



NA-MIC

National Alliance for Medical Image Computing

<http://na-mic.org>

fMRI Data Analysis

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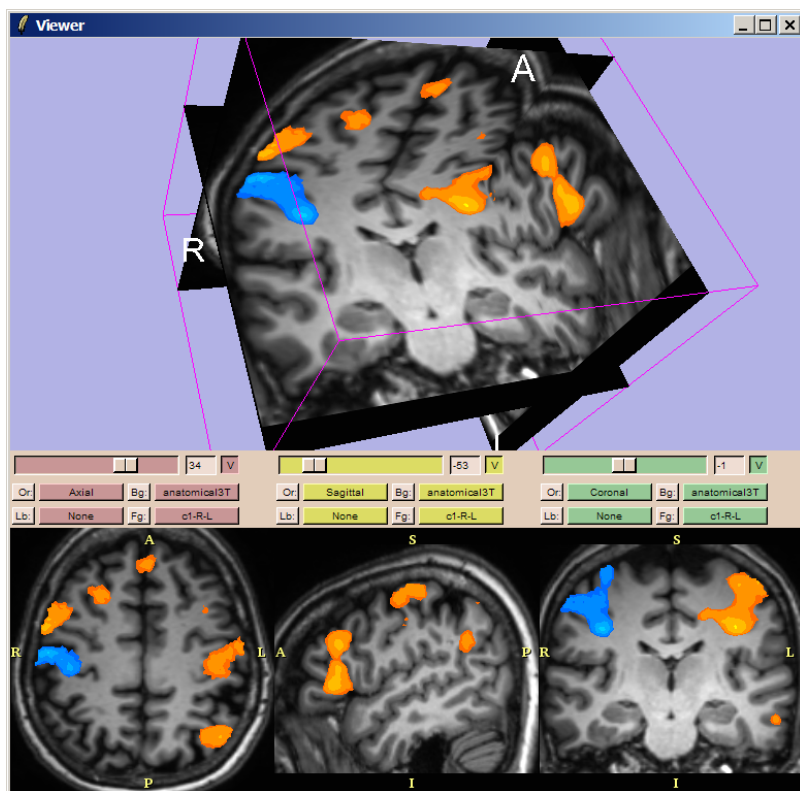


Disclaimer

It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.



Goal of the tutorial



Guiding you step by step through the process of using the fMRIEngine to **analyze fMRI data** and **visualize results** within Slicer. A sensory motor paradigm was used for the tutorial dataset.



fMRI engine Module

The fMRIEngine is:

- An **open-source package** for analyzing and visualizing brain activations supporting the file formats DICOM, ANALYZE, and NIfTI.
- A **developing framework** for a suite of activation detection algorithms and inference engines; currently it provides a linear modeling detector.
- A **research prototype**: the full save/reload functionalities are under development. There are no capabilities at this time to do the fMRI pre-processing steps.



Prerequisites

This tutorial assumes that you have already completed Slicer Basics:

- Loading and Viewing Data (Slicer Training 1)
- Saving Data (Slicer Training 7)

Supporting material:

www.na-mic.org/Wiki/index.php/Slicer:Workshops:User_Training_101



Computer Resources

- This tutorial guides you through a full fMRI analysis of a real fMRI timeseries to get users familiar with the interface and workflow.
- You have the option of using either
 - a full-dataset (90 time pts) [fMRI-long-dataset.zip](#) for which your computer must have adequate processing speed and RAM (we recommend at least 3GB) or
 - a truncated portion (30 time pts) [fMRI-short-dataset.zip](#) of the full dataset, that requires at least 1GB RAM.
- The short dataset contains the first 30 time points of the full dataset.

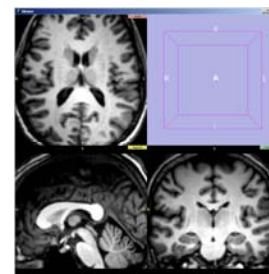
Please use the appropriate dataset for your computer.



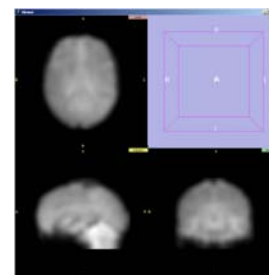
Tutorial datasets

The fMRI tutorial dataset is composed of

Structural scans(anatomical3T.img)



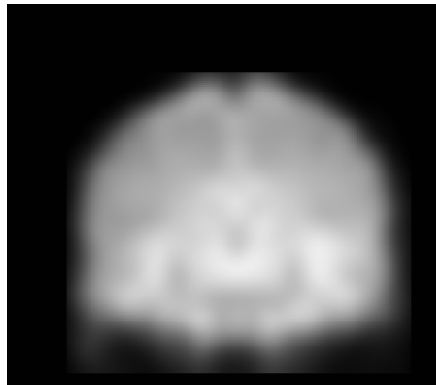
Functional scans.....(functionalxx.img)



www.na-mic.org/Wiki/index.php/Slicer:Workshops:User_Training_101



fMRI Data pre-processing (SPM)



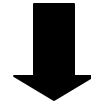
Realignment



Motion Correction



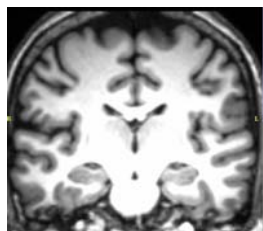
Normalization to MNI



Smoothing



Data description



Structural (MPRAGE): ANALYZE format
135 slices
1.0 mm x 1.0 mm x 1.0 mm voxels
Normalized to MNI



Pre-processed Functional (EPI): NIfTI format
68 slices
2.0 mm x 2.0 mm x 2.0 mm voxels
Repetition Time TR = 2s



Paradigm description

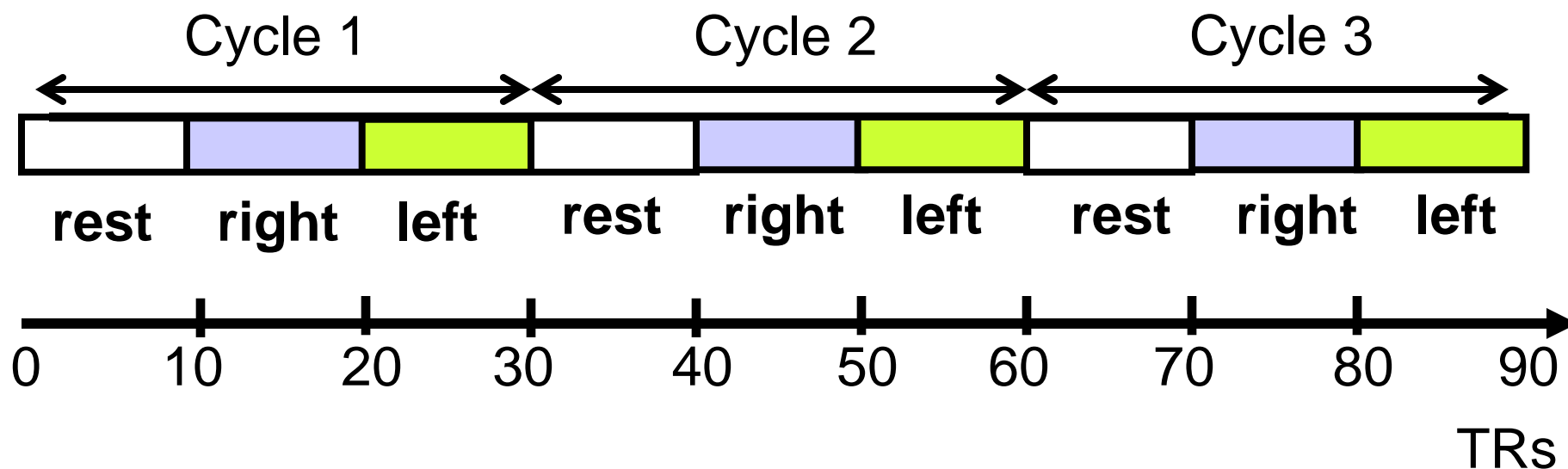
- Finger sequencing fMRI task to elicit **activation** in the hand regions of the **primary sensory motor cortex**
- Block design motor paradigm
- Subject touches thumb to fingers sequentially within block (thumb touches first through fourth finger)
- Subject alternates left and right hand



Paradigm design

Three cycles

rest | right hand | left hand

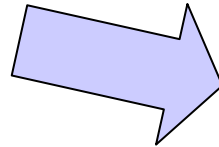




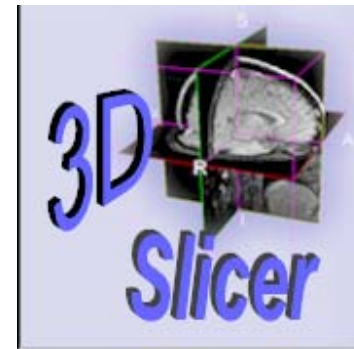
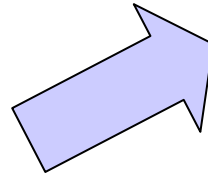
fMRI Engine compatibilities

SPM

SPM fMRI pre-processing



FSL fMRI pre-processing



3DSlicer fMRI full analysis
and visualization



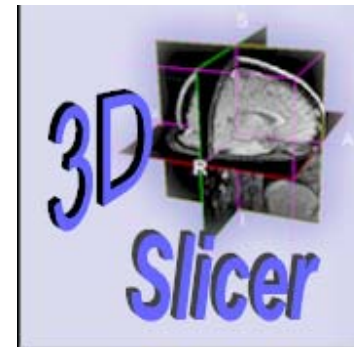
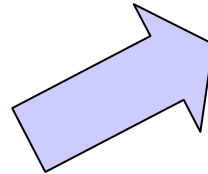
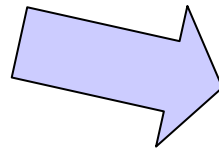
fMRI Engine compatibilities

SPM

SPM fMRI **full** analysis



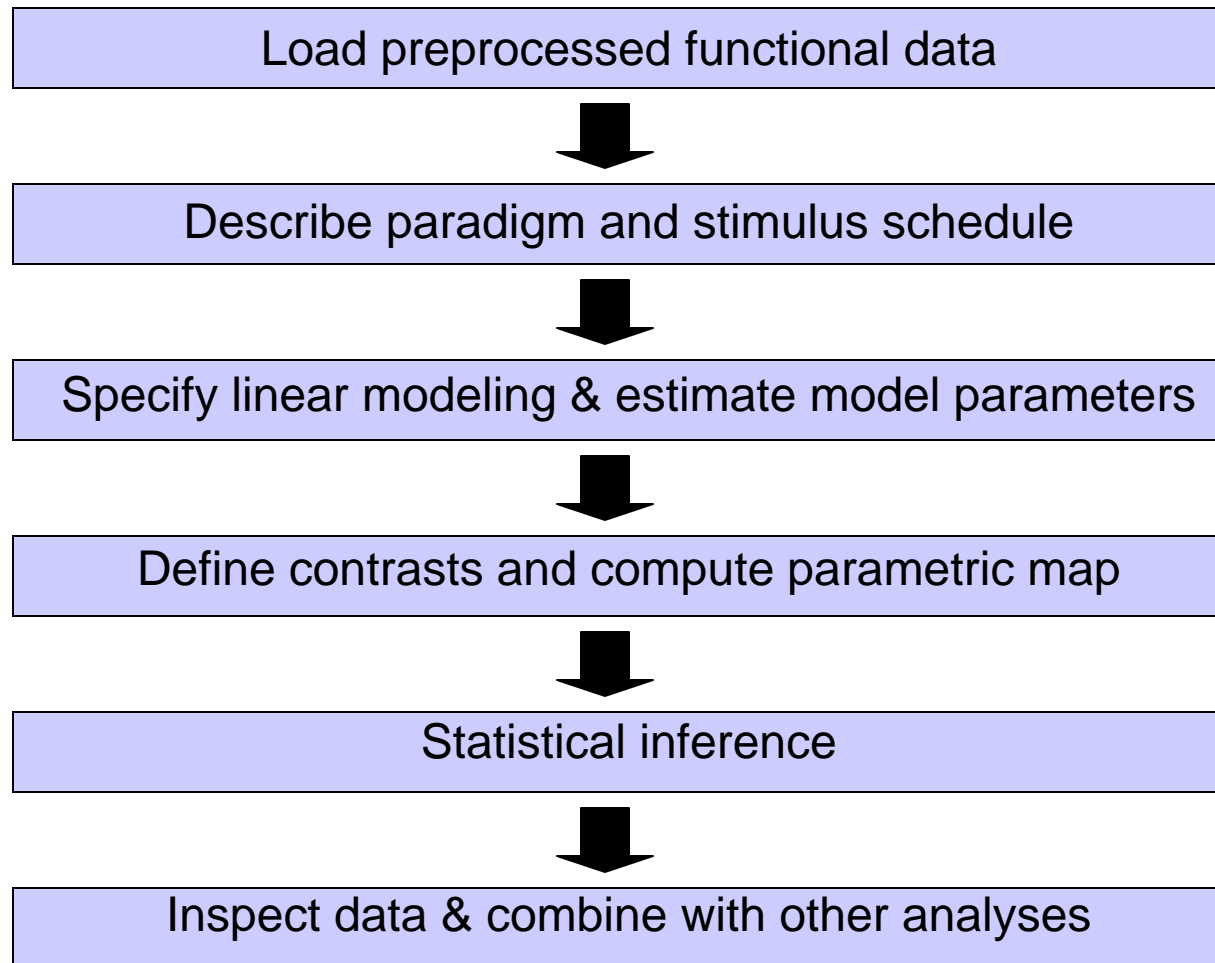
FSL fMRI **full** analysis



3DSlicer visualization
and modeling



fMRIEngine workflow





Overview

Part 1: Loading and Previewing Data

Part 2: Describing stimulus schedule

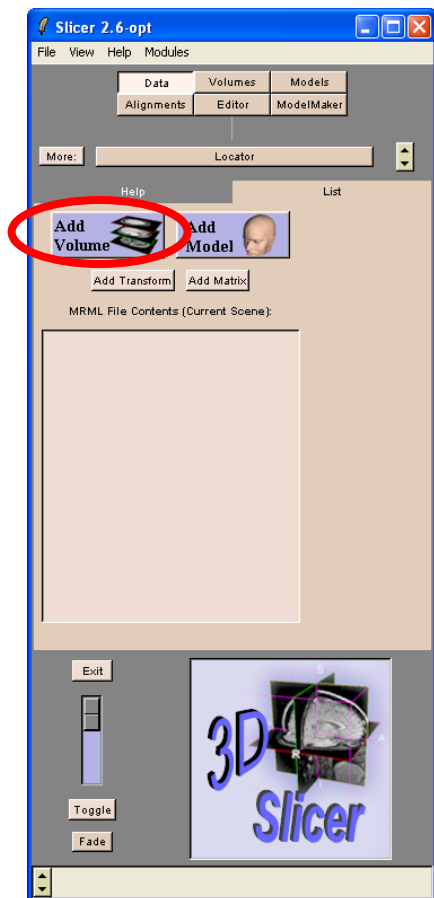
Part 3: Linear modeling & estimation

Part 4: Contrasts & computing SPMs

Part 5: Inference & inspection



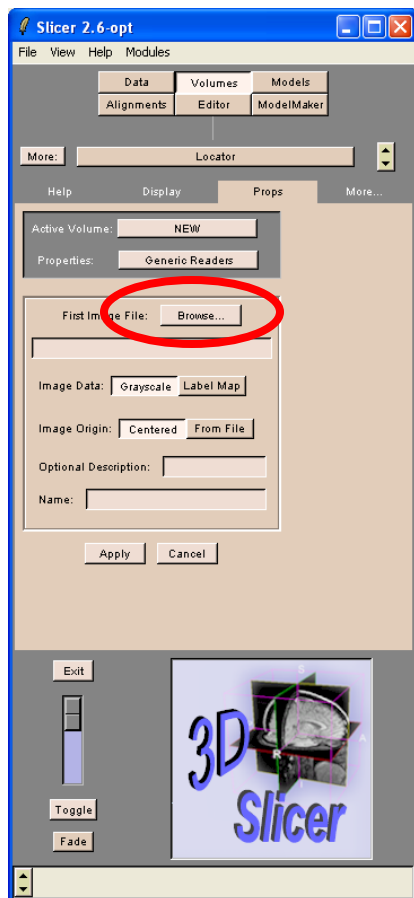
Loading the structural dataset



Click on Add Volume in the main menu



Loading the structural dataset



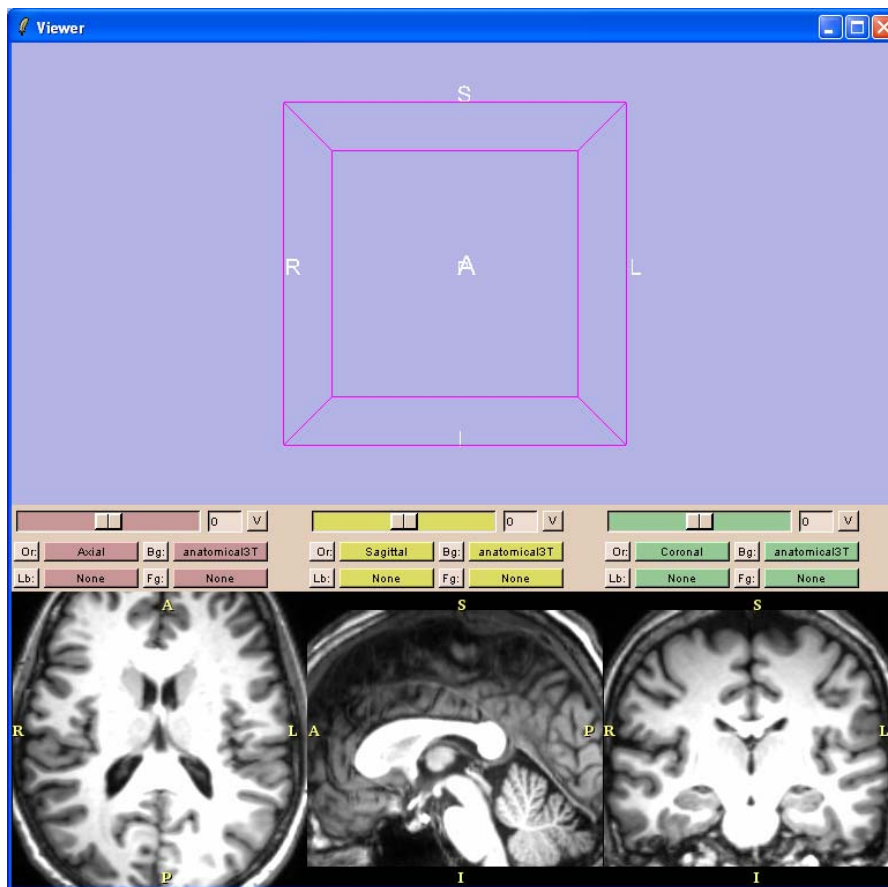
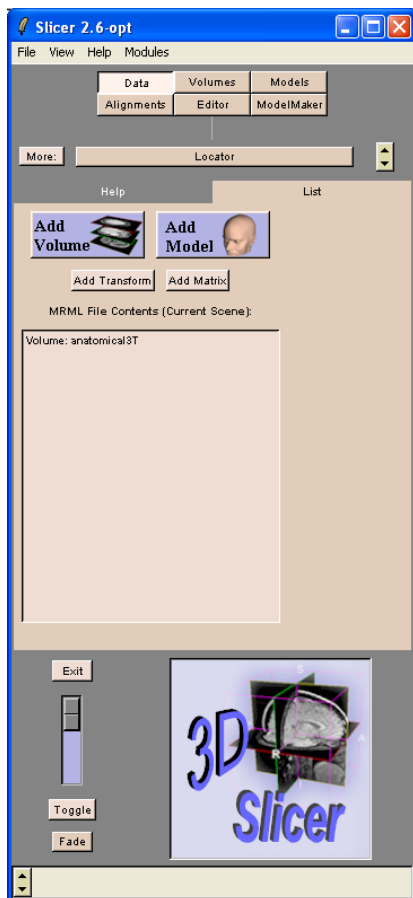
Select the reader Generic Reader in the Props Panel of the module Volumes.

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

The anatomical volume in the short and long datasets are identical.

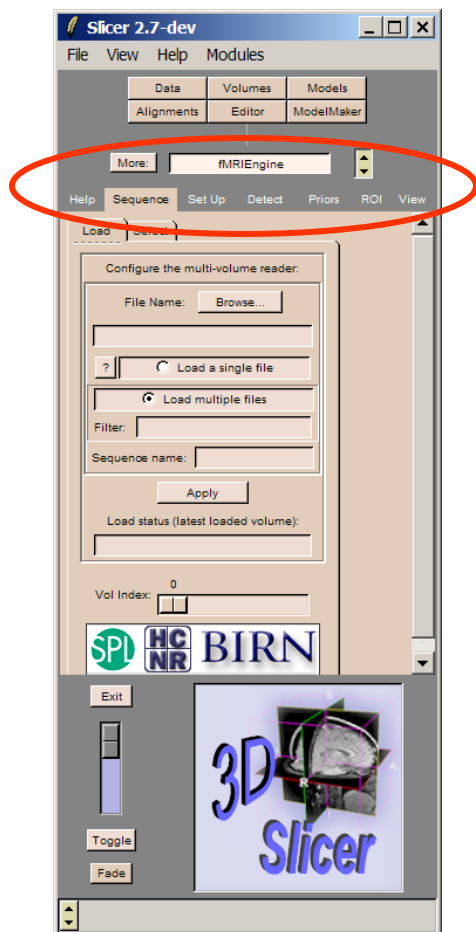


Loading the structural dataset





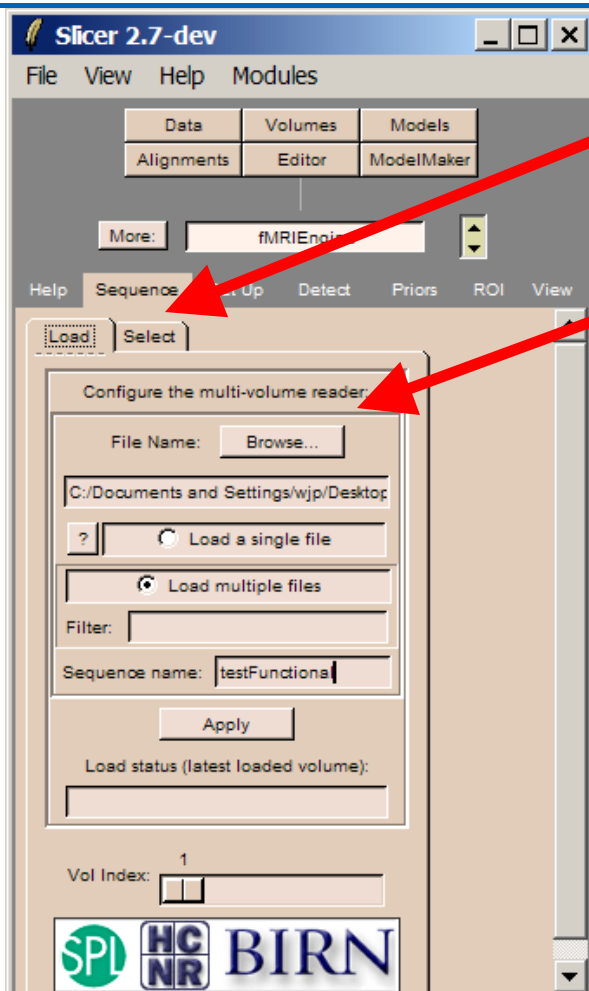
fMRI Engine



Select Modules in the main menu
Select Application → fMRIEngine



Load Image Sequence



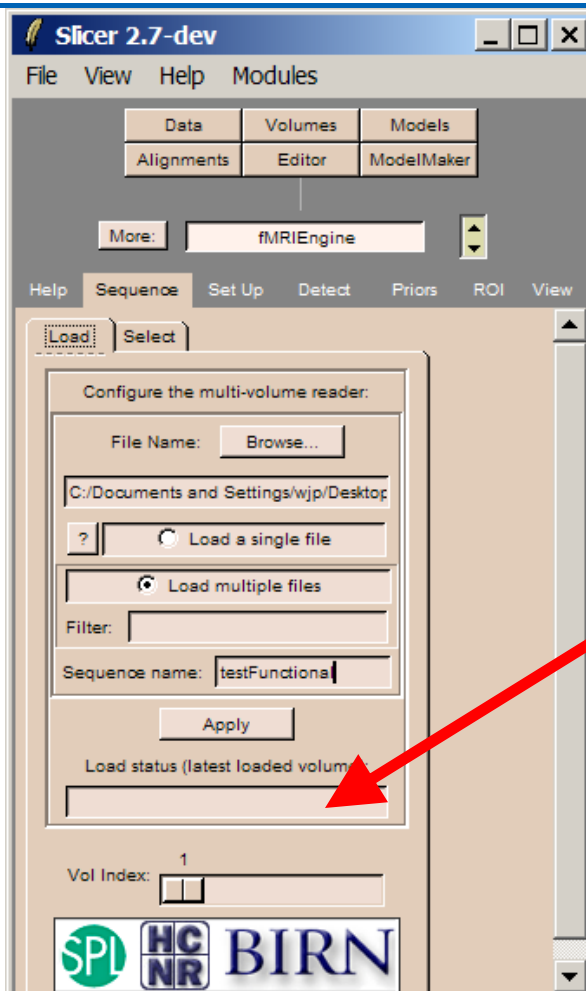
Pick Sequence → Load tab

Click on Browse and select the file functional01.hdr from either dataset.
Select Load Multiple Files

Enter the sequence name testFunctional and click on Apply.



