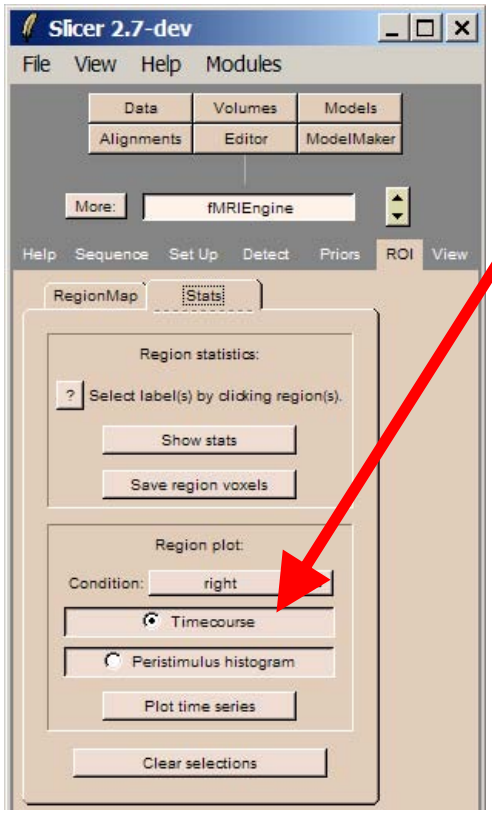

Click Show stats to display the statistics for the selected regions

# Region Statistics




A window displays the statistics for the selected region(s)

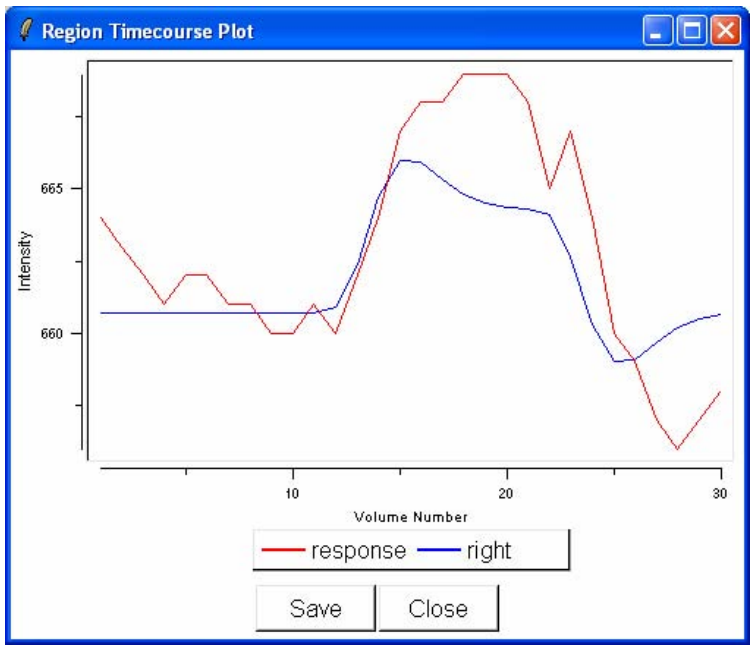
# Region timecourse



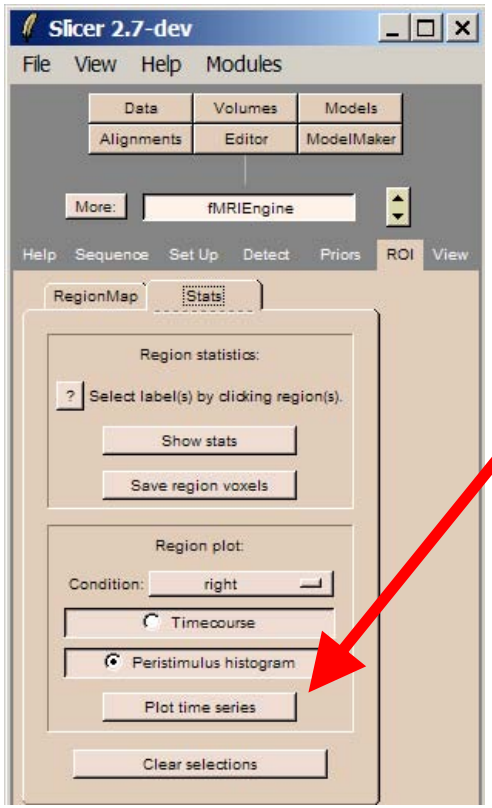

Select Timecourse plot option and click Plot time series for this region.

# Region timecourse

A window displays the region timecourse plot.

