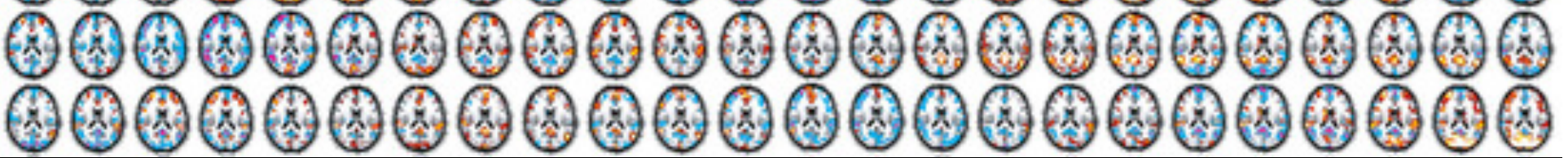


MATLAB TUTORIAL

How to Analyze fMRI on SPM

Independent Study in Psychology
Fall 2011

fMRI Datasets



Face fMRI Dataset:

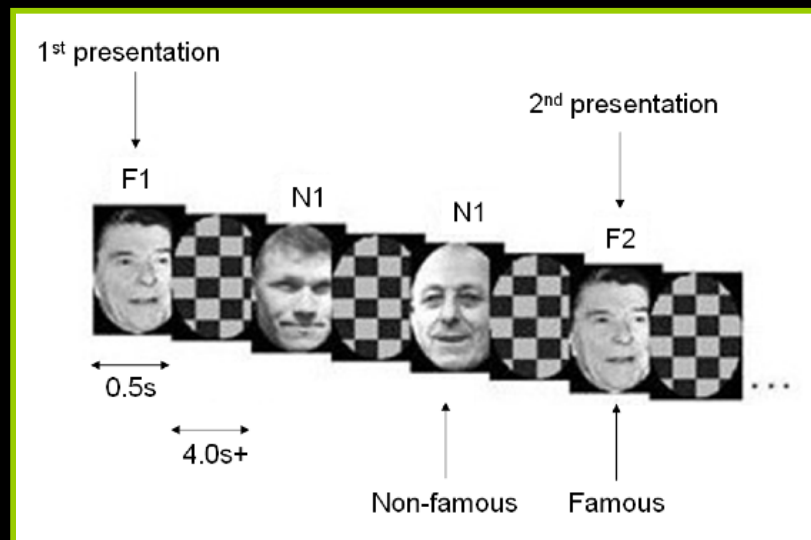
http://www.fil.ion.ucl.ac.uk/spm/data/face_rep/

Face Group fMRI Dataset:

http://www.fil.ion.ucl.ac.uk/spm/data/face_rfx/spm2_face_rfx.doc

Paradigm

- Randomized presentation of 26 famous and 26 non-famous grayscale photographs
- Each face required a judgment denoting whether or not the face was famous

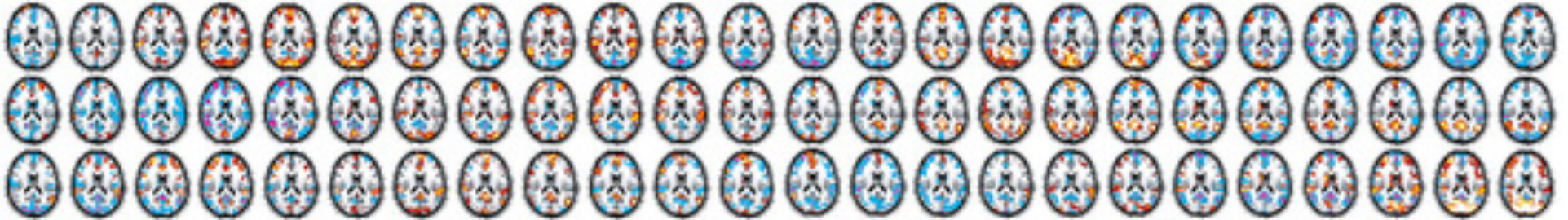


fMRI Data Collection

- Images were acquired using continuous Echo-Planar Imaging (EPI)
 - TE = 40 ms
 - TR = 2 s
 - 24 descending slices
 - 64 x 64 3 x 3 mm²
 - 3 mm thick
 - 1.5 mm gap

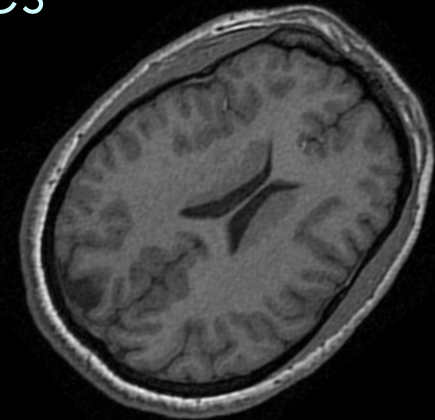


fMRI First-Level Data Analysis

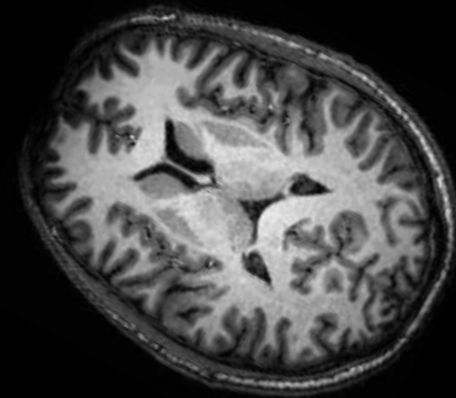


fMRI Data Files

- 351 Analyze format functional images
 - sM03953_0005_*.img



- Analyze format structural images
 - sM03953.img

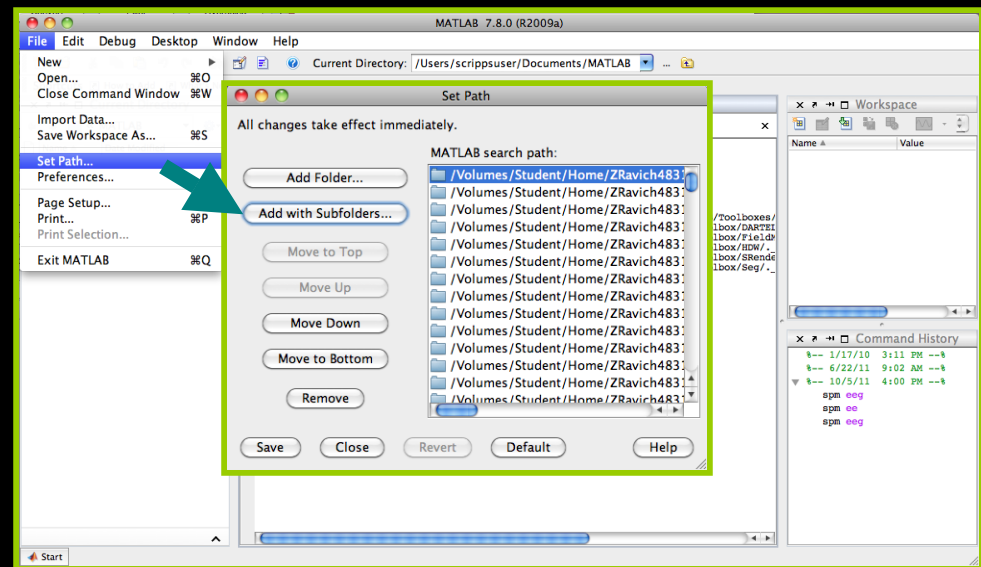


***Create 2 subdirectories:
1) jobs and 2) categorical***

Step 1

Getting Started

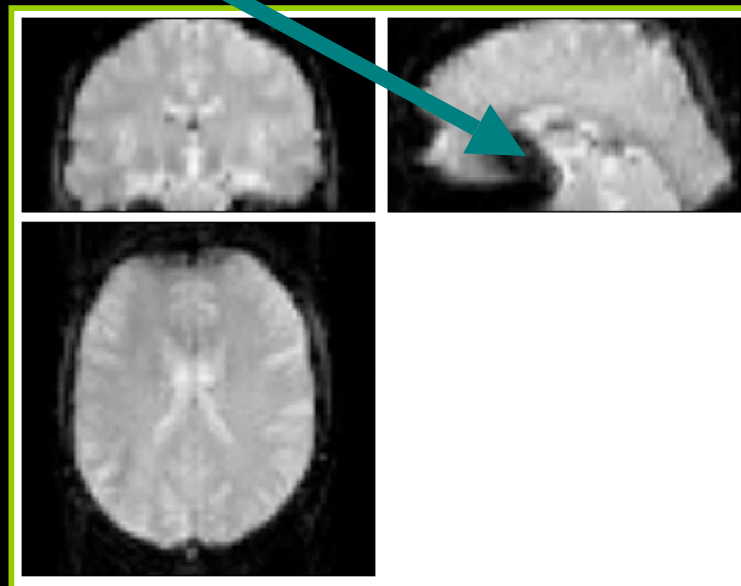
- Open up MATLAB
- Go to “File” → “Set Path” → “Add with Subfolders” → Select the dataset folder (i.e., Home\ZoeRavich4831\MATLAB\Datasets)
 - “Do you want to save this path for future reference?”; Click “No”
- Go to the Command Window and type “spm_fmri” to open up the fMRI GUI



Step 2

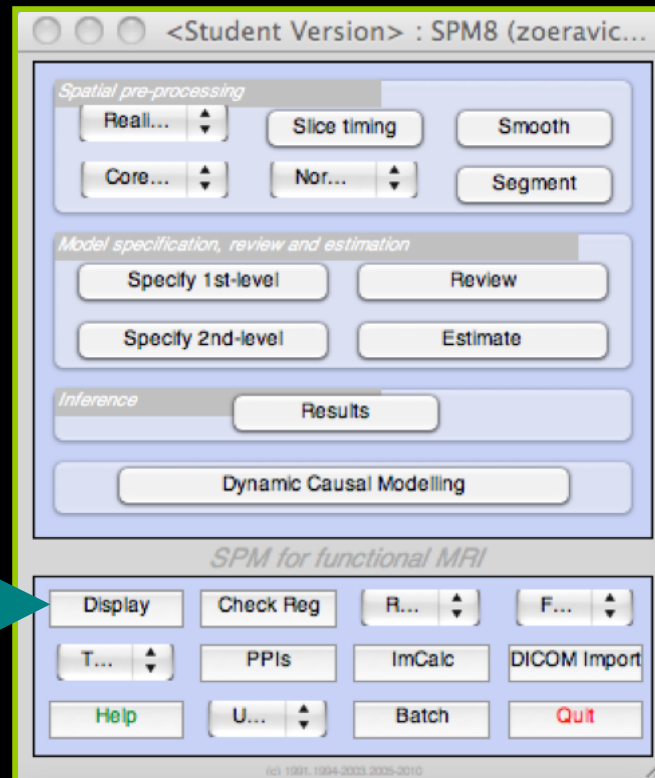
Display

- Press the DISPLAY button
 - Select the first functional image
 - Note orbitofrontal and inferior temporal drop-out and ghosting

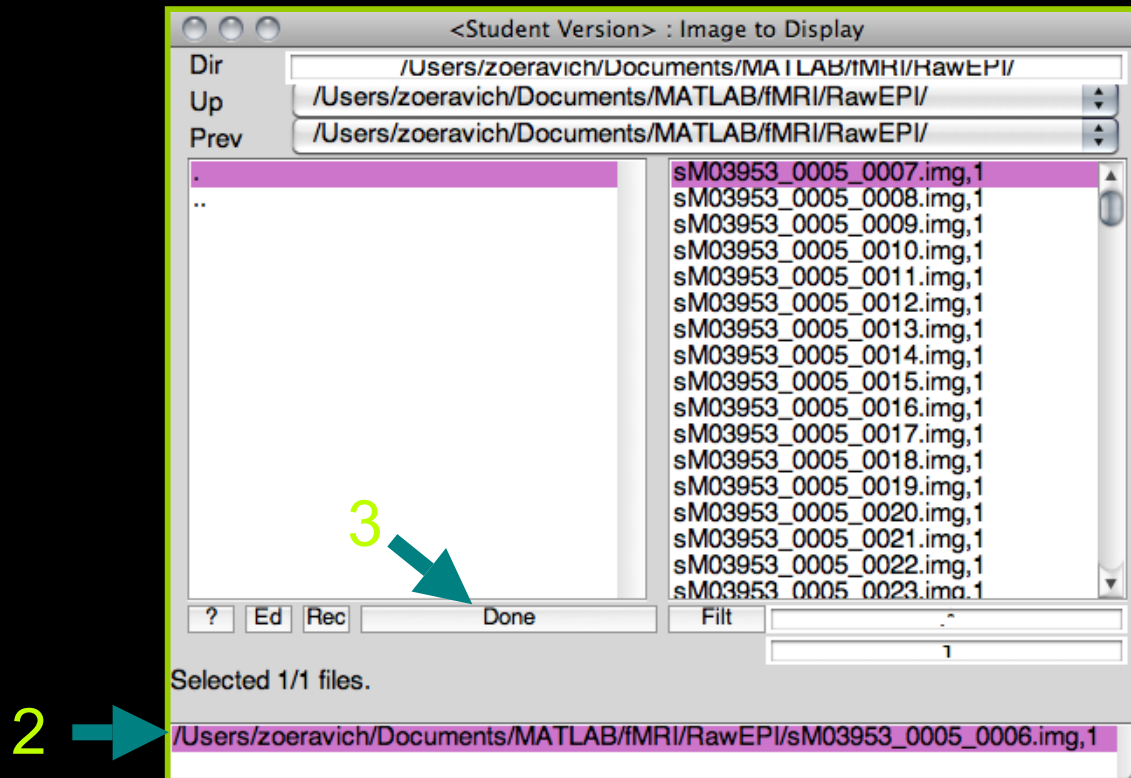


Step 2

Display

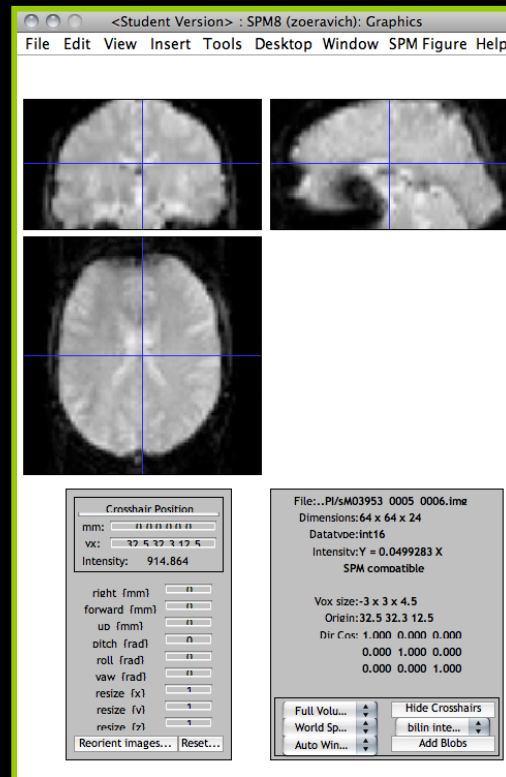


Step 2 Display



Step 2

Display



Step 3

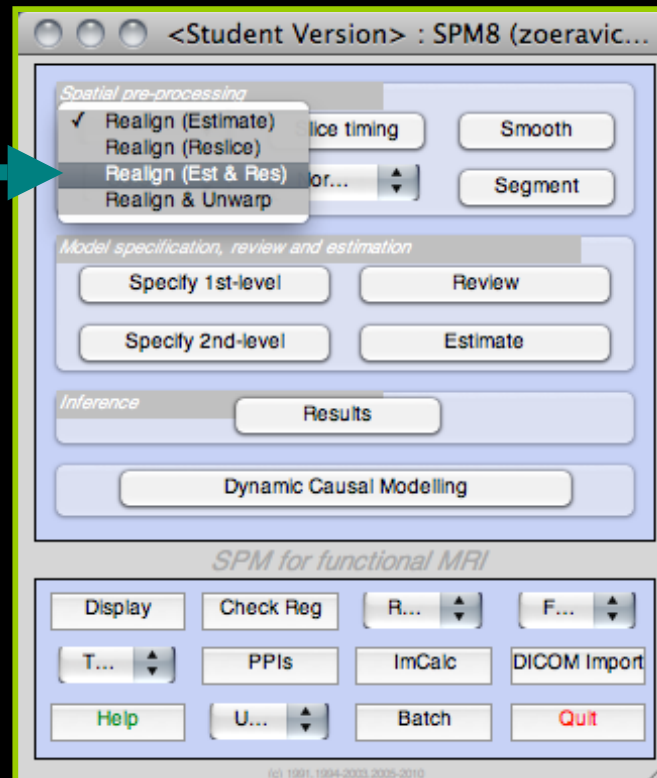
Realignment

- Select REALIGN (EST & RES) from the “Realign” drop-down menu
 - Highlight “Data” and select “New Session”; then highlight the newly created “Session” option
 - Select “Specify Files” and choose all of the functional images using the filter $\wedge s.*$
 - Save the job as realign.mat
 - Press the “Run” button
- New files: rsM03953_0005_*.img, meansM03953_0005_0006.img (the mean image), and rp_sM03953_0005_0006.txt (the realignment parameters; copy into the DIR/jobs directory)

Step 3

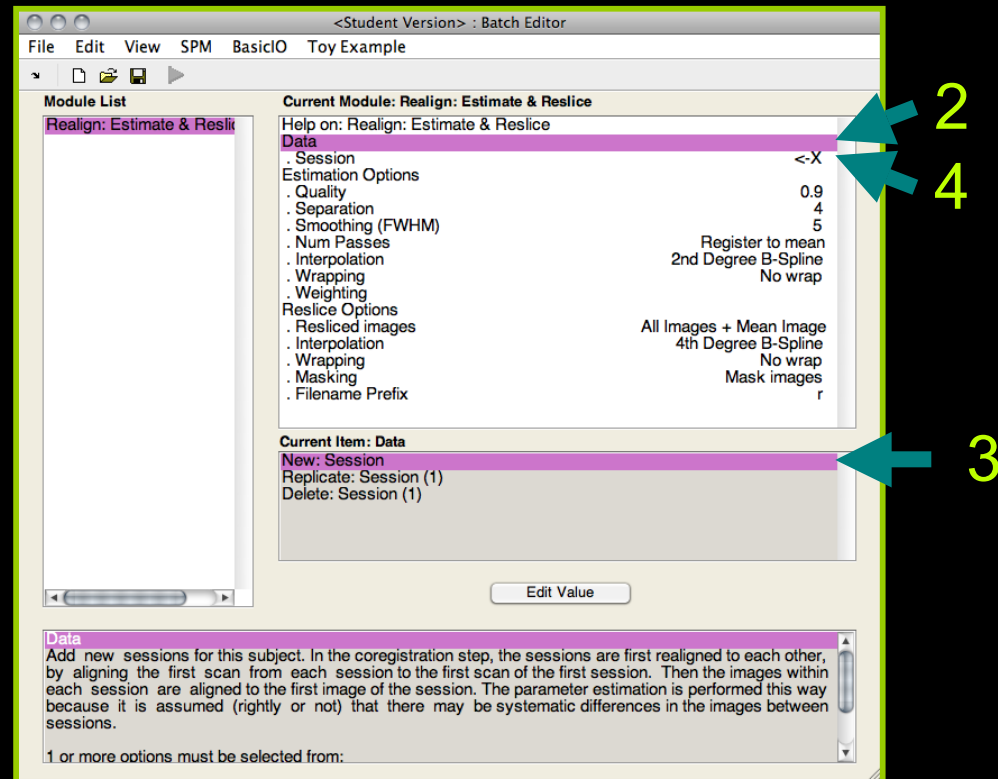
Realignment

1 →

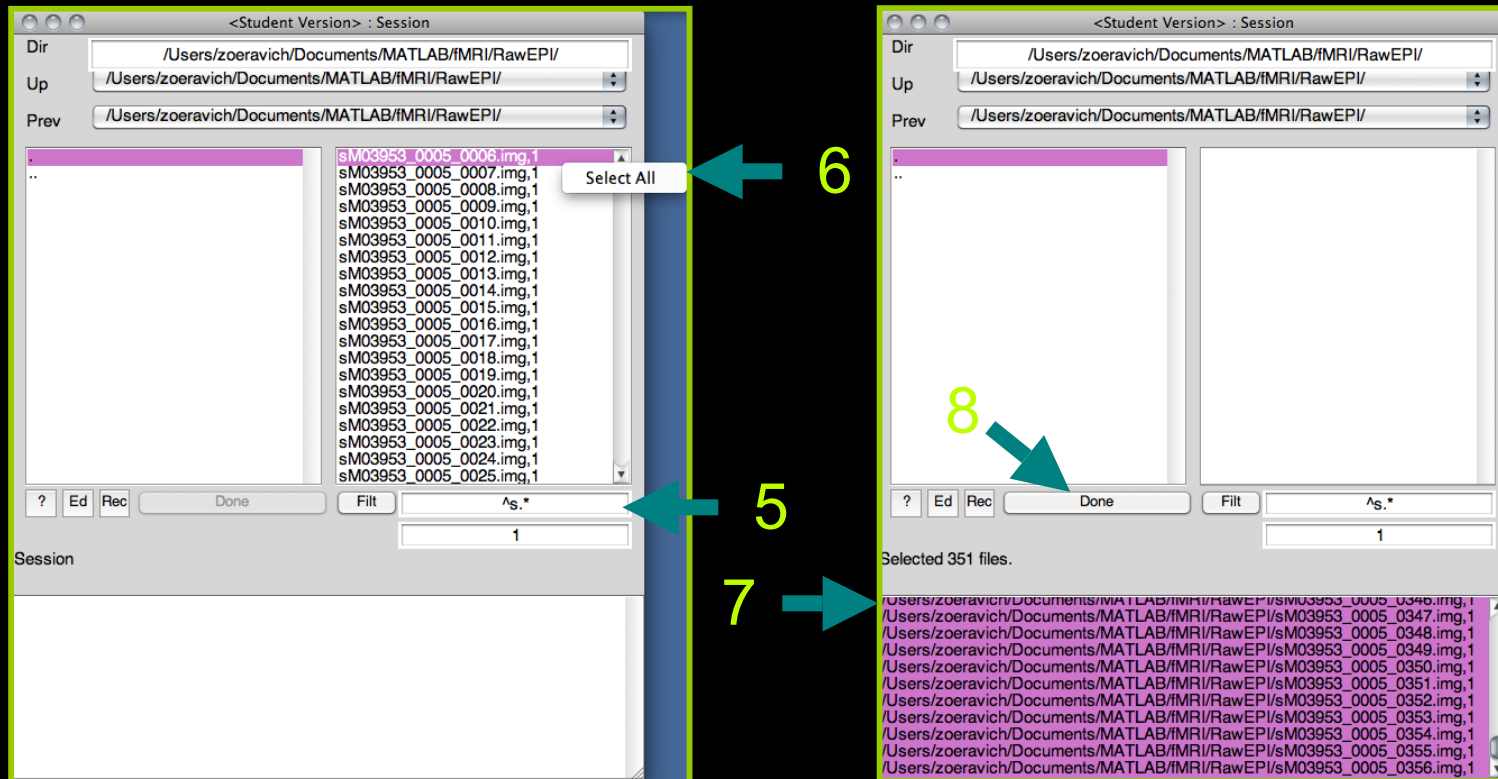


Step 3

Realignment

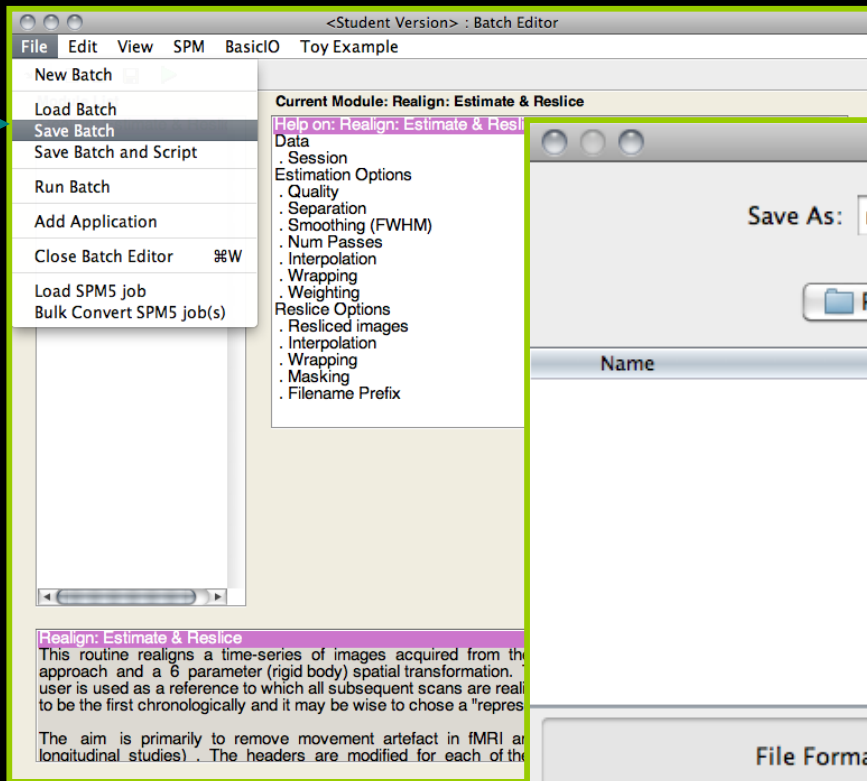


Step 3 Realignment

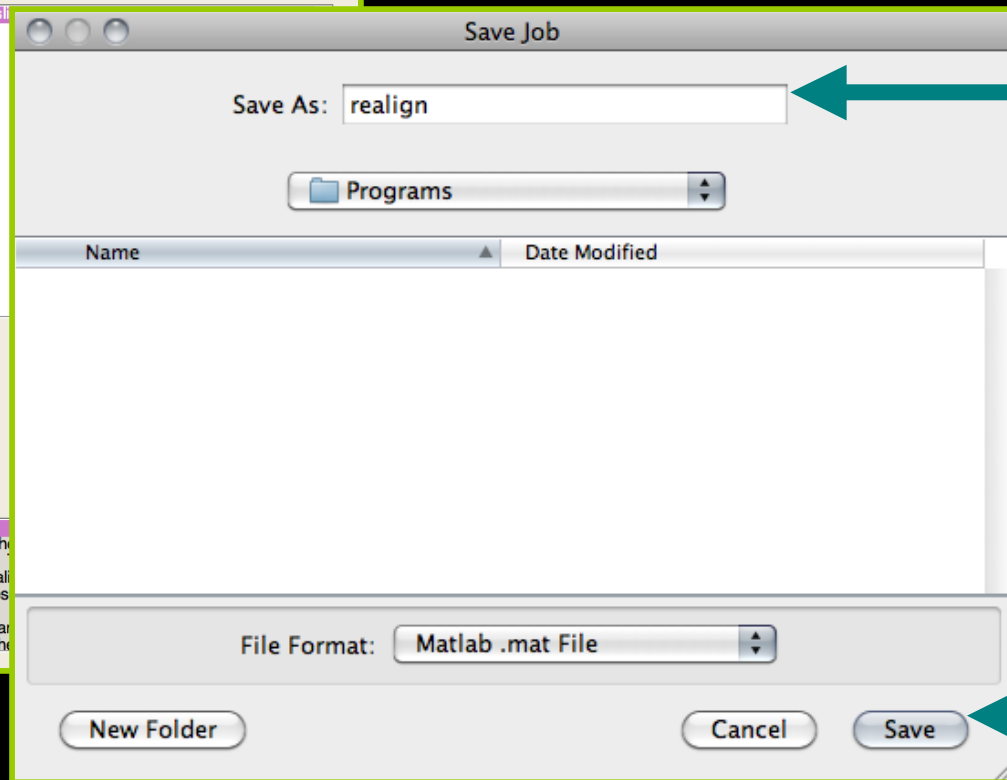


Step 3 Realignment

9



10



11

Step 3 Realignment

12

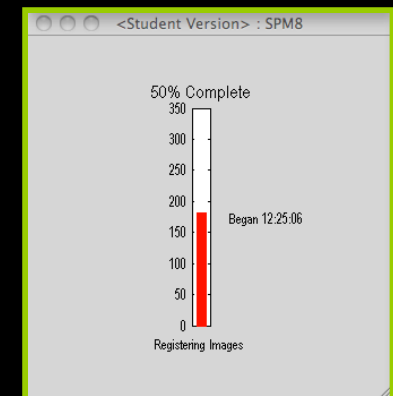
The screenshot shows the SPM Batch Editor window with the 'Realign: Estimate & Reslice' module selected. A green arrow points to the 'Run' button (a green play icon) in the toolbar. The interface is divided into several sections:

- Module List:** A list of modules with 'Realign: Estimate & Reslice' highlighted.
- Current Module: Realign: Estimate & Reslice:** A configuration panel with the following settings:
 - Help on: Realign: Estimate & Reslice
 - Data: 351 files
 - Estimation Options:
 - Quality: 0.9
 - Separation: 4
 - Smoothing (FWHM): 5
 - Num Passes: Register to mean
 - Interpolation: 2nd Degree B-Spline
 - Wrapping: No wrap
 - Weighting:
 - Reslice Options:
 - Resliced images: All Images + Mean Image
 - Interpolation: 4th Degree B-Spline
 - Wrapping: No wrap
 - Masking: Mask images
 - Filename Prefix: r
- Help on: Realign: Estimate & Reslice:** A text area containing the following text:

This routine realigns a time-series of images acquired from the same subject using a least squares approach and a 6 parameter (rigid body) spatial transformation. The first image in the list specified by the user is used as a reference to which all subsequent scans are realigned. The reference scan does not have to be the first chronologically and it may be wise to choose a "representative scan" in this role.