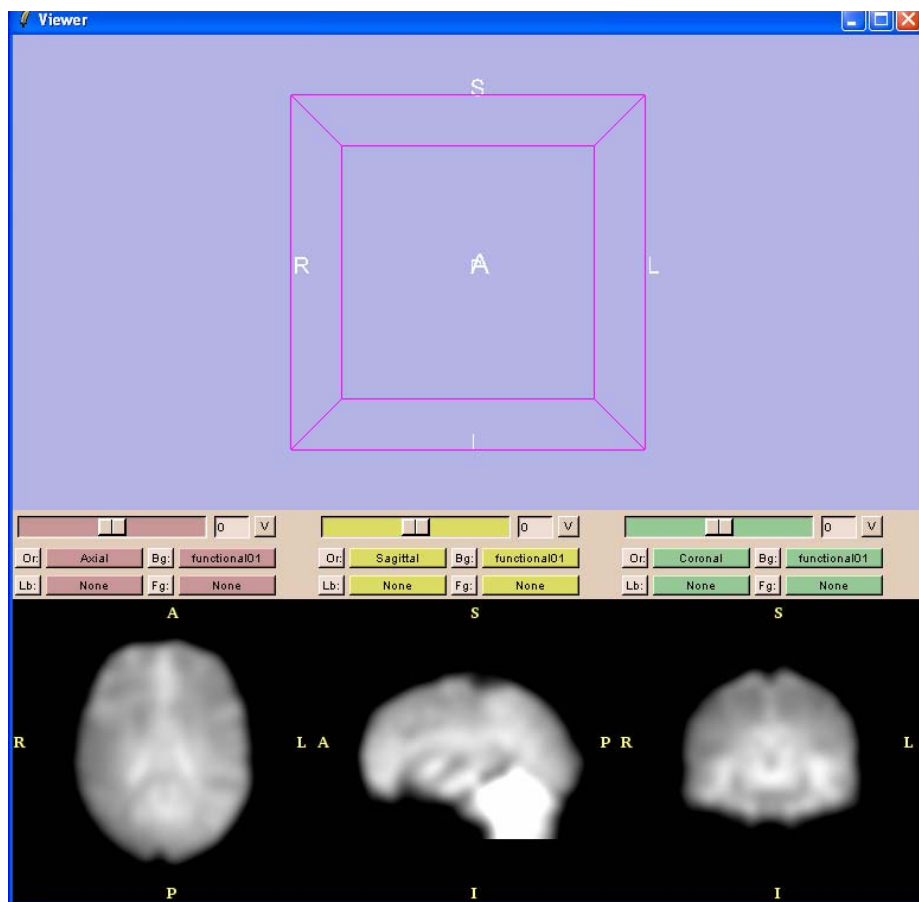
Load Image Sequence



Slicer displays the load status of the 30 (short dataset) or 90 (long dataset) functional volumes.



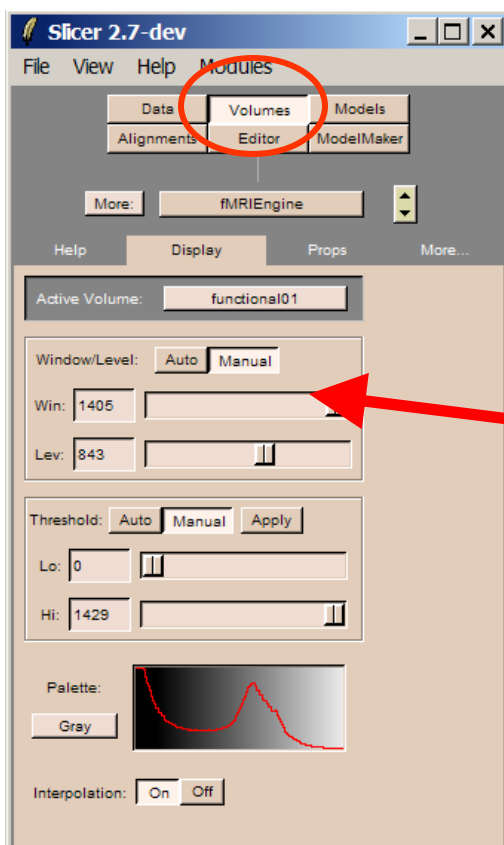
Load Image Sequence



Slicer loads the functional volumes in the Viewer.



Set Image Display

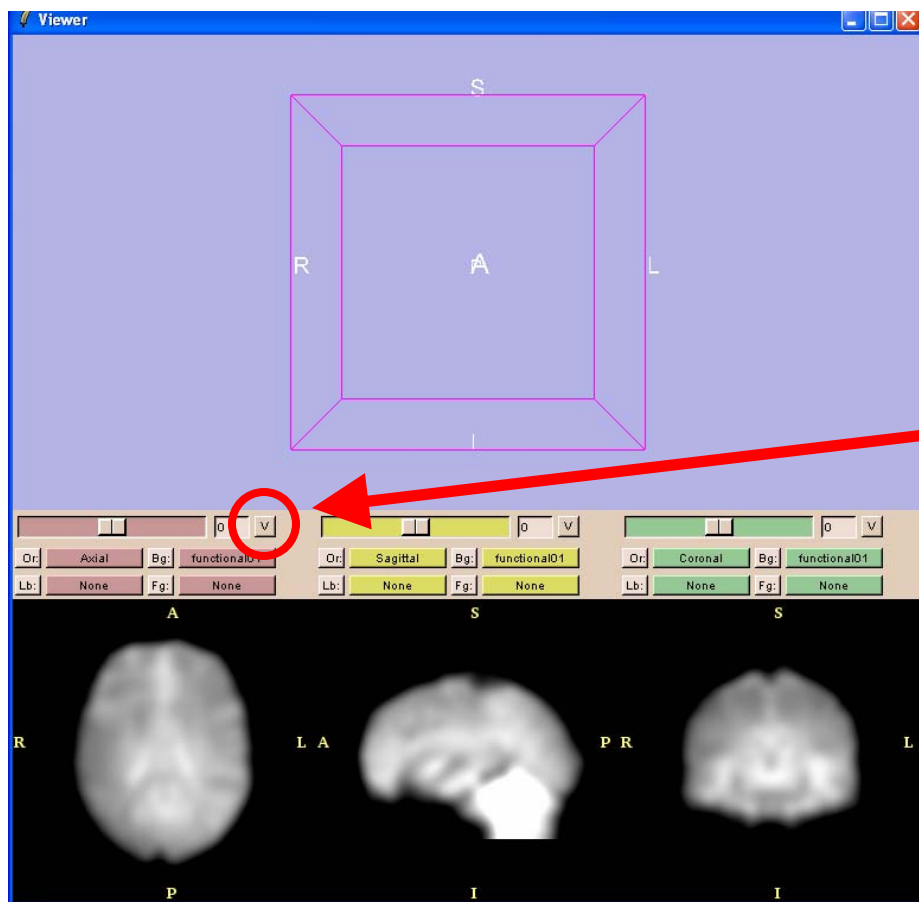


Click on the module Volumes,
and select the panel Display

Adjust Win and Lev to get best
display of image data



Set Image Display

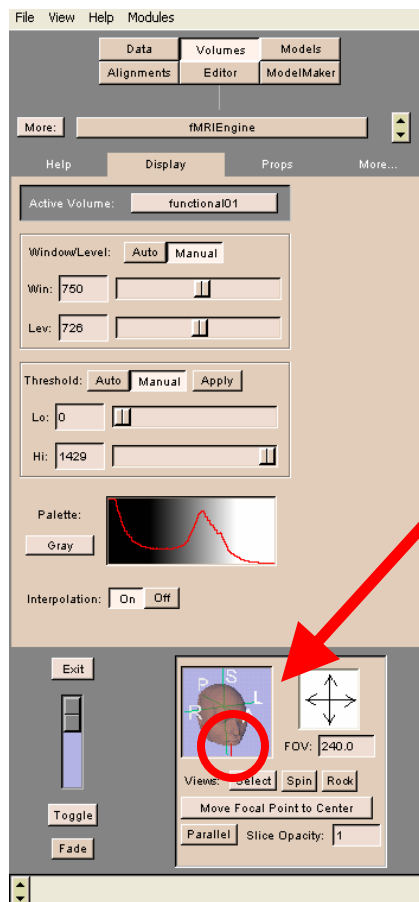


Slicer updates the Window and Level settings.

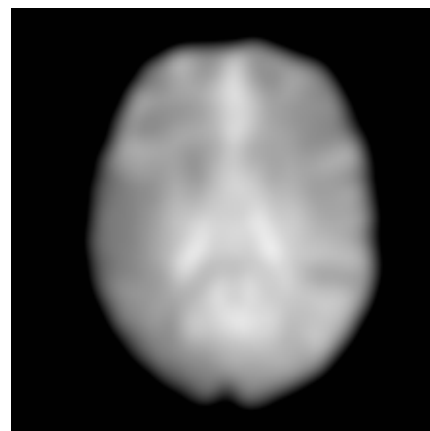
Click on the V button to display the axial slice in the Viewer.



Set Image Display

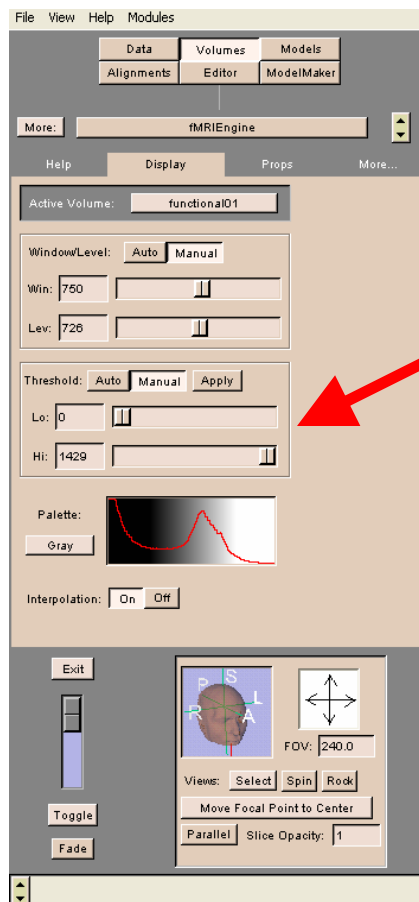


Click on the letter I in the control window to display the Inferior view.





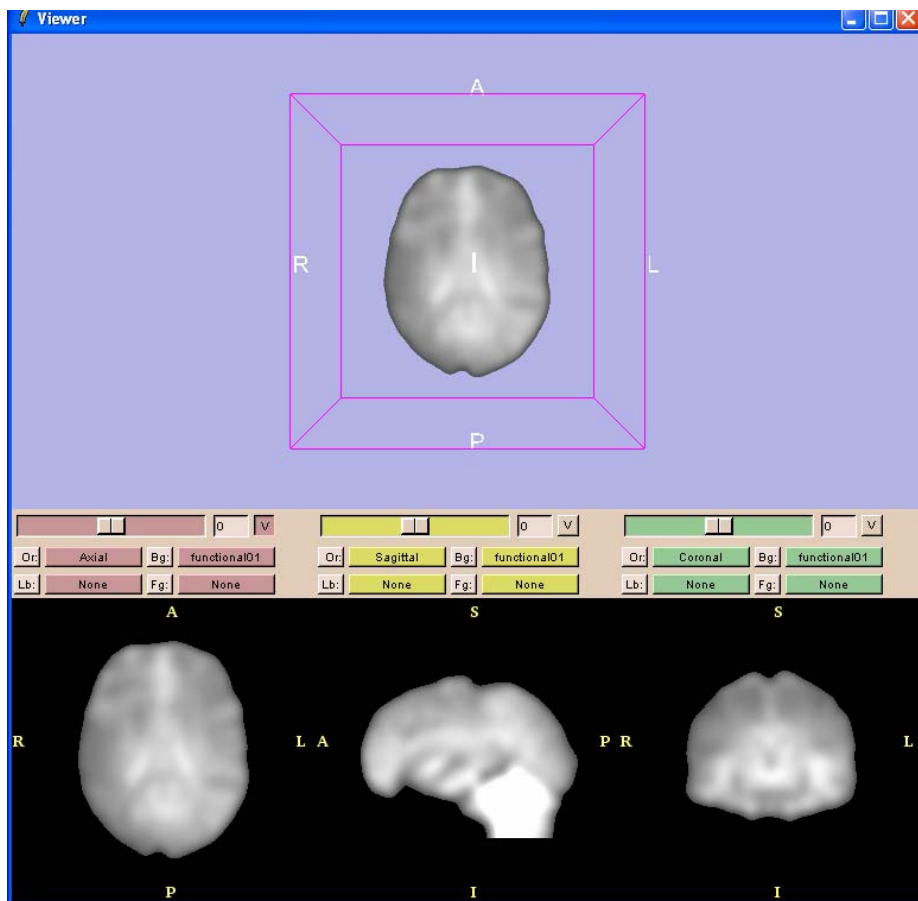
Set Image Display



Adjust the low threshold Lo to mask out background



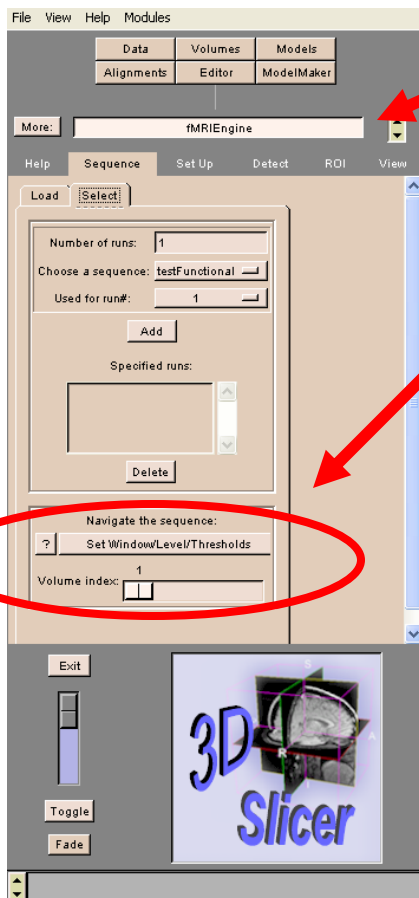
Set Image Display



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



Set Sequence Display



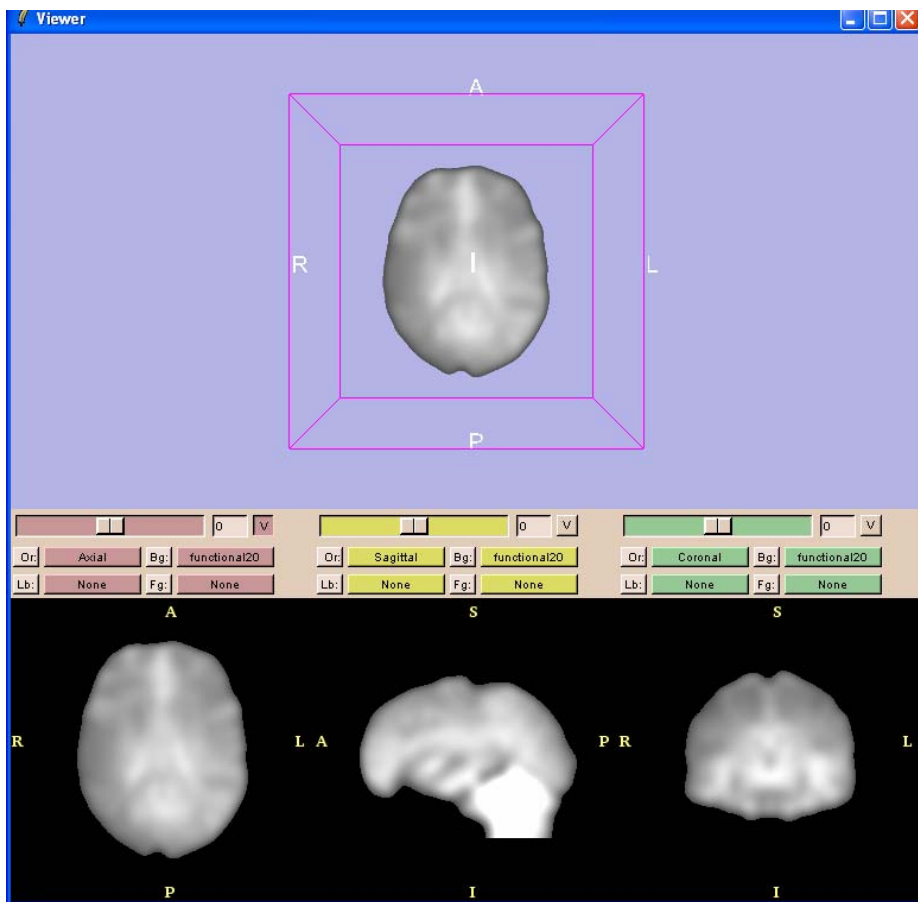
Click on fMRIEngine, select the panel Sequence, and pick the tab Select

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

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



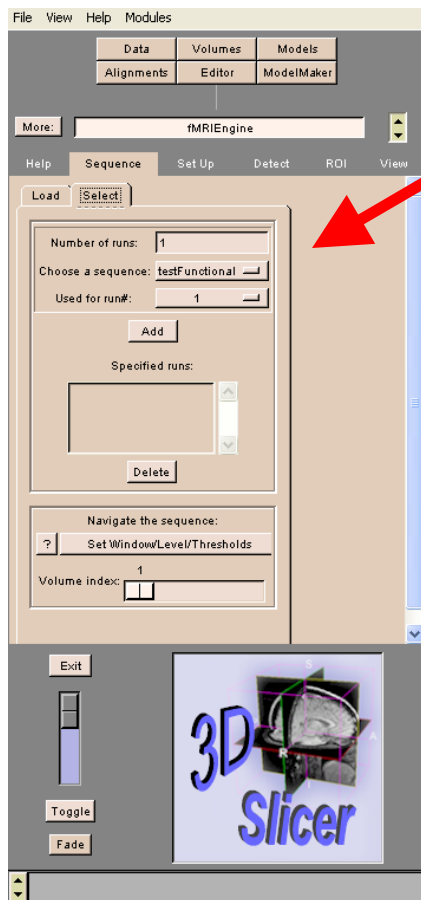
Inspect Image Display



Slicer displays the volumes of the sequence.



Select Image Sequence

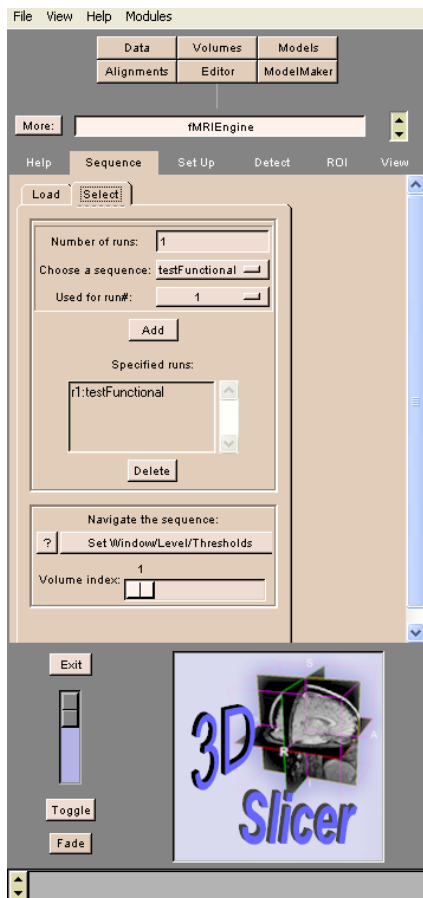


Specify the number of runs = 1,
select the sequence testFunctional

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



Select Image Sequence



Slicer assigns the sequence to run 1



Overview

Part 1: Loading and Previewing Data

Part 2: Describing stimulus schedule

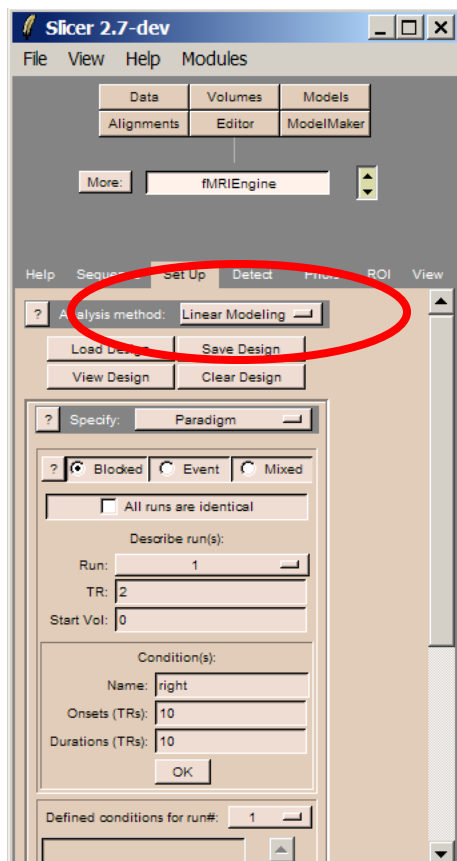
Part 3: Linear modeling & estimation

Part 4: Contrasts & computing SPMs

Part 5: Inference & inspection



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

$$Y = BX + e$$

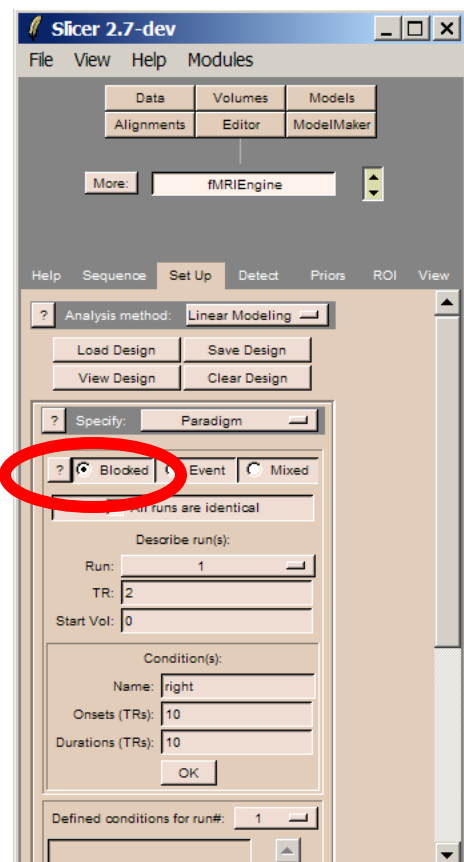
B = set of experimental parameters

Y = Observed data

X = Design Matrix e = noise



Stimulus schedule



Select the design type
Blocked



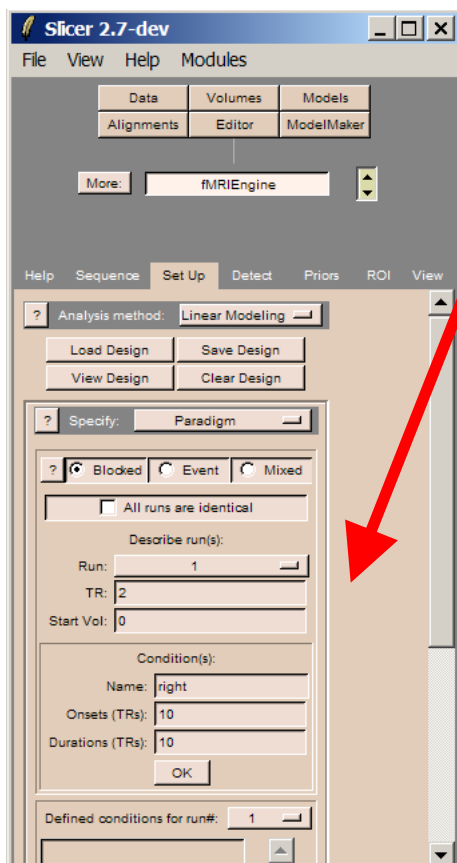
Paradigm timing parameters

- 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



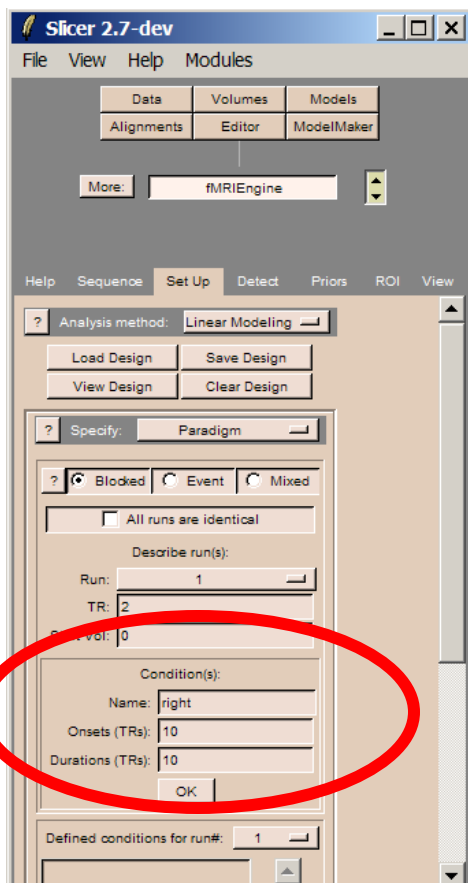
Stimulus schedule



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



Stimulus schedule



Enter the schedule for the first condition

Short dataset:

Name = right

Onset = 10

Durations = 10

Long dataset:

Name = right

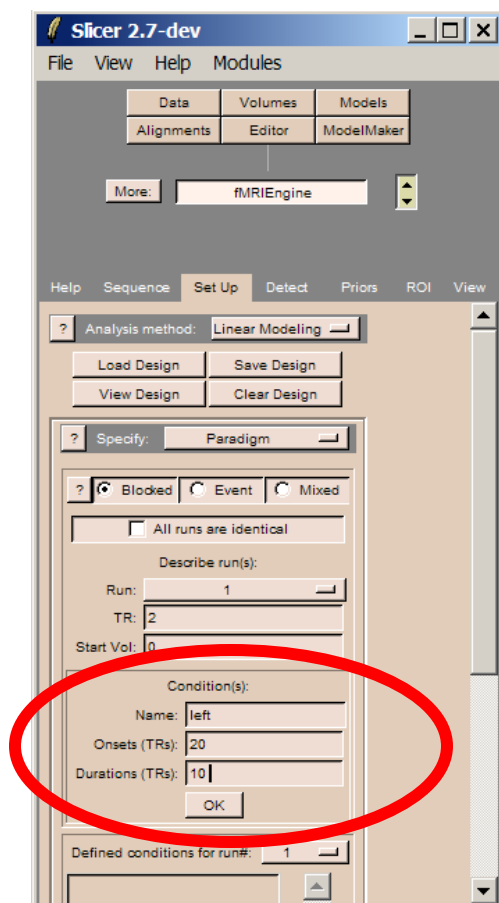
Onset = 10 40 70

Durations = 10 10 10

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



Stimulus schedule



Enter the schedule for the second condition

Short dataset:

Name = left

Onset = 20

Durations = 10

Long dataset:

Name = left

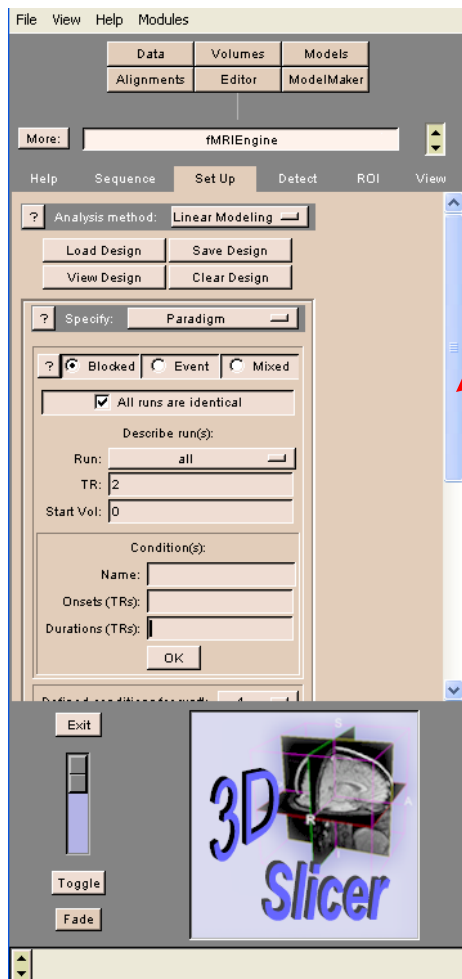
Onset = 20 50 80

Durations = 10 10 10

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



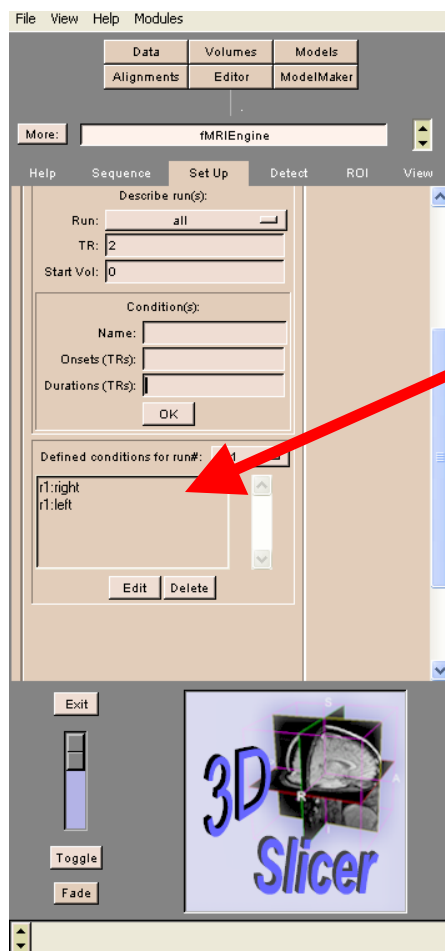
Stimulus schedule



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



Overview

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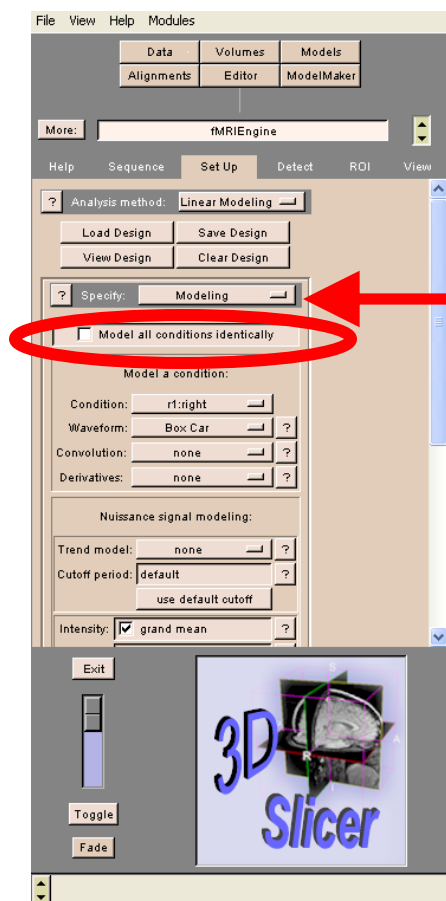
Part 3: Linear modeling & estimation

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Part 5: Inference & inspection



Model a Condition

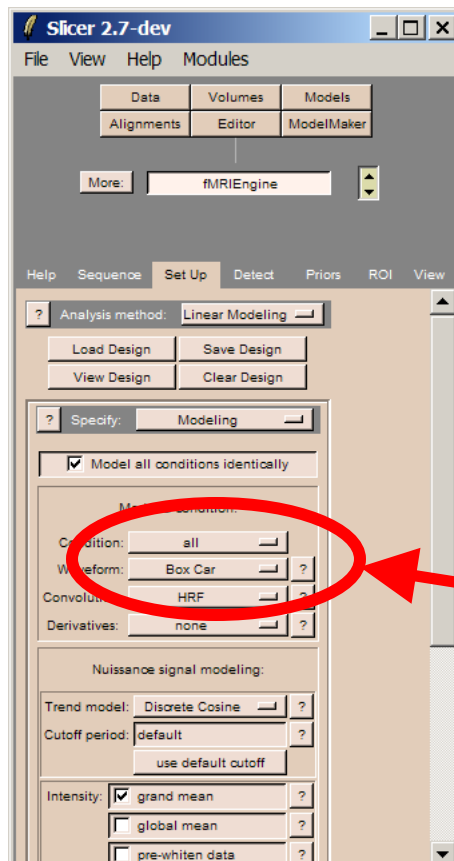


Select Specify Modeling

Click on Model all conditions identically



Model a Condition

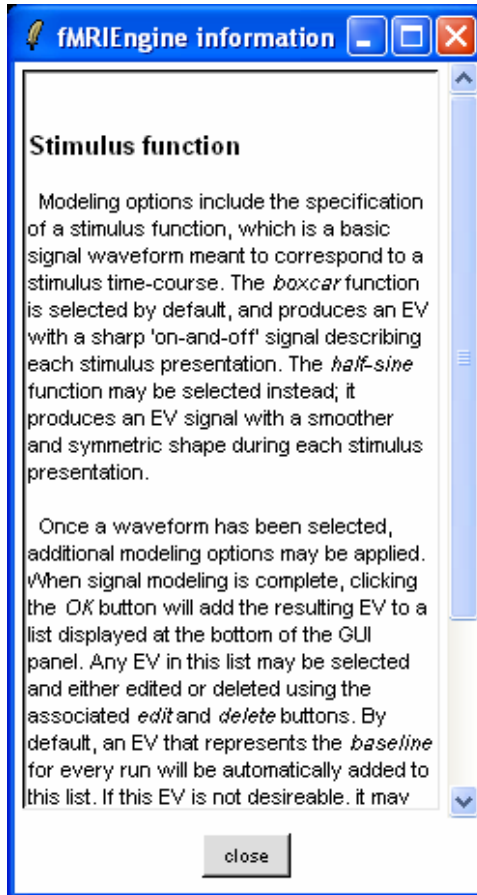


Select
Condition: all
Waveform: BoxCar

Click on the question mark
next to Waveform for
detailed description
of the modeling option.



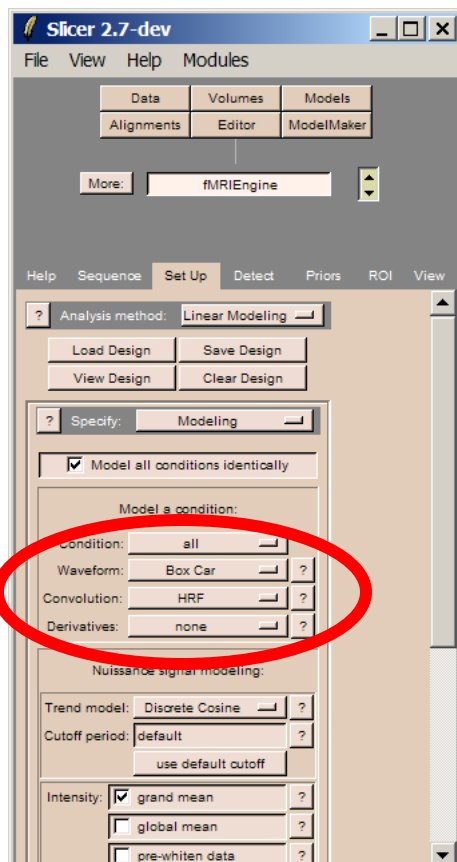
Model a Condition



Slicer displays a detailed description of the Stimulus function.



Model a Condition

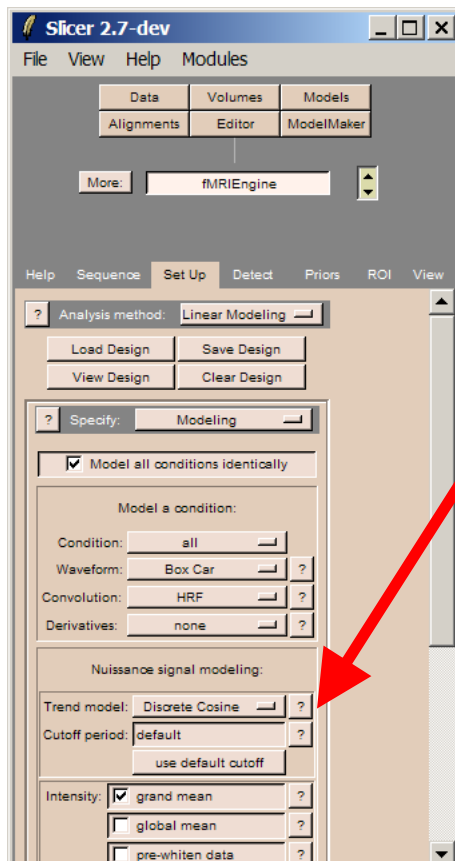


Select

- Convolution: HRF (Hemodynamic Response Function)
- Derivatives: none



Nuisance Signal Modeling

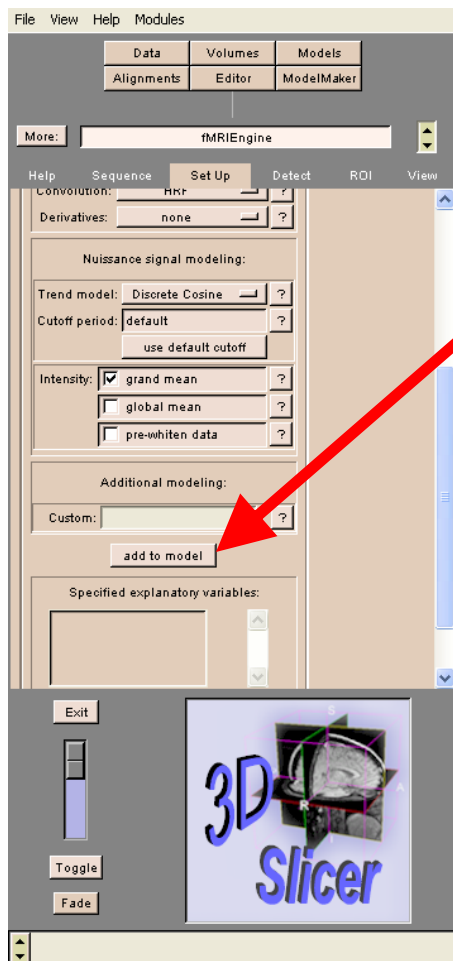


On the subpanel Nuisance signal modeling, select
Trend model: Discrete Cosine
Cutoff period: default

Click on use default cutoff



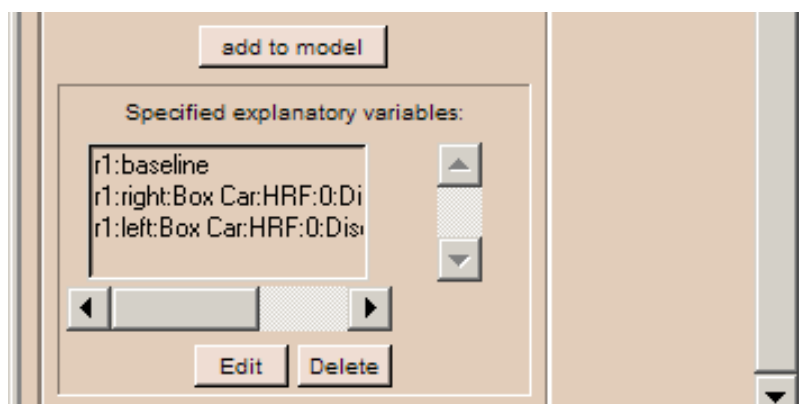
Nuisance Signal Modeling



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



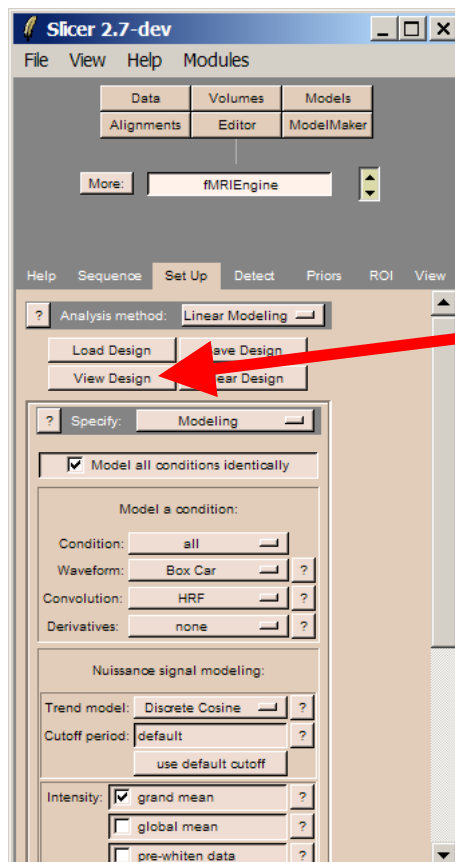
Nuisance Signal Modeling



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



View Design Matrix

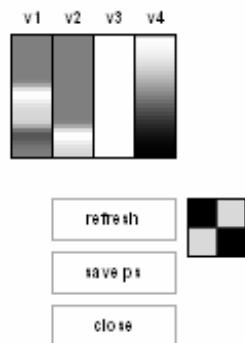


Click View Design to display the design matrix

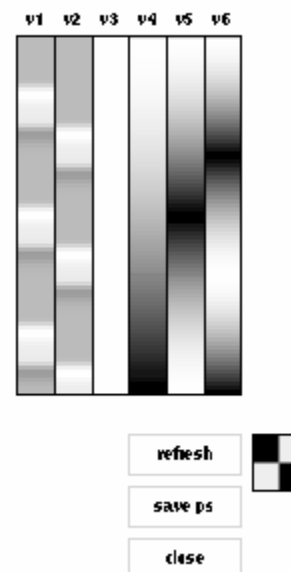


View Design Matrix

A window displaying the model design appears.



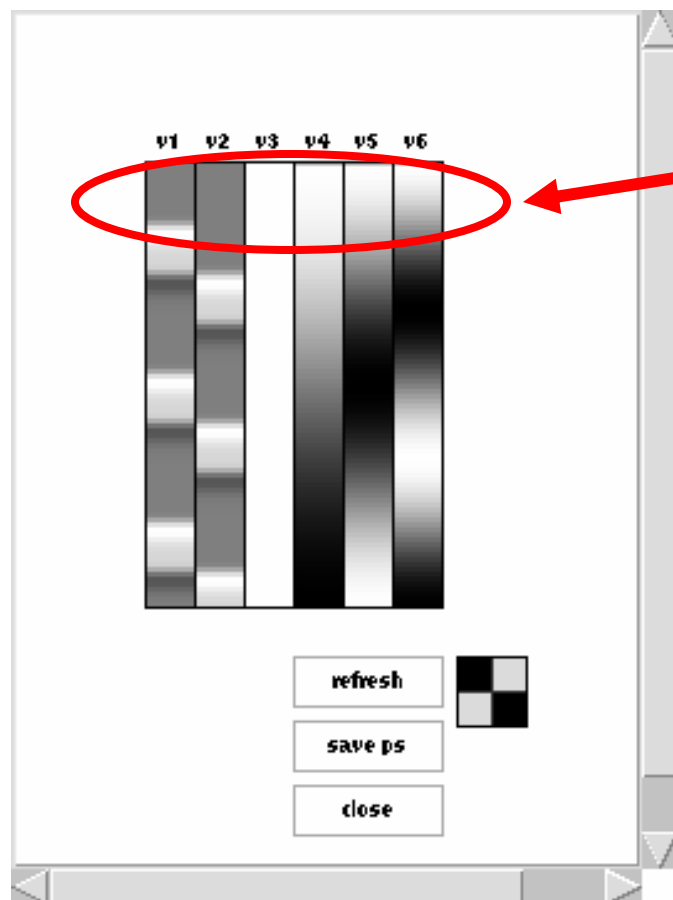
Short dataset



Long dataset



Design Matrix

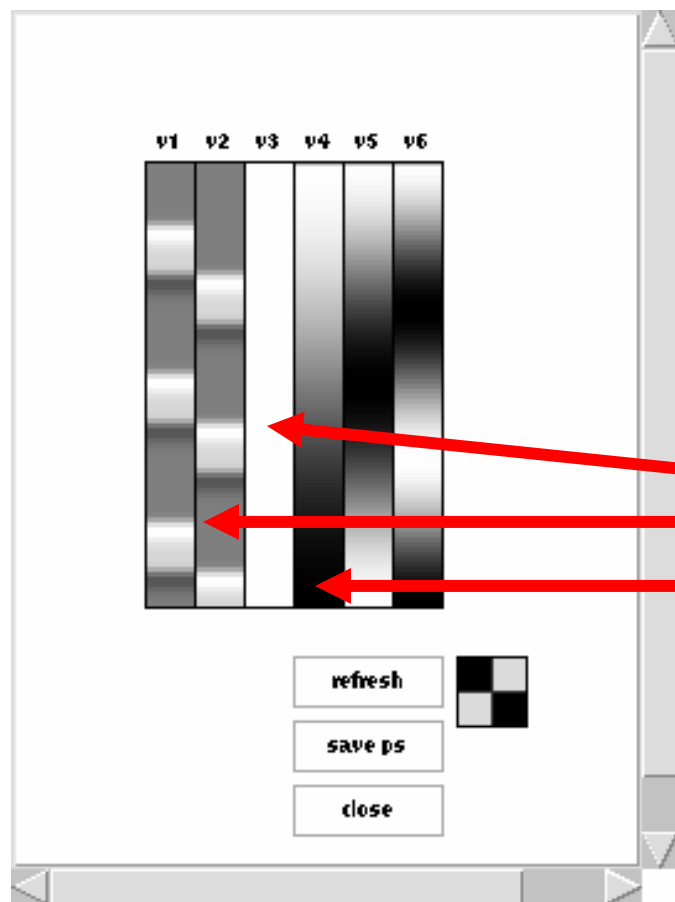


Move the mouse from left to right over the columns of the matrix to display the characteristics of the modeled conditions.

v1 = left modeled condition
v2 = right modeled condition
v3 = baseline
v4,v5,v6 = low frequency noise



Design Matrix

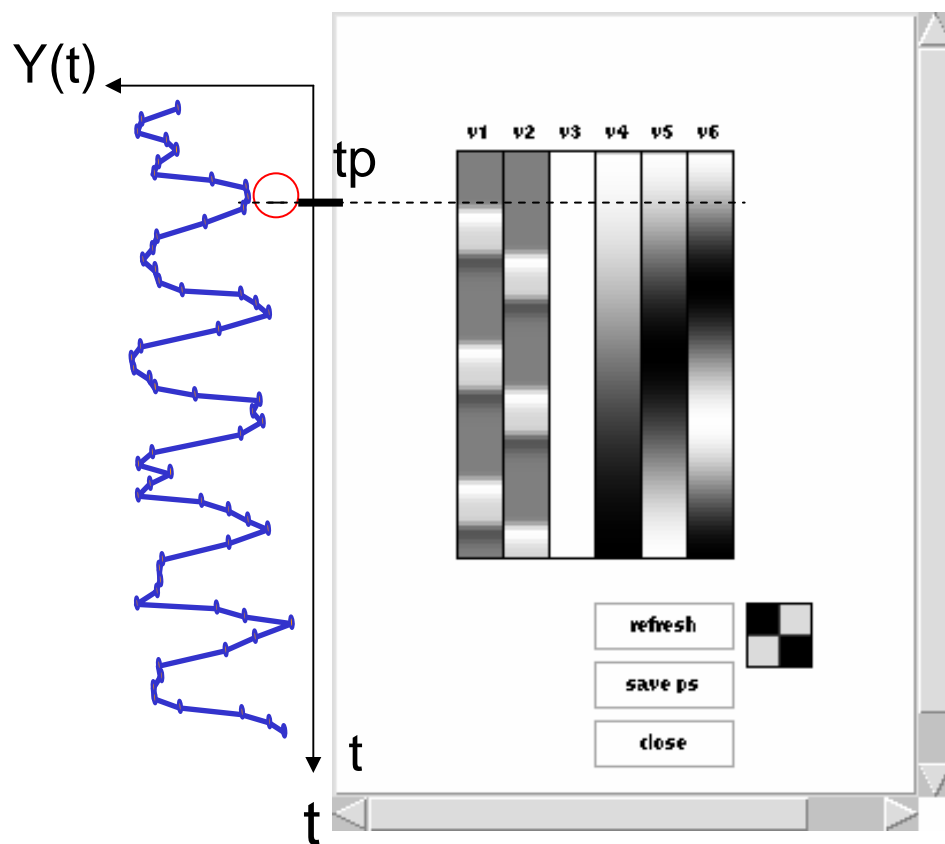


Observe the different values of the signal intensity in the matrix.