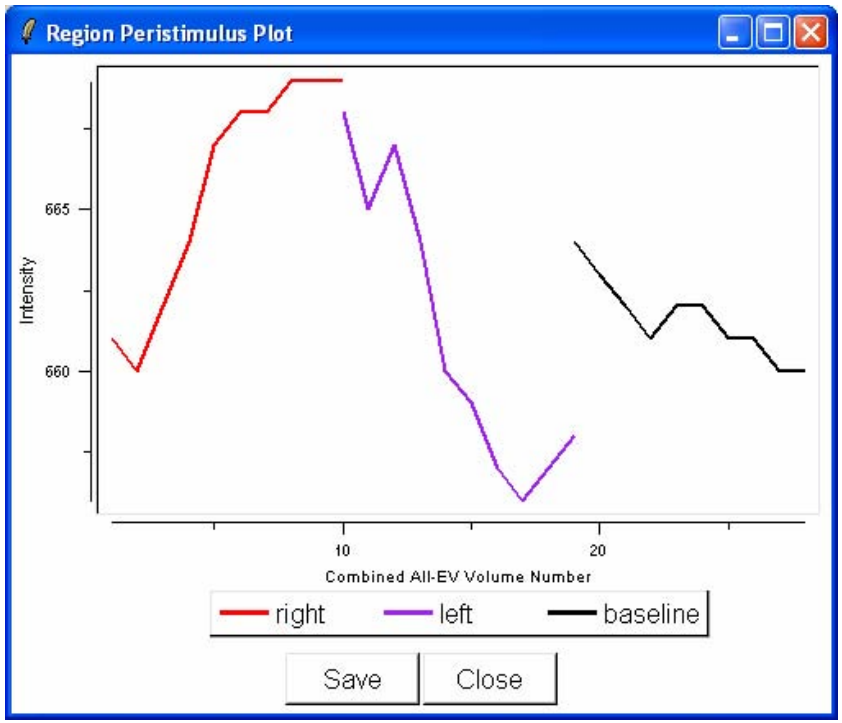


# Region Peristimulus Plot



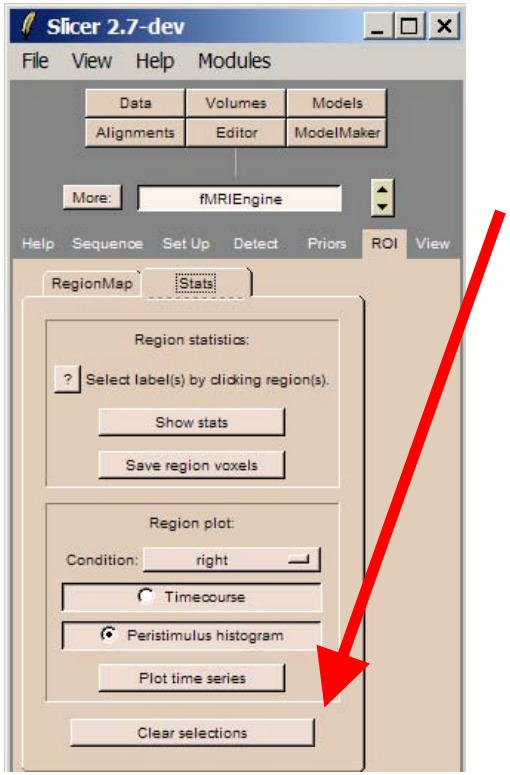

Select Peristimulus histogram and click Plot time series for this region

# Region Peristimulus Plot




A window displays the Region Peristimulus Plot

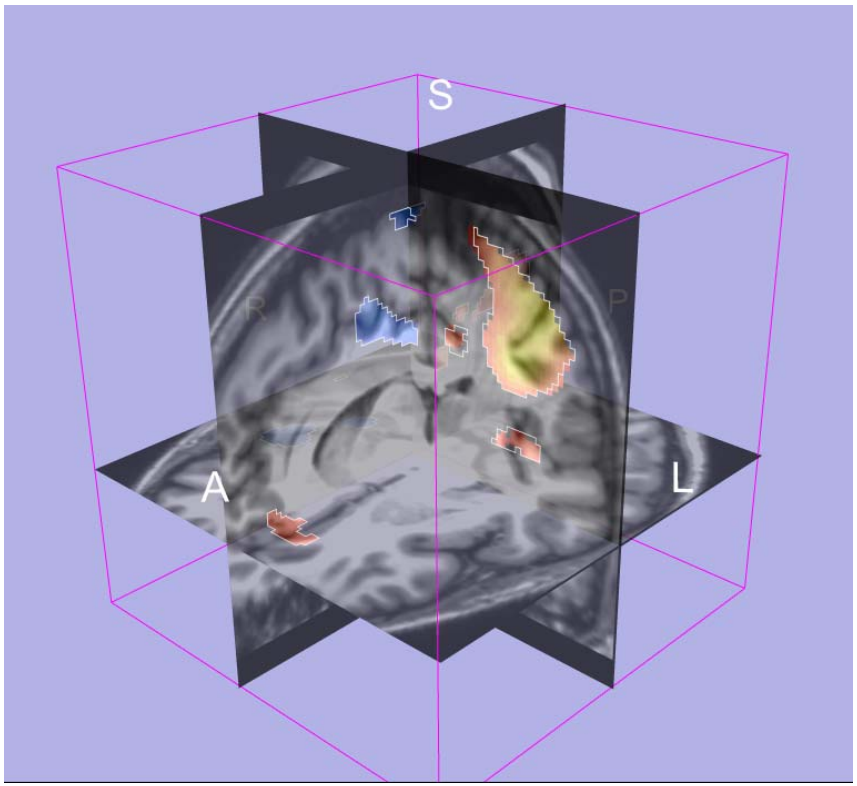
# Visualization




Click on Clear selections and display the structural image in the background (Bg) and activation map in the foreground (Fg).

# Visualization

Fade in the activation volume for a good view of combined data



# Conclusion

- Real clinical situations are not straightforward
- Image orientation, encoding and contents are decisive for correct data analysis
- fMRI studies are highly interdisciplinary

# The Life Cycle of Medical Imaging Data

Image: NIH

Acquisition

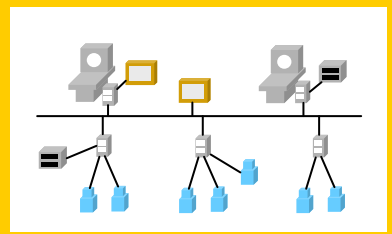
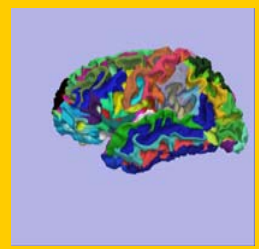


Image by MIT OpenCourseWare.

Storage

Display



Analysis