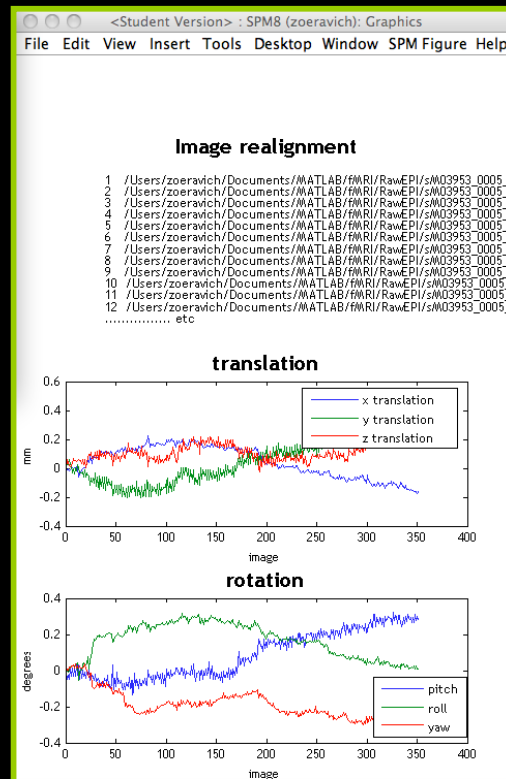
The aim is primarily to remove movement artefact in fMRI and PET time-series (or more generally longitudinal studies). The headers are modified for each of the input images, such that they reflect the

Processing...



Step 3

Realignment



Step 4

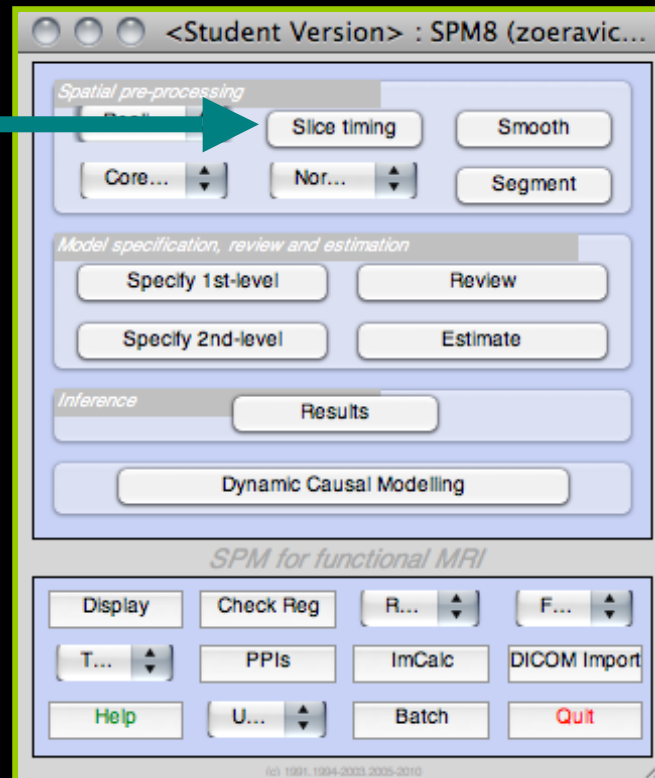
Slice Timing Correction

- Press the SLICE TIMING button
 - Highlight “Data” and select “New Sessions”
 - Select “Specify Files” and choose all of the 351 realigned functional images using the filter $\wedge r.*$
 - “Number of Slices”; Type “24”
 - “TR”; Type “2”
 - “TA”; Type “2 - 2/24”
 - “Slice order”; Type “24:-1:1”
 - “Reference Slice”; Type “12”
 - Save the job as slice_timing.mat
 - Press the “Run” button
- New files: arsM03953_0005_*.img

Step 4

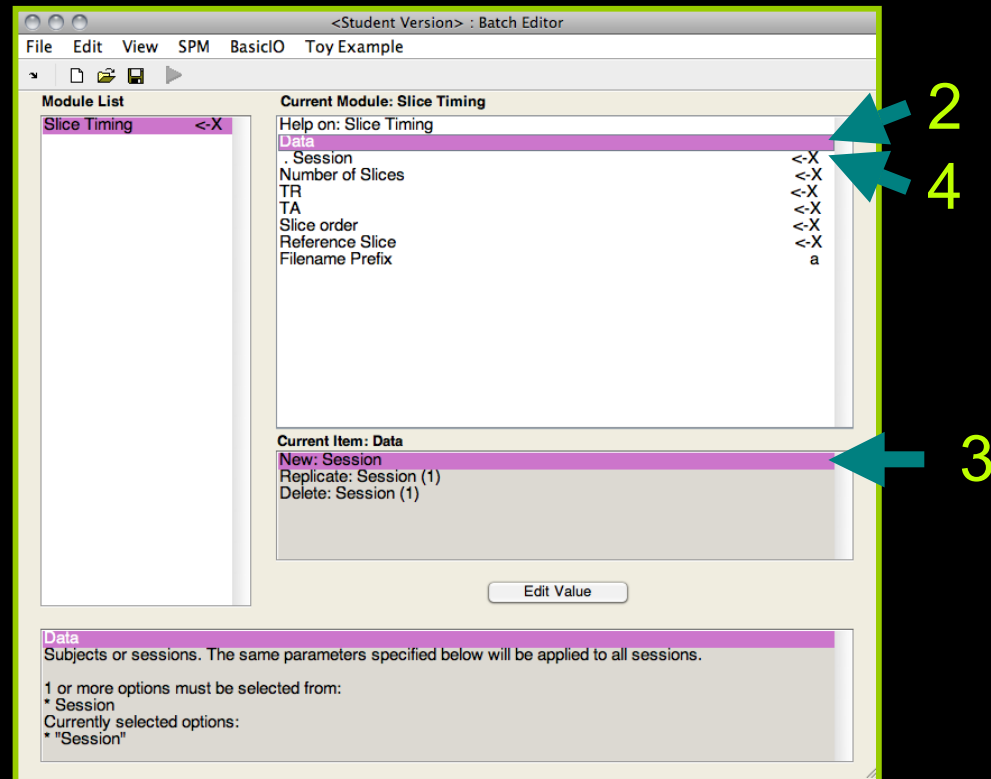
Slice Timing Correction

1



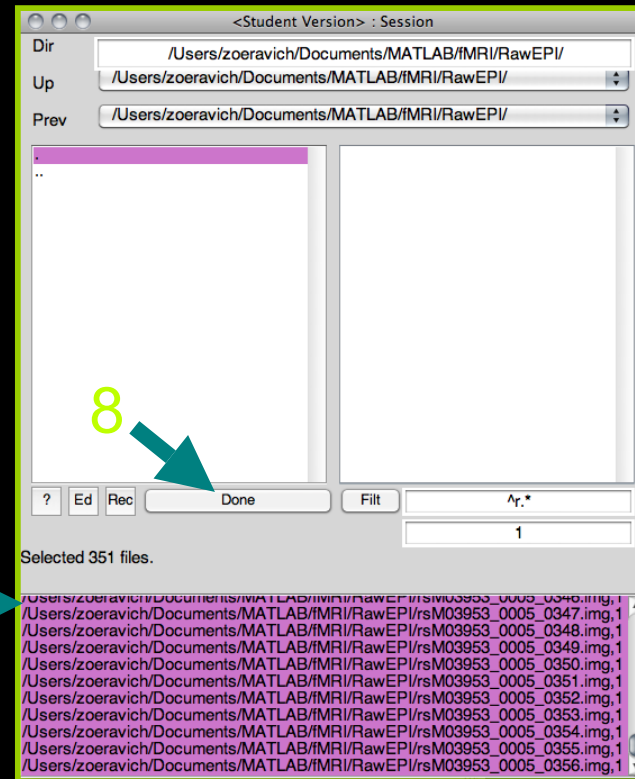
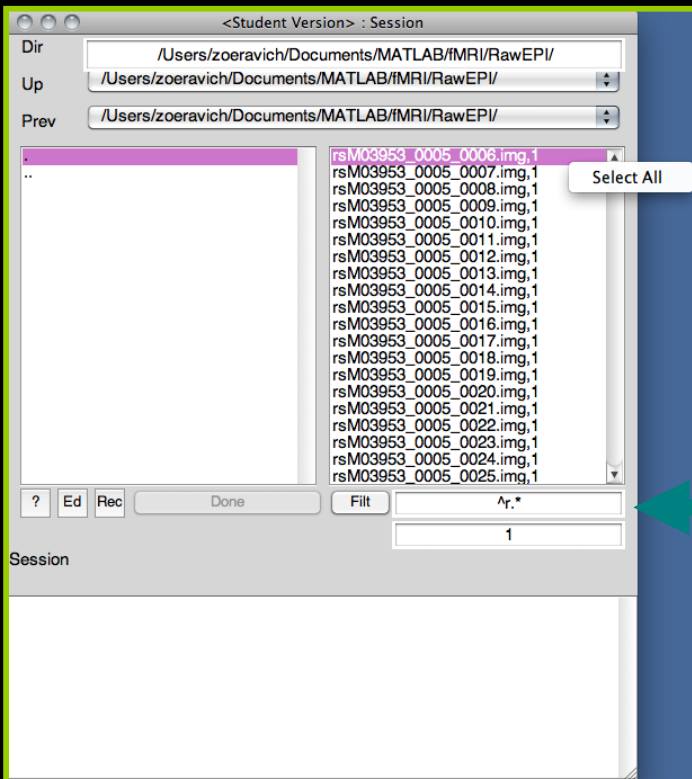
Step 4

Slice Timing Correction



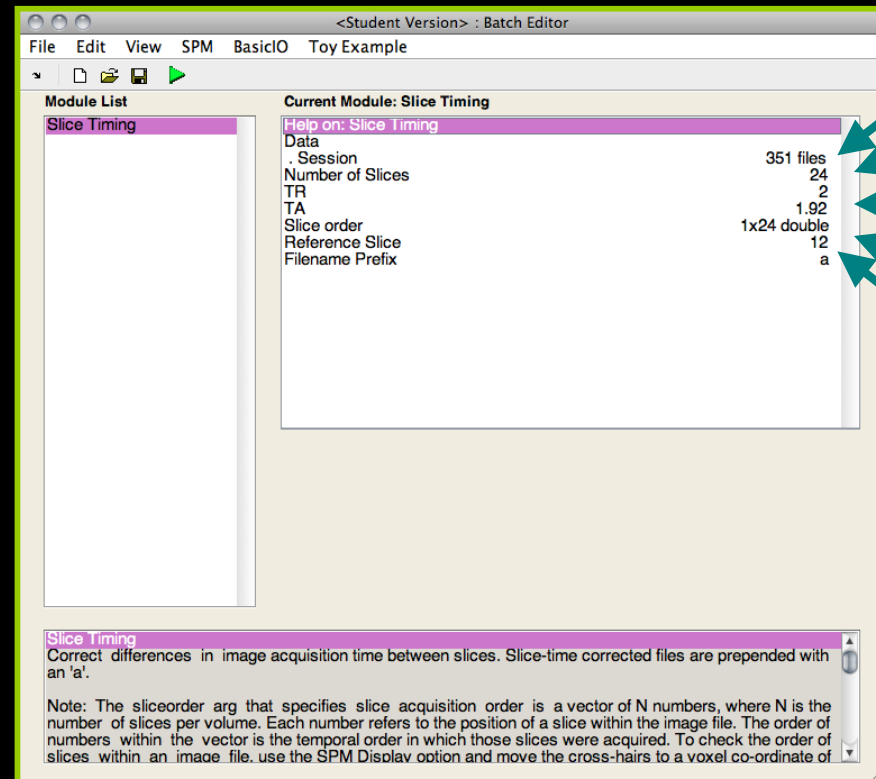
Step 4

Slice Timing Correction



Step 4

Slice Timing Correction



Step 4

Slice Timing Correction

The image shows two overlapping windows from the SPM software. The background window is the 'Batch Editor' for the 'Slice Timing' module. A yellow arrow labeled '14' points to the 'File' menu, which is open and showing options like 'New Batch', 'Load Batch', 'Save Batch', 'Run Batch', etc. The foreground window is the 'Save Job' dialog box. A yellow arrow labeled '15' points to the 'Save As' text field, which contains the text 'slice_timing'. Below this, there is a folder selection dropdown set to 'Programs' and a file list showing 'realign.mat' with a date of 'Tuesday, October 18, 2011 12:10 PM'. At the bottom of the dialog, the 'File Format' is set to 'Matlab .mat File'. A yellow arrow labeled '16' points to the 'Save' button.

14

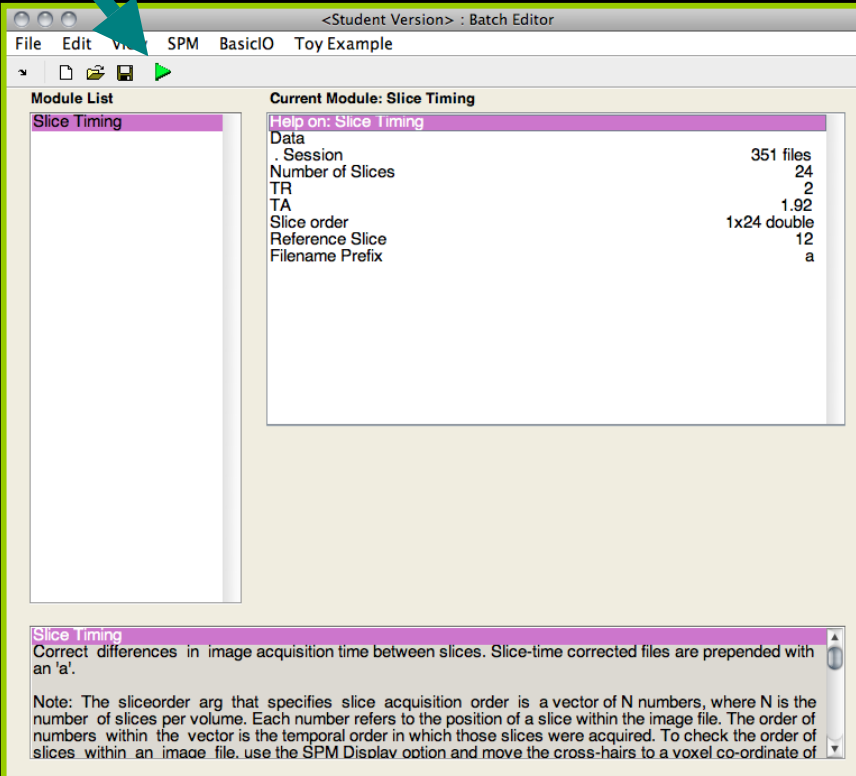
15

16

Step 4

Slice Timing Correction

17



<Student Version> : Batch Editor

File Edit View SPM BasicIO Toy Example

Module List

- Slice Timing

Current Module: Slice Timing

Help on: Slice Timing

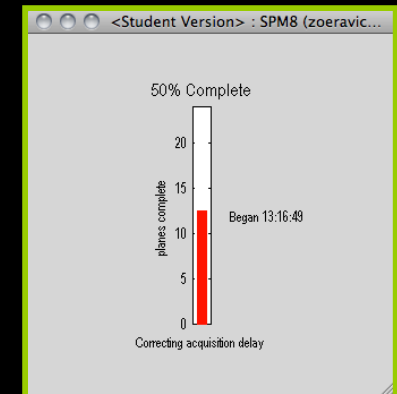
Data	
. Session	351 files
Number of Slices	24
TR	2
TA	1.92
Slice order	1x24 double
Reference Slice	12
Filename Prefix	a

Slice Timing

Correct differences in image acquisition time between slices. Slice-time corrected files are prepended with an 'a'.

Note: The sliceorder arg that specifies slice acquisition order is a vector of N numbers, where N is the number of slices per volume. Each number refers to the position of a slice within the image file. The order of numbers within the vector is the temporal order in which those slices were acquired. To check the order of slices within an image file, use the SPM Display option and move the cross-hairs to a voxel co-ordinate of

Processing...



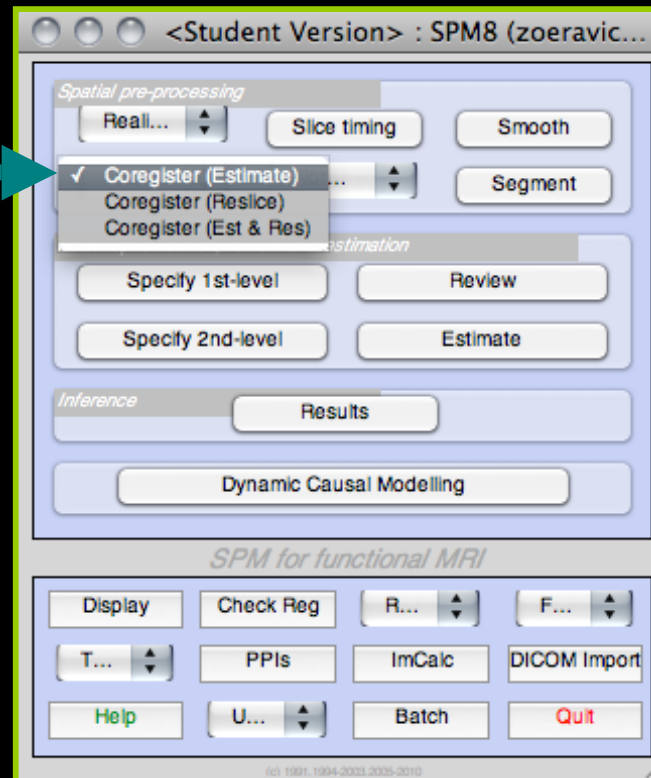
Step 5

Coregistration

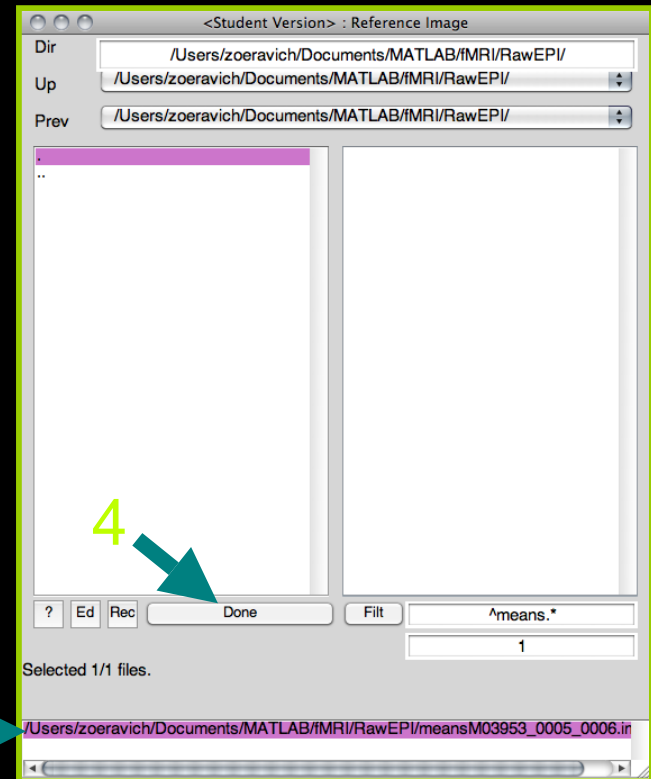
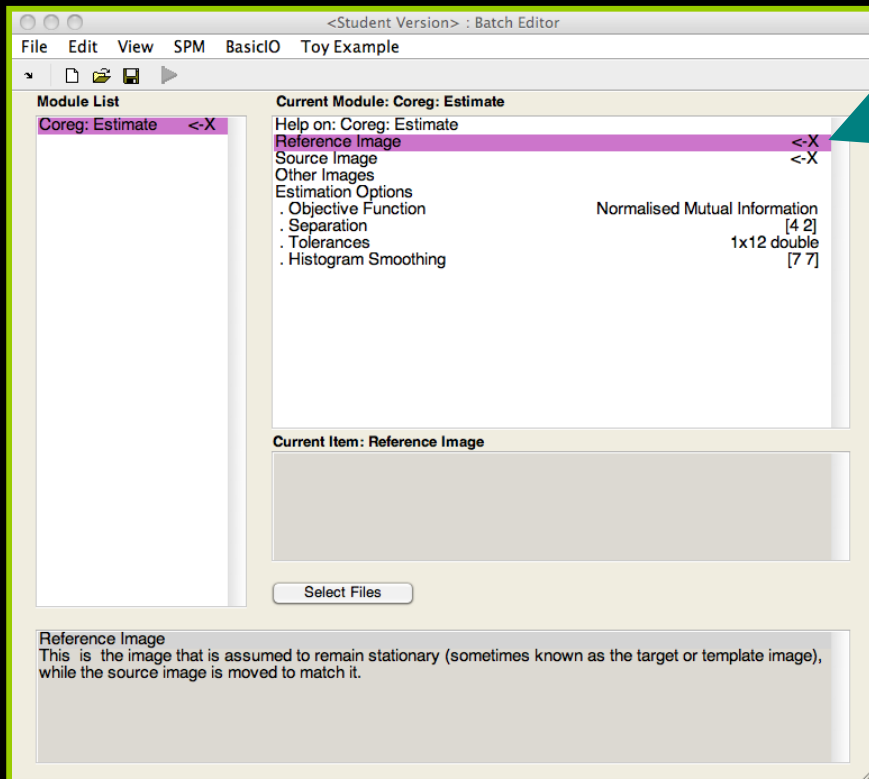
- Select COREGISTER (ESTIMATE) from the “Coregister” drop-down menu
 - Highlight “Reference Image” and select the meansM03953_0007.img file
 - Highlight “Source Image” and select the sM03953_0007.img file
 - Save the job as coreg.mat
 - Press the “Run” button
- New files: sM03953_0007.img

Step 5 Coregistration

1 →

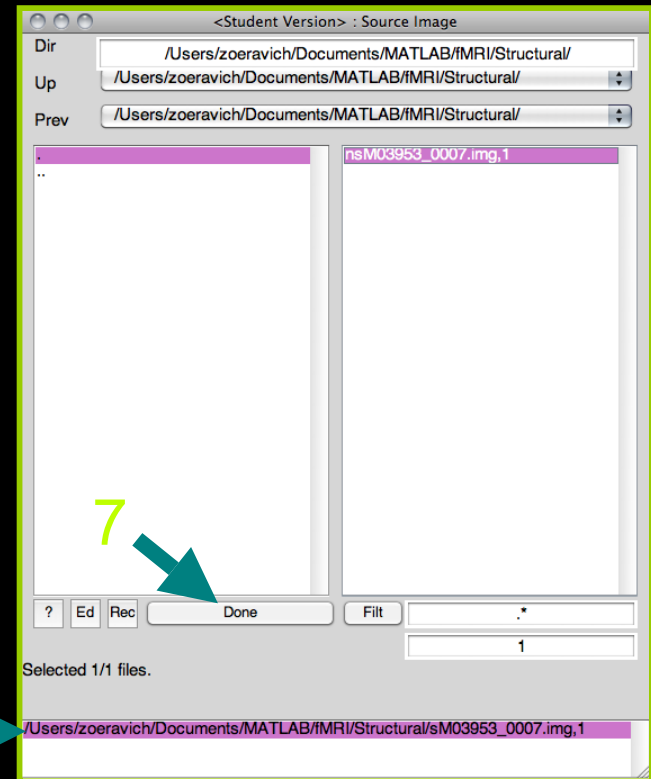
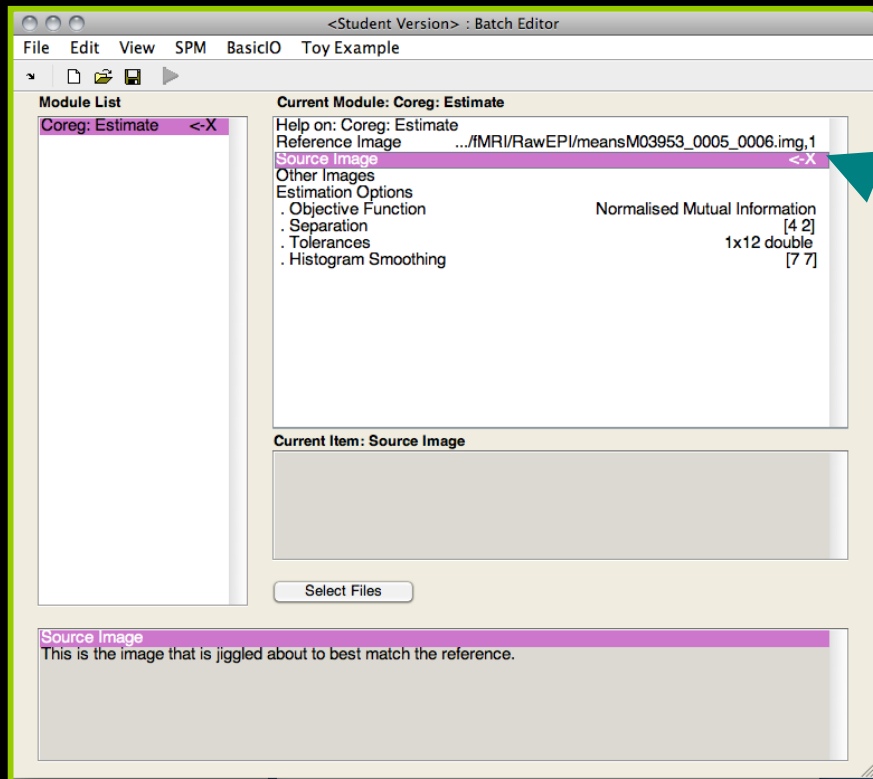


Step 5 Coregistration



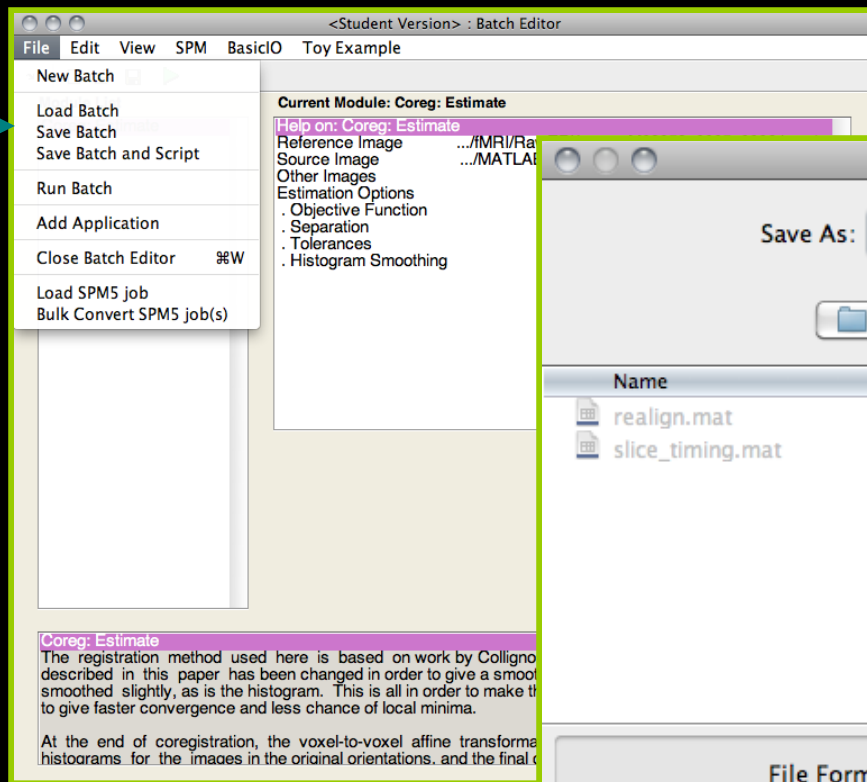
Step 5

Coregistration

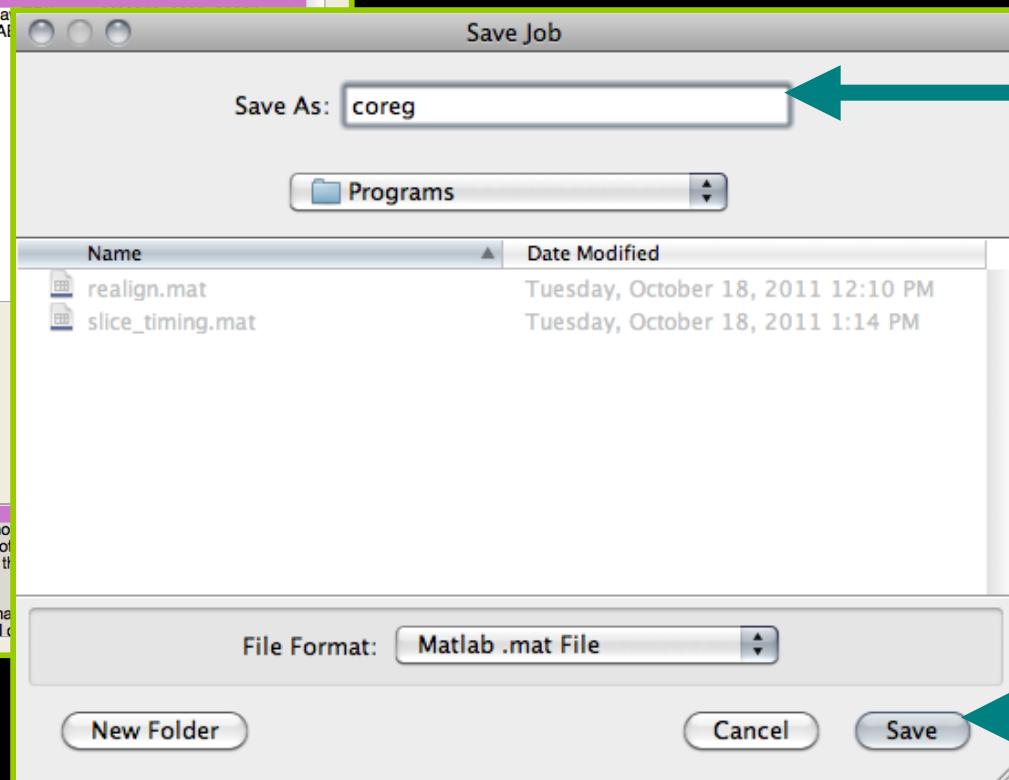


Step 5 Coregistration

8



9



10

Step 5 Coregistration

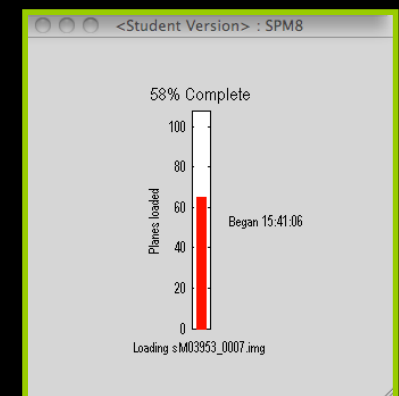
11

The screenshot shows the SPM Batch Editor window with the 'Coreg: Estimate' module selected. The interface includes a menu bar (File, Edit, View, SPM, BasicIO, Toy Example), a toolbar, and a main workspace. The 'Module List' on the left shows 'Coreg: Estimate' selected. The 'Current Module: Coreg: Estimate' panel displays the following configuration:

- Reference Image: .../fMRI/RawEPI/meansM03953_0005_0006.img, 1
- Source Image: .../MATLAB/fMRI/Structural/sM03953_0007.img, 1
- Other Images: (empty)
- Estimation Options:
 - . Objective Function: Normalised Mutual Information
 - . Separation: [4 2]
 - . Tolerances: 1x12 double
 - . Histogram Smoothing: [7 7]

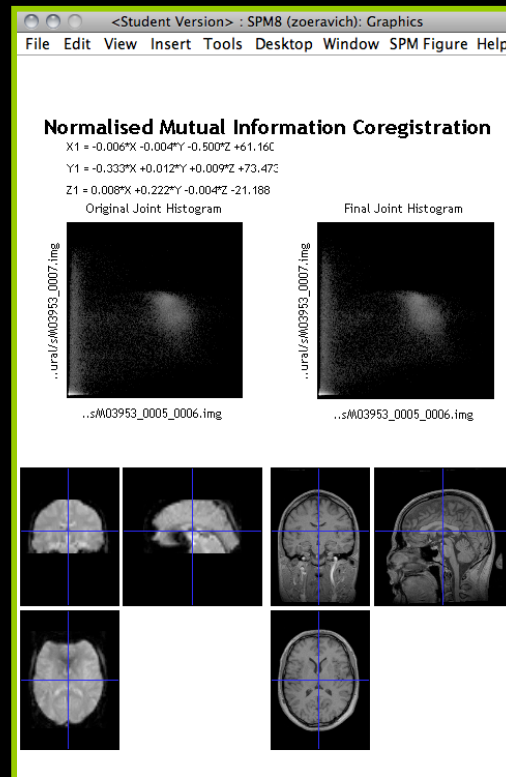
Below the configuration panel, a text box provides details about the registration method used, based on Collignon et al. work, and notes that the images are smoothed slightly. It also states that at the end of coregistration, the voxel-to-voxel affine transformation matrix and histograms for the images in their original and final orientations will be displayed.