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



Design Matrix



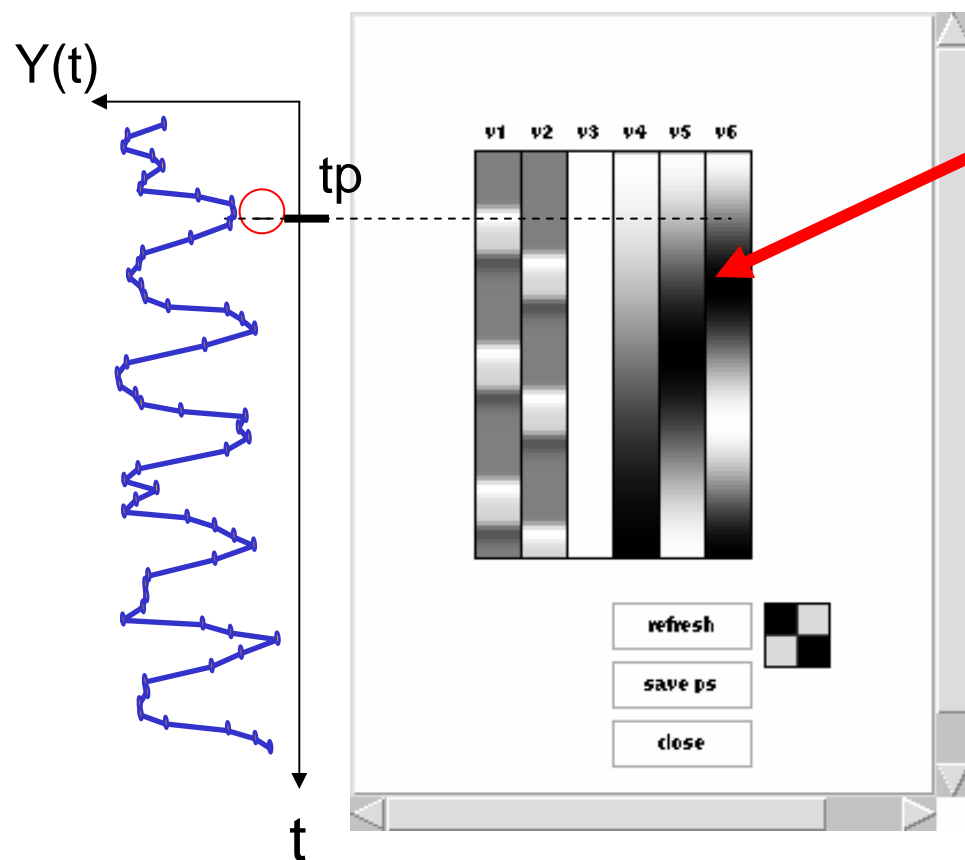
Each column represents the contribution from each condition we might see in a voxel time course.

Modeled Signal

$$Y(tp) = b_1 v_1(tp) + b_2 v_2(tp) + b_3 v_3(tp) + b_4 v_4(tp) + b_5 v_5(tp) + b_6 v_6(tp)$$



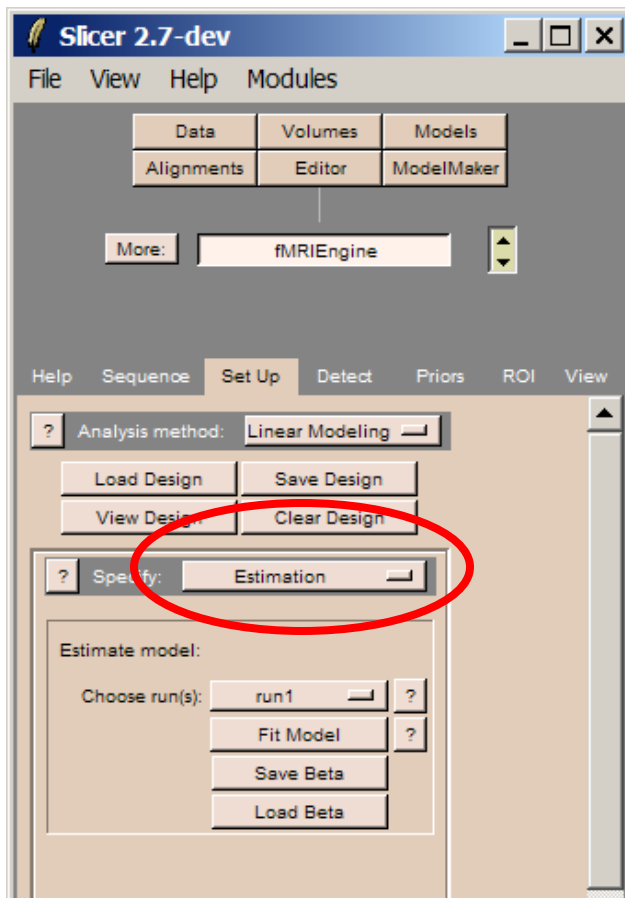
Design Matrix



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



Estimation

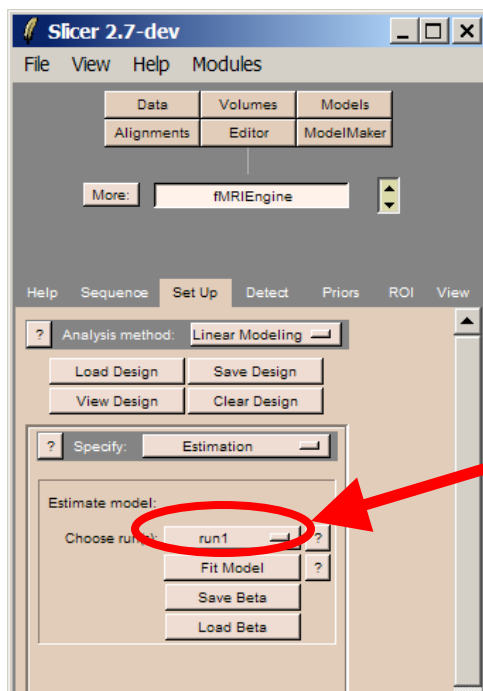


Select Specify Estimation to estimate B and e at every voxel:

$$Y = BX + e$$



Estimating model parameters

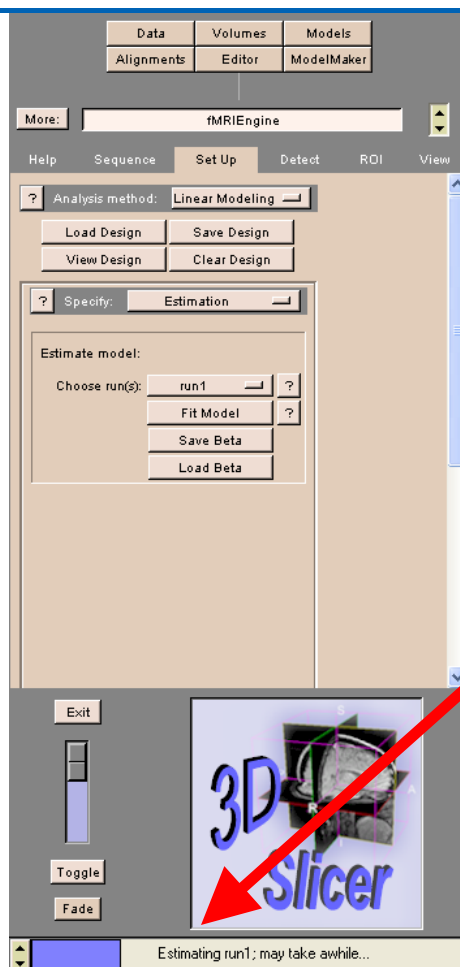


The Estimation panel appears

Select run1 and click on Fit Model



Estimating model parameters



Slicer shows the progress of model estimation



Overview

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Part 2: Describing stimulus schedule

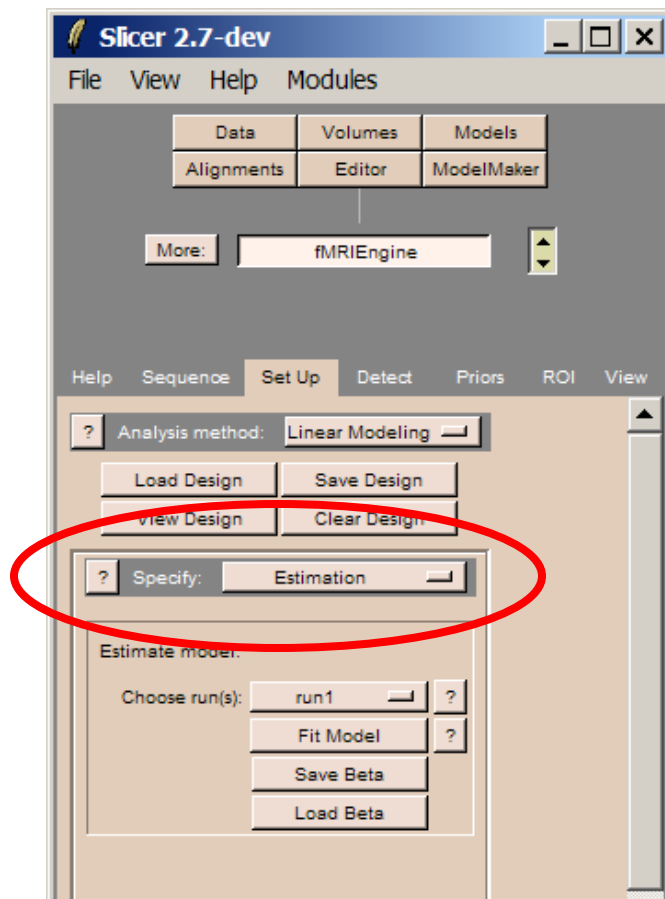
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Part 5: Inference & inspection



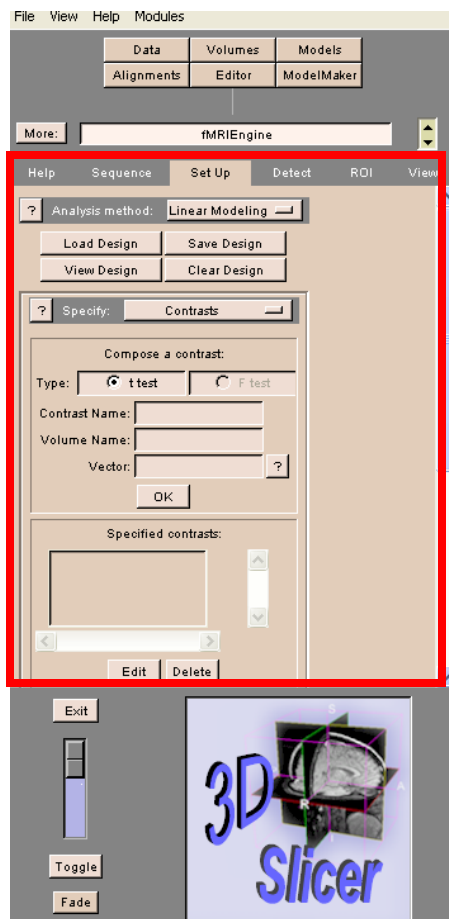
Specify Contrasts



In the SetUp panel, select Specify → Contrasts



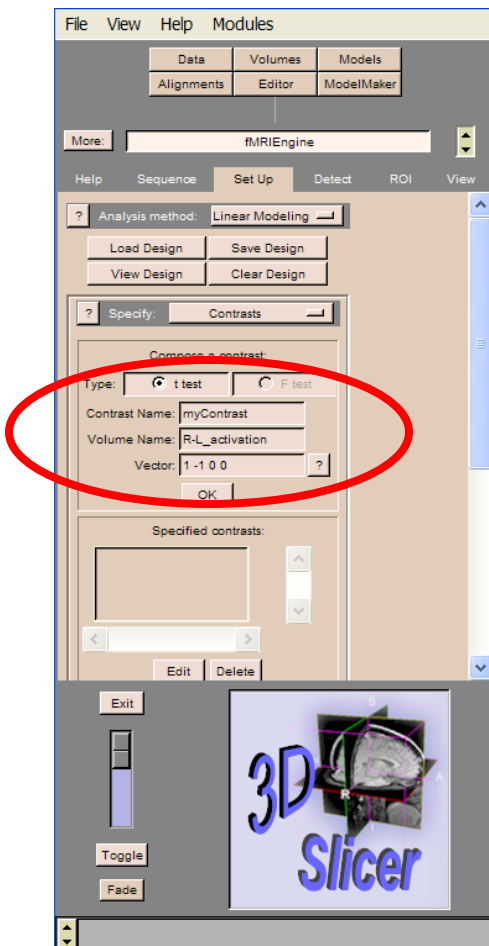
Specify Contrasts



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

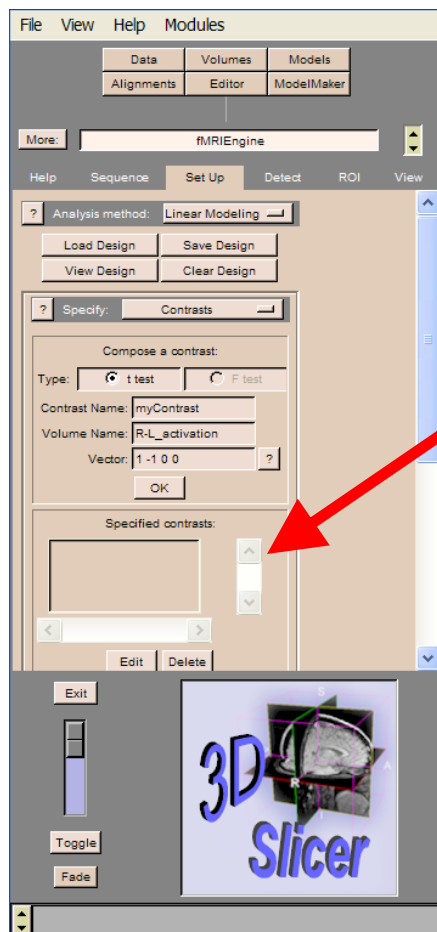


Contrast Vector

- Encoding of the effect that you want to test
- A contrast component per column in the design matrix (trailing zeros may be omitted)
 $1\ 0\ 0\ 0\ 0\ 0 \rightarrow$ test for whether there is any effect for the right hand
 $1\ -1\ 0\ 0\ 0\ 0 \rightarrow$ statistically contrast the effect for the right and left hand



Specify Contrasts



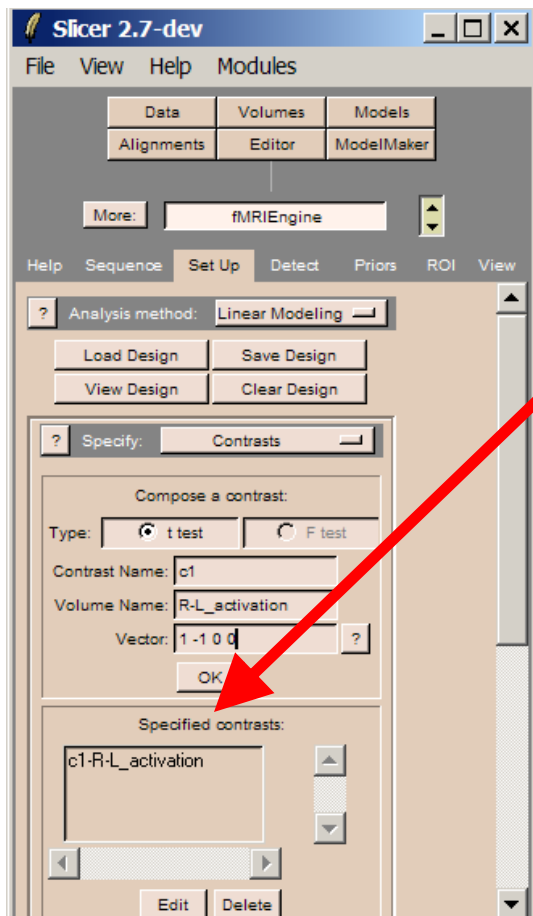
Select the statistical test t-test

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



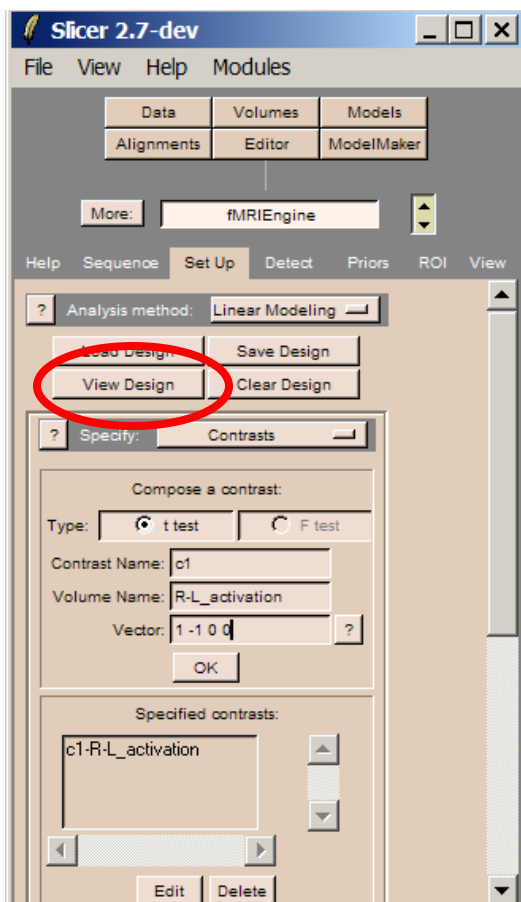
Specify Contrasts



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



Check contrasts & model

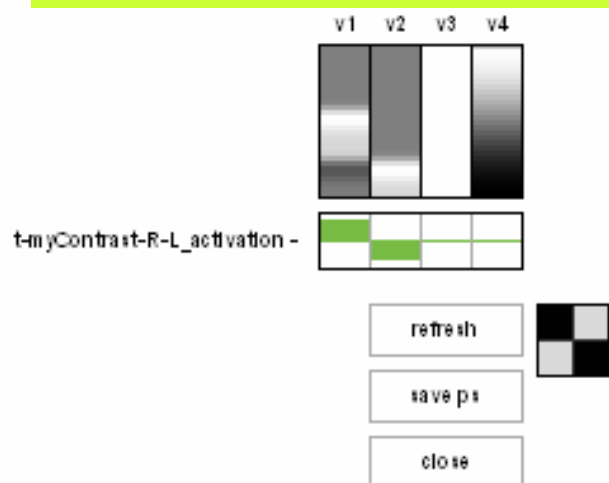


Click on View Design to display the Design matrix

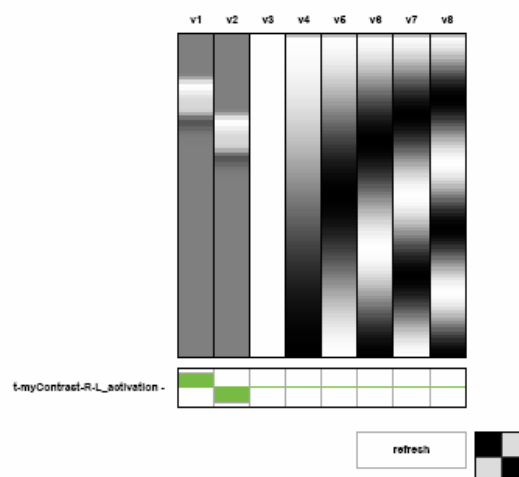


Design Matrix

A window displaying the design matrix and contrast vector appears.



Short dataset

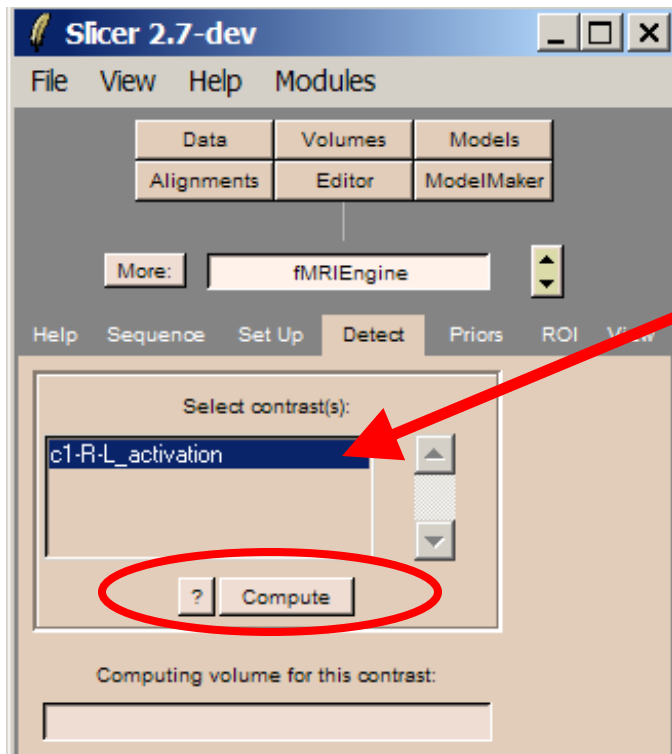


Long dataset

Check that the contrast and model are correct.



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)



Overview

Part 1: Loading and Previewing Data

Part 2: Describing stimulus schedule

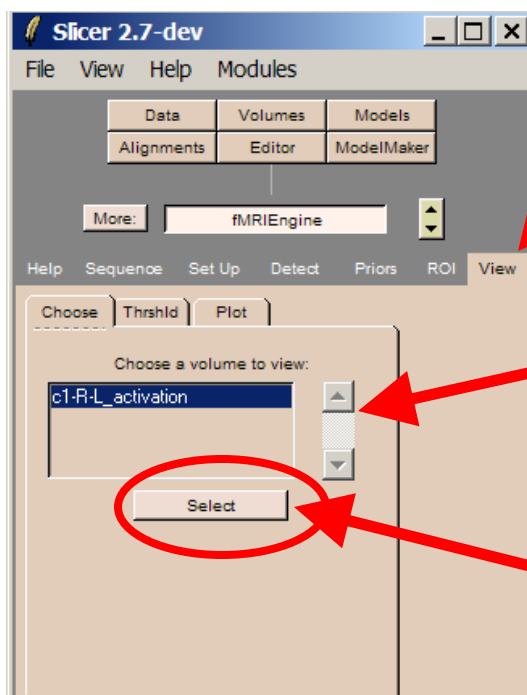
Part 3: Linear modeling & estimation

Part 4: Contrasts & computing SPMs

Part 5: Inference & inspection



Select the activation volume



Click on the View Tab

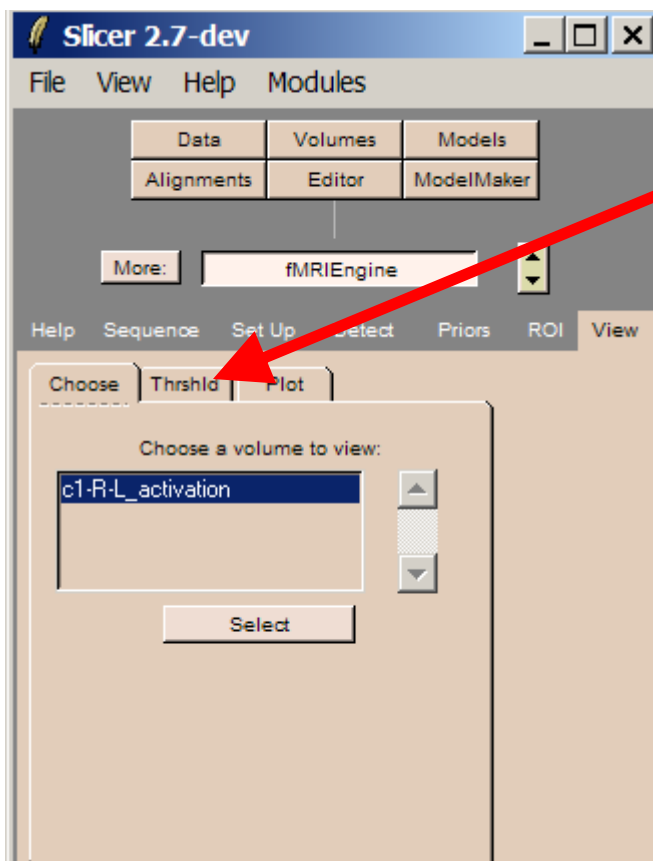
Select the subpanel Choose

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

Click on Select



Threshold

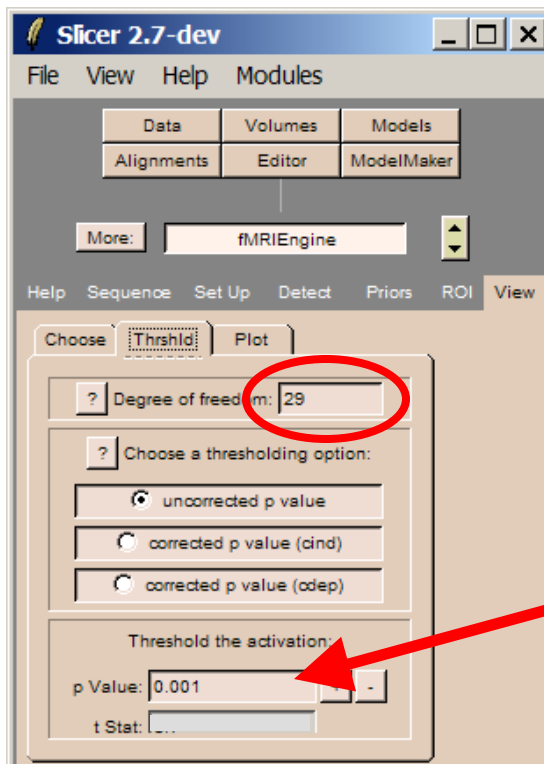


Click on the Threshold Tab

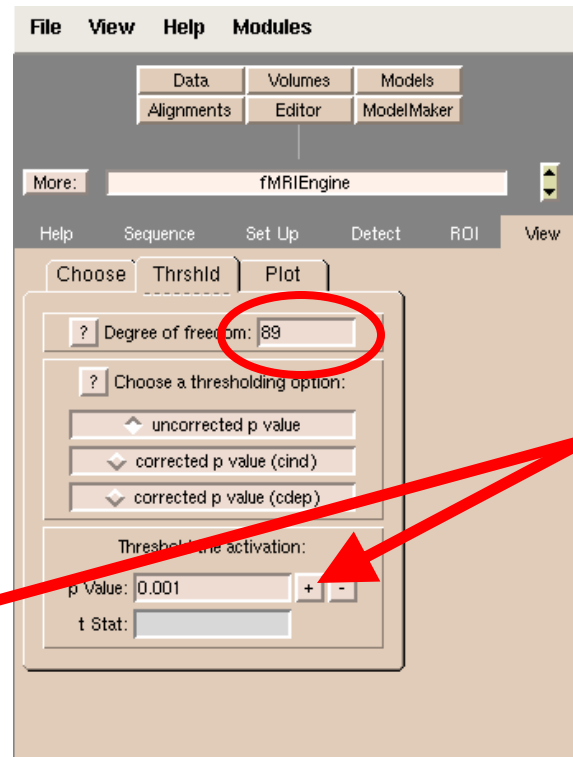


Threshold

Slicer indicates the degree of freedom (DoF): $N_{vol}-1$



Short dataset
DoF=29



Long dataset
DoF=89

Specify the p-Value
threshold 0.001 and
hit Enter



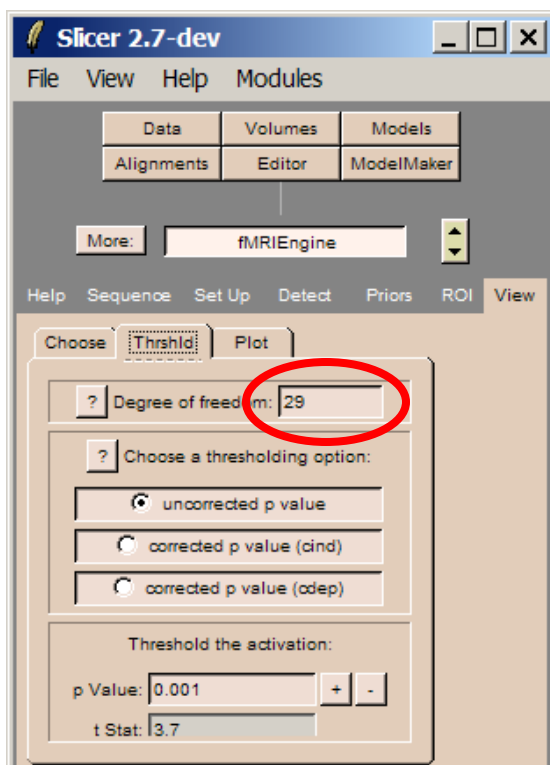
Null hypothesis

- H₀: there is no difference between the right hand condition and left hand condition on the fMRI signal. This is tested at each voxel.
- If the resulting probability is lower than the experiment's alpha value ($p < 0.001$), the null hypothesis can be rejected.