Processing...



Step 5

Coregistration



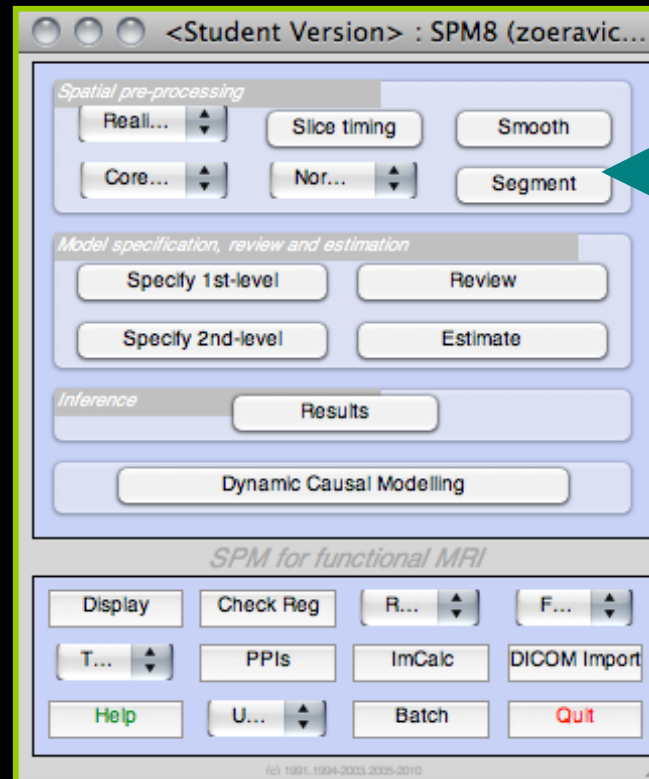
Step 6

Segmentation

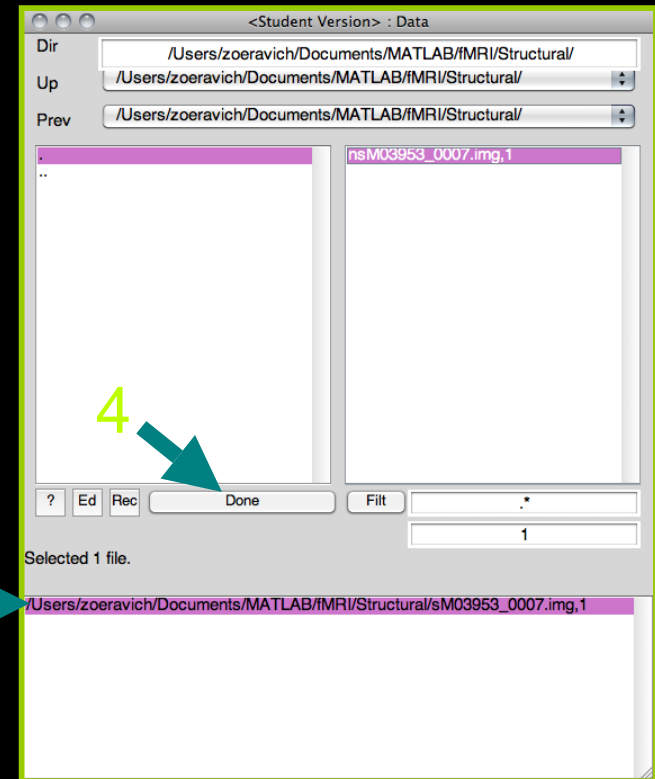
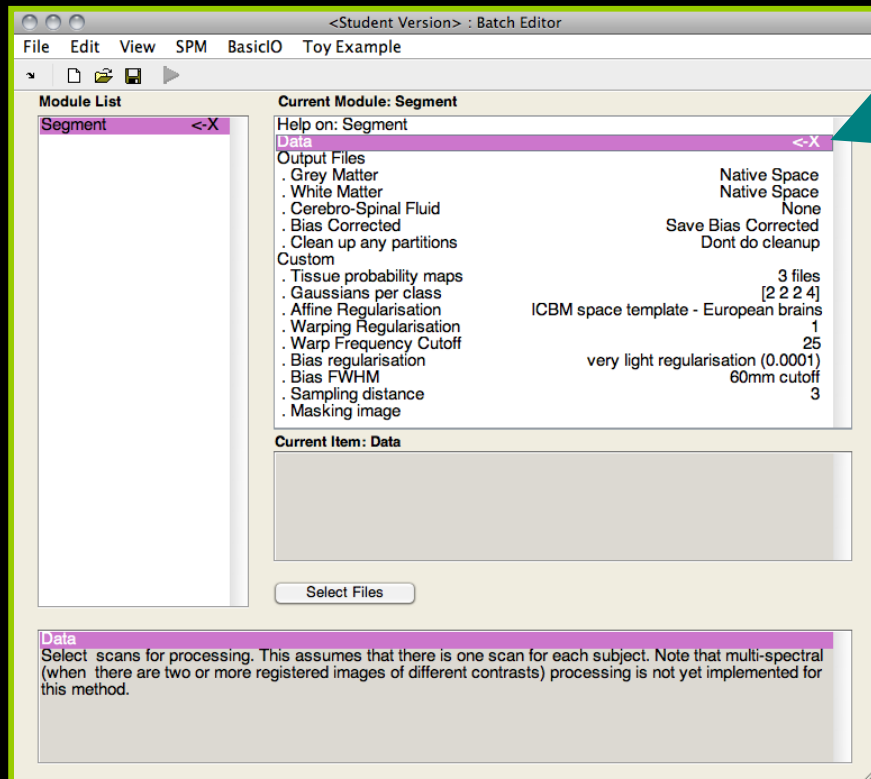
- Press the SEGMENT button
 - Highlight “Data” and select the coregistered sM03953_0007.img file
 - Save the job as segment.mat
 - Press the “Run” button
- New files: msM03953_0007.img, c*sM03953_0007.img (the gray matter and white matter images) and sM03953_0007_seg_sn.mat (the spatial normalisation)
- Press the CHECK REG button
 - Select the grey matter, white mater, and original structural images

Step 6

Segmentation



Step 6 Segmentation



Step 6

Segmentation

The image shows two overlapping windows from the SPM software. The background window is the 'Batch Editor' with a menu open. The foreground window is the 'Save Job' dialog box. A yellow '5' with an arrow points to the 'Save Batch' menu item. A yellow '6' with an arrow points to the 'Save As' text field in the dialog box, which contains the word 'segment'. A yellow '7' with an arrow points to the 'Save' button at the bottom right of the dialog box. The 'Save Job' dialog also shows a file list with columns for 'Name' and 'Date Modified', and a 'File Format' dropdown set to 'Matlab .mat File'.

5 →

6 →

7 →

Batch Editor Menu:

- New Batch
- Load Batch
- Save Batch
- Save Batch and Script
- Run Batch
- Add Application
- Close Batch Editor ⌘W
- Load SPM5 job
- Bulk Convert SPM5 job(s)

Current Module: Segment

Help on: Segment

Data

Output Files

- . Grey Matter
- . White Matter
- . Cerebro-Spinal Fluid
- . Bias Corrected
- . Clean up any partitions

Custom

- . Tissue probability maps
- . Gaussians per class
- . Affine Regularisation
- . Warping Regularisation
- . Warp Frequency Cutoff
- . Bias regularisation
- . Bias FWHM
- . Sampling distance
- . Masking image

Segment

Segment, bias correct and spatially normalise - all in the same correcting, spatially normalising or segmenting your data. Not is usually because the images were poorly aligned beforehar manually reposition the images so that the AC is close to coord orientation is within a few degrees of the tissue probability map da

Save Job

Save As: segment

Programs

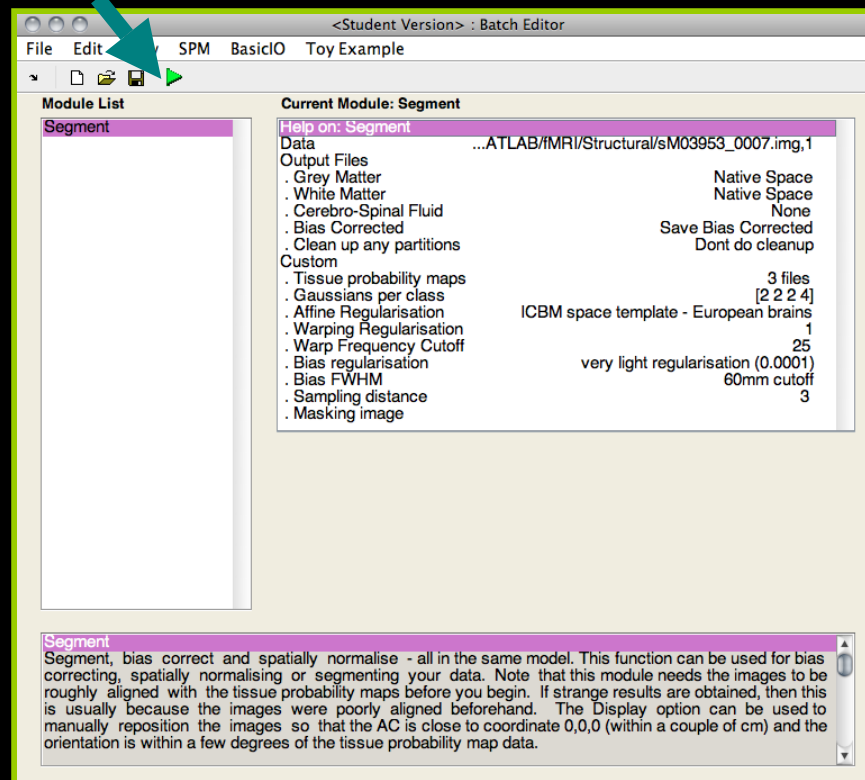
Name	Date Modified
coreg.mat	Tuesday, October 18, 2011 3:40 PM
realign.mat	Tuesday, October 18, 2011 12:10 PM
slice_timing.mat	Tuesday, October 18, 2011 1:14 PM

File Format: Matlab .mat File

New Folder Cancel Save

Step 6 Segmentation

8



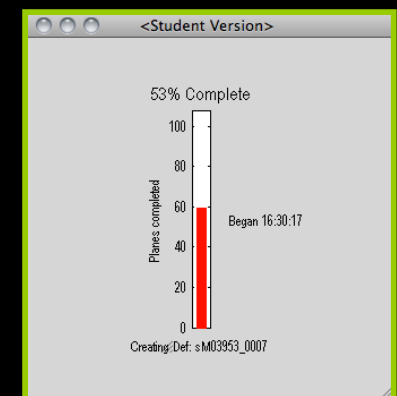
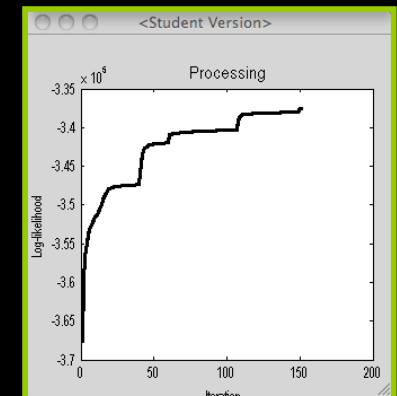
The screenshot shows the SPM Batch Editor window titled '<Student Version> : Batch Editor'. The menu bar includes 'File', 'Edit', 'SPM', 'BasicIO', and 'Toy Example'. A green arrow points to the 'Run' button (a green play icon) in the toolbar. The 'Module List' on the left shows 'Segment' selected. The 'Current Module: Segment' panel displays the following configuration:

- Help on: Segment
- Data: ...ATLAB/MRI/Structural/sM03953_0007.img,1
- Output Files: Native Space
- . Grey Matter: Native Space
- . White Matter: Native Space
- . Cerebro-Spinal Fluid: None
- . Bias Corrected: Save Bias Corrected
- . Clean up any partitions: Dont do cleanup
- Custom: 3 files
- . Tissue probability maps: [2 2 2 4]
- . Gaussians per class: ICBM space template - European brains
- . Affine Regularisation: 1
- . Warping Regularisation: 25
- . Warp Frequency Cutoff: very light regularisation (0.0001)
- . Bias regularisation: 60mm cutoff
- . Bias FWHM: 3
- . Sampling distance: 3
- . Masking image:

Below the configuration panel, a description for the 'Segment' module is provided:

Segment
Segment, bias correct and spatially normalise - all in the same model. This function can be used for bias correcting, spatially normalising or segmenting your data. Note that this module needs the images to be roughly aligned with the tissue probability maps before you begin. If strange results are obtained, then this is usually because the images were poorly aligned beforehand. The Display option can be used to manually reposition the images so that the AC is close to coordinate 0,0,0 (within a couple of cm) and the orientation is within a few degrees of the tissue probability map data.

Processing...

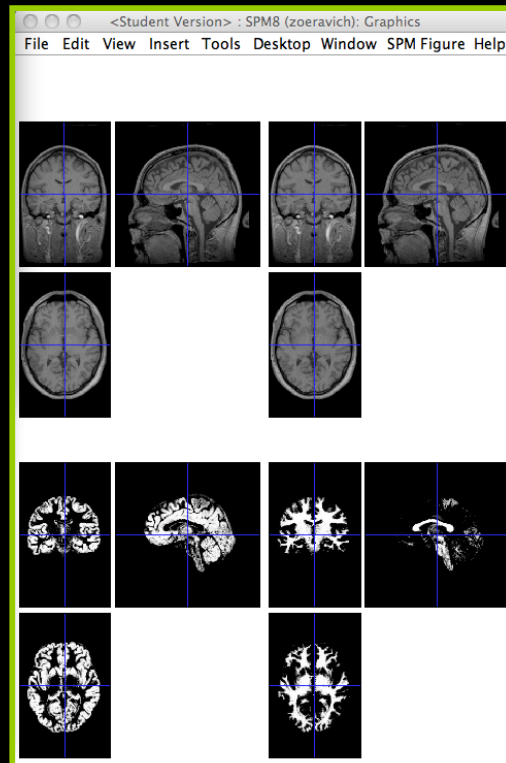


Step 6 Segmentation

The image shows the SPM8 software interface for the Segmentation step. The main window is titled "<Student Version> : SPM8 (zoeravic...)". It has several sections: "Spatial pre-processing" with buttons for "Reall...", "Slice timing", "Smooth", "Core...", "Nor...", and "Segment"; "Model specification, review and estimation" with buttons for "Specify 1st-level", "Review", "Specify 2nd-level", and "Estimate"; "Inference" with a "Results" button; and "SPM for functional MRI" with buttons for "Display", "Check Reg", "R...", "F...", "T...", "PPis", "ImCalc", "DICO", "Help", "U...", and "Batch". A yellow box highlights the "Display" button, with a yellow arrow labeled "9" pointing to it. Overlaid on this is a dialog box titled "<Student Version> : Images to Display". It shows a directory path: "/Users/zoeravich/Documents/MATLAB/fMRI/Structural/". Below the path are buttons for "?", "Ed", "Rec", "Done", and "Filt". A list of files is shown, with "nsM03953_0007.img,1" selected. A yellow arrow labeled "11" points to the "Done" button. Below the list, it says "Selected 4/1-15 files." and lists four files: "/Users/zoeravich/Documents/MATLAB/fMRI/Structural/sM03953_0007.img,1", "/Users/zoeravich/Documents/MATLAB/fMRI/Structural/msM03953_0007.img,1", "/Users/zoeravich/Documents/MATLAB/fMRI/Structural/c1sM03953_0007.img,1", and "/Users/zoeravich/Documents/MATLAB/fMRI/Structural/c2sM03953_0007.img,1". A yellow box highlights the last two files, with a yellow arrow labeled "10" pointing to them.

Step 6

Segmentation



Step 7

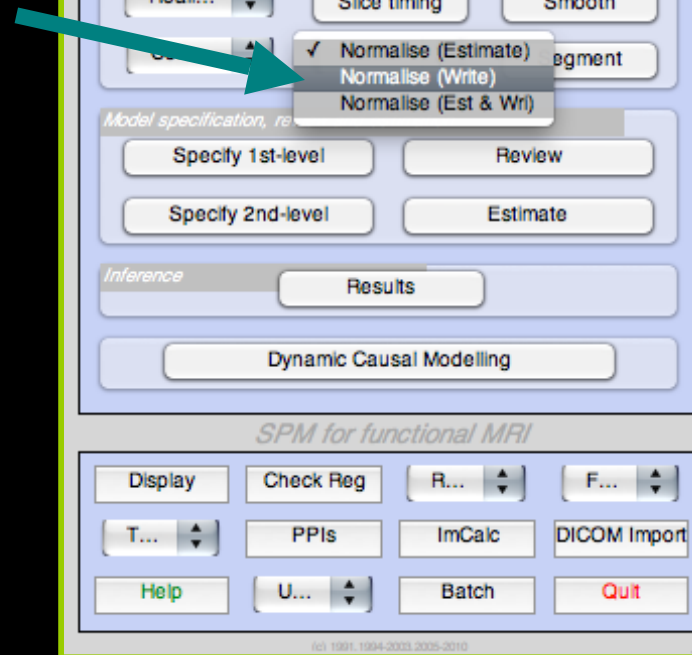
Normalise

- Select NORMALISE (WRITE) from the “Normalise” drop-down menu
 - Highlight “Data” and select “New Subject”
 - Open “Subject”, highlight “Parameter File”, and select the sM03953_0007_seg_sn.mat file
 - Highlight “Images to Write” and select ^ar.* files as well as the meansM03953_0005_006.img file
 - Open “Writing Options” and change “Voxel sizes” to [3 3 3]
 - Save the job as normalise.mat
 - Press the “Run” button
- New files: warsM03953_0005_*.img

Step 7

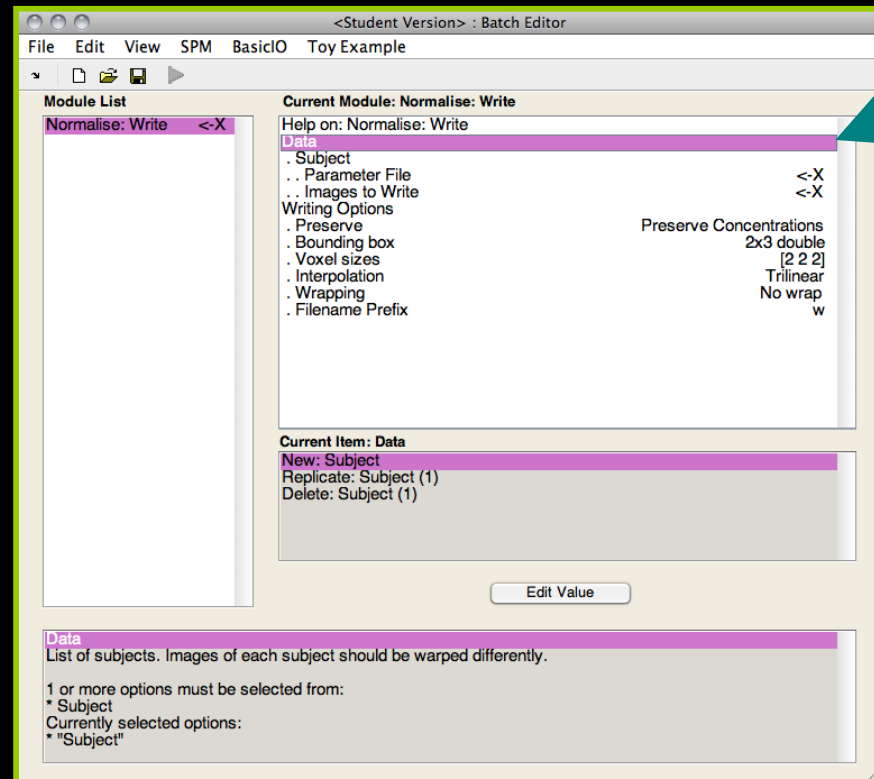
Normalise

1

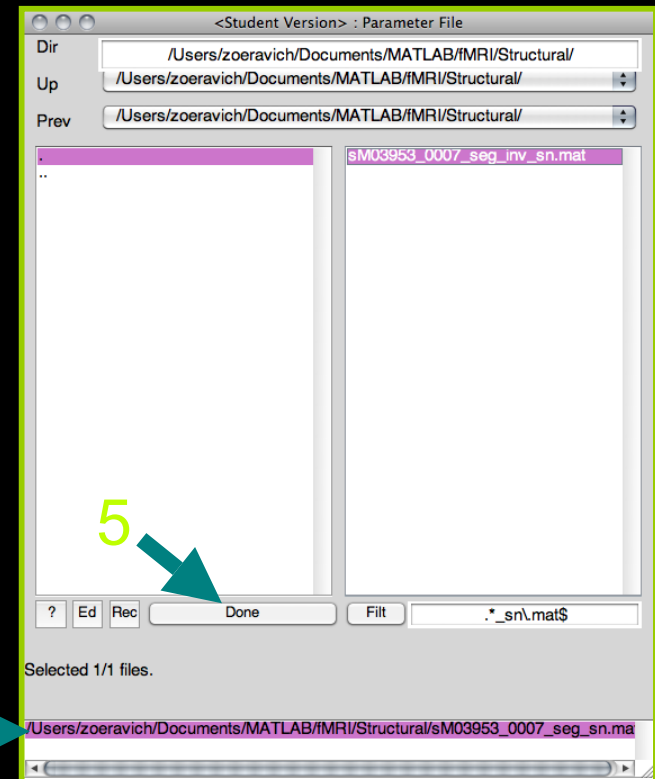
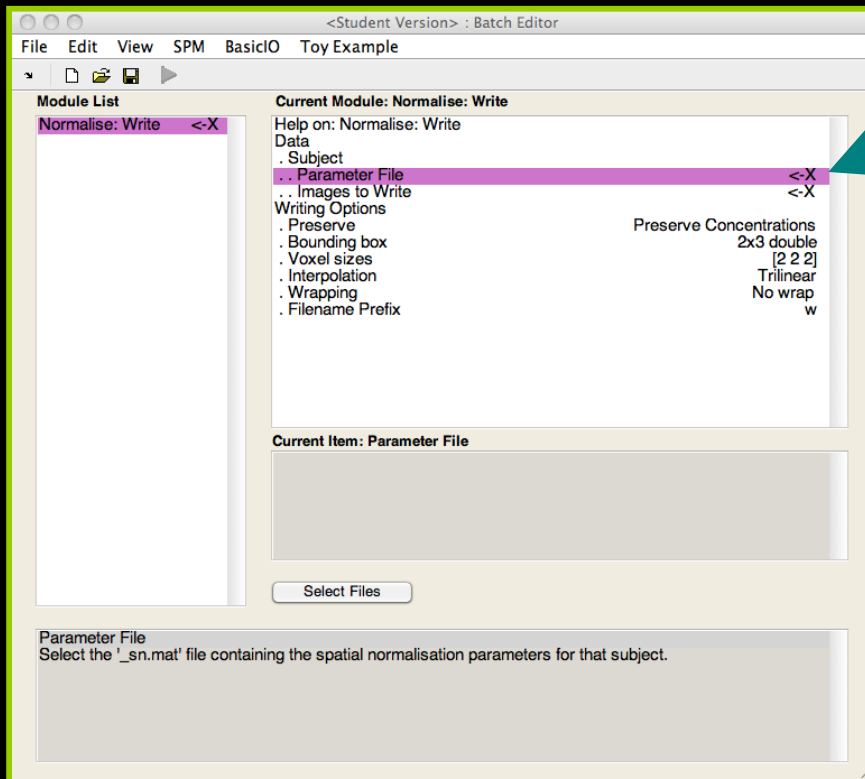


Step 7

Normalise

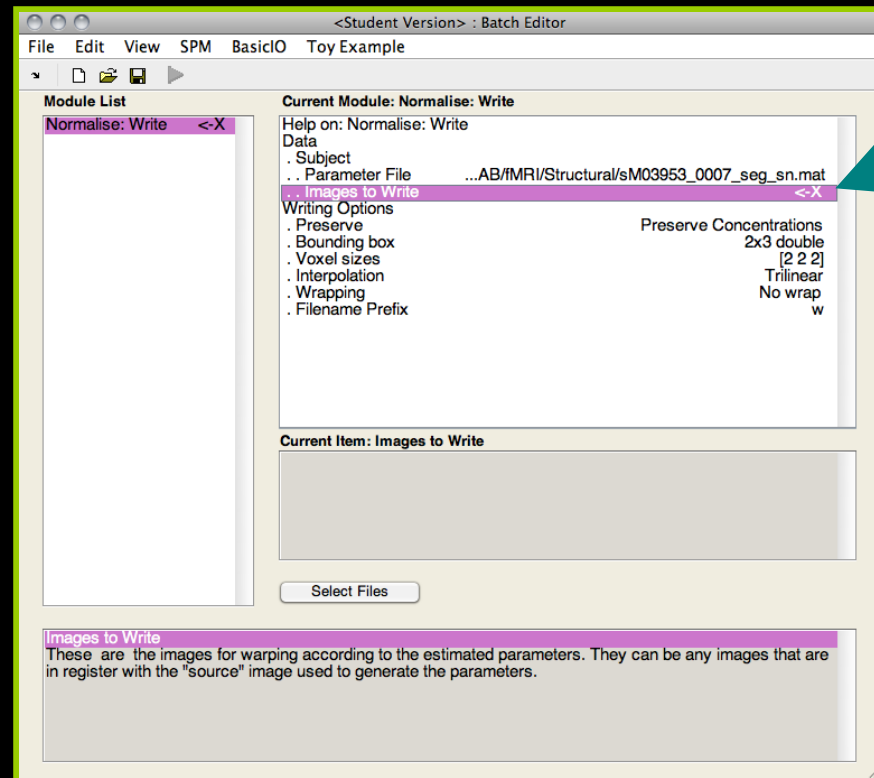


Step 7 Normalise

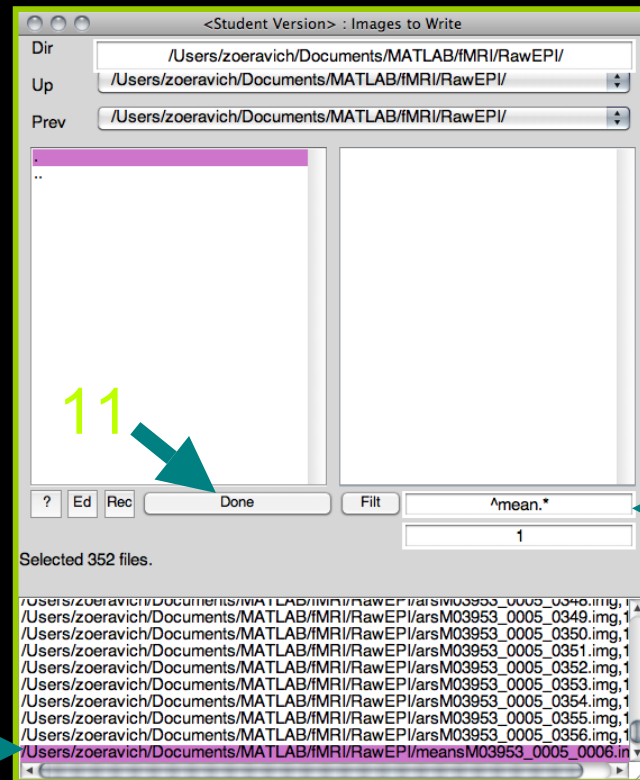
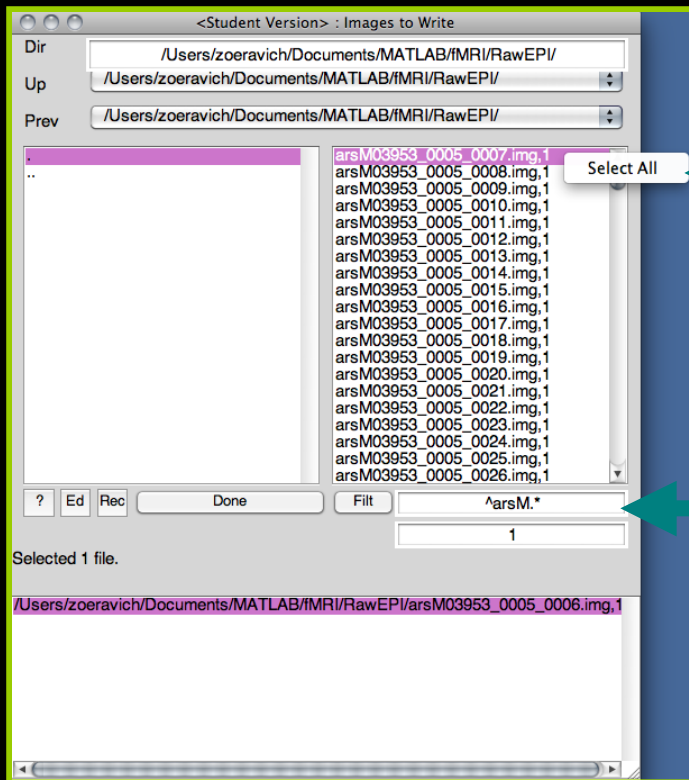


Step 7

Normalise



Step 7 Normalise



Step 7 Normalise

The image shows a screenshot of the SPM Batch Editor interface. The main window is titled "<Student Version> : Batch Editor" and contains a "Module List" on the left and a "Current Module: Normalise: Write" panel on the right. The "Current Module" panel shows various options for the Normalise: Write process, including "Voxel sizes" which is currently set to [2 2 2]. A yellow arrow labeled "12" points to the "Voxel sizes" field. A second yellow arrow labeled "13" points to the "Voxel sizes" field in the "Voxel sizes" dialog box. The dialog box is titled "<Student Version> : Voxel sizes" and contains the text "Enter a value." and "To clear a value, clear the input field and accept." Below this text is an input field containing the value "3 3 3". A yellow arrow labeled "14" points to the "OK" button in the dialog box. The dialog box also includes a "Cancel" button.

12

13

14

Step 7 Normalise

The image shows two overlapping windows from a software application. The background window is the 'Batch Editor' with a menu open. The foreground window is the 'Save Job' dialog box.

15 → Points to the 'Save Batch' option in the Batch Editor menu.

→ Points to the 'normalise' text in the 'Save As:' field of the Save Job dialog.

16 → Points to the 'normalise' text in the 'Save As:' field of the Save Job dialog.

→ Points to the 'Save' button in the Save Job dialog.

17 → Points to the 'Save' button in the Save Job dialog.

Save Job Dialog Content:

Save As: normalise

Programs

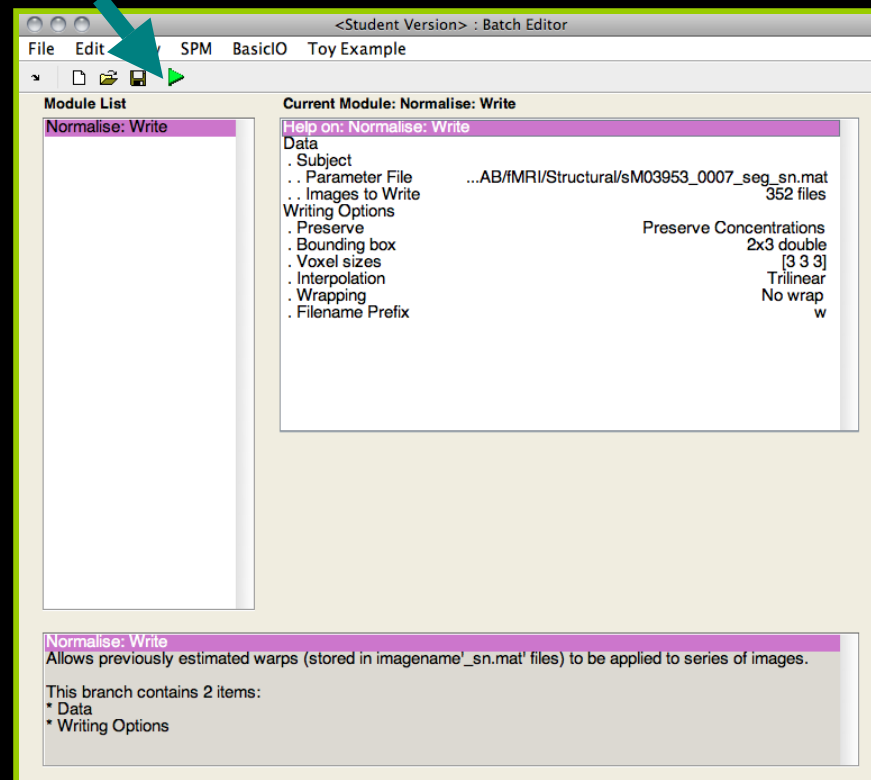
Name	Date Modified
coreg.mat	Tuesday, October 18, 2011 3:40 PM
realign.mat	Tuesday, October 18, 2011 12:10 PM
segment.mat	Tuesday, October 18, 2011 4:25 PM
slice_timing.mat	Tuesday, October 18, 2011 1:14 PM

File Format: Matlab .mat File

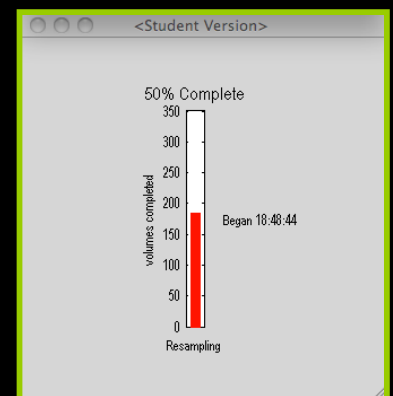
New Folder Cancel Save

Step 7 Normalise

18



Processing...



Step 7

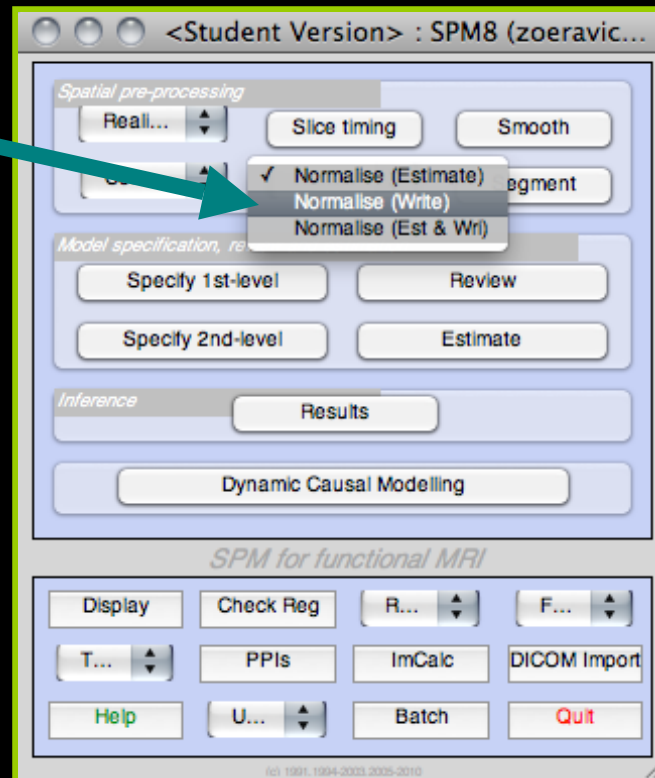
Normalise (Optional)

- Select NORMALISE (WRITE) from the “Normalise” drop-down menu
 - Highlight “Data” and select “New Subject”
 - Open “Subject”, highlight “Parameter File”, and select the sM03953_0007_seg_sn.mat file
 - Highlight “Images to Write” and select the msM03953_0005_007.img file
 - Open “Writing Options” and change “Voxel sizes” to [1 1 1]
 - Save the job as norm_struct.mat
 - Press the “Run” button
- New files: warsM03953_0005_*.img

Step 7

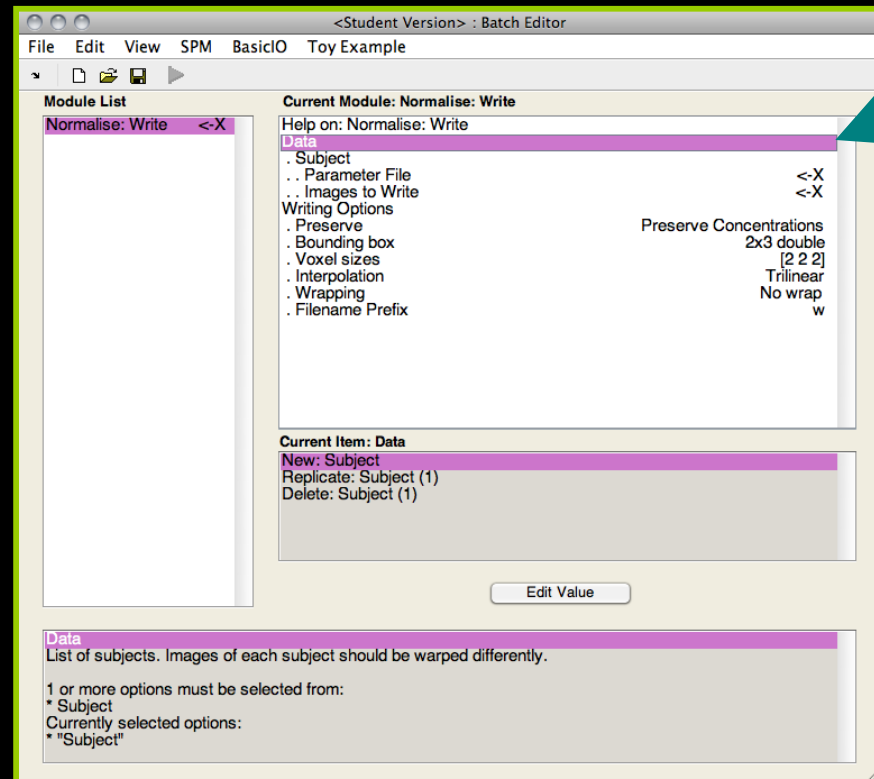
Normalise (Optional)

1



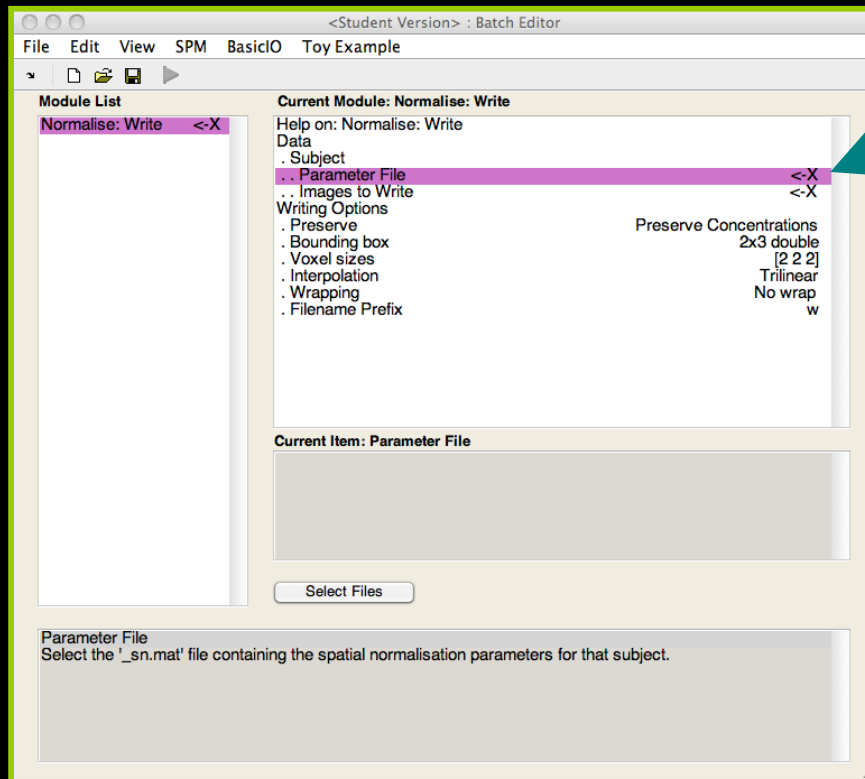
Step 7

Normalise (Optional)

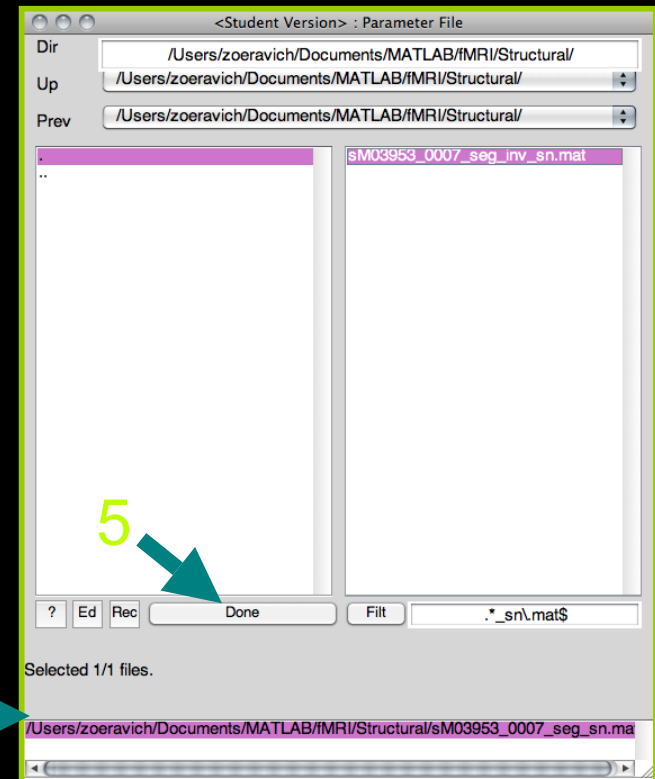


Step 7

Normalise (Optional)



3

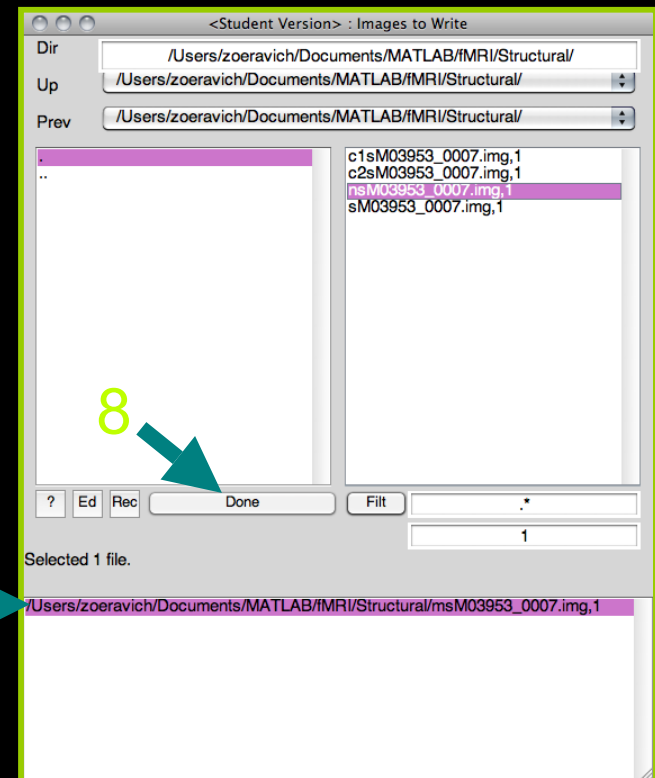
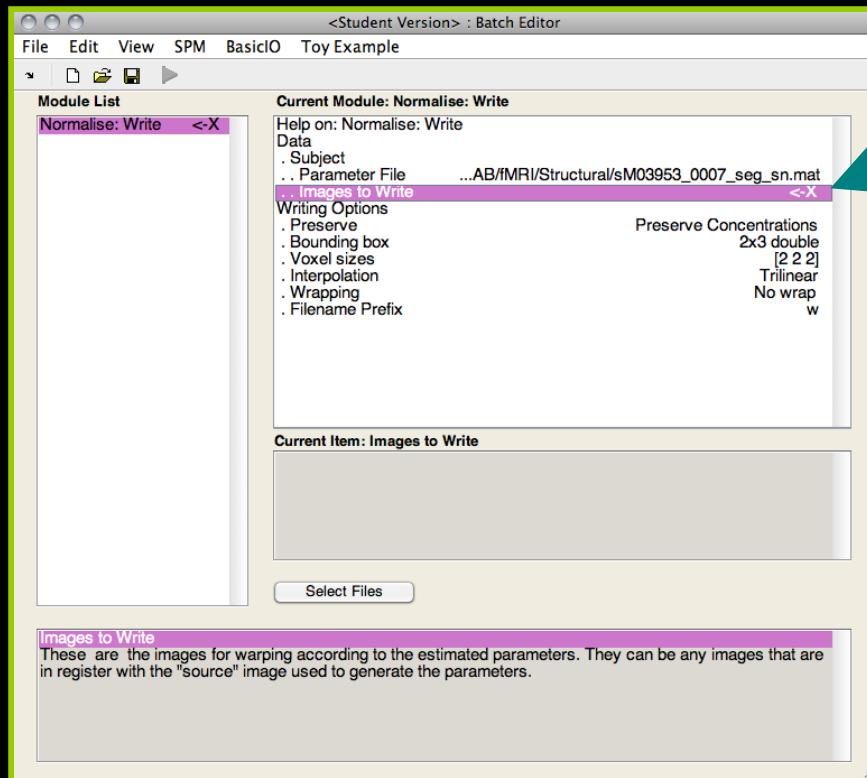


5

4

Step 7

Normalise (Optional)



Step 7

Normalise (Optional)

The image shows a screenshot of the SPM Batch Editor interface. The main window is titled "<Student Version> : Batch Editor" and contains a "Module List" on the left and a "Current Module: Normalise: Write" configuration panel on the right. The "Voxel sizes" option is highlighted in the configuration panel, with a yellow arrow labeled "9" pointing to it. Below the configuration panel, a "Current Item" section shows the value "2 2 2".

A dialog box titled "<Student Version> : Voxel sizes" is overlaid on the main window. It contains the text "Enter a value." and "To clear a value, clear the input field and accept." Below this is an input field containing the text "1 1 1|", with a yellow arrow labeled "10" pointing to it. At the bottom right of the dialog box are "OK" and "Cancel" buttons, with a yellow arrow labeled "11" pointing to the "OK" button.

Voxel sizes
The voxel sizes (x, y & z, in mm) of the volume. This item has a default value, set via a call to `@(val)spm_get_defaults('normalise.write.voxel_sizes')`. Evaluated statements are entered. An 1-by-3 array must be entered.

Step 7

Normalise (Optional)

The image shows two overlapping windows from a software application. The background window is the 'Batch Editor' with a menu open. The foreground window is the 'Save Job' dialog box.

12 → points to the 'Save Batch' option in the Batch Editor menu.

13 → points to the 'Save As:' text field in the 'Save Job' dialog, which contains the text 'norm.struct'.

14 → points to the 'Save' button in the 'Save Job' dialog.

The 'Save Job' dialog shows a file list with the following columns: Name and Date Modified.

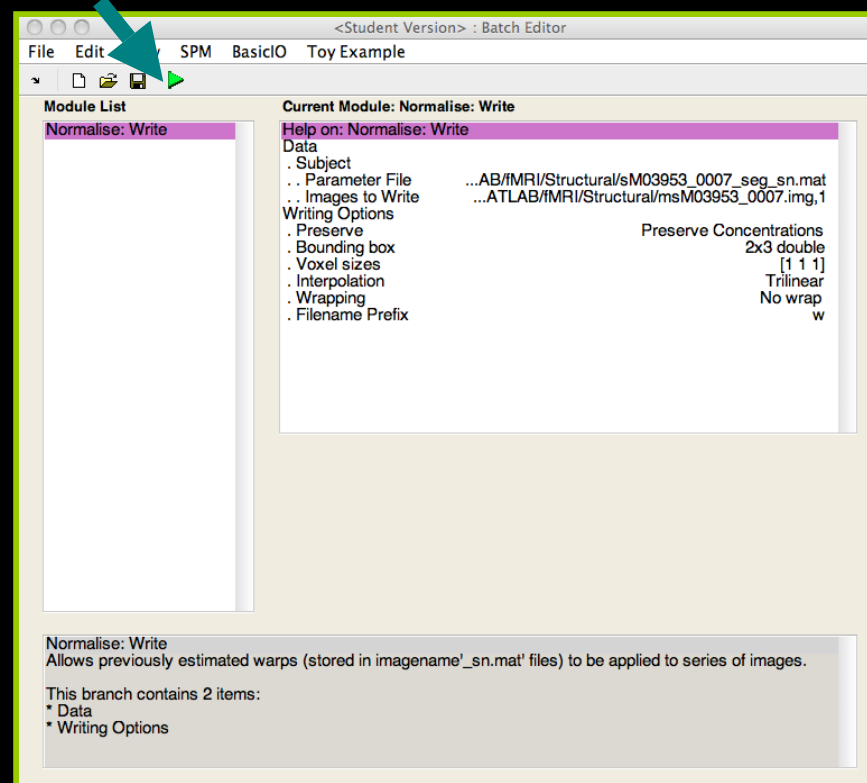
Name	Date Modified
coreg.mat	Tuesday, October 18, 2011 3:40 PM
normalise.mat	Tuesday, October 18, 2011 6:46 PM
realign.mat	Tuesday, October 18, 2011 12:10 PM
segment.mat	Tuesday, October 18, 2011 4:25 PM
slice_timing.mat	Tuesday, October 18, 2011 1:14 PM

The 'File Format' dropdown in the dialog is set to 'Matlab .mat File'.

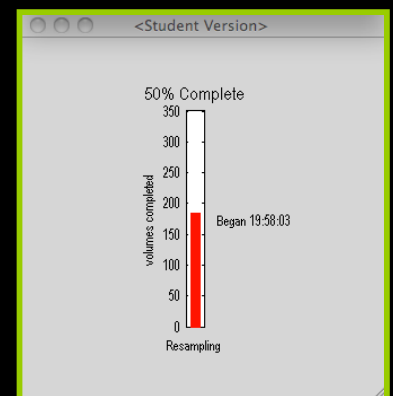
Step 7

Normalise (Optional)

15



Processing...



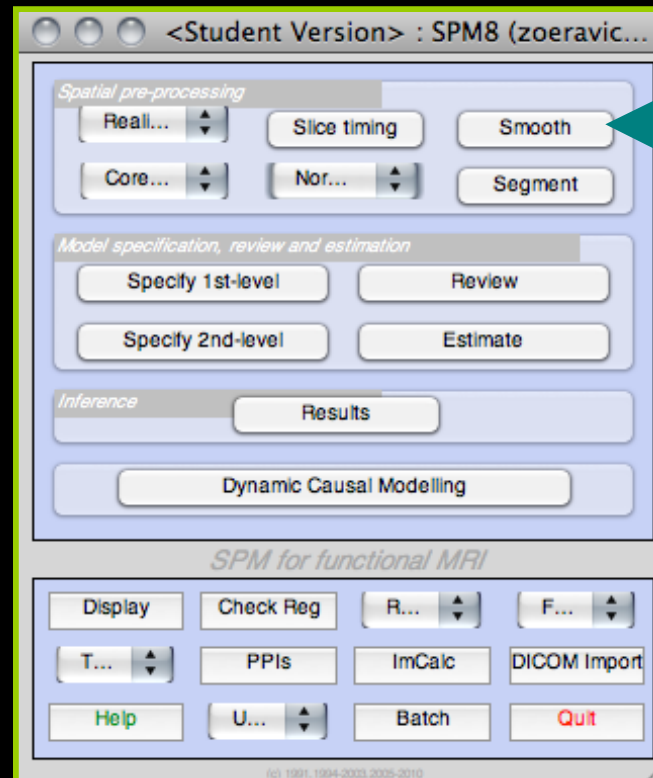
Step 8

Smoothing

- Press the SMOOTH button
 - Highlight “Images to Smooth” and select \wedge wms.* files
 - Save the job as smooth.mat
 - Press the “Run” button
- New files: swmsM03953_0005_*.img

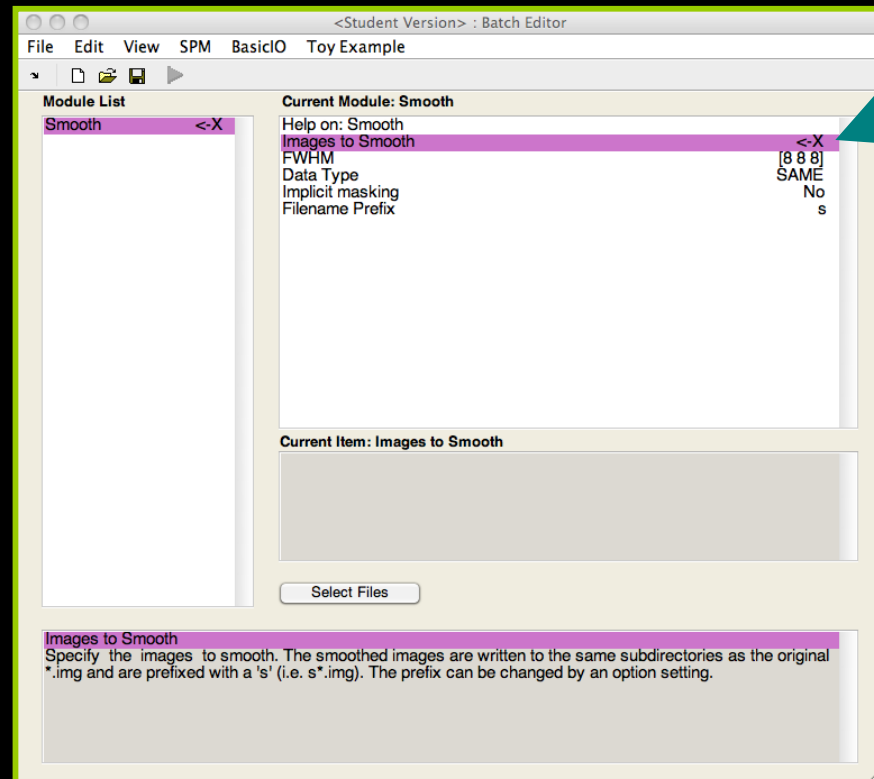
Step 8

Smoothing

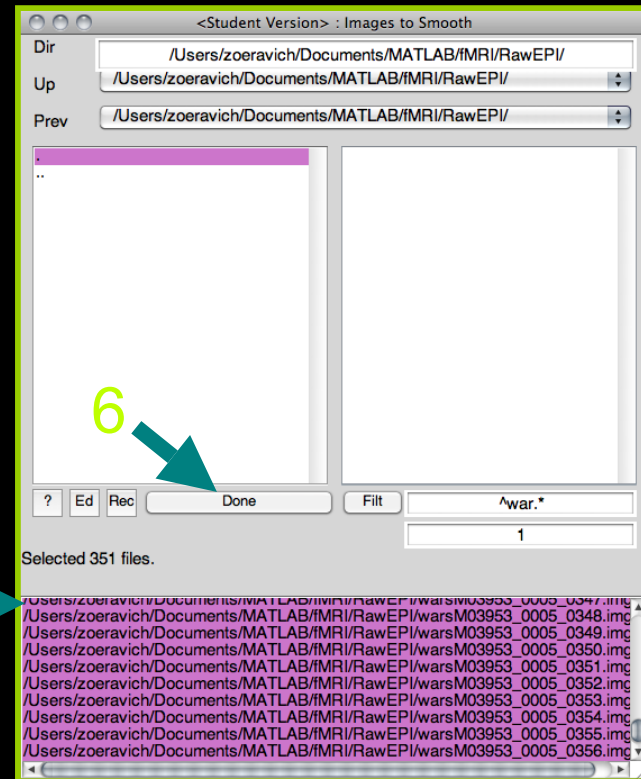
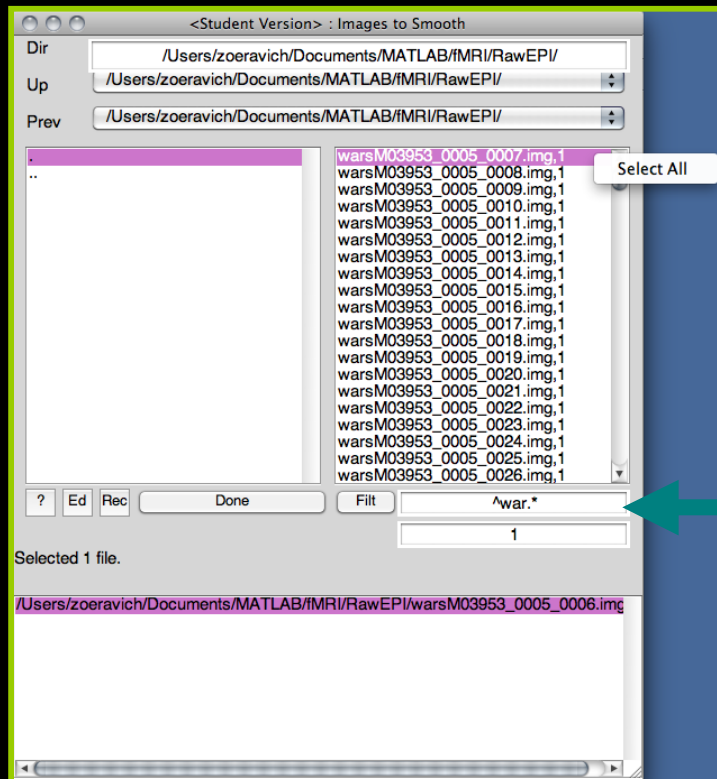