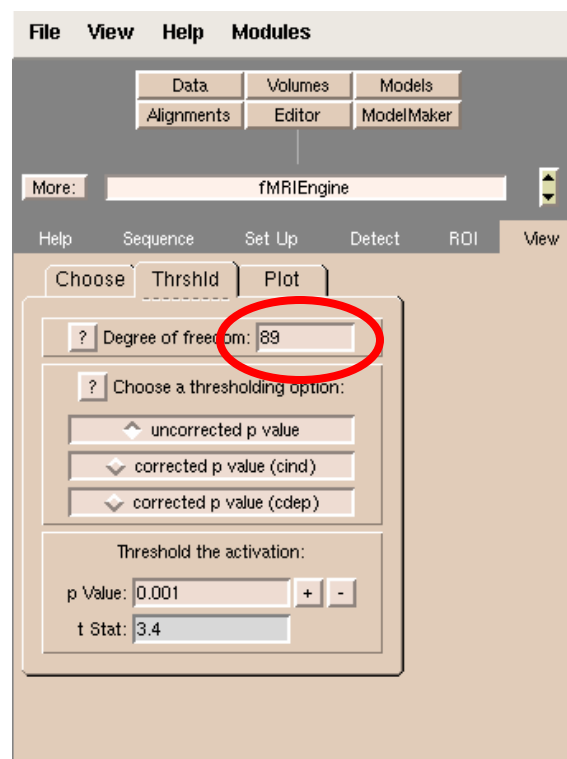
Threshold

Slicer calculates the corresponding threshold t Stat



Short dataset

t Stat = 3.7



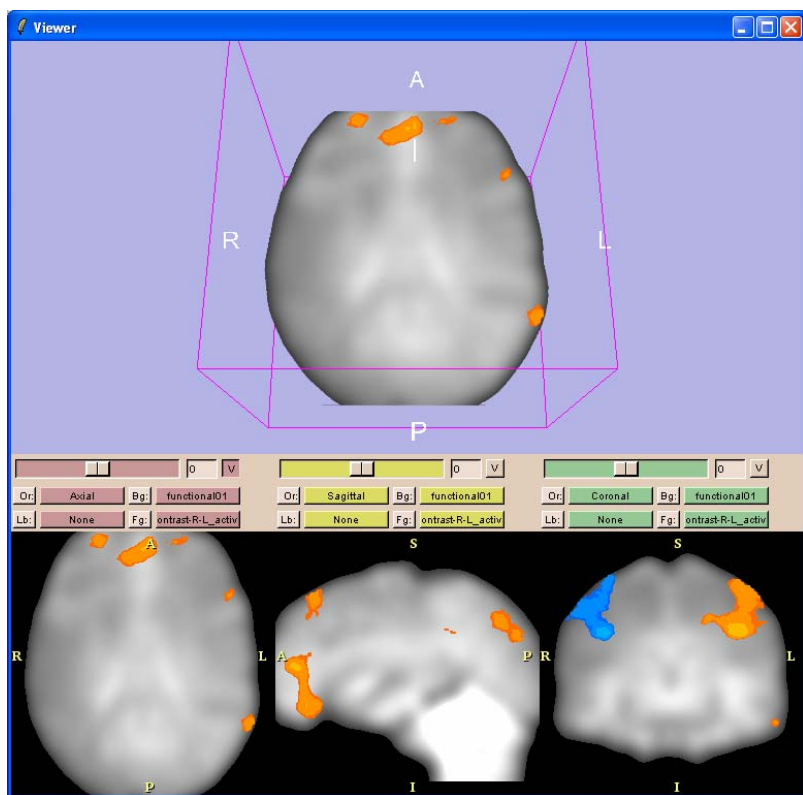
Long dataset

t Stat = 3.4

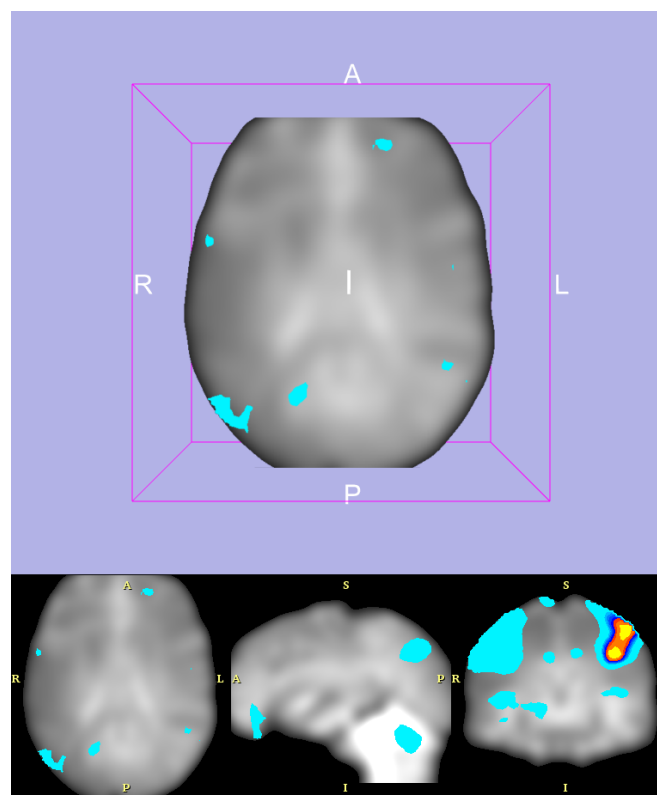


Activation map

Slicer displays the activation map overlaid on the fMRI images



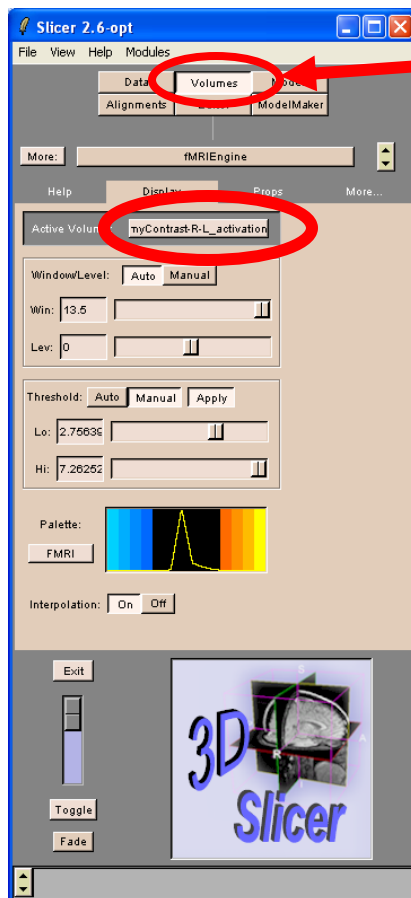
Short dataset



Long dataset



fMRI color palette



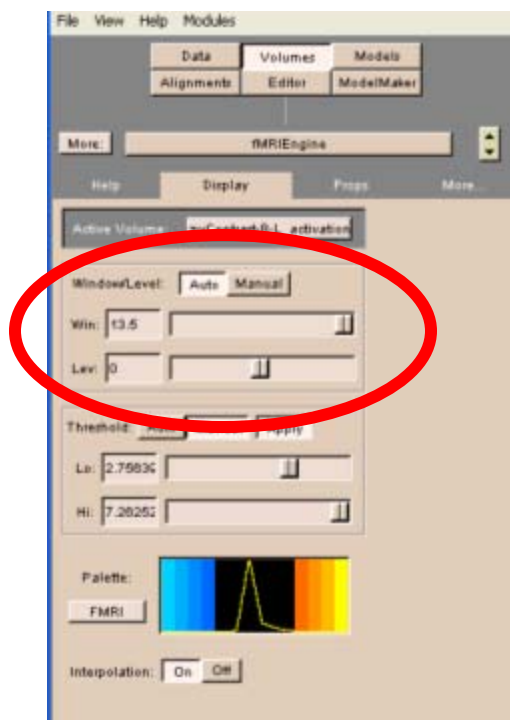
Click on the module Volumes

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



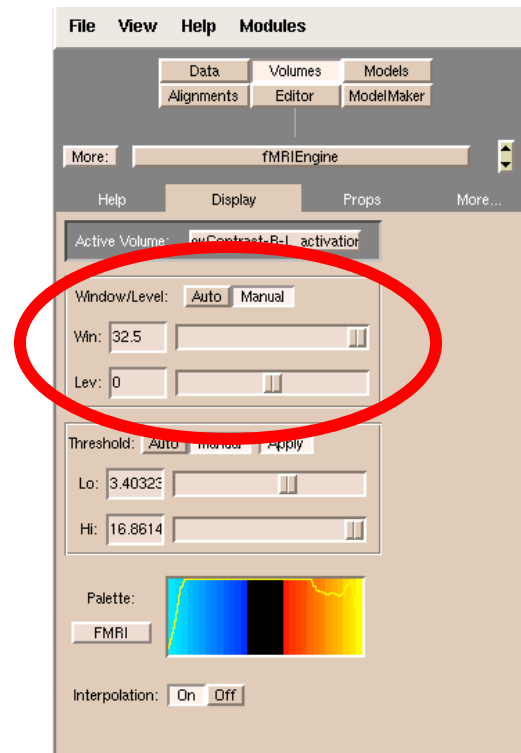
fMRI color palette

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



Short dataset

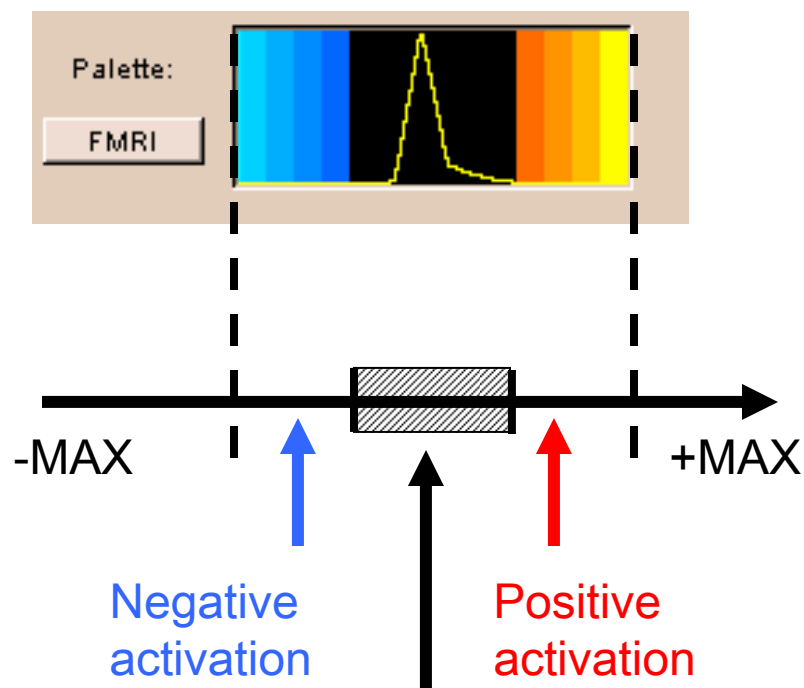
<http://na-mic.org> *Large Computing*



Long dataset

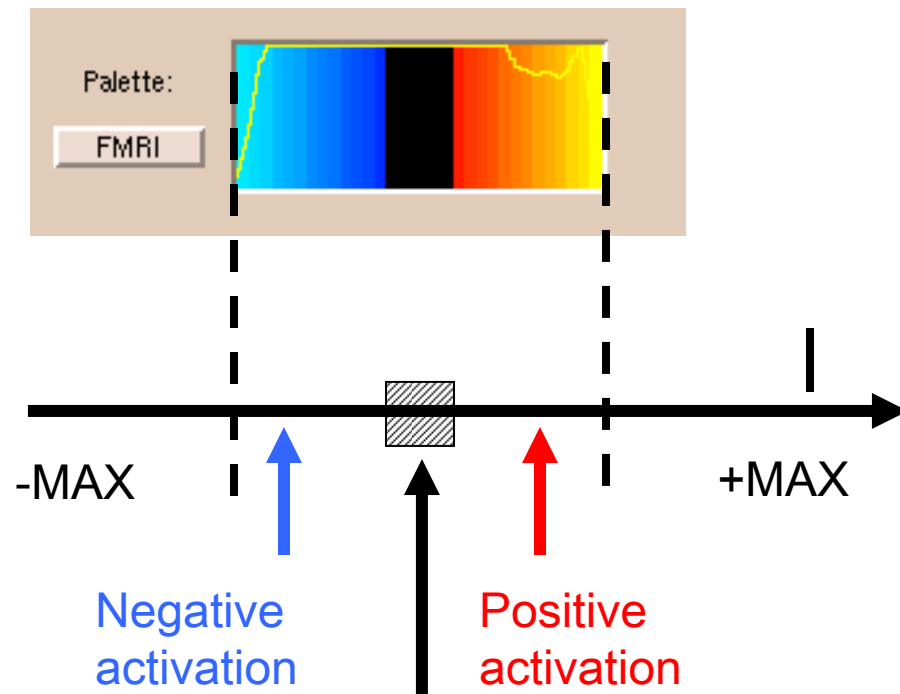


fMRI color palette



No statistical significance

Short dataset



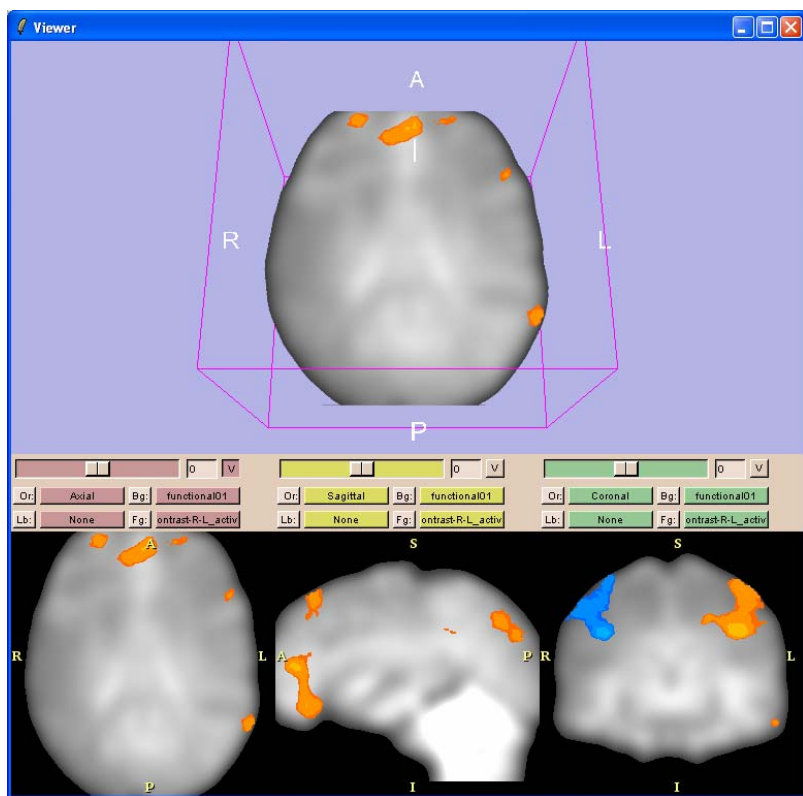
No statistical significance

Long dataset

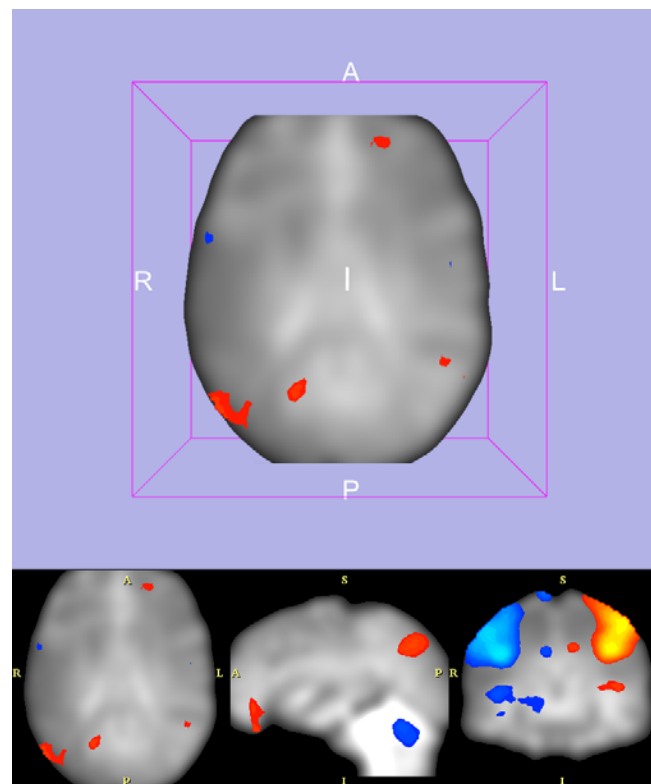


Activation map

Slicer displays the activation map overlaid on the fMRI images



Short dataset

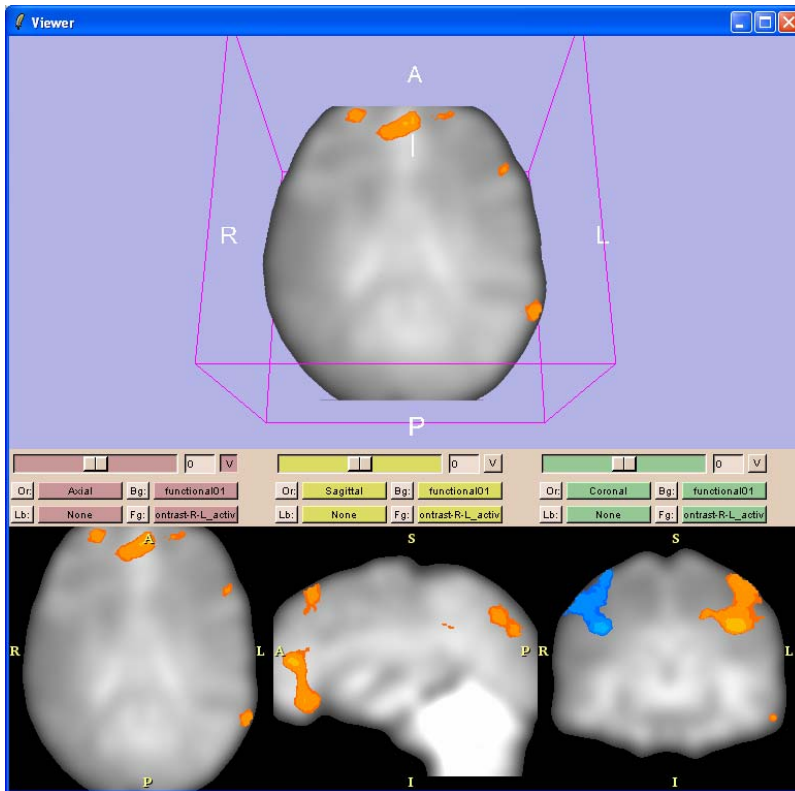


Long dataset

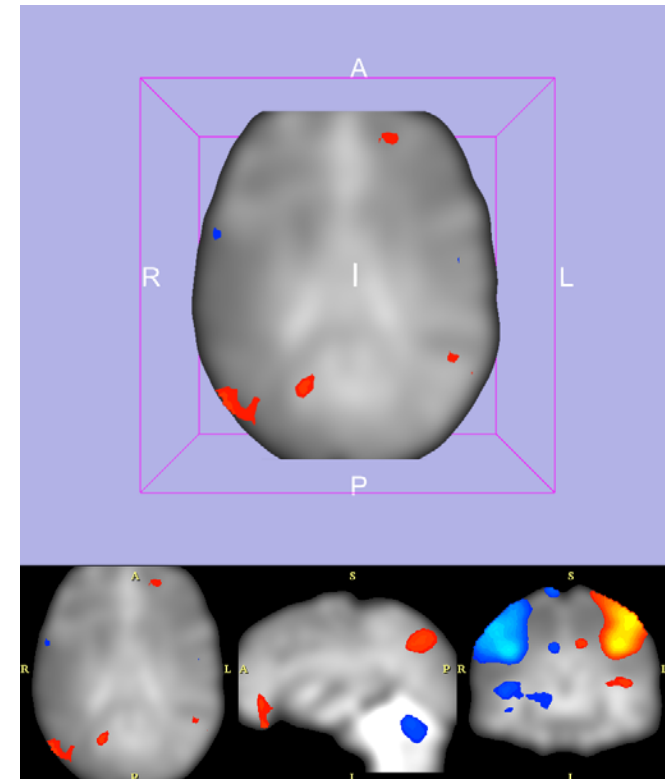


Visualize

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



Short dataset

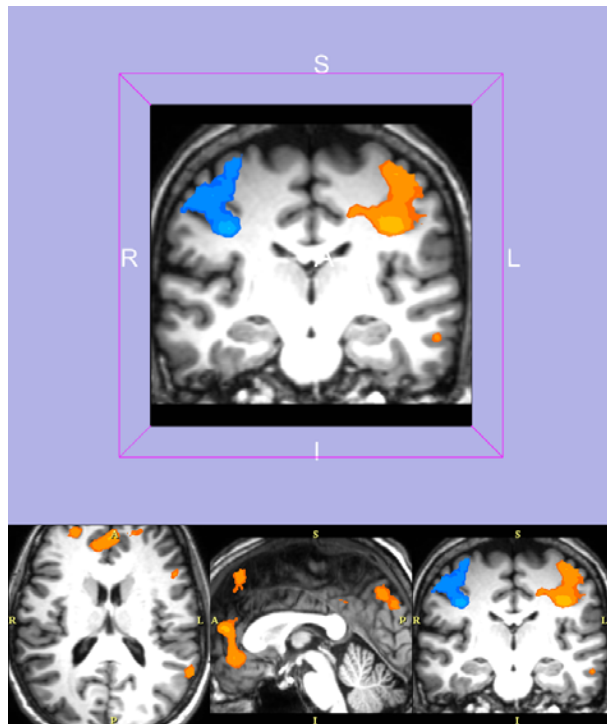


Long dataset

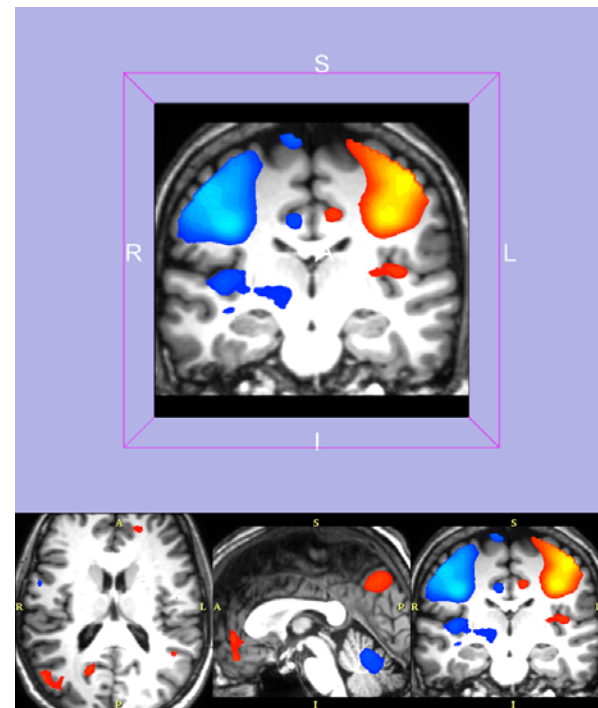


Visualize

Slicer displays the activation map superimposed on the anatomical images.



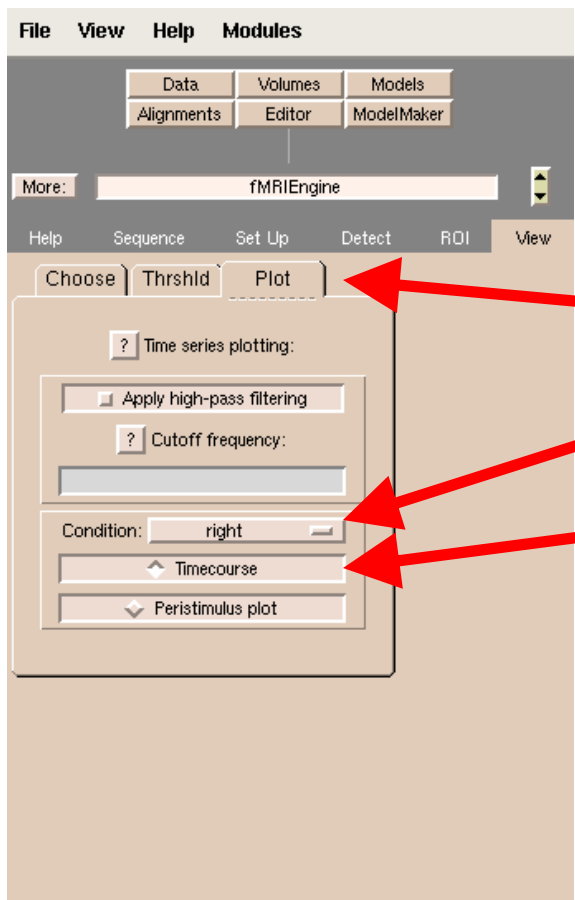
Short dataset



Long dataset



Inspect



Pick the tab Plot and select the condition = right

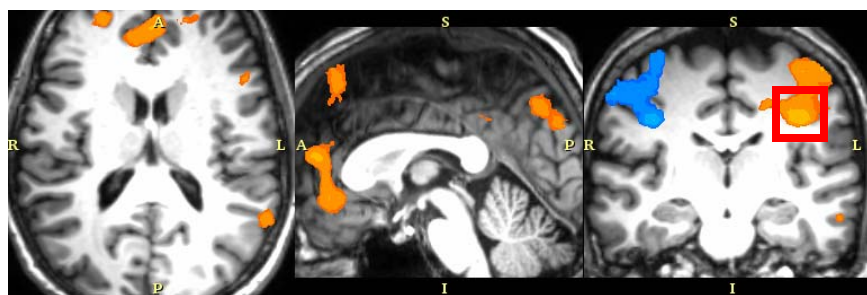
Select Timecourse plot option



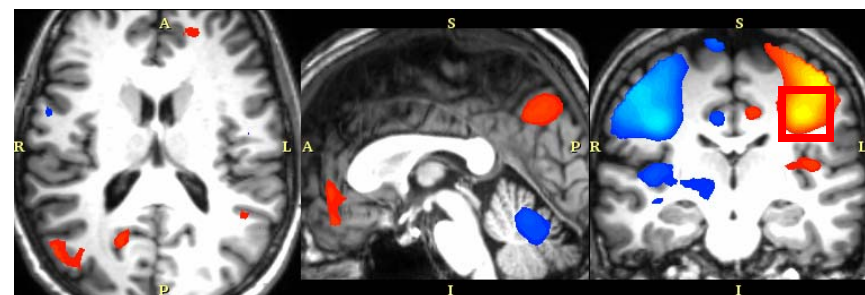
Inspect

Mouse over labelled area in Slice Window and left click on the pixel $R = -40$ $A = 0$ $S = 20$, which is highly significant in the activation map.

The left-hemisphere of the subject is shown on the right side of the image, in radiological convention.



Short dataset

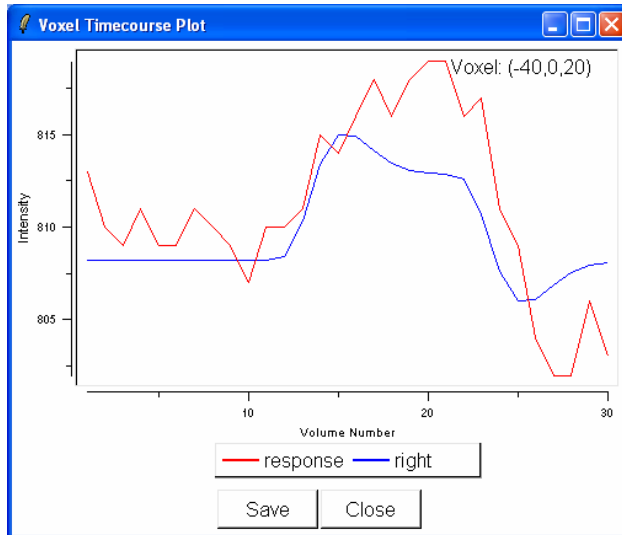
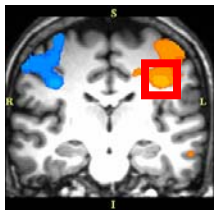


Long dataset

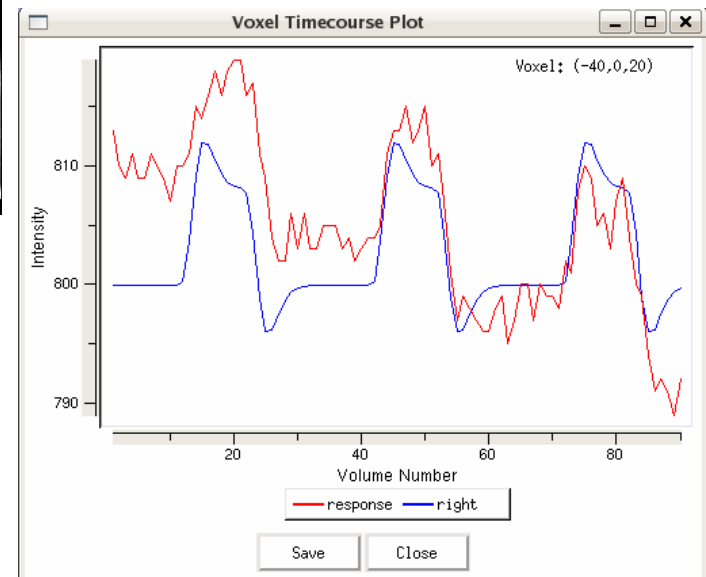
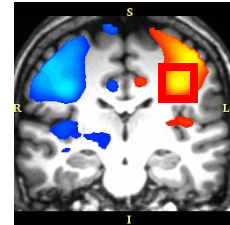


Voxel Timecourse

Slicer displays the voxel's actual timecourse (response) plotted with the modeled condition (right *hand*) for the selected voxel.



Short dataset



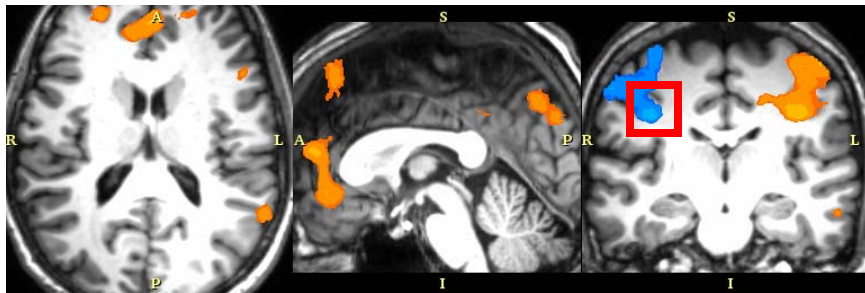
Long dataset

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

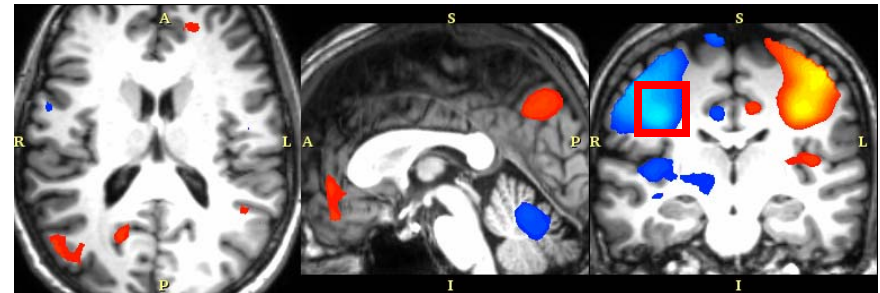


Inspect

Mouse over labelled area in Slice Window and left click on the pixel $R = 40$ $A = 0$ $S = 20$, which is highly significant in the opposite direction.



Short dataset

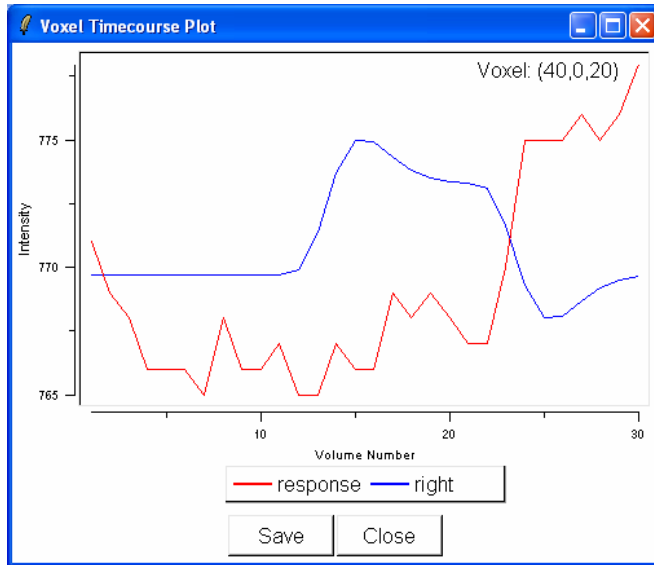
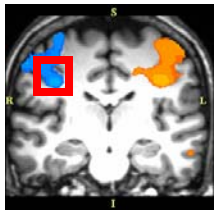


Long dataset

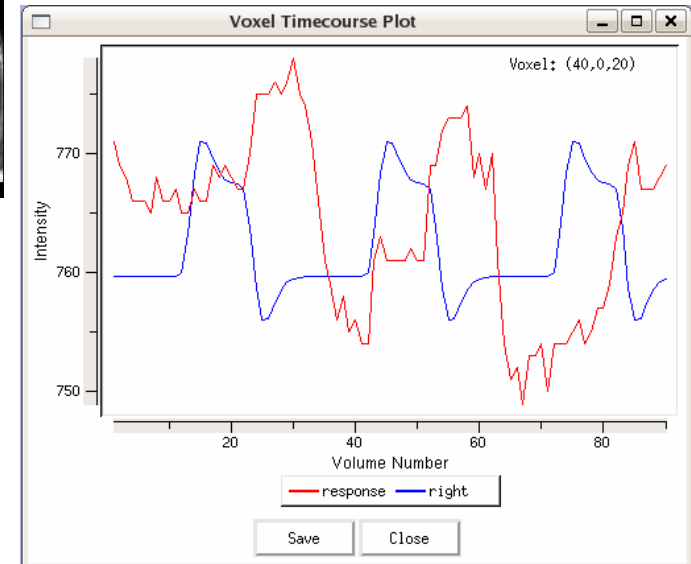
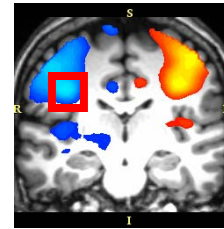


Voxel Timecourse

Slicer displays the voxel's timecourse plotted with the modeled condition for the selected voxel



Short dataset

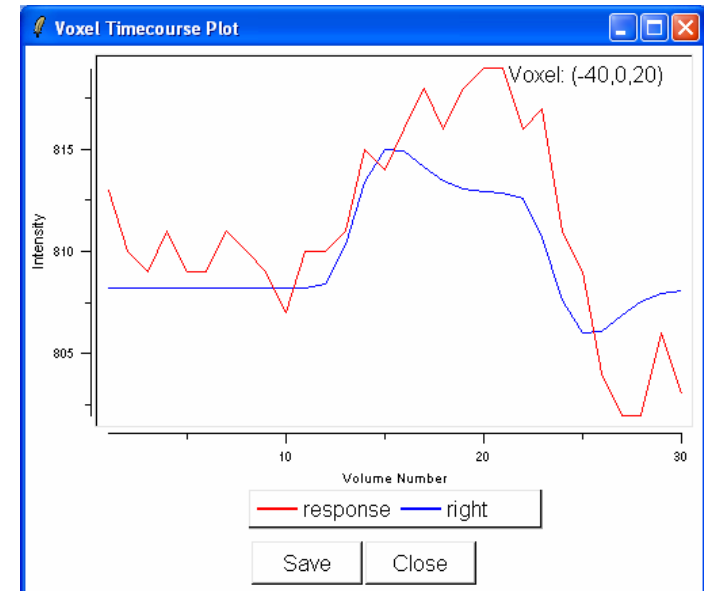
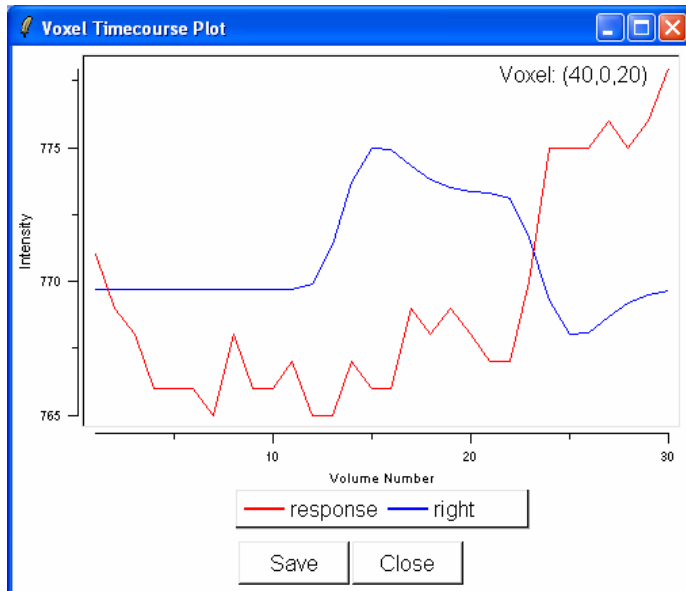
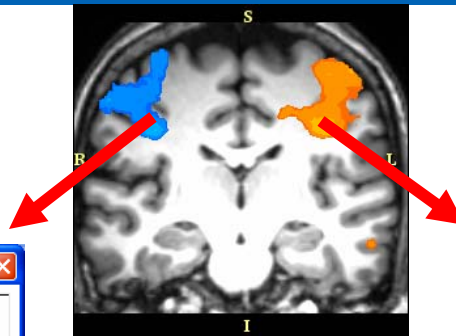


Long dataset

If we were plotting the left hand condition, what correlation would be observed?