Step 8

Smoothing



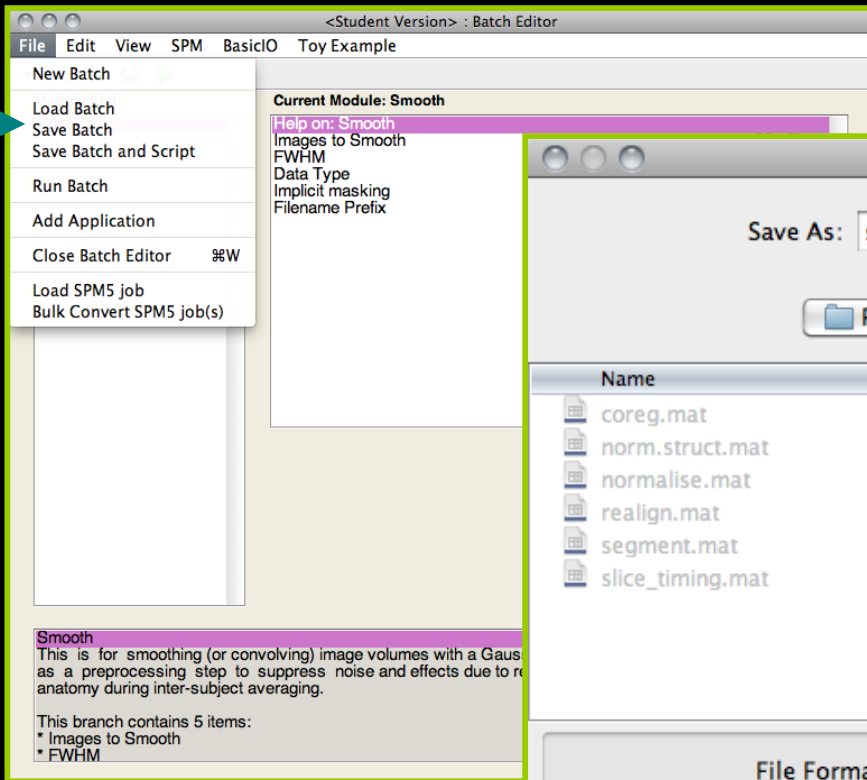
Step 8 Smoothing



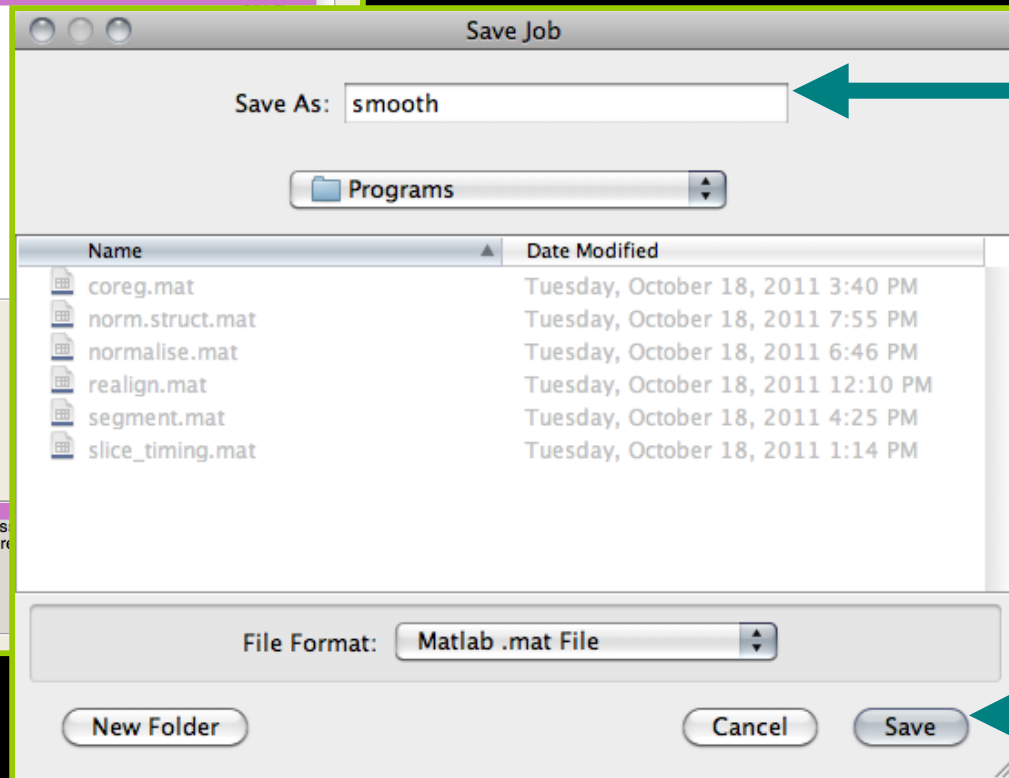
Step 8

Smoothing

7



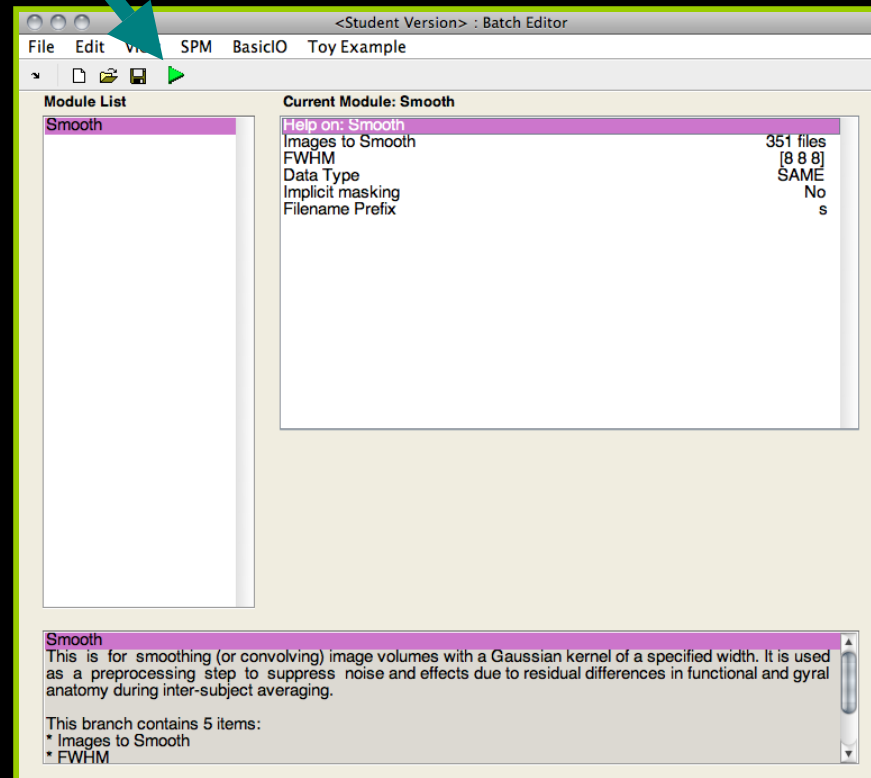
8



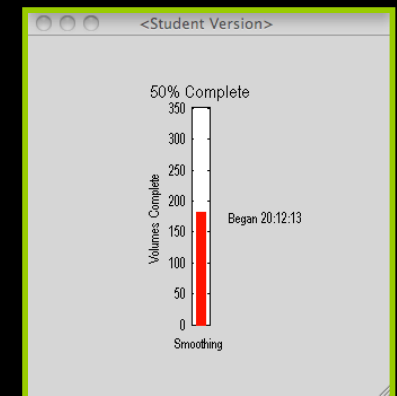
9

Step 8 Smoothing

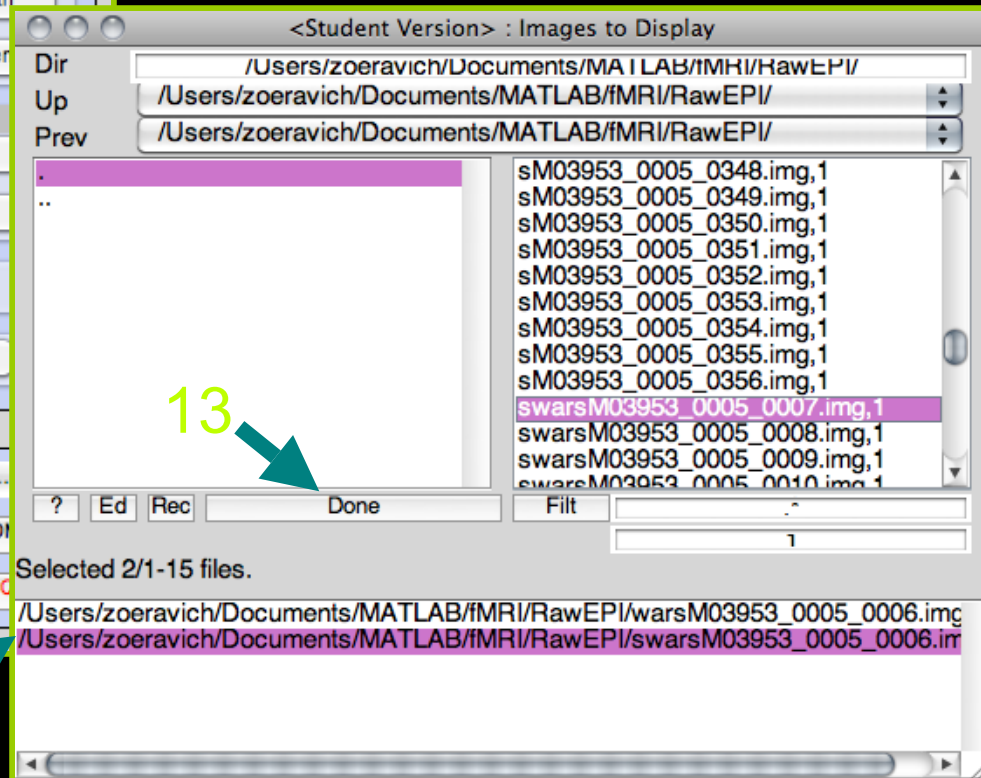
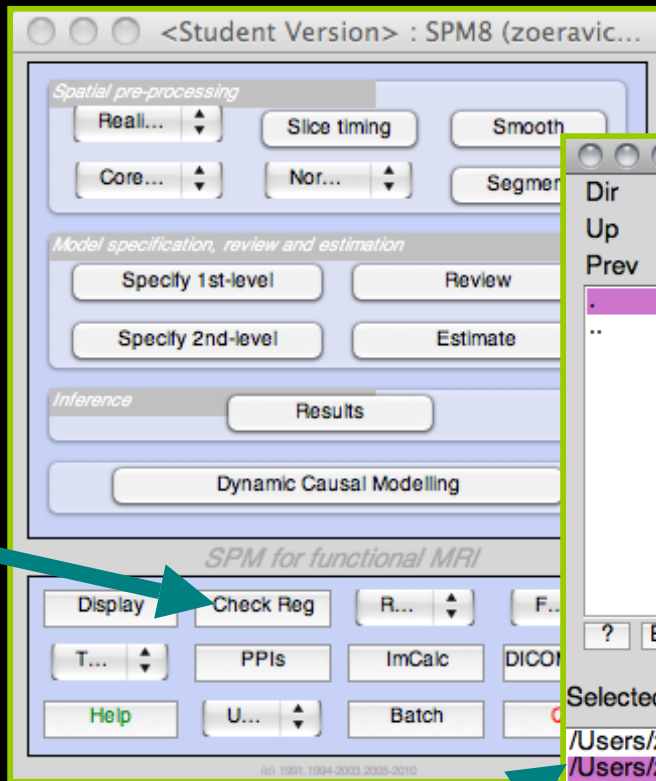
10



Processing...



Step 8 Smoothing



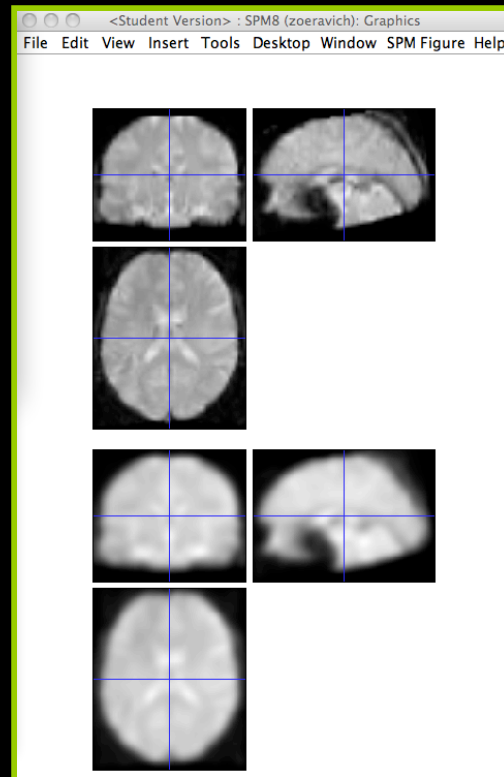
11

13

12

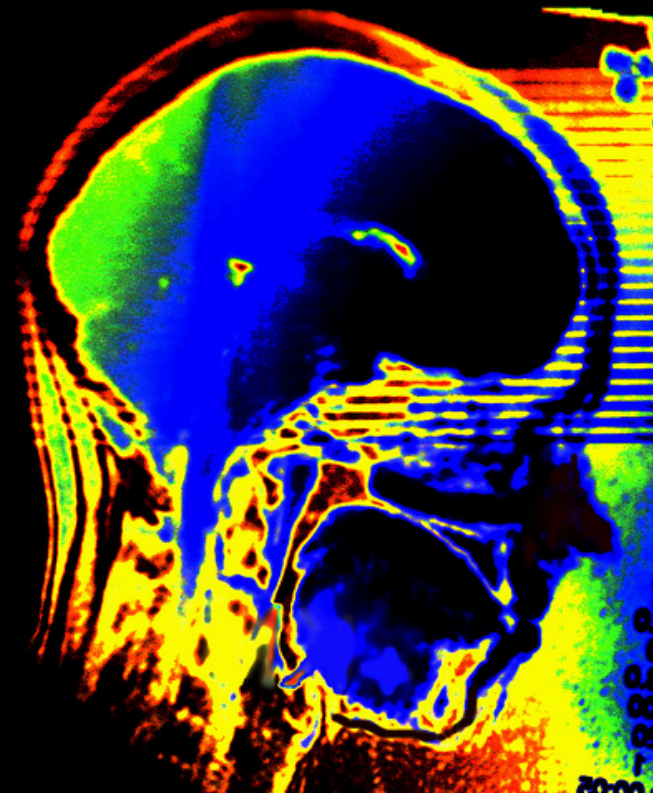
Step 8

Smoothing



Modelling Overview

1. Specify First Level
2. Estimate
3. Inference for Categorical Design
4. Statistical Tables
5. F-Contrasts
6. Testing Effects of Movement



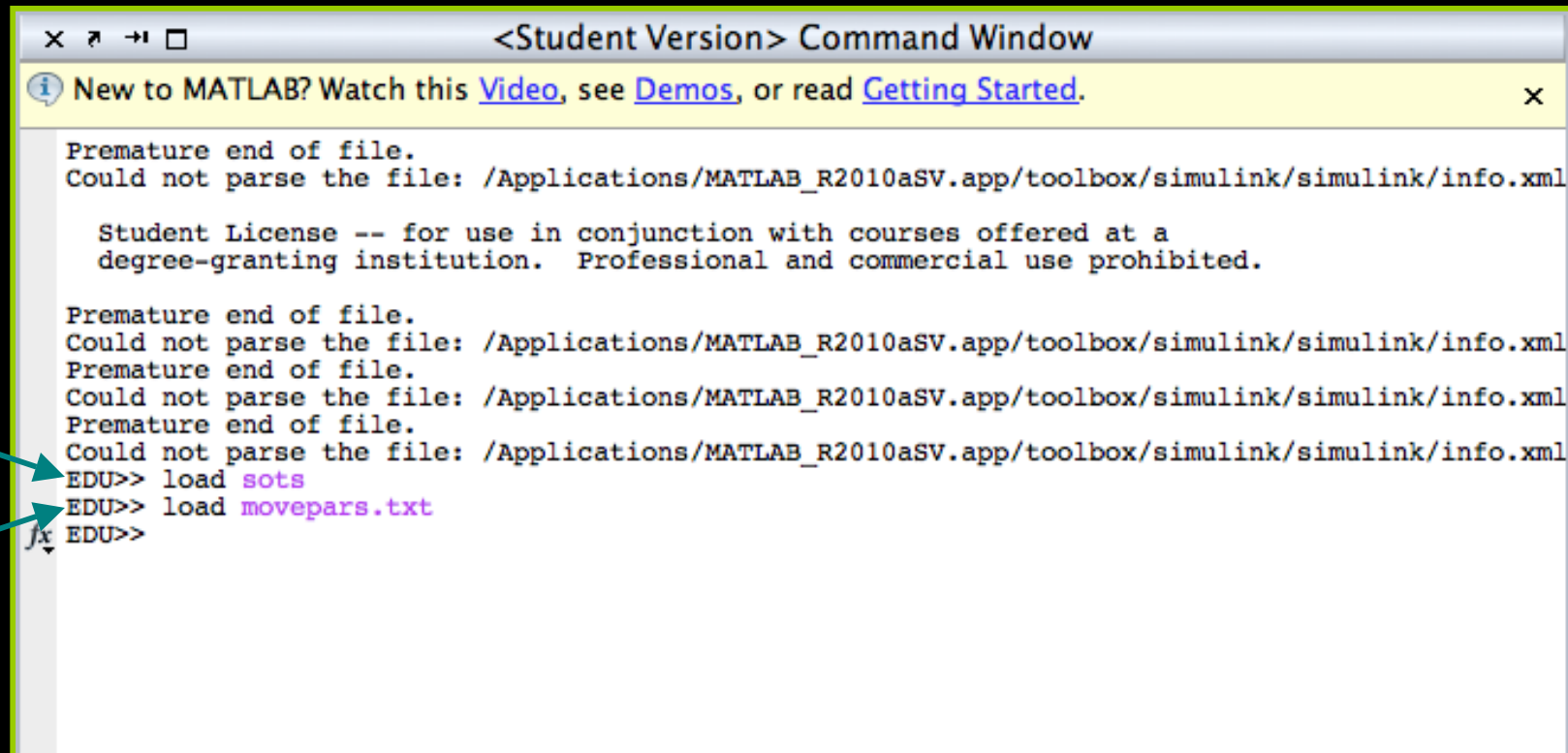
Step 9

Specify First-Level (Part 1)

- At the MATLAB command prompt, type “load sots” and then “moveparts.txt”
- Press the SPECIFY 1ST-LEVEL button
 - Highlight “Units for design” in the “Timing parameters” section and select “Scans”
 - “Interscan interval”; Type “2”
 - “Microtime resolution”; Type “24”
 - “Microtime onset”; Type “12”
 - Highlight “Data and Design” and select “New Subject/Session”; then highlight “Scans” and use the ^swar.* filter to choose 351 functional images

Step 9

Specify First-Level (Part 1)



The screenshot shows a MATLAB Command Window titled "<Student Version> Command Window". At the top, there is a yellow banner with an information icon and the text: "New to MATLAB? Watch this [Video](#), see [Demos](#), or read [Getting Started](#)." Below this, the window contains several lines of text. The first line is "Premature end of file." followed by "Could not parse the file: /Applications/MATLAB_R2010aSV.app/toolbox/simulink/simulink/info.xml". This is followed by a license notice: "Student License -- for use in conjunction with courses offered at a degree-granting institution. Professional and commercial use prohibited." Below the license notice, the same error message and file path are repeated. At the bottom, there are three lines of command input: "EDU>> load sots", "EDU>> load movepars.txt", and "EDU>>".

```
<Student Version> Command Window
New to MATLAB? Watch this Video, see Demos, or read Getting Started.
Premature end of file.
Could not parse the file: /Applications/MATLAB_R2010aSV.app/toolbox/simulink/simulink/info.xml

Student License -- for use in conjunction with courses offered at a
degree-granting institution. Professional and commercial use prohibited.

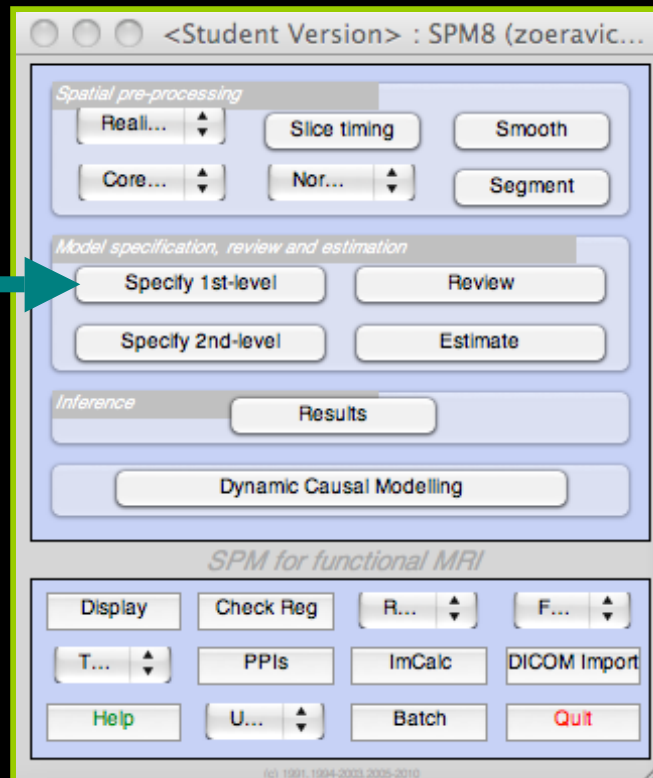
Premature end of file.
Could not parse the file: /Applications/MATLAB_R2010aSV.app/toolbox/simulink/simulink/info.xml
Premature end of file.
Could not parse the file: /Applications/MATLAB_R2010aSV.app/toolbox/simulink/simulink/info.xml
Premature end of file.
Could not parse the file: /Applications/MATLAB_R2010aSV.app/toolbox/simulink/simulink/info.xml
EDU>> load sots
EDU>> load movepars.txt
EDU>>
```

1 →
2 →

Step 9

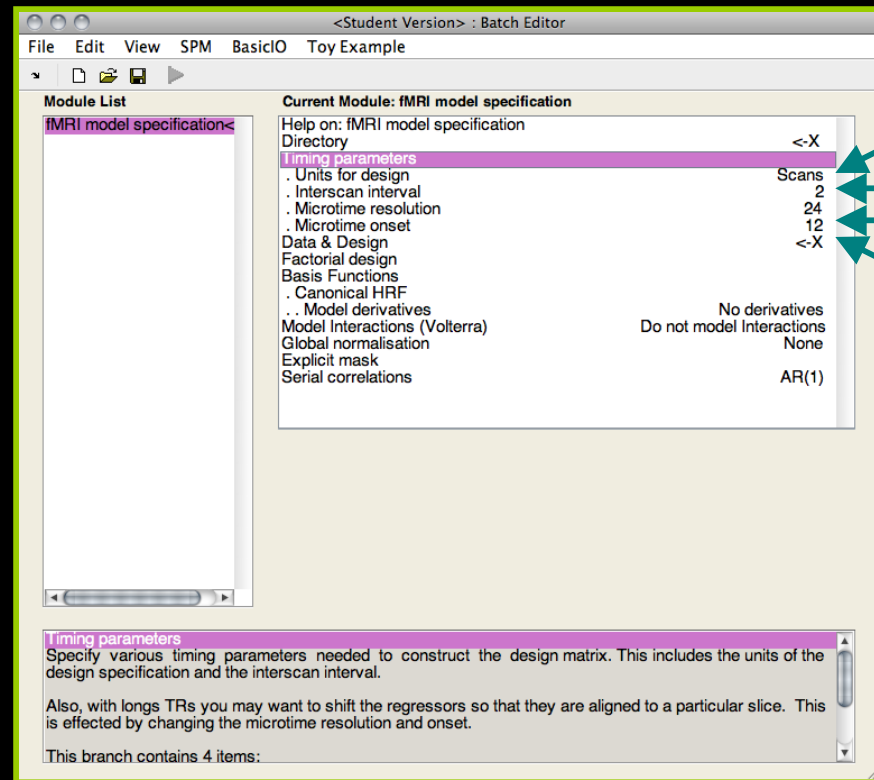
Specify First-Level (Part 1)

3



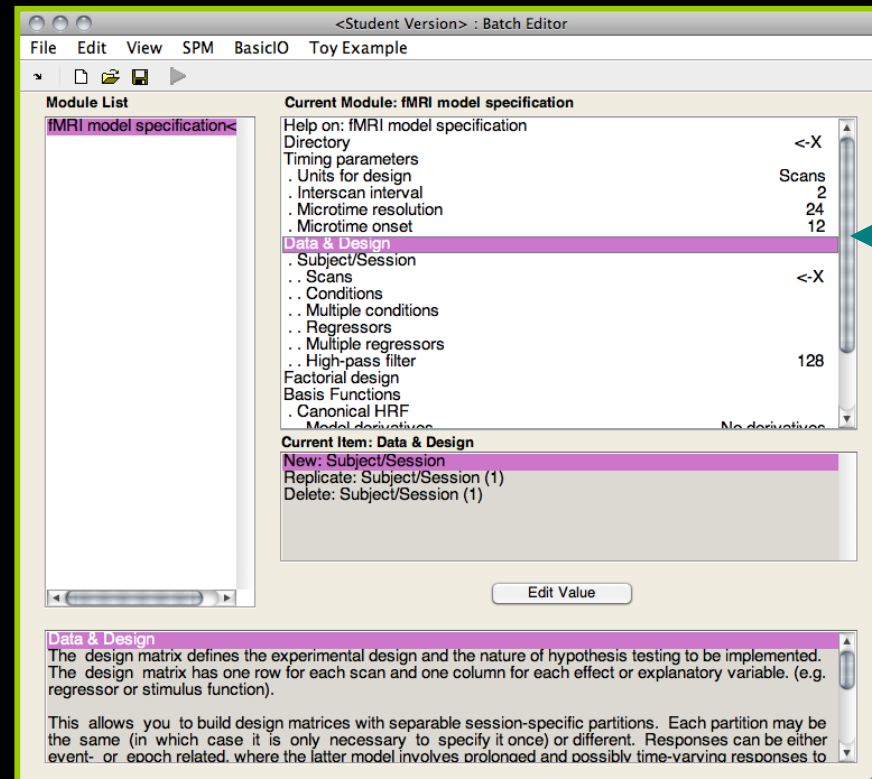
Step 9

Specify First-Level (Part 1)



Step 9

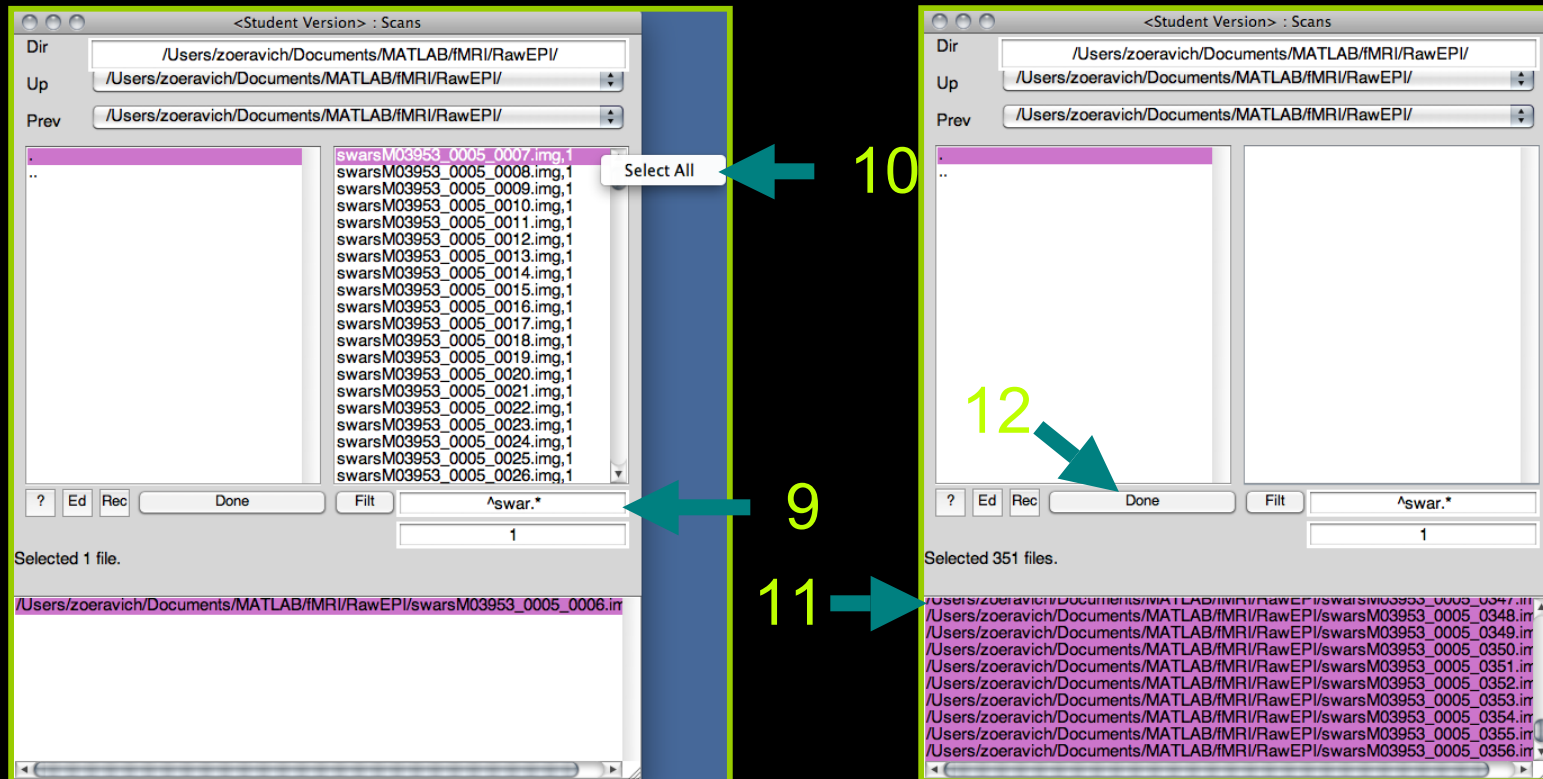
Specify First-Level (Part 1)



8

Step 9

Specify First-Level (Part 1)



Step 9

Specify First-Level (Part 2)

- Highlight “Conditions”, select “New condition”, and open the newly created “Condition” option
 - “Name”; Type “N1”
 - “Onsets”; Type “ $\text{set}\{1\}$ ”
 - “Durations”; Type “0”
- Highlight “Conditions”, select “Replicate condition”, and then open the newly created “Condition” option
 - “Name”; Type “N2”
 - “Onsets”; Type “ $\text{set}\{2\}$ ”

Step 9

Specify First-Level (Part 2)

13

14

15

16

17

18

<Student Version> : Batch Editor

File Edit View SPM BasicIO Toy Example

Module List

fMRI model specification<

Current Module: fMRI model specification

Help on: fMRI model specification

Directory

Timing parameters

- . Units for design
- . Interscan interval
- . Microtime resolution
- . Microtime onset

Data & Design

- . Subject/Session
- . Scans
- . Conditions

Current Item: Conditions

New: Condition

Replicate: Condition (1)

Delete: Condition (1)

Edit Value

Conditions

You are allowed to combine both event- and epoch-related responses in the same model. Any number of condition (event or epoch) types can be specified. Epoch and event-related responses are modeled in exactly the same way by specifying their onsets (in terms of onset times). Events are specified with a duration of 0. If you enter a single number for the durations that all trials conform to this duration. For factorial designs, one can later associate conditions with the appropriate levels of experimental factors.

<Student Version> : Batch Editor

File Edit View SPM BasicIO Toy Example

Module List

fMRI model specification<

Current Module: fMRI model specification

Help on: fMRI model specification

Directory

Timing parameters

- . Units for design Scans
- . Interscan interval 2
- . Microtime resolution 24
- . Microtime onset 12

Data & Design

- . Subject/Session
- . Scans 351 files
- . Conditions
- . Condition

Condition

- . Name N1
- . Onsets 26x1 double
- . Durations 0
- . Time Modulation No Time Modulation
- . Parametric Modulations
- . Multiple conditions
- . Regressors

Condition

An array of input functions is constructed, specifying occurrence events or epochs (or both). These are convolved with a basis set at a later stage to give regressors that enter into the design matrix. Interactions of evoked responses with some parameter (time or a specified variate) enter at this stage as additional columns in the design matrix with each trial multiplied by the [expansion of the] trial-specific parameter. The 0th order expansion is simply the main effect in the first column.

This branch contains 5 items:

Step 9

Specify First-Level (Part 2)

19



20



Module List

Current Module: fMRI model specification

Help on: fMRI model specification

Directory

- Timing parameters
 - . Units for design
 - . Interscan interval
 - . Microtime resolution
 - . Microtime onset
- Data & Design
 - . Subject/Session
 - . Scans
- . Conditions
- ... Condition
- ... Name
- ... Onsets
- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- .. Multiple conditions
- ... Regressors

Current Item: Conditions

- New: Condition
- Replicate: Condition (1)
- Delete: Condition (1)

Conditions

You are allowed to combine both event- and epoch-related responses in the same model. Any number of condition (event or epoch) types can be specified. Epoch and event-related responses are modeled in exactly the same way by specifying their onsets [in terms of onset times]. Events are specified with a duration of 0. If you enter a single number for the duration that all trials conform to this duration. For factorial designs, one can later associate conditions with the appropriate levels of experimental factors.

Module List

Current Module: fMRI model specification

- .. Scans 351 files
- .. Conditions
- ... Condition
- ... Name N1
- ... Onsets 26x1 double 0
- ... Durations No Time Modulation
- ... Time Modulation
- ... Parametric Modulations
- ... Condition
- ... Name N2
- ... Onsets 26x1 double 0
- ... Durations No Time Modulation
- ... Time Modulation
- ... Parametric Modulations
- .. Multiple conditions
- .. Regressors
- .. Multiple regressors
- .. High-pass filter 128
- Factorial design

Condition

An array of input functions is constructed, specifying occurrence events or epochs (or both). These are convolved with a basis set at a later stage to give regressors that enter into the design matrix. Interactions of evoked responses with some parameter (time or a specified variate) enter at this stage as additional columns in the design matrix with each trial multiplied by the [expansion of the] trial-specific parameter. The 0th order expansion is simply the main effect in the first column.

This branch contains 5 items:

21

22

23

24



Step 9

Specify First-Level (Part 3)

- Highlight “Conditions”, select “Replicate condition”, and then open the newly created “Condition” option
 - “Name”; Type “F1”
 - “Onsets”; Type “sot{3}”
- Highlight “Conditions”, select “Replicate condition”, and then open the newly created “Condition” option
 - “Name”; Type “F2”
 - “Onsets”; Type “sot{4}”
- Highlight “Multiple Regressions” and select the movepars.txt file

Step 9

Specify First-Level (Part 3)

25

Module List

Current Module: fMRI model specification

- .. Scans
- .. Conditions
- ... Condition
- ... Name
- ... Onsets
- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- .. Condition
- ... Name
- ... Onsets
- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- .. Multiple conditions
- .. Regressors
- .. Multiple regressors
- .. High-pass filter
- Factorial design

Current Item: Conditions

New: Condition

Replicate: Condition (1)

Replicate: Condition (2)

Delete: Condition (1)

Delete: Condition (2)

Conditions

You are allowed to combine both event- and epoch-related responses in the same model. Any number of condition (event or epoch) types can be specified. Epoch and event-related responses are modeled in exactly the same way by specifying their onsets (in terms of onset times) and durations. Events are specified with a duration of 0. If you enter a single number for the duration, that all trials conform to this duration. For factorial designs, one can later associate conditions with the appropriate levels of experimental factors.

26

Module List

Current Module: fMRI model specification

- ... Parametric Modulations
- .. Condition
- ... Name
- ... Onsets
- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- .. Condition
- ... Name
- ... Onsets
- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- .. Multiple conditions
- .. Regressors
- .. Multiple regressors
- .. High-pass filter
- Factorial design
- Basic Functions

Name

Onsets

Durations

Time Modulation

Parametric Modulations

Condition

Name

Onsets

Durations

Time Modulation

Parametric Modulations

Multiple conditions

Regressors

Multiple regressors

High-pass filter

Factorial design

Basic Functions

N2

26x1 double

0

No Time Modulation

F1

26x1 double

0

No Time Modulation

128

Condition

An array of input functions is constructed, specifying occurrence events or epochs (or both). These are convolved with a basis set at a later stage to give regressors that enter into the design matrix. Interactions of evoked responses with some parameter (time or a specified variate) enter at this stage as additional columns in the design matrix with each trial multiplied by the [expansion of the] trial-specific parameter. The 0th order expansion is simply the main effect in the first column.

This branch contains 5 items:

27

28

29

30

Step 9

Specify First-Level (Part 3)

31



32



Conditions
 You are allowed to combine both event- and epoch-related responses in the same model. Any number of condition (event or epoch) types can be specified. Epoch and event-related responses are modeled in exactly the same way by specifying their onsets [in terms of onset times] and durations. Events are specified with a duration of 0. If you enter a single number for the duration that all trials conform to this duration. For factorial designs, one can later associate conditions with the appropriate levels of experimental factors.

Condition
 An array of input functions is constructed, specifying occurrence events or epochs (or both). These are convolved with a basis set at a later stage to give regressors that enter into the design matrix. Interactions of evoked responses with some parameter (time or a specified variate) enter at this stage as additional columns in the design matrix with each trial multiplied by the [expansion of the] trial-specific parameter. The 0th order expansion is simply the main effect in the first column.

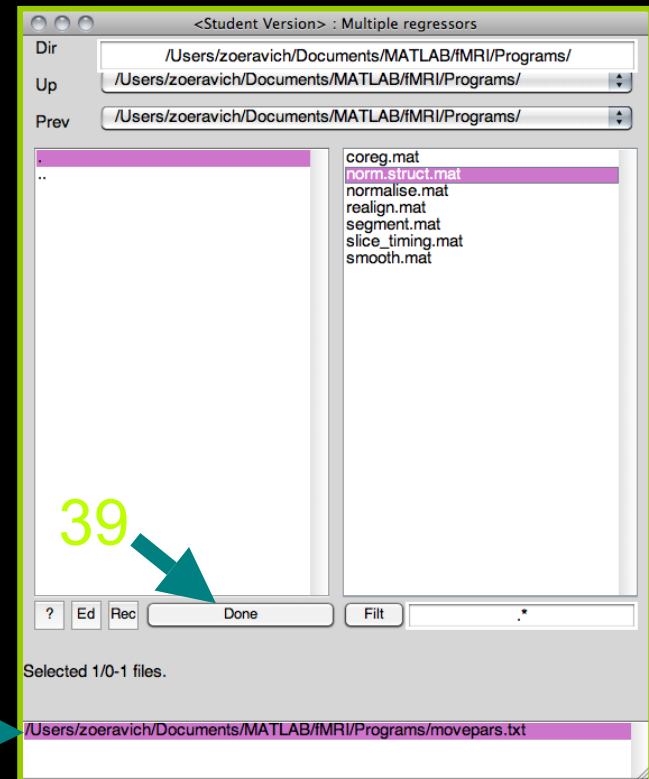
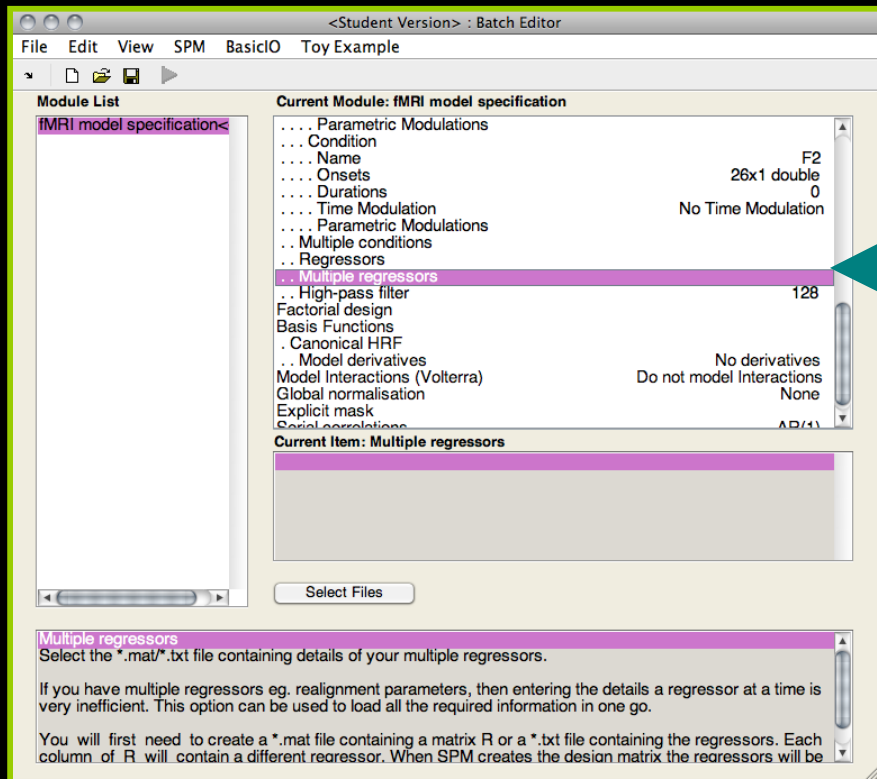
This branch contains 5 items:

33
34
35
36



Step 9

Specify First-Level (Part 3)



Step 9

Specify First-Level (Part 4)

- Highlight “Factorial Design”, select “New Factor”, and open the newly created “Factor” option
 - “Name”; Type “Fam”
 - “Levels”; Type “2”
- Highlight “Factorial Design”, select “New Factor”, and then open the newly created “Factor” option
 - “Name”; Type “Rep”
 - “Levels”; Type “2”
- Highlight “Basis Functions” and select “Canonical HRF”; choose “Model derivatives” and then “Time and Dispersion derivatives”

Step 9

Specify First-Level (Part 4)

40



41



<Student Version> : Batch Editor
File Edit View SPM BasicIO Toy Example

Module List
fMRI model specification-<

Current Module: fMRI model specification

- ... Parametric Modulations
- ... Condition
- ... Name
- ... Onsets
- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- ... Multiple conditions
- ... Regressors
- ... Multiple regressors .../MATLAB/IMRI/Prog
- ... High-pass filter
- Factorial design**
- ... Factor
- ... Name
- ... Levels
- Basis Functions
- ... Canonical HRF
- ... Model derivatives
- Model Interactions (Malters)

Current Item: Factorial design

- New: Factor**
- Replicate: Factor (1)
- Delete: Factor (1)

Edit Value

Factorial design
If you have a factorial design then SPM can automatically generate the contrasts needed for main effects and interactions.

This includes the F-contrasts necessary to test for these effects at the within-subject level and the simple contrasts necessary to generate the contrast images for a between-subject analysis.

<Student Version> : Batch Editor
File Edit View SPM BasicIO Toy Example

Module List
fMRI model specification-<

Current Module: fMRI model specification

- ... Parametric Modulations
- ... Condition
- ... Name F2
- ... Onsets 26x1 double
- ... Durations 0
- ... Time Modulation No Time Modulation
- ... Parametric Modulations
- ... Multiple conditions
- ... Regressors
- ... Multiple regressors .../MATLAB/IMRI/Programs/movepars.txt
- ... High-pass filter 128
- Factorial design
- Factor**
- ... Name Fam
- ... Levels 2
- Basis Functions
- ... Canonical HRF
- ... Model derivatives No derivatives
- Model Interactions (Malters) Do not model interactions

Current Item: Factor

- Factor**
- Add a new factor to your experimental design

This branch contains 2 items:

- * Name
- * Levels

42

43



Step 9

Specify First-Level (Part 4)

44



45



<Student Version> : Batch Editor
File Edit View SPM BasicIO Toy Example

Module List
fMRI model specification-<

Current Module: fMRI model specification

- ... Parametric Modulations
- ... Condition
- ... Name
- ... Onsets
- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- ... Multiple conditions
- ... Regressors
- ... Multiple regressors .../MATLAB/IMRI/Prog
- ... High-pass filter
- Factorial design**
- ... Factor
- ... Name
- ... Levels
- Basis Functions
- ... Canonical HRF
- ... Model derivatives
- Model Interactions (Matters)

Current Item: Factorial design

- New: Factor
- Replicate: Factor (1)
- Delete: Factor (1)

Edit Value

Factorial design
If you have a factorial design then SPM can automatically generate the contrasts needed to test for main effects and interactions.

This includes the F-contrasts necessary to test for these effects at the within-subject level and the simple contrasts necessary to generate the contrast images for a between-subject analysis.

<Student Version> : Batch Editor
File Edit View SPM BasicIO Toy Example

Module List
fMRI model specification-<

Current Module: fMRI model specification

- ... Parametric Modulations
- ... Condition
- ... Name
- ... Onsets 26x1 double
- ... Durations 0
- ... Time Modulation No Time Modulation
- ... Parametric Modulations
- ... Multiple conditions
- ... Regressors
- ... Multiple regressors .../MATLAB/IMRI/Programs/movepars.txt
- ... High-pass filter 128
- Factorial design
- ... Factor
- ... Name Fam
- ... Levels 2
- Factor**
- ... Name Rep
- ... Levels 2
- Basis Functions

Factor
Add a new factor to your experimental design

This branch contains 2 items:

- Name
- Levels

46

47



Step 9

Specify First-Level (Part 4)

48



49



Batch Editor - <Student Version> : Toy Example

File Edit View SPM BasicIO Toy Example

Module List

Current Module: fMRI model specification

- ... Durations
- ... Time Modulation
- ... Parametric Modulations
- ... Multiple conditions
- ... Regressors
- ... Multiple regressors
- ... High-pass filter
- Factorial design
 - Factor
 - .. Name
 - .. Levels
 - Factor
 - .. Name
 - .. Levels
- Basis Functions**
- .. Canonical HRF
- .. Model derivatives
- Model Interactions (Volterra) Do not model interactions
- Global Normalization

Current Item: Basis Functions

- Canonical HRF**
- Fourier Set
- Fourier Set (Hanning)
- Gamma Functions
- Finite Impulse Response

Edit Value

Basis Functions

The most common choice of basis function is the Canonical HRF with or without derivatives.

One of the following options must be selected:

- * Canonical HRF
- * Fourier Set
- * Fourier Set (Hanning)

Batch Editor - <Student Version> : Toy Example

File Edit View SPM BasicIO Toy Example

Module List

Current Module: fMRI model specification

- ... Durations 0
- ... Time Modulation No Time Modulation
- ... Parametric Modulations
- ... Multiple conditions
- ... Regressors
- ... Multiple regressors .../MATLAB/IMRI/Programs/movepars.txt
- ... High-pass filter 128
- Factorial design
 - Factor
 - .. Name Fam
 - .. Levels 2
 - Factor
 - .. Name Rep
 - .. Levels 2
- Basis Functions
 - .. Canonical HRF
 - Model derivatives** Time and Dispersion derivatives
 - Model Interactions (Volterra) Do not model interactions
 - Global Normalization None

Current Item: Model derivatives

- No derivatives
- Time derivatives
- Time and Dispersion derivatives**

Edit Value

Model derivatives

Model HRF Derivatives. The canonical HRF combined with time and dispersion derivatives comprise an 'informed' basis set, as the shape of the canonical response conforms to the hemodynamic response that is commonly observed. The incorporation of the derivative terms allow for variations in subject-to-subject and voxel-to-voxel responses. The time derivative allows the peak response to vary by plus or minus a second and the dispersion derivative allows the width of the response to vary. The informed basis set requires an SPM(F) for inference. T-contrasts over just the canonical are perfectly valid but assume constant delay/dispersion. The informed basis set compares favourably with eq. FIR bases on many data sets.

50



51



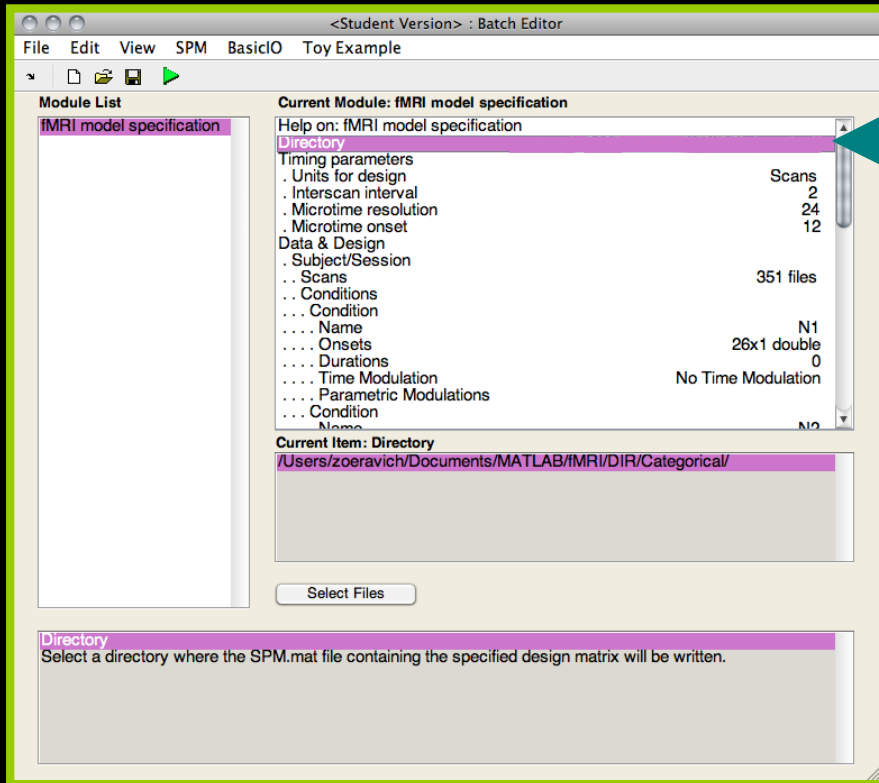
Step 9

Specify First-Level (Part 5)

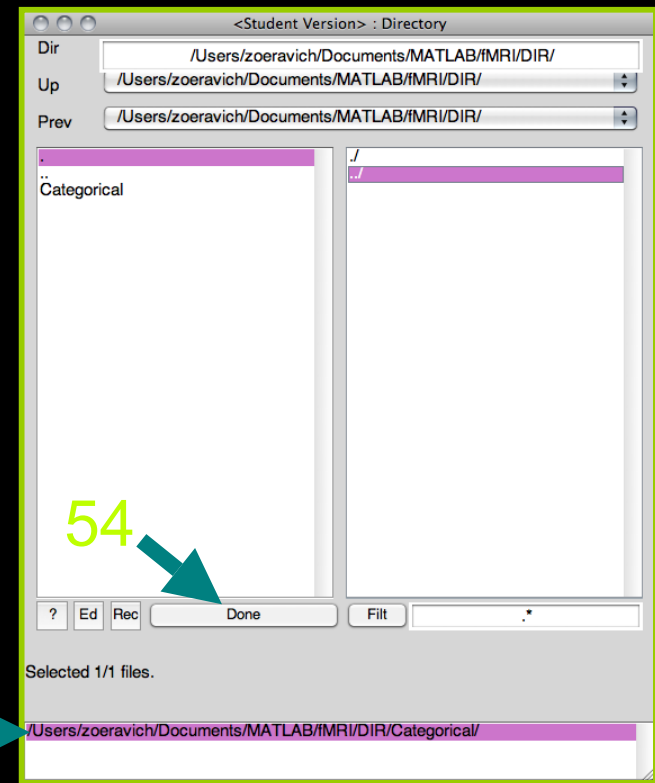
- Highlight “Directory” and select the DIR/categorical directory
- Save the job as categorical_spec.mat
- Press the “Run” button
- Press the REVIEW button (it is advisable to check the model specification)
 - Under the “Design” tab, select the first item “Design Matrix”
 - “Explore” → “Session 1” → “N1”

Step 9

Specify First-Level (Part 5)



52



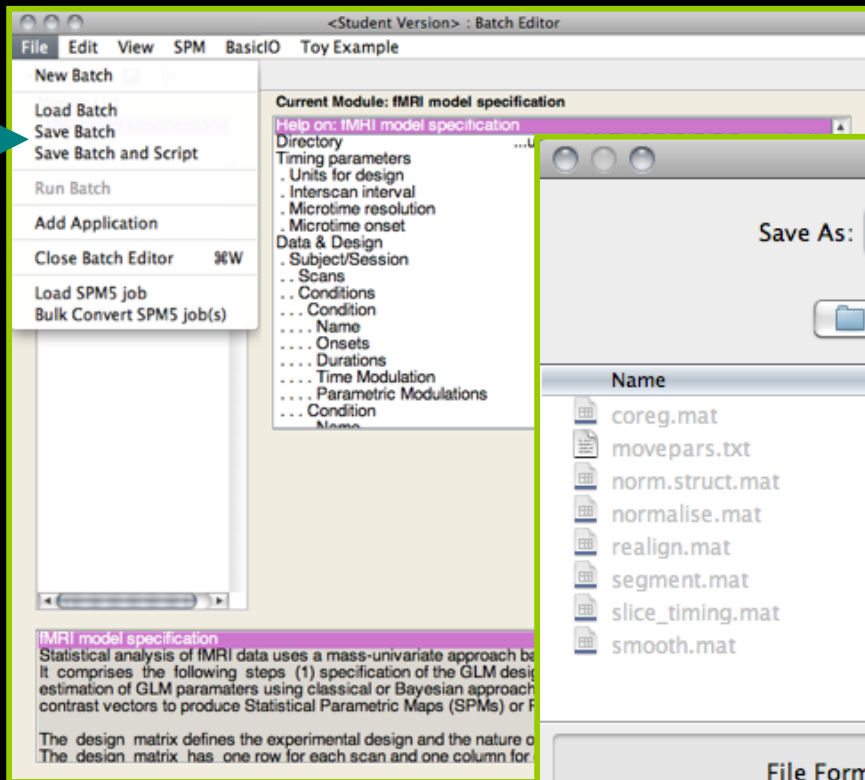
54

53

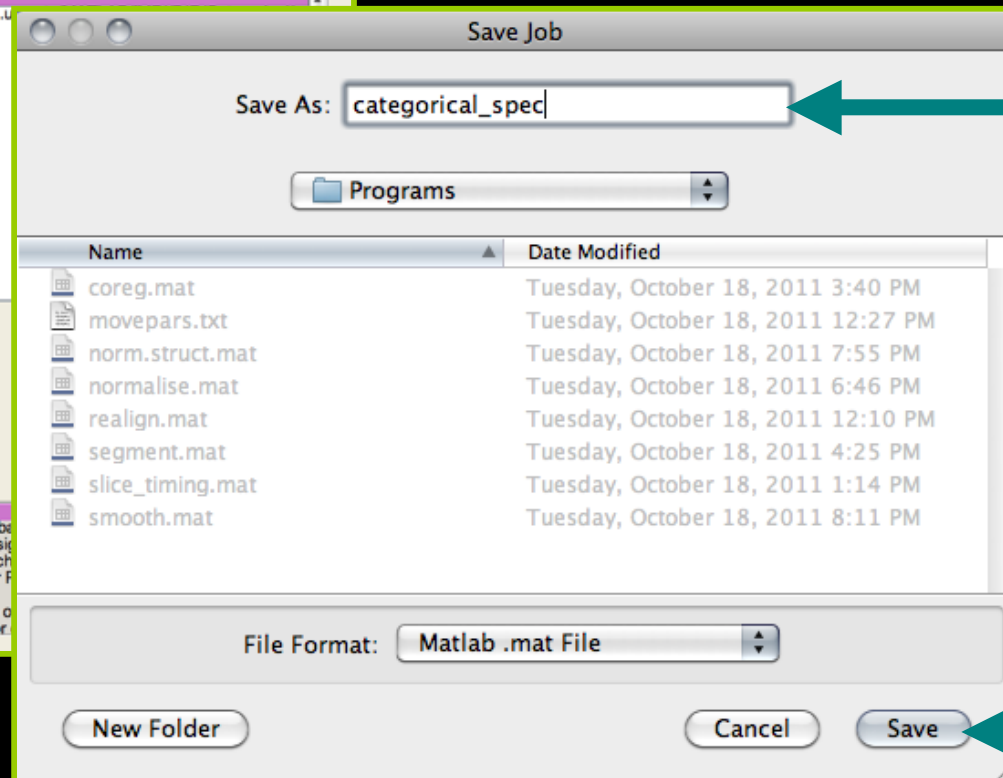
Step 9

Specify First-Level (Part 5)

55 →



→ 56

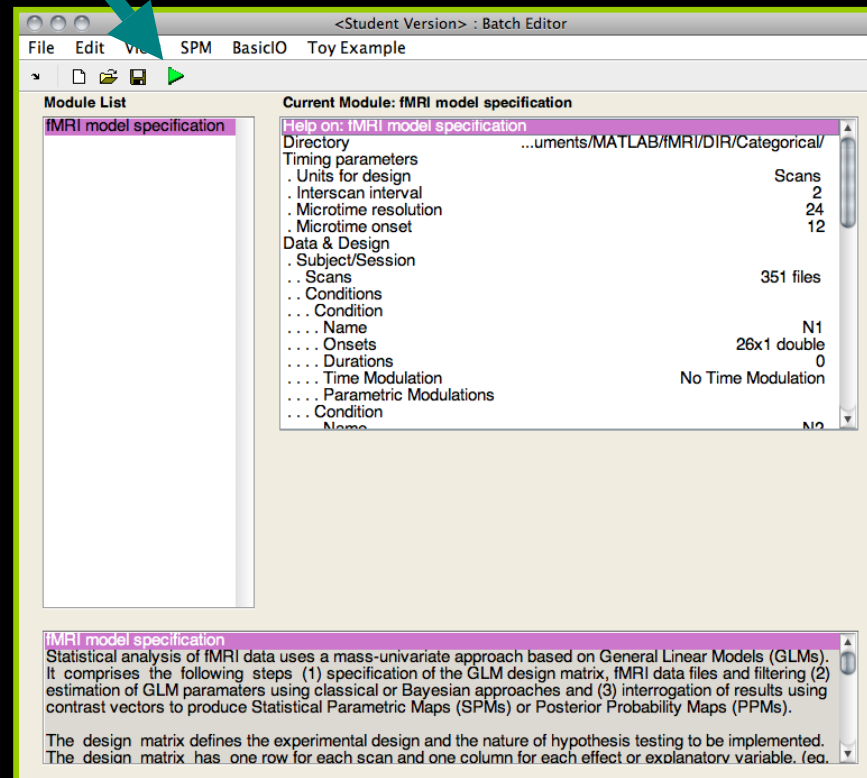


→ 57

Step 9

Specify First-Level (Part 5)

58



The screenshot shows the SPM Batch Editor window with the 'fMRI model specification' module selected. The interface includes a menu bar (File, Edit, View, SPM, BasicIO, Toy Example), a toolbar, and a main workspace. The workspace is divided into three sections: a 'Module List' on the left, a 'Current Module: fMRI model specification' panel in the center, and a help text area at the bottom.