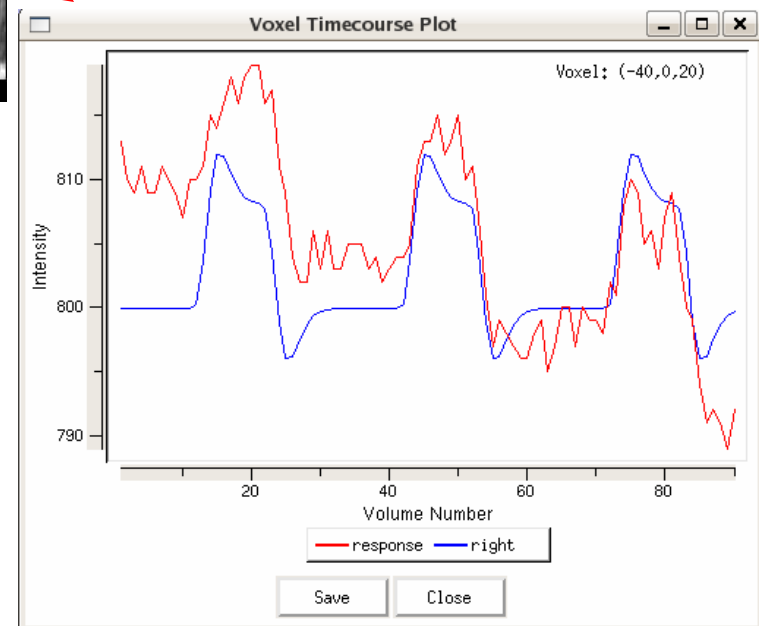
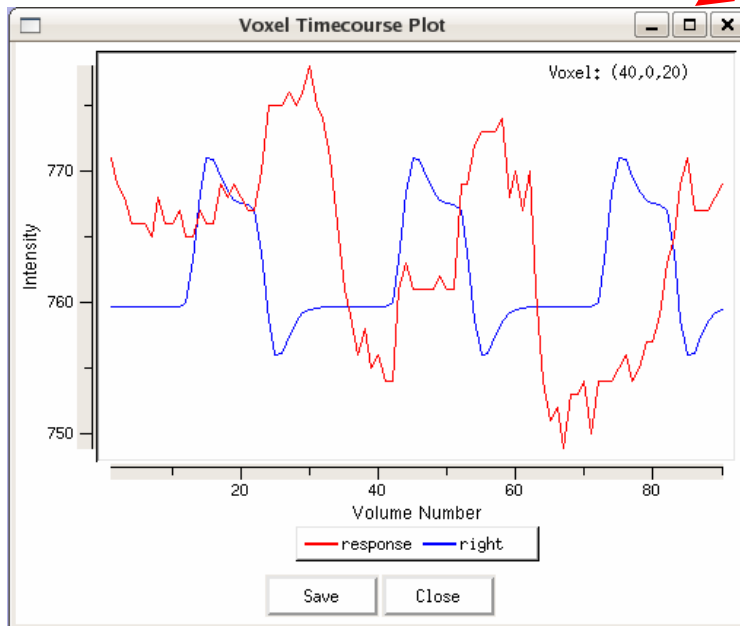
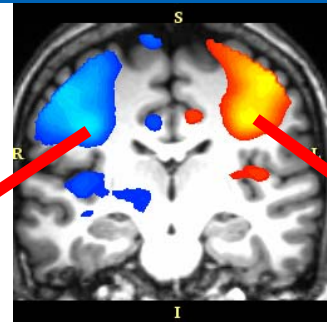
Contralateral side vs Ipsilateral side (short dataset)



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



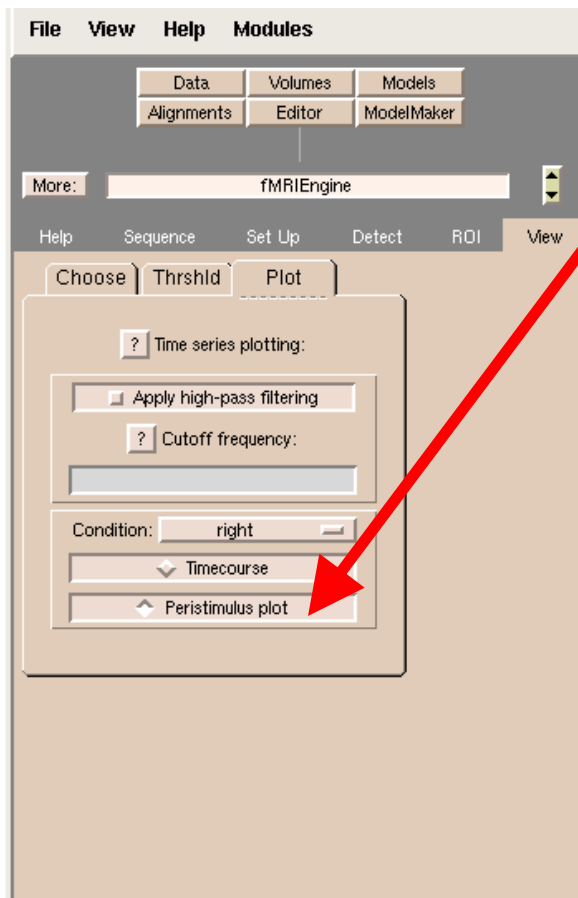
Contralateral side vs Ipsilateral side (long dataset)



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



Inspect

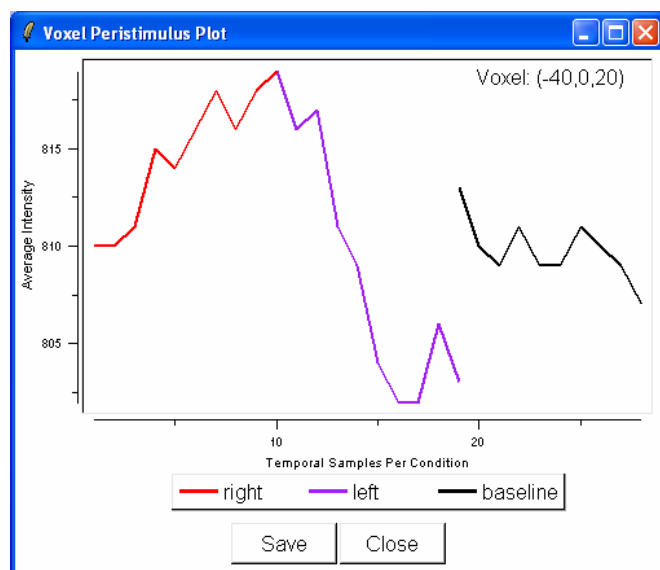
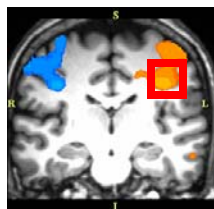


Select Peristimulus plot option and click on the voxel (-40,0,20) in the positive activation region

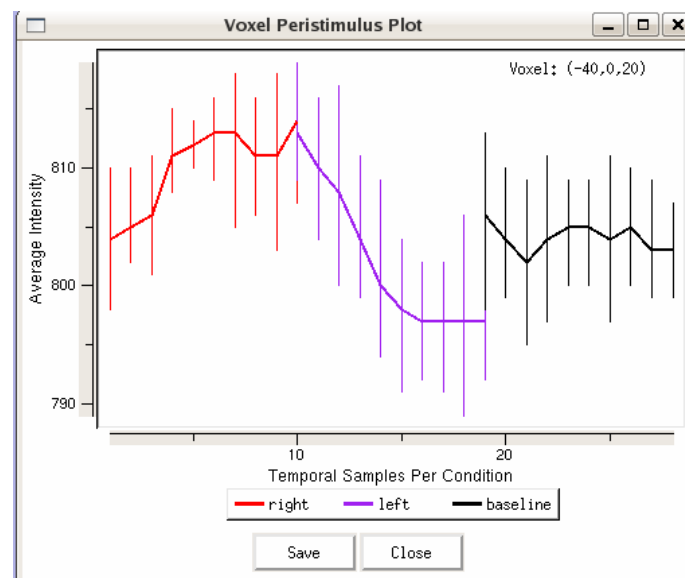
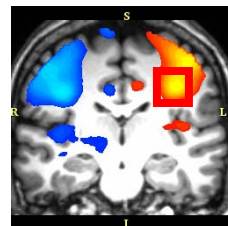


Voxel Peristimulus Plot

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



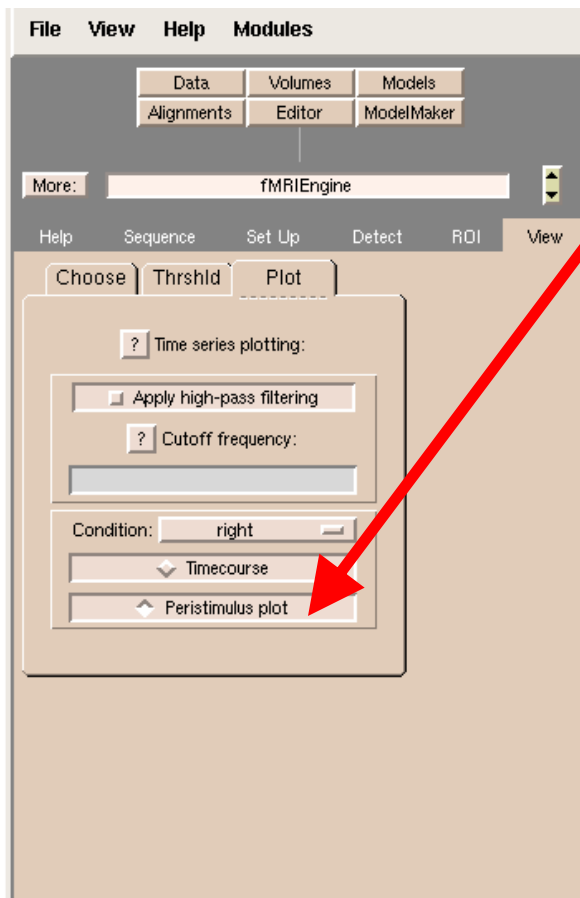
Short dataset



Long dataset



Inspect

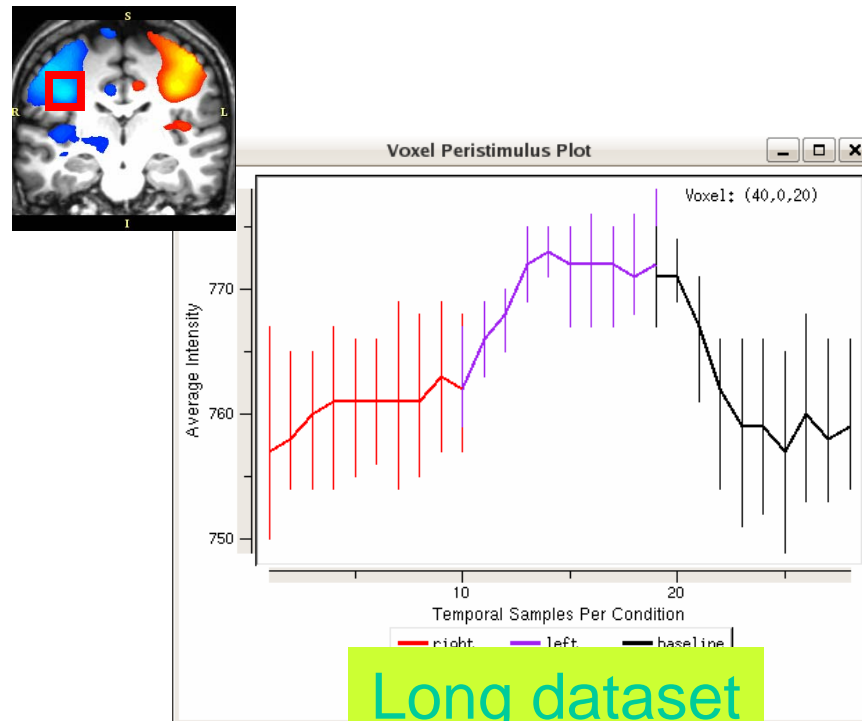
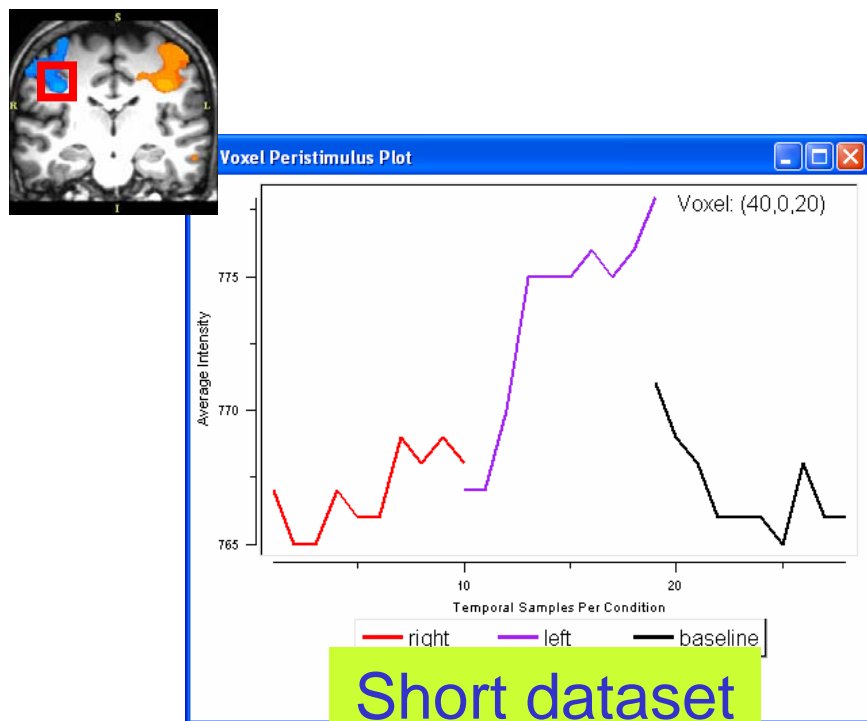


Select Peristimulus histogram option and click on the voxel in the negative activation region (40,0,20)



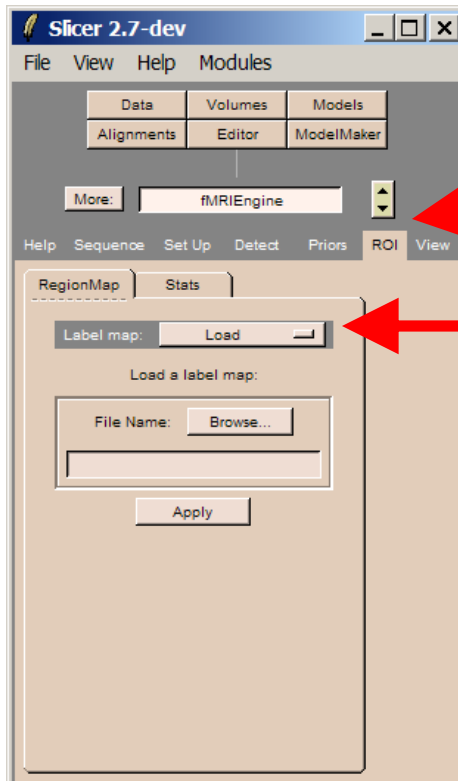
Voxel Peristimulus Plot

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





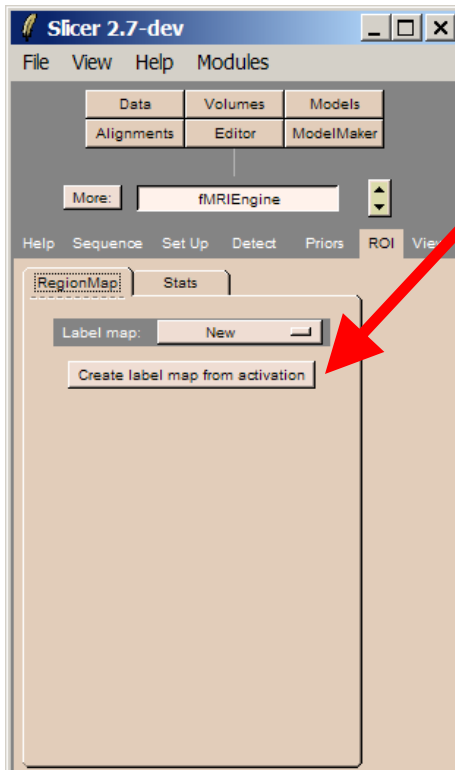
Activation-based region of interest



Select the ROI panel and RegionMap tab
Choose New Activation from Label map



Activation-based region of interest

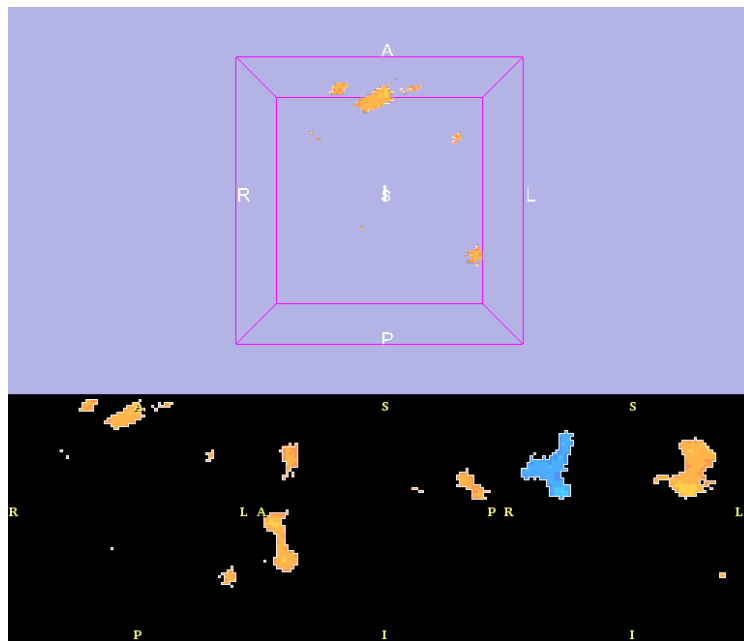


Click Create label map from activation, and wait while activation “blobs” are labelled

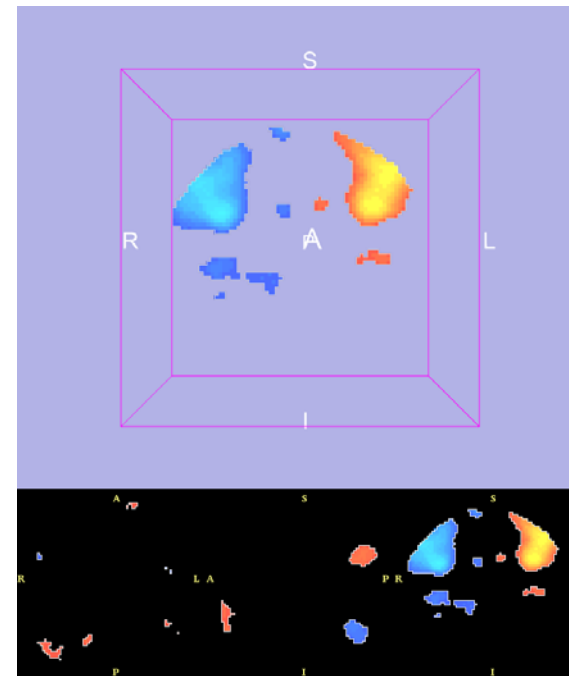


Activation-based region of interest

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



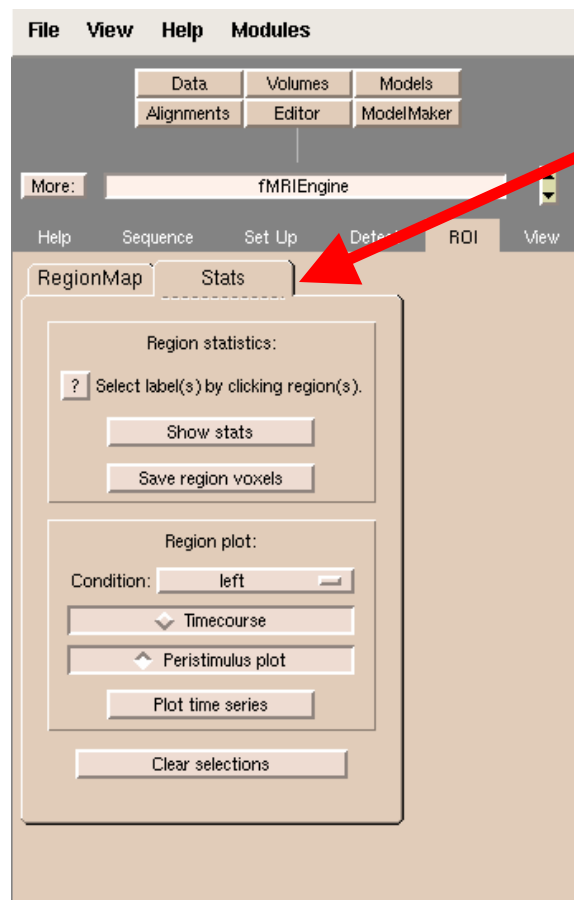
Short dataset



Long dataset



Region Statistics



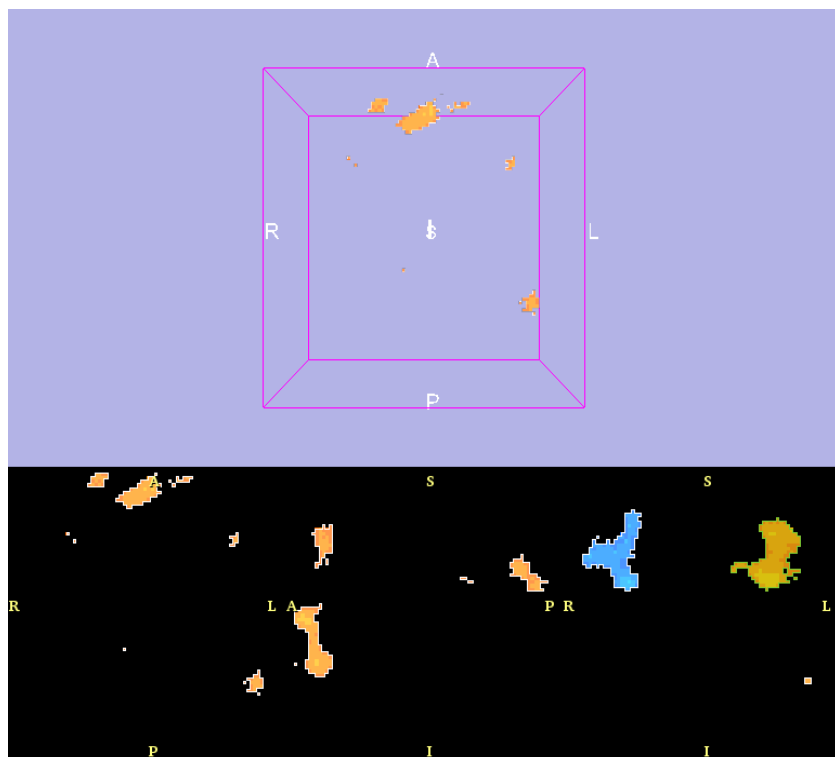
Select the subtab Stats
Select one or multiple regions in the left hemisphere to include in analysis by clicking in Slice Window.

Select the condition right.

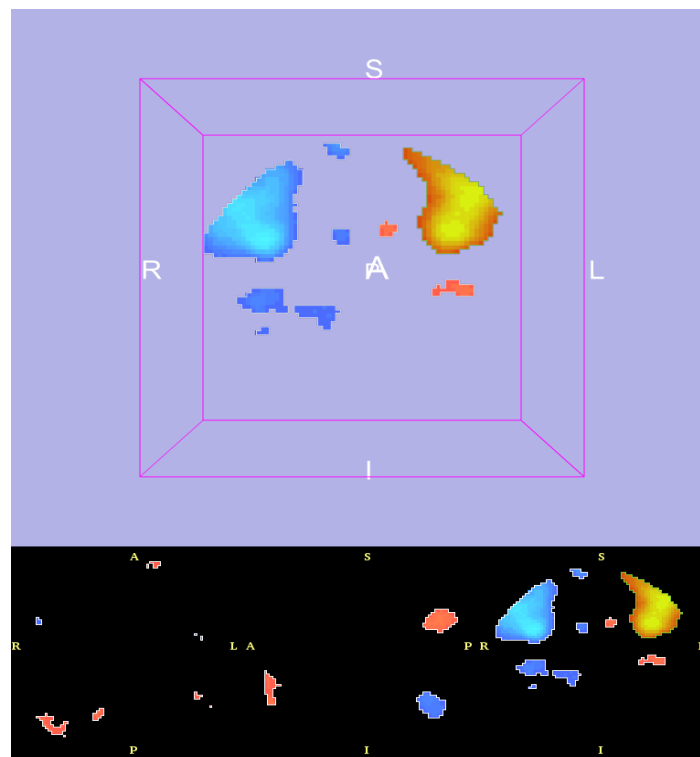


Region Statistics

The selected regions appear in green.



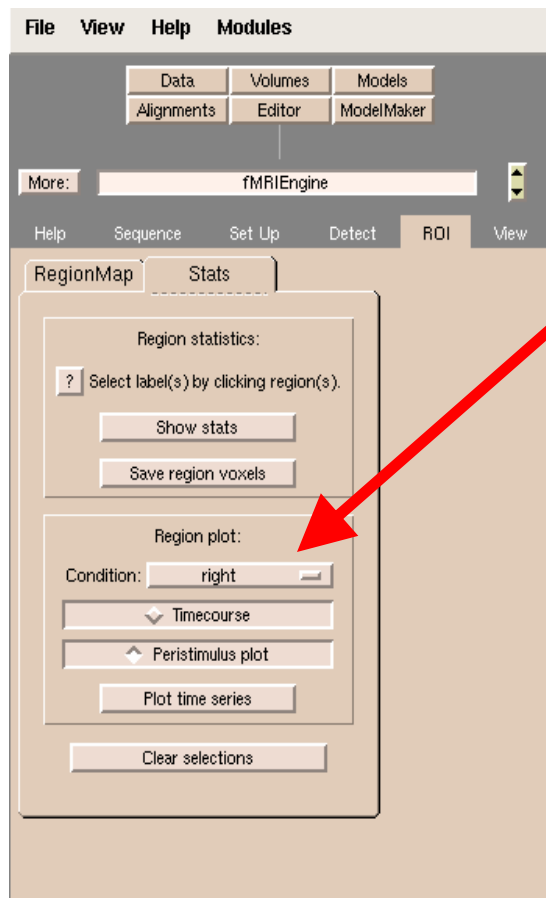
Short dataset



Long dataset



Region Statistics

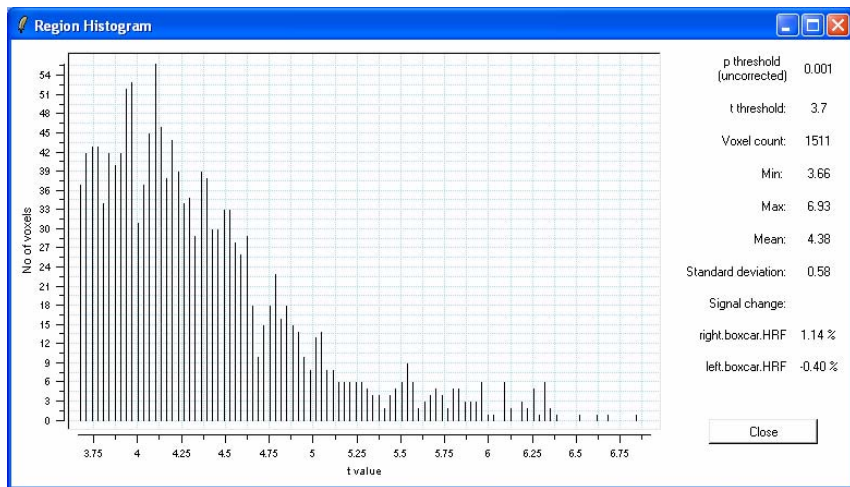


Click Show stats to display the statistics for the selected regions

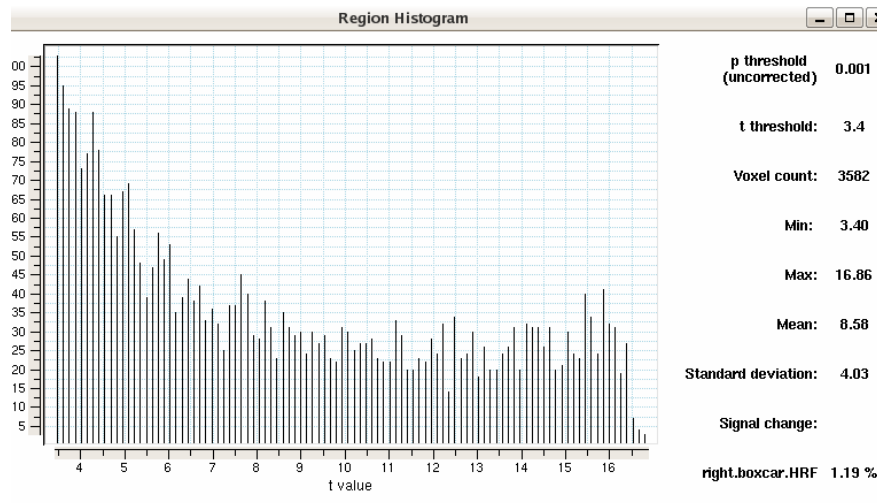


Region Statistics

Slicer displays the statistics for the selected region(s)



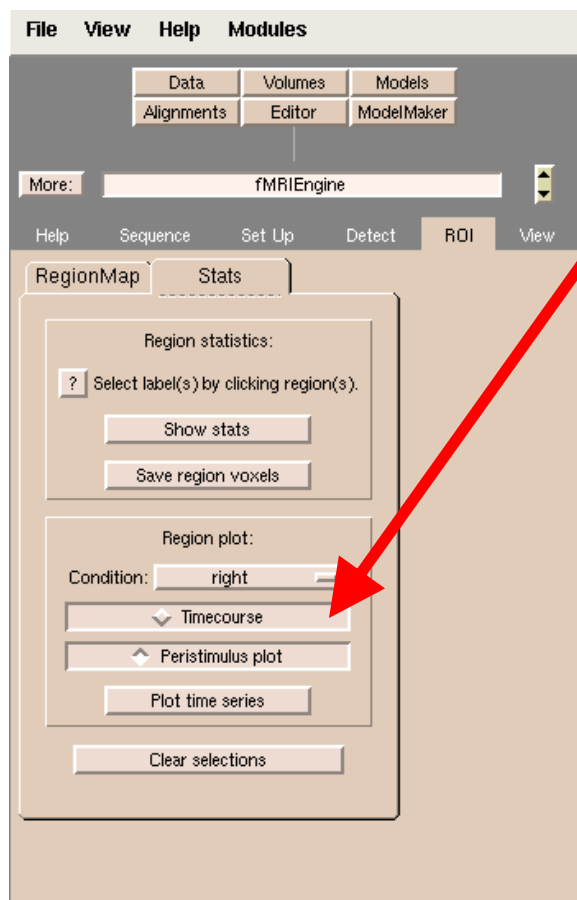
Short dataset



Long dataset



Region Timecourse

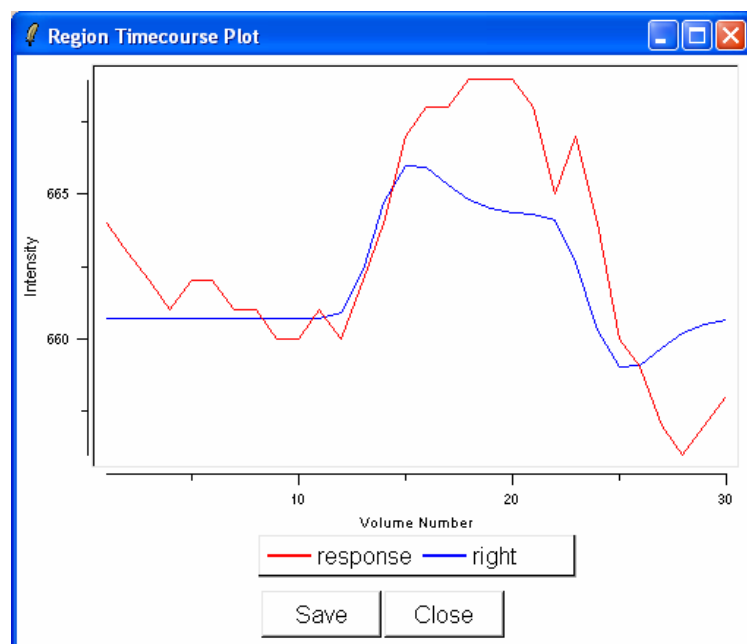


Select Timecourse plot option and click on Plot time series for this region.

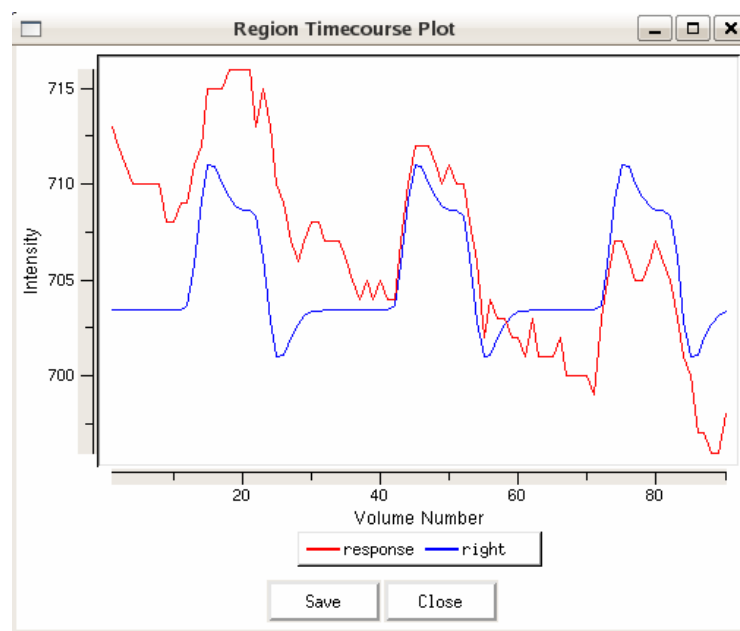


Region Timecourse

Slicer displays the region timecourse plot



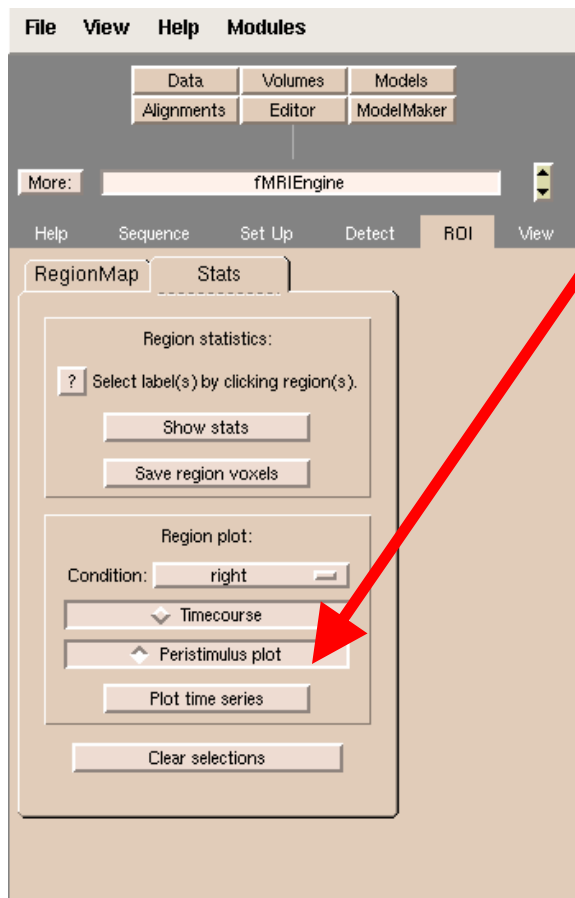
Short dataset



Long dataset



Region Peristimulus Plot

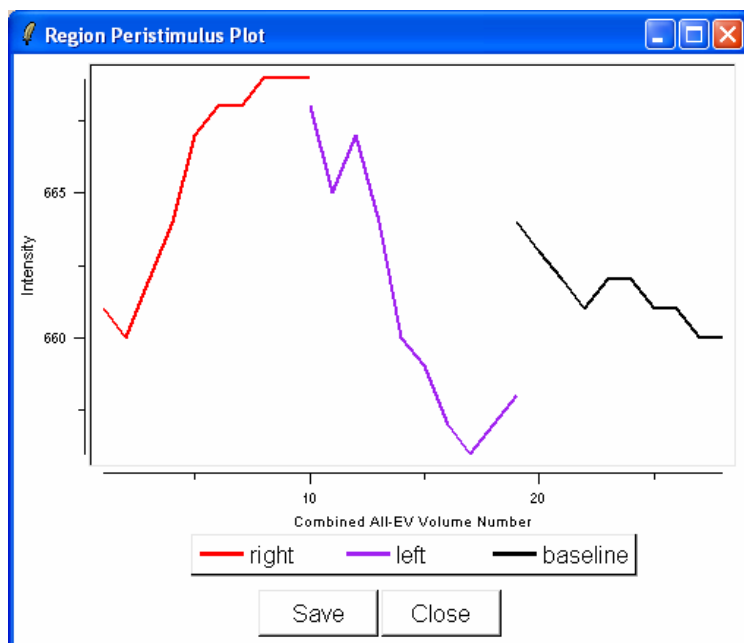


Select Peristimulus plot and click Plot time series for this region.

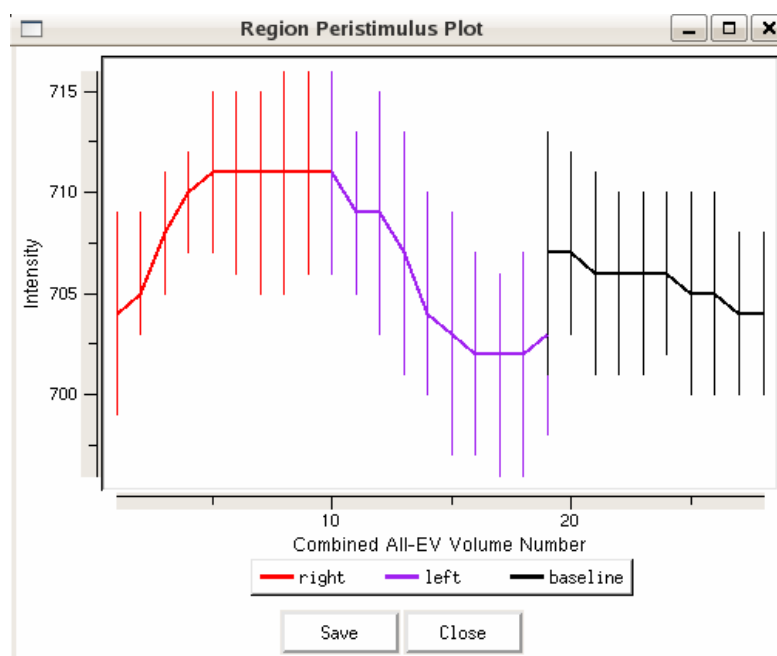


Region Peristimulus Plot

Slicer displays the Region Peristimulus Plot



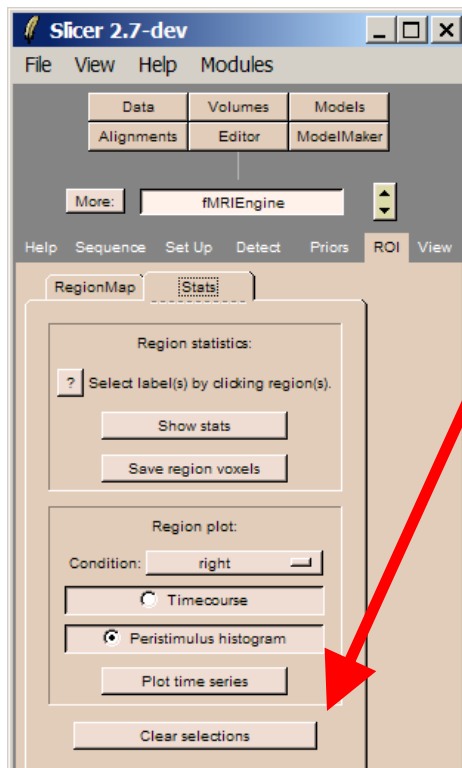
Short dataset



Long dataset



3D Visualization

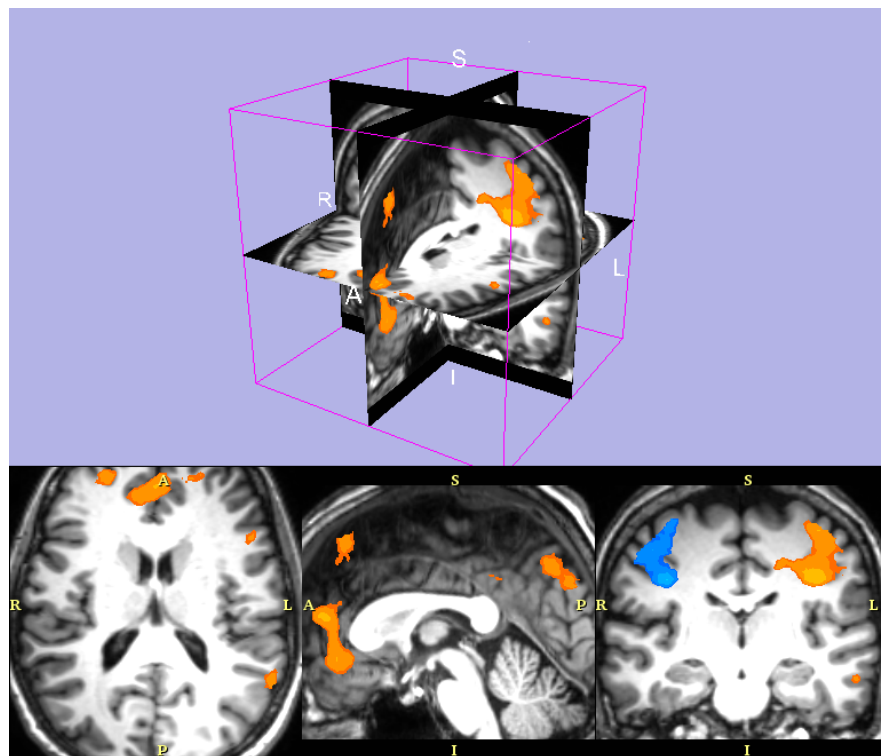


Click on Clear selections and display the structural volume anatomical3T in the background (Bg) and the activation map myContrast-R-L_activation in the foreground (Fg).

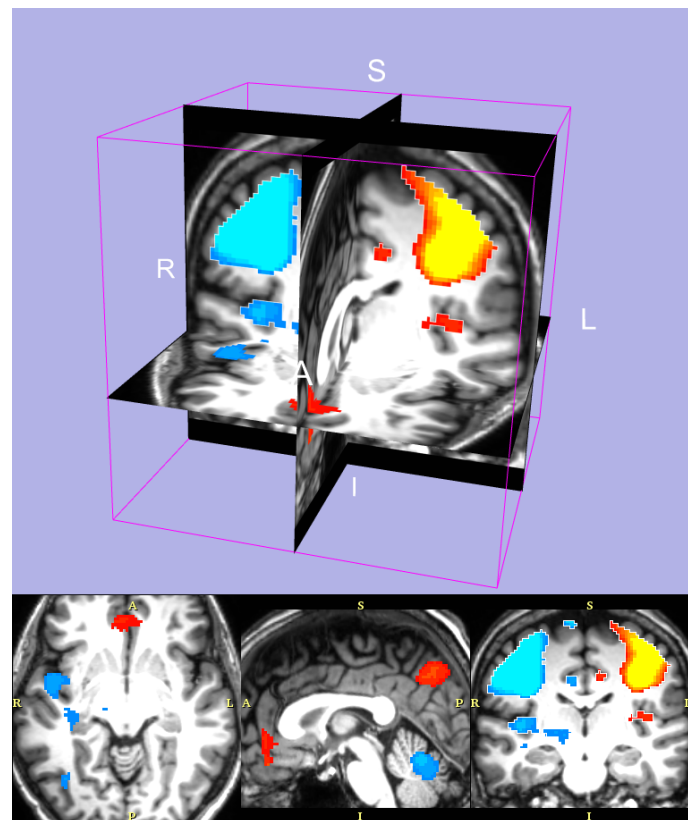
Display three anatomical slices in the 3D Viewer.



3D Visualization



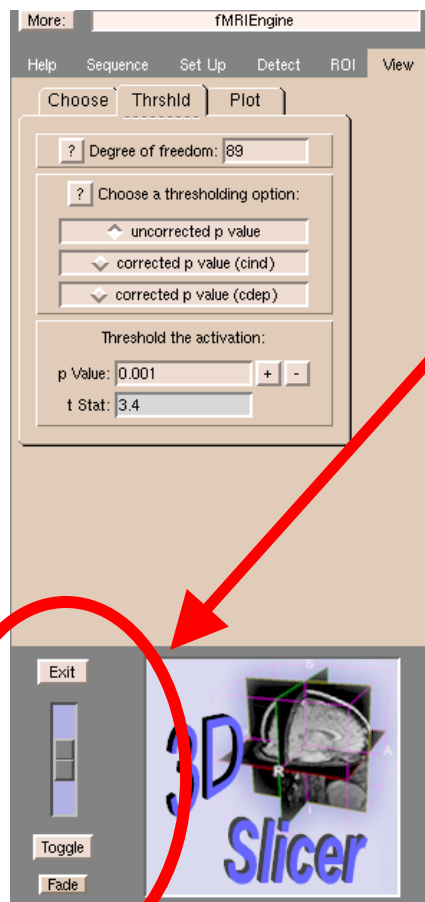
Short dataset



Long dataset



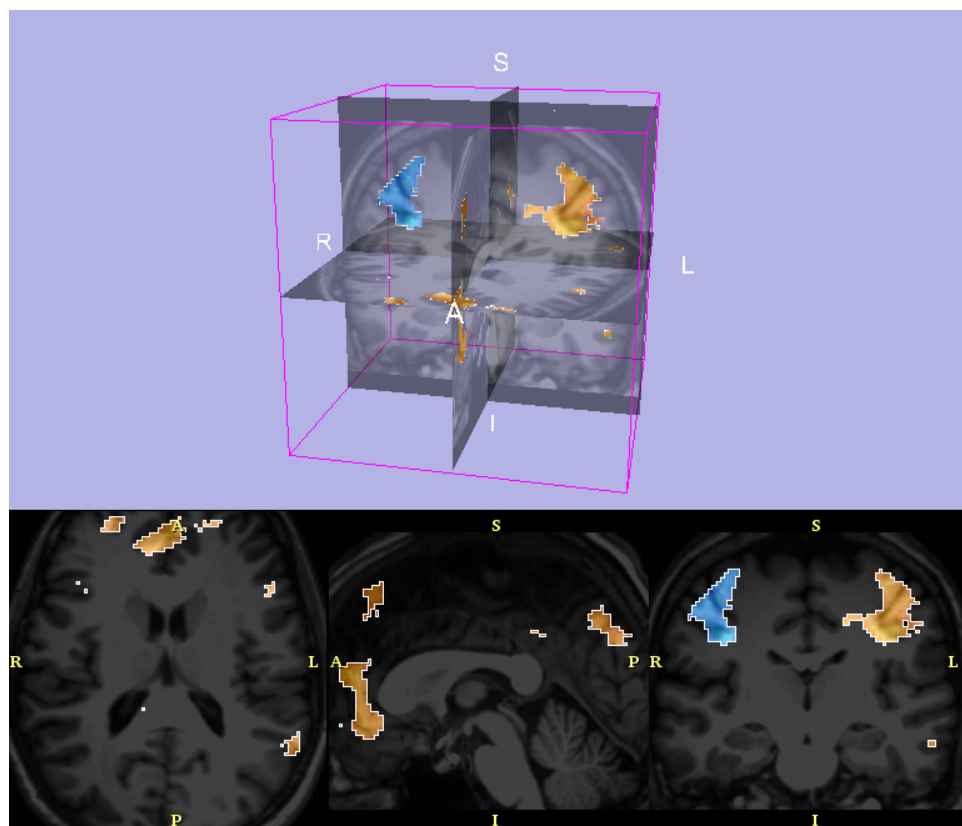
3D Visualization



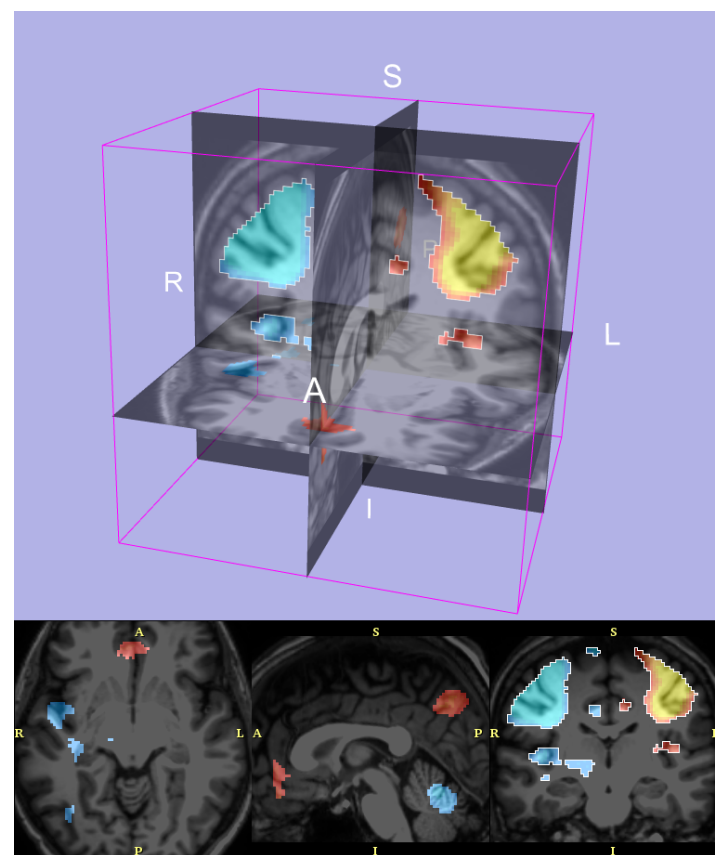
Fade in the activation volume for a good view of combined data



3D Visualization



Short dataset



Long dataset



Conclusion

- Analysis and visualization of fMRI data
- Framework activation detection algorithms and inference engines
- Open-Source environment