Module List

- fMRI model specification

Current Module: fMRI model specification

Help on: fMRI model specification

Directory: ...uments/MATLAB/fMRI/DIR/Categorical/

Timing parameters

. Units for design	Scans
. Interscan interval	2
. Microtime resolution	24
. Microtime onset	12

Data & Design

. Subject/Session	
.. Scans	351 files
.. Conditions	
... Condition	
... Name	N1
... Onsets	26x1 double
... Durations	0
... Time Modulation	No Time Modulation
... Parametric Modulations	
... Condition	
... Name	N2

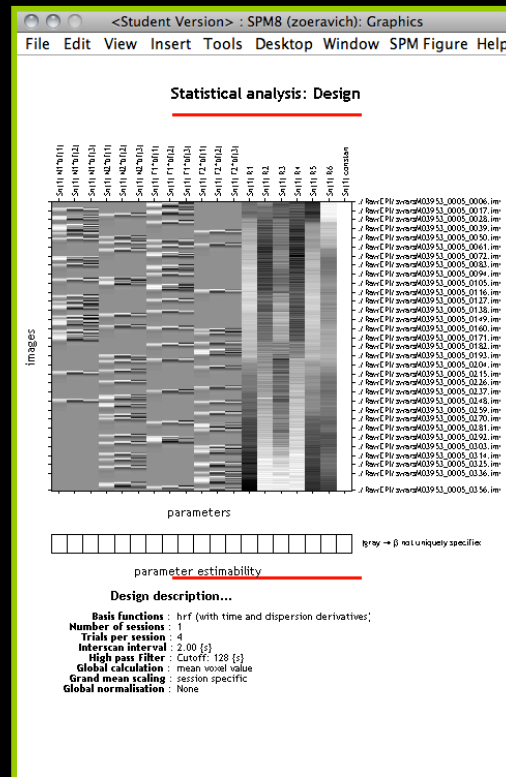
fMRI model specification

Statistical analysis of fMRI data uses a mass-univariate approach based on General Linear Models (GLMs). It comprises the following steps (1) specification of the GLM design matrix, fMRI data files and filtering (2) estimation of GLM parameters using classical or Bayesian approaches and (3) interrogation of results using contrast vectors to produce Statistical Parametric Maps (SPMs) or Posterior Probability Maps (PPMs).

The design matrix defines the experimental design and the nature of hypothesis testing to be implemented. The design matrix has one row for each scan and one column for each effect or explanatory variable. (eq.

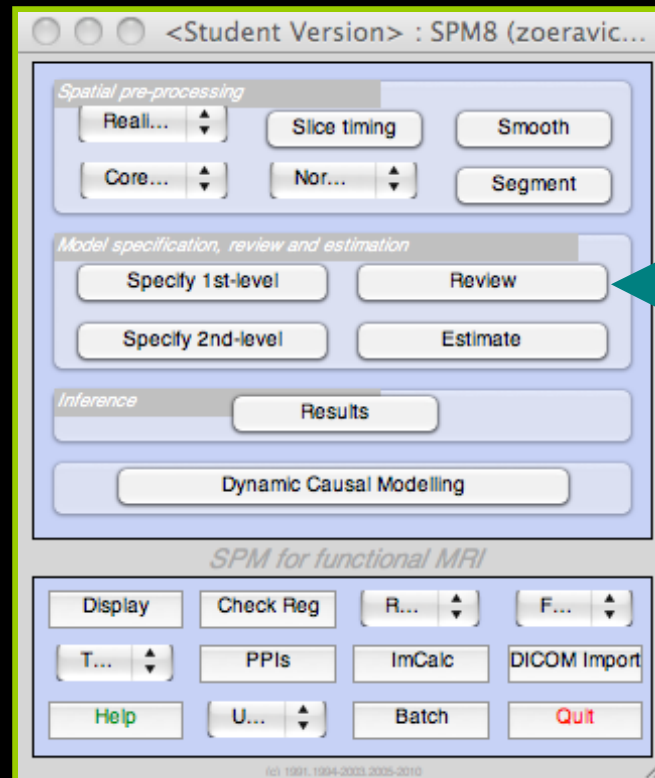
Step 9

Specify First-Level (Part 5)



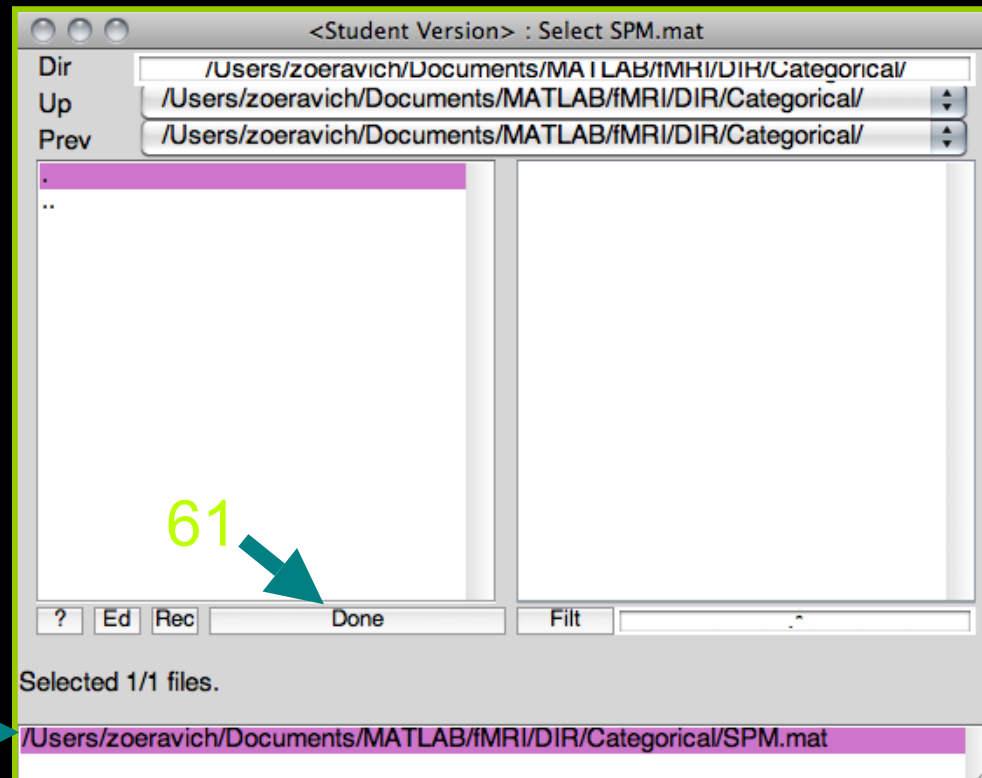
Step 9

Specify First-Level (Part 5)



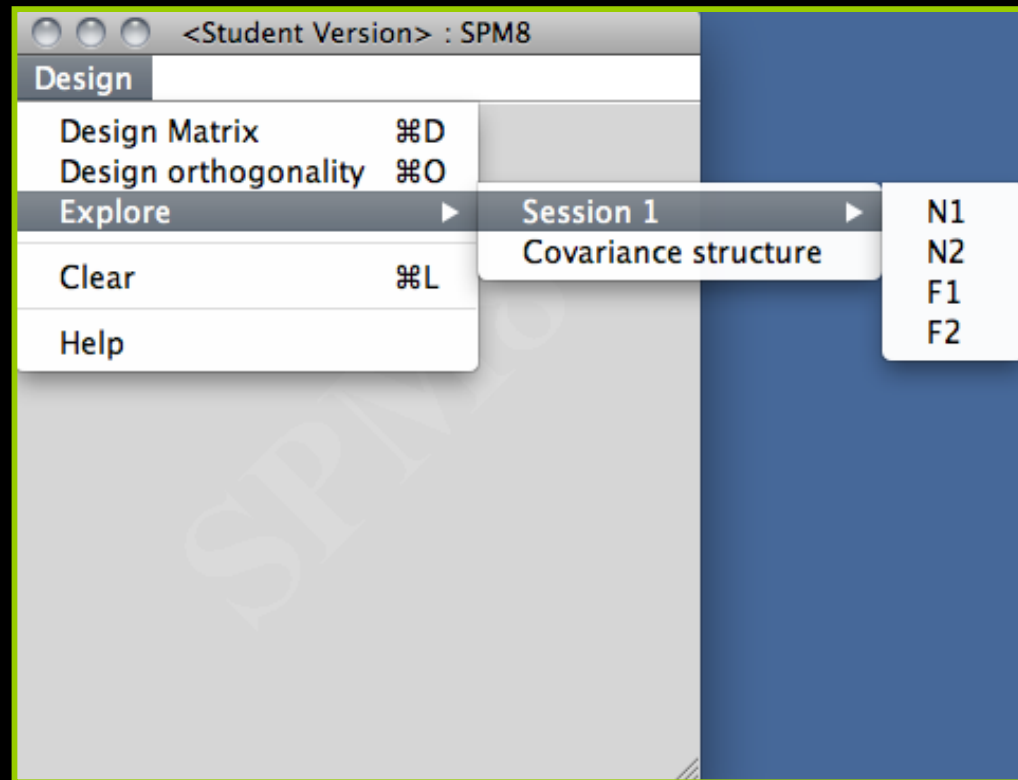
Step 9

Specify First-Level (Part 5)



Step 9

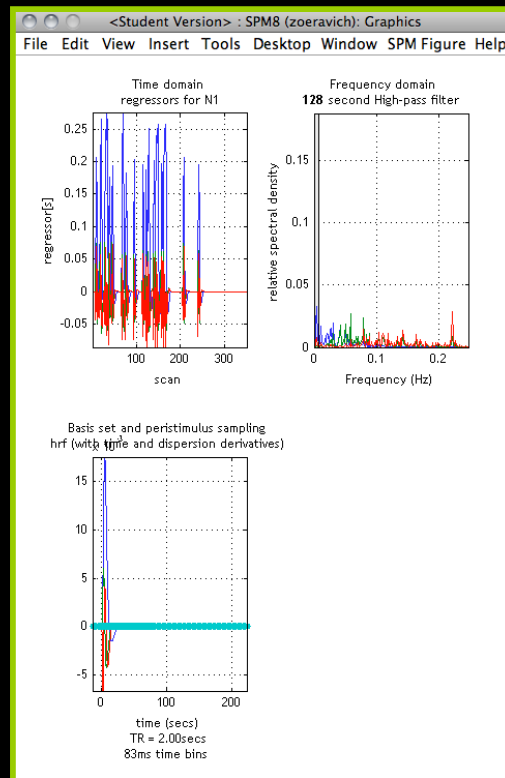
Specify First-Level (Part 5)



62

Step 9

Specify First-Level (Part 5)

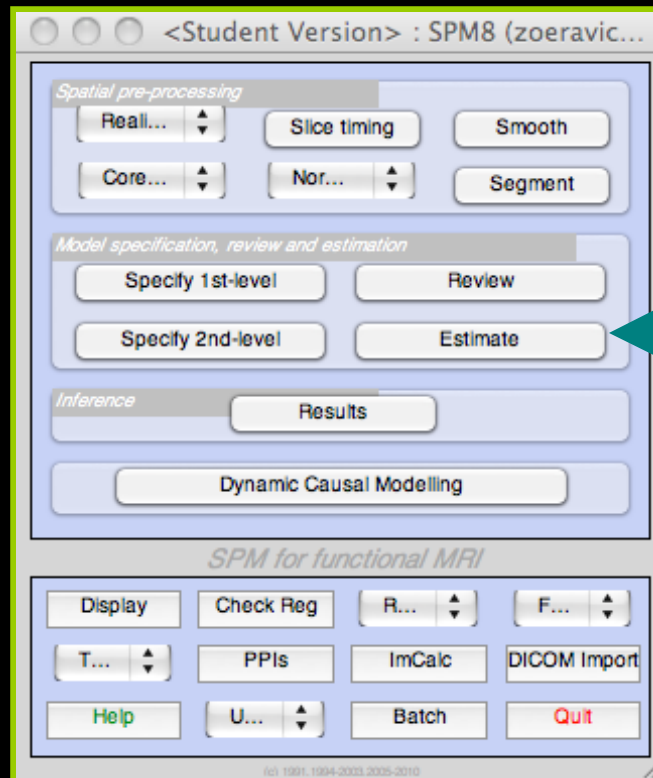


Step 10

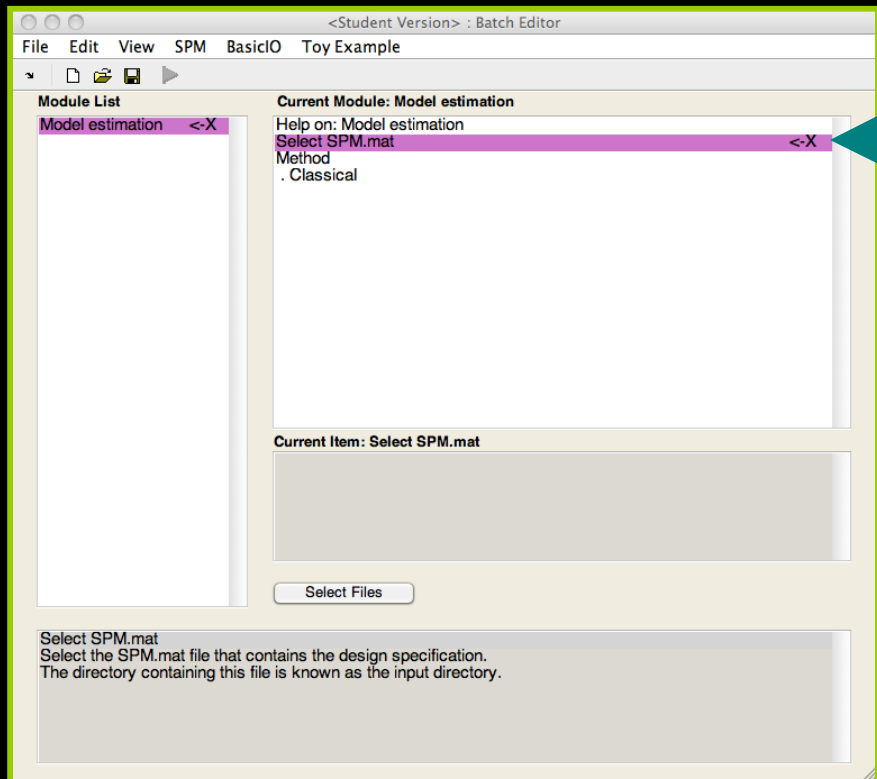
Estimate

- Press the ESTIMATE button
 - Highlight “Select SPM.mat” and select the SPM.mat file saved in the DIR/categorical directory
 - Save the job as categorical_est.job
 - Press the “Run” button

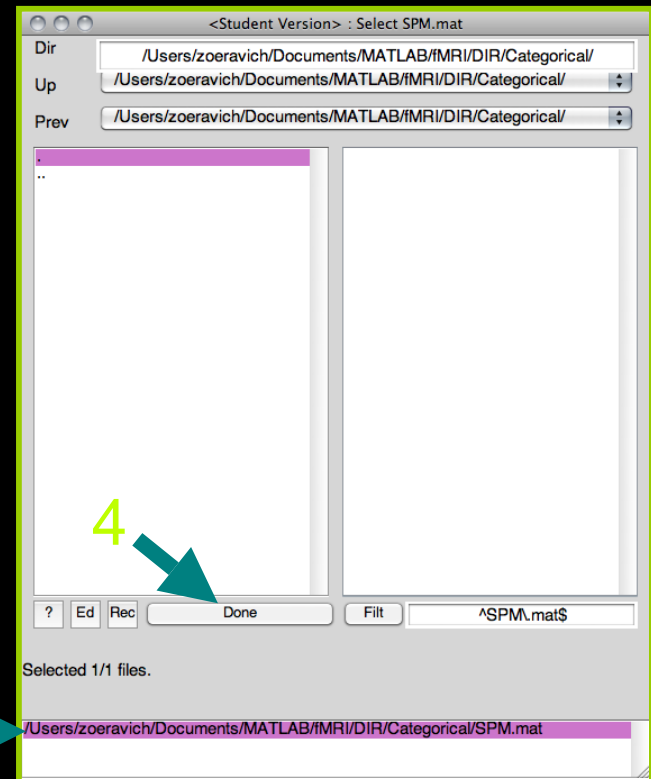
Step 10 Estimate



Step 10 Estimate



2

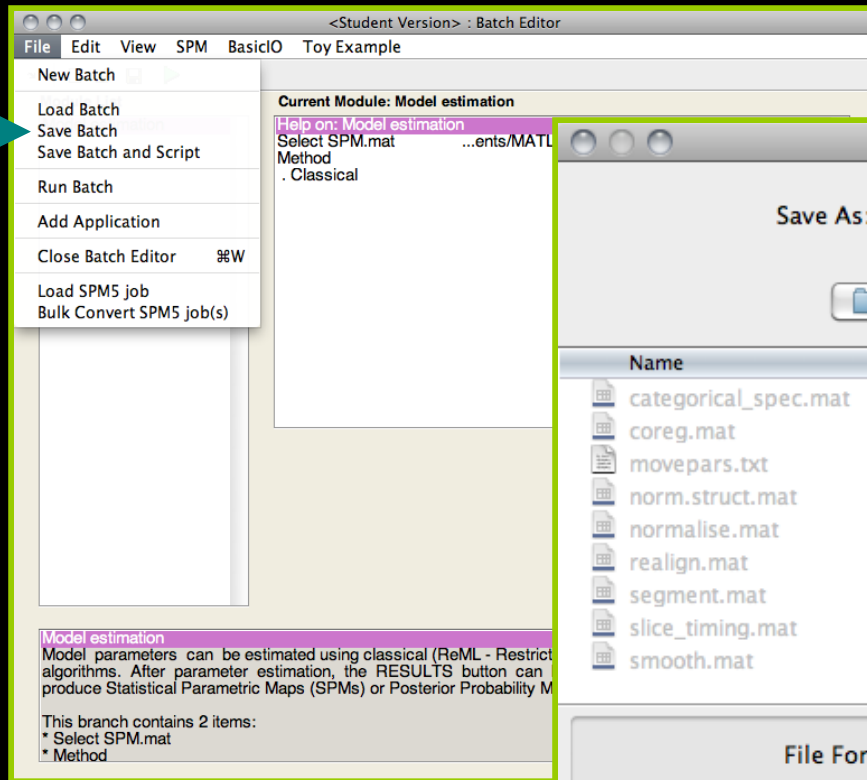


4

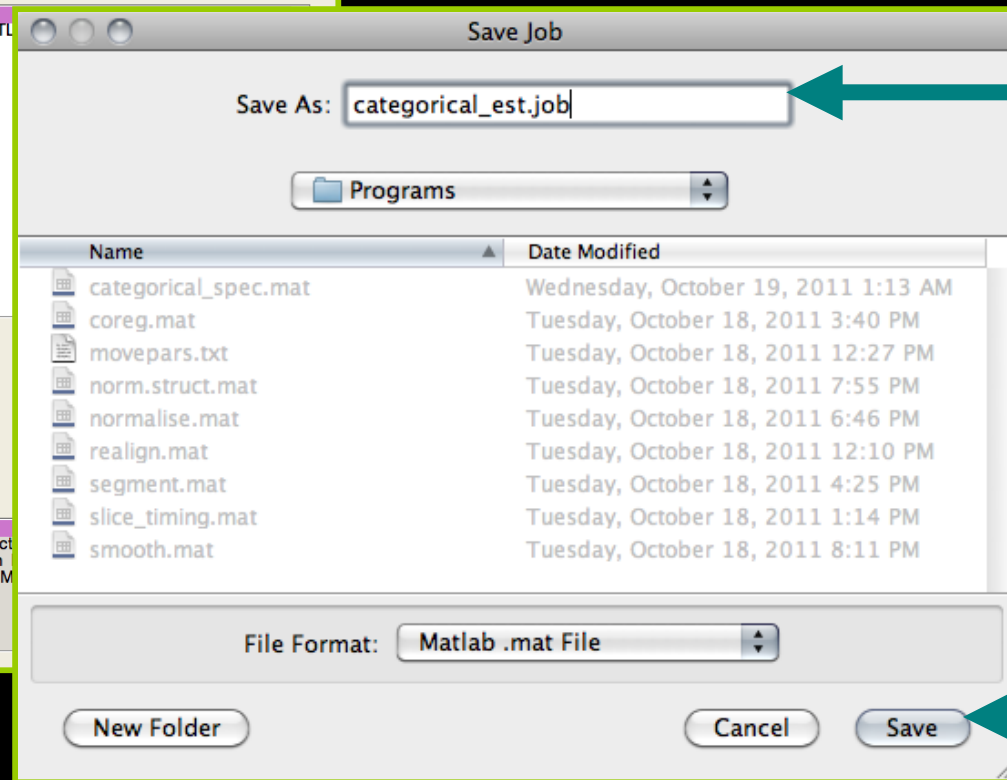
3

Step 10 Estimate

5



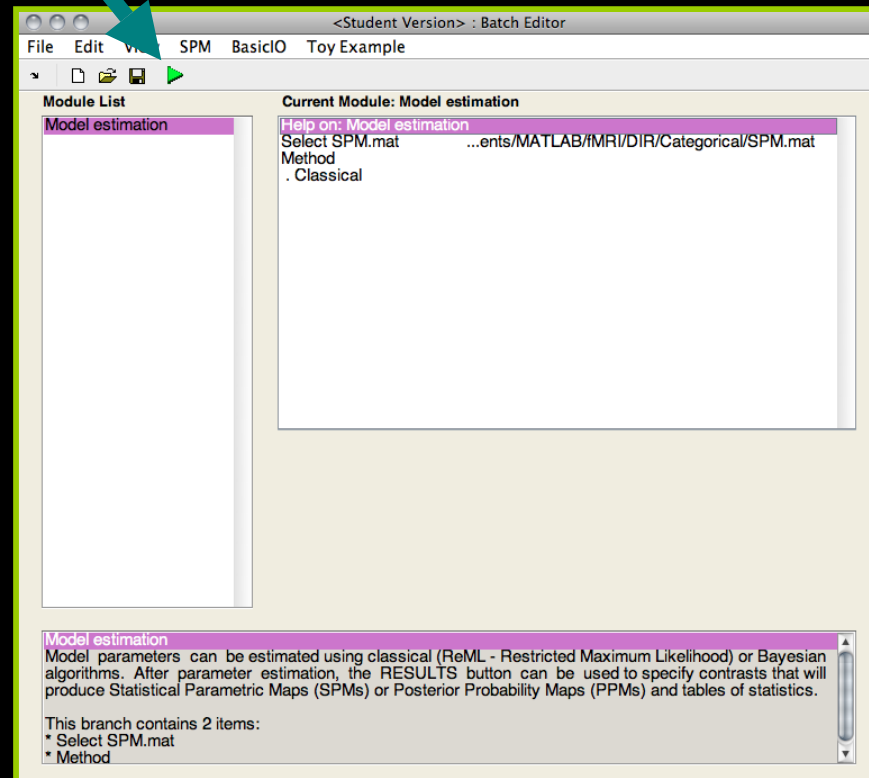
6



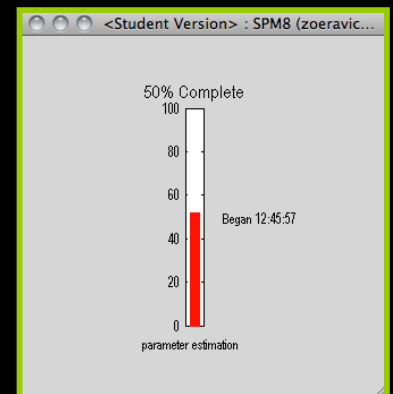
7

Step 10 Estimate

8



Processing...



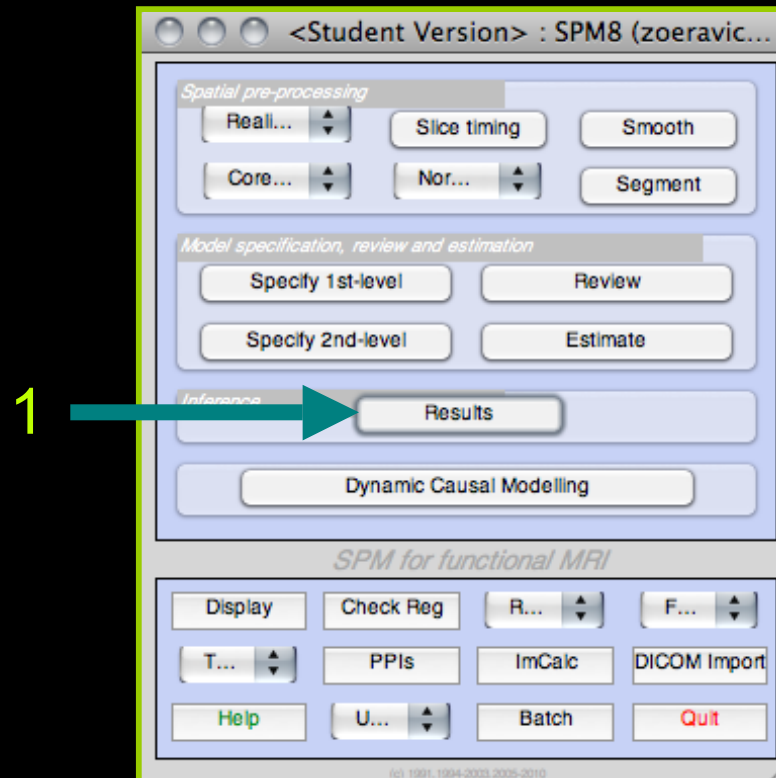
Step 11

Inference for Categorical Design

- Press the RESULTS button
 - Select the SPM.mat file saved in the DIR/categorical directory, choose contrast number 5, and then press “Done”
 - “Mask with other contrast?”; Click “No”
 - “Title for comparison?”; Type “Canonical HRF: Faces > Baseline”
 - “p value adjustment to control”; Click “FWE”
 - “Corrected p value (family-wise error)”; Accept the default value, “0.05”
 - “Extent threshold {voxels}”; Accept the default value, “0”

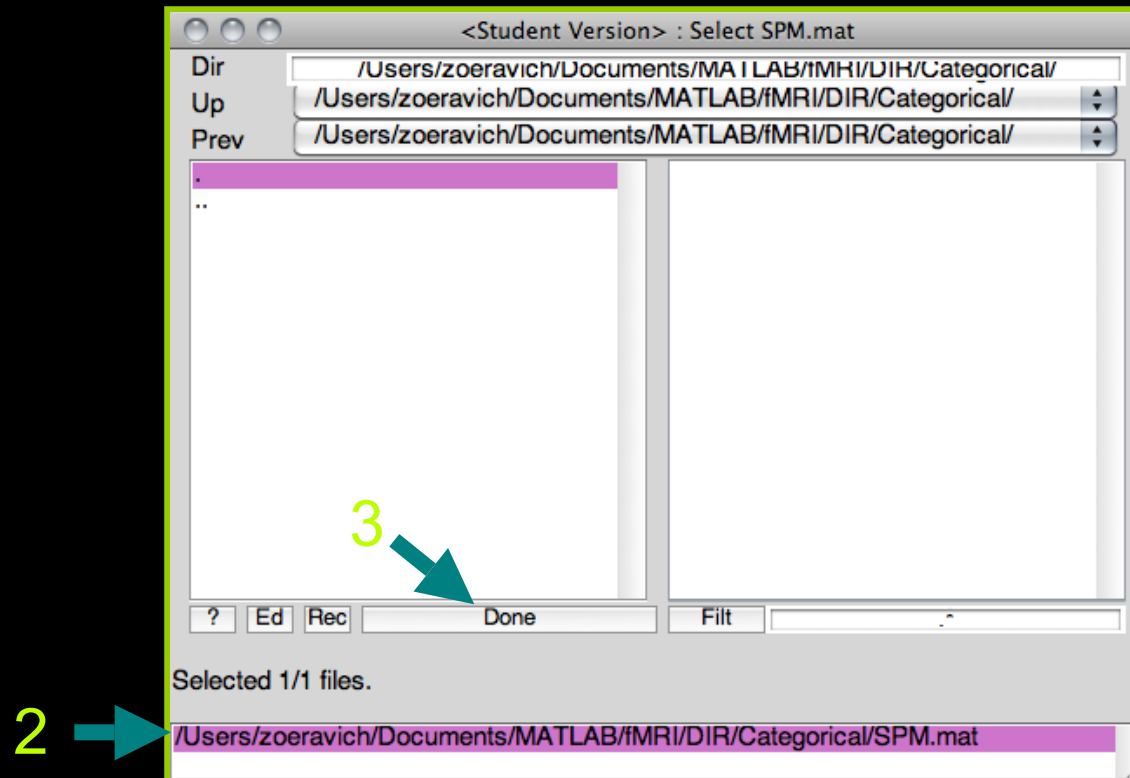
Step 11

Inference for Categorical Design



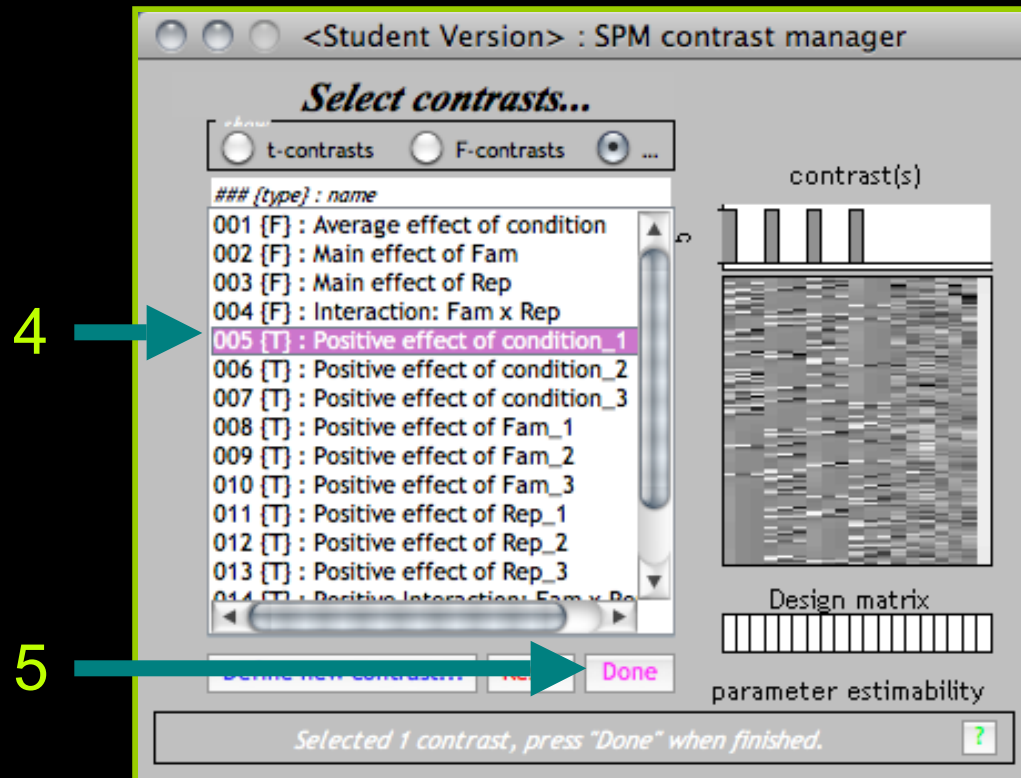
Step 11

Inference for Categorical Design



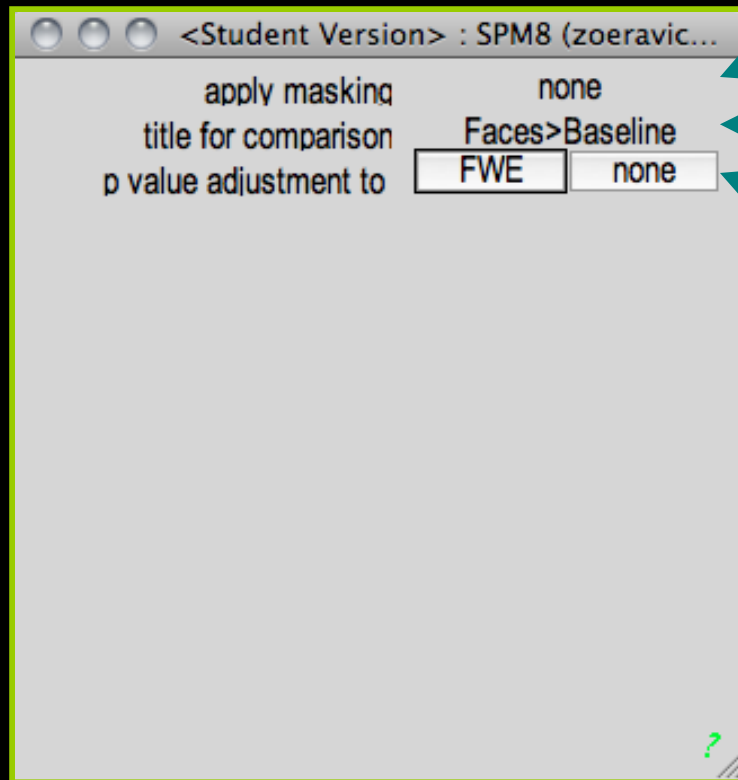
Step 11

Inference for Categorical Design



Step 11

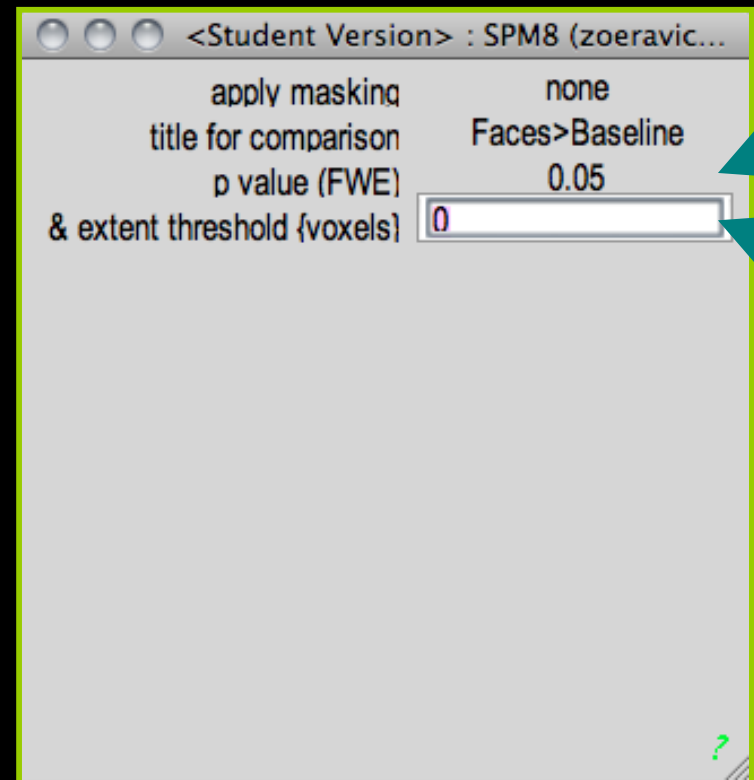
Inference for Categorical Design



6

7

8

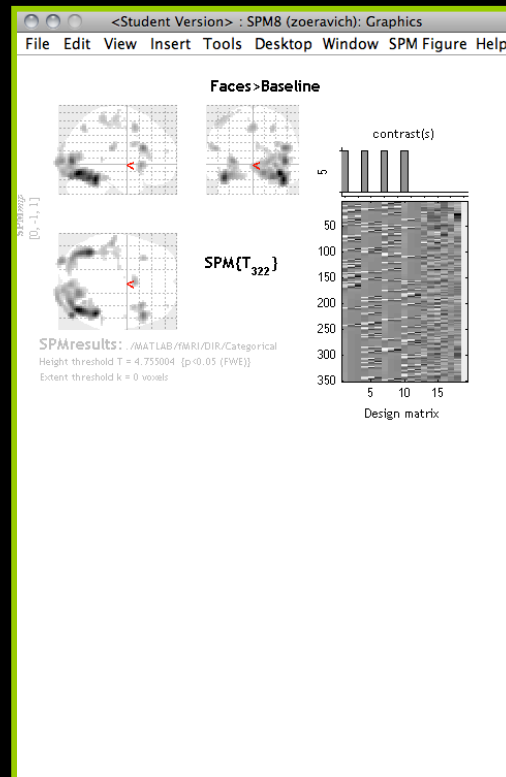


9

10

Step 11

Inference for Categorical Design

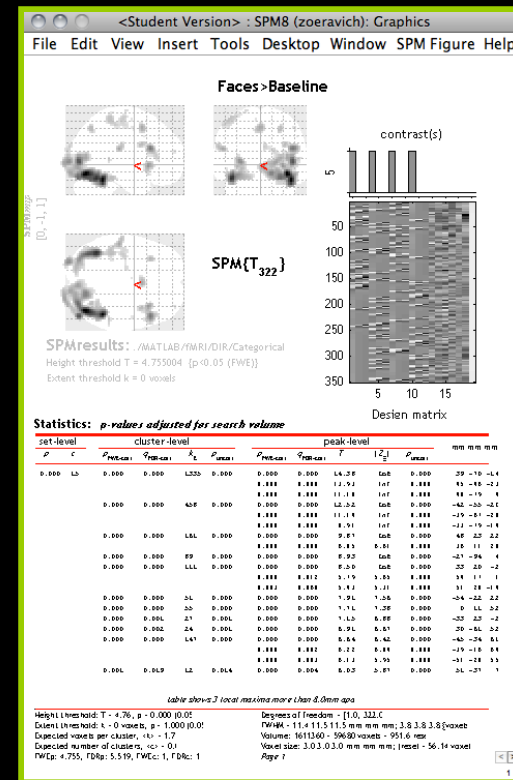
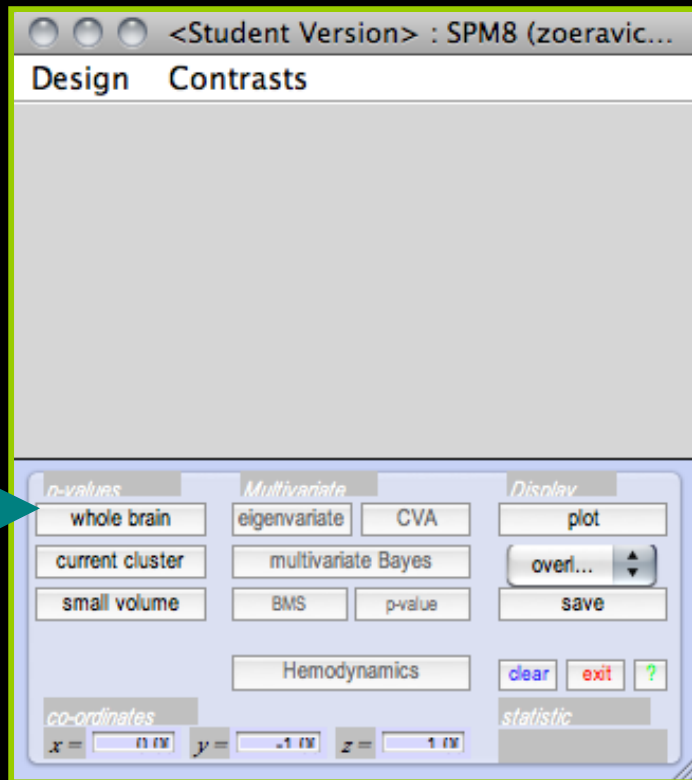


Step 12

Statistical Tables

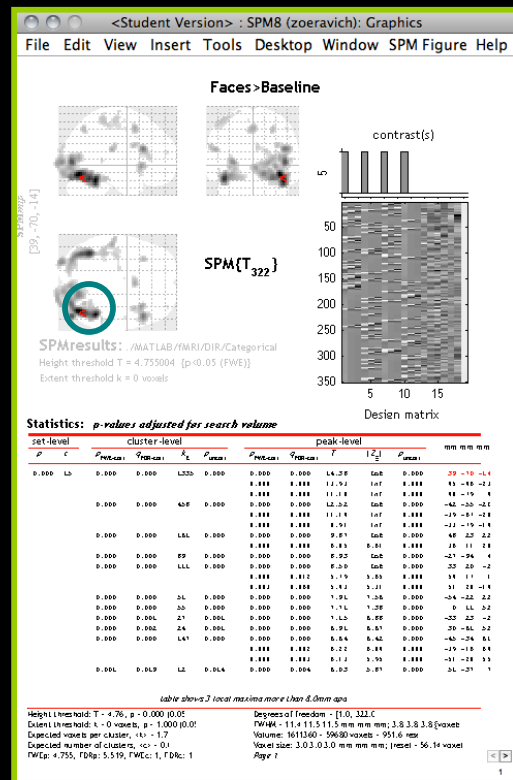
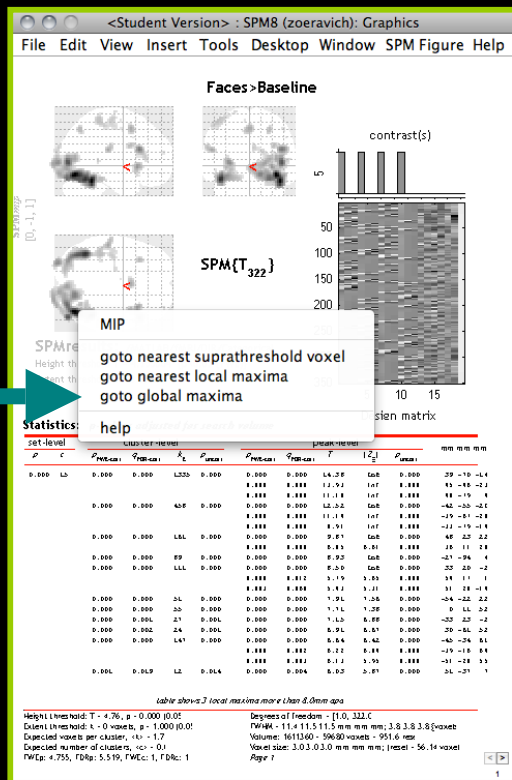
- Press the WHOLE BRAIN button in the p-values section of the interactive window
 - **x, y, z (mm)** (coordinates in MNI space for each maximum)
 - **Peak-level** (chance of finding a peak with this or a greater height)
 - **Cluster-level** (chance of finding a cluster with this many or a greater number of voxels)
 - **Set-level** (chance of finding this or a greater number of clusters in the search volume)
- Right-click on the MIP and select “goto global maxima” (e.g., [39 -70 -14])

Step 12 Statistical Tables



Step 12 Statistical Tables

2



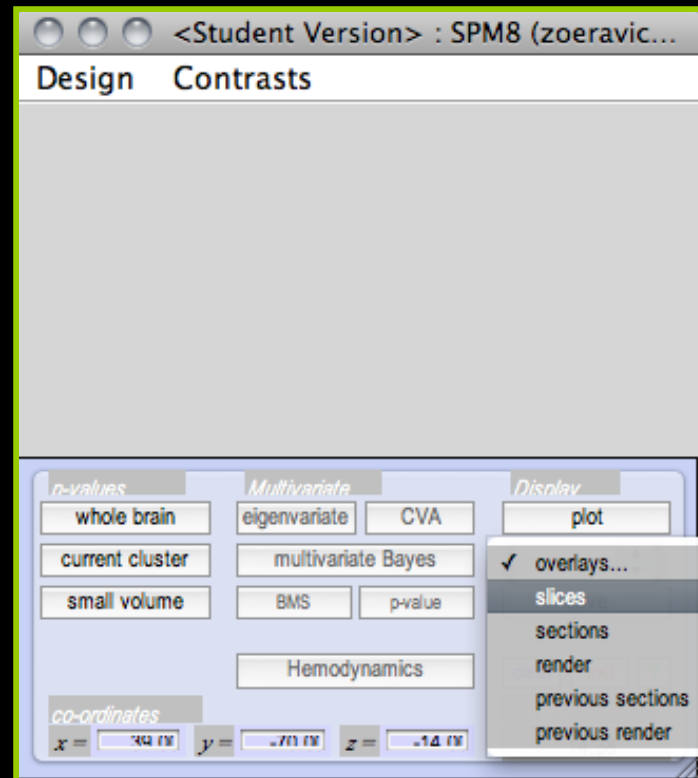
Step 12

Statistical Tables (Optional)

- Select SLICES from the “Overlays” drop-down menu
 - Select the wmeansM03953_0005_0006.img file and then press “Done”
- Click the PLOT button
 - “Plot”; Click “Contrast of estimates and 90% C.I.”
 - “Which contrast?...”; Click “Average effect of condition”

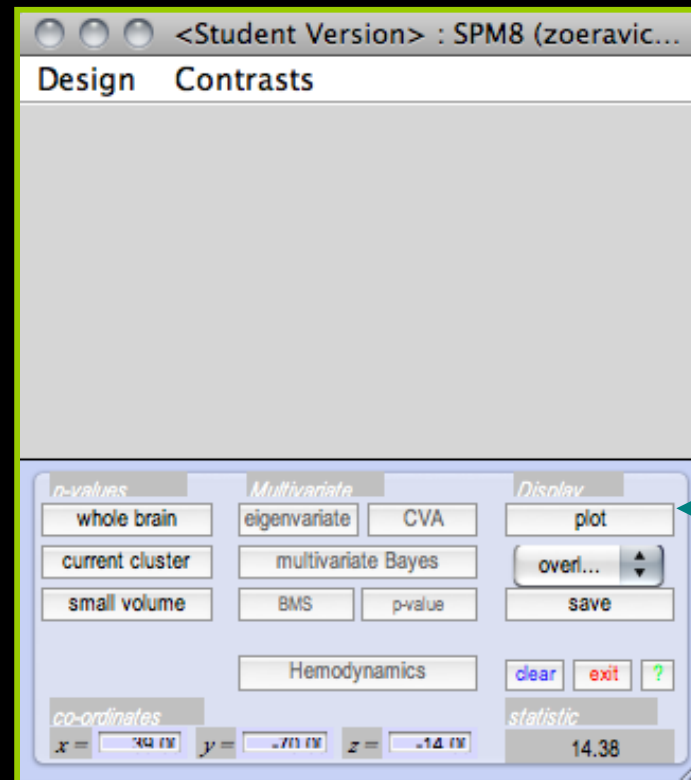
Step 12

Statistical Tables (Optional)



Step 12

Statistical Tables (Optional)

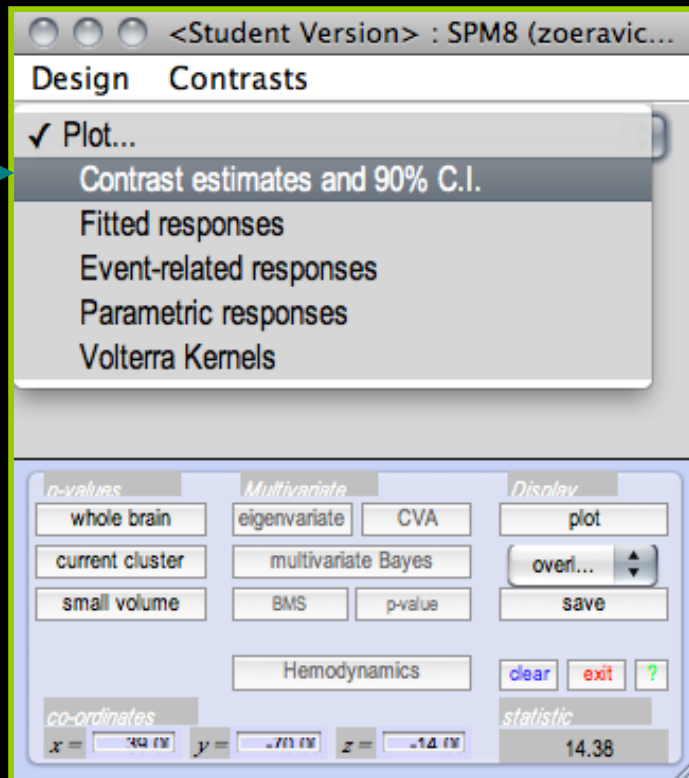


6

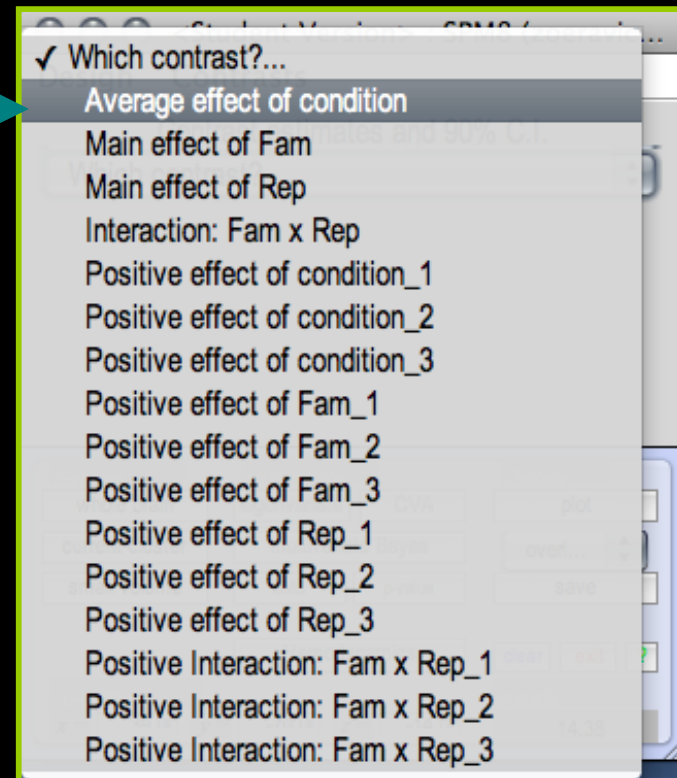
Step 12

Statistical Tables (Optional)

7 →

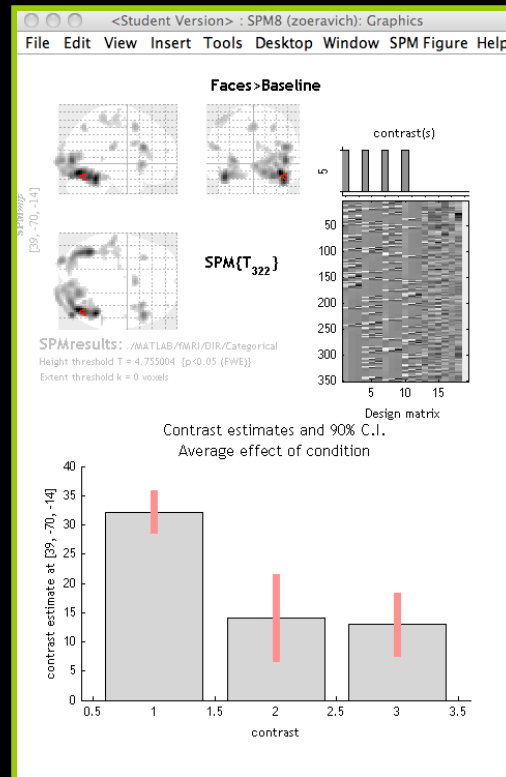


8 →



Step 12

Statistical Tables (Optional)



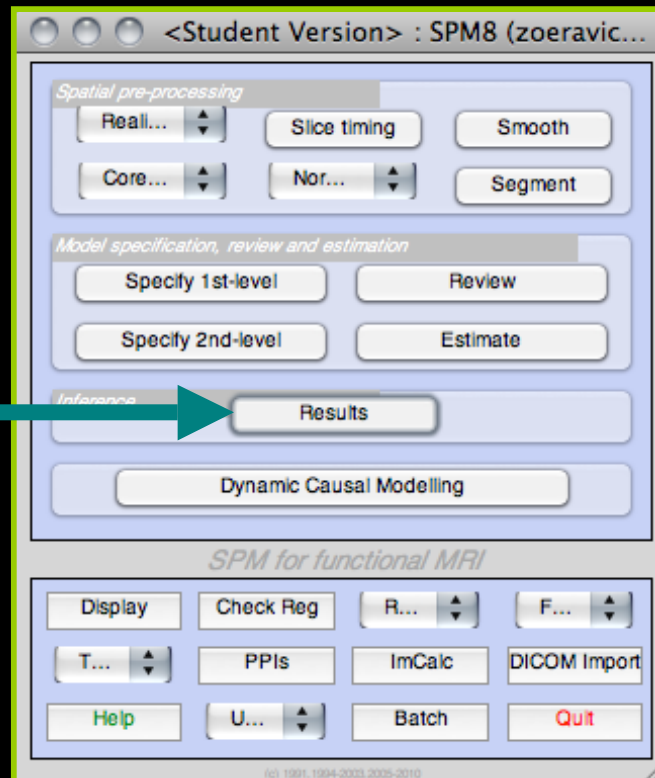
Step 13

F-Contrasts

- Press the RESULTS button
 - Select the SPM.mat file saved in the DIR/categorical directory
 - Select the “F-contrast” toggle, choose contrast number 3, and then press “Done”
 - “Mask with other contrast?”; Click “Yes” and select contrast 5
 - “Uncorrected mask p-value?”; Enter “0.001”
 - “Nature of mask?”; Click “Inclusive”
 - “Title for comparison?”; Click “Main effect of Rep...”
 - “p value adjustment to control”; Click “None”
 - “Threshold (F or p value)”; Accept the default value, “0.001”
 - “Extent threshold {voxels}”; Accept the default value, “0”

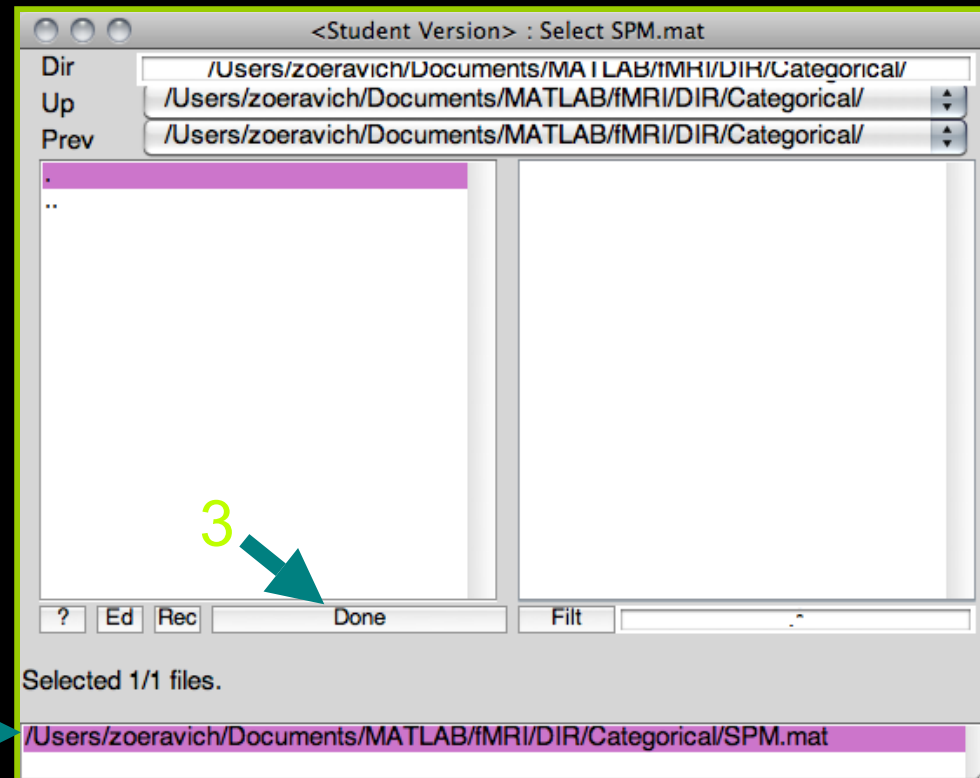
Step 13

F-Contrasts



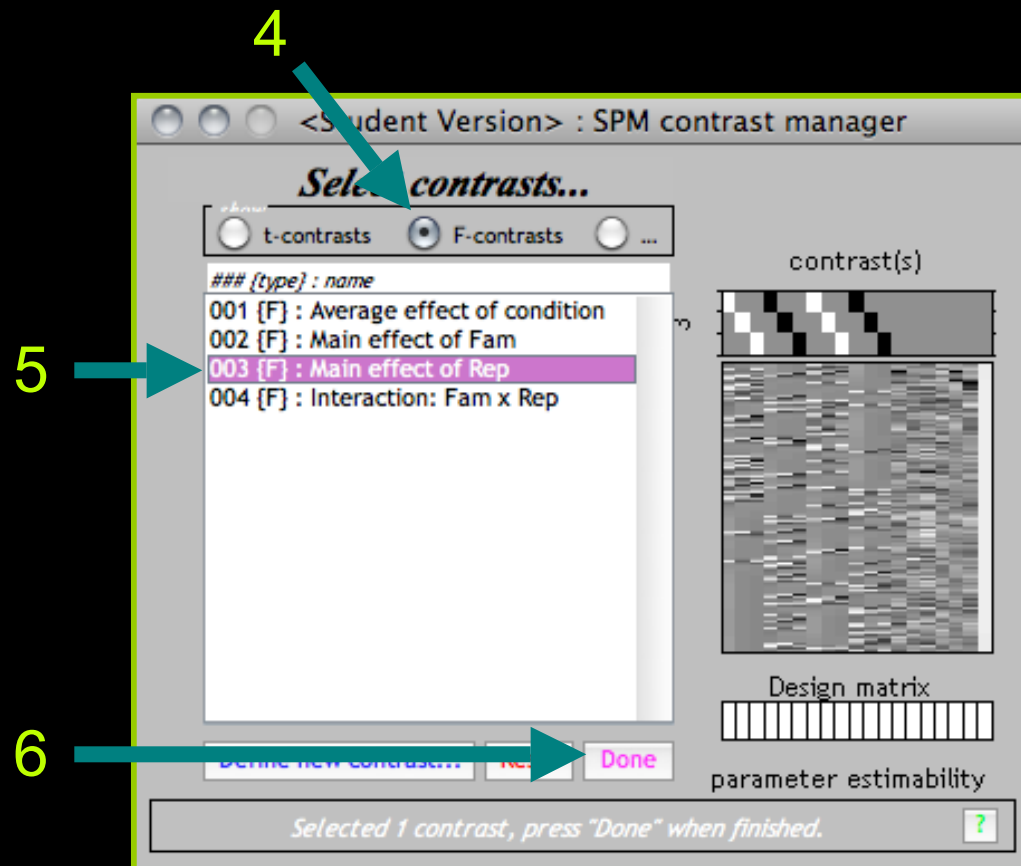
Step 13

F-Contrasts



Step 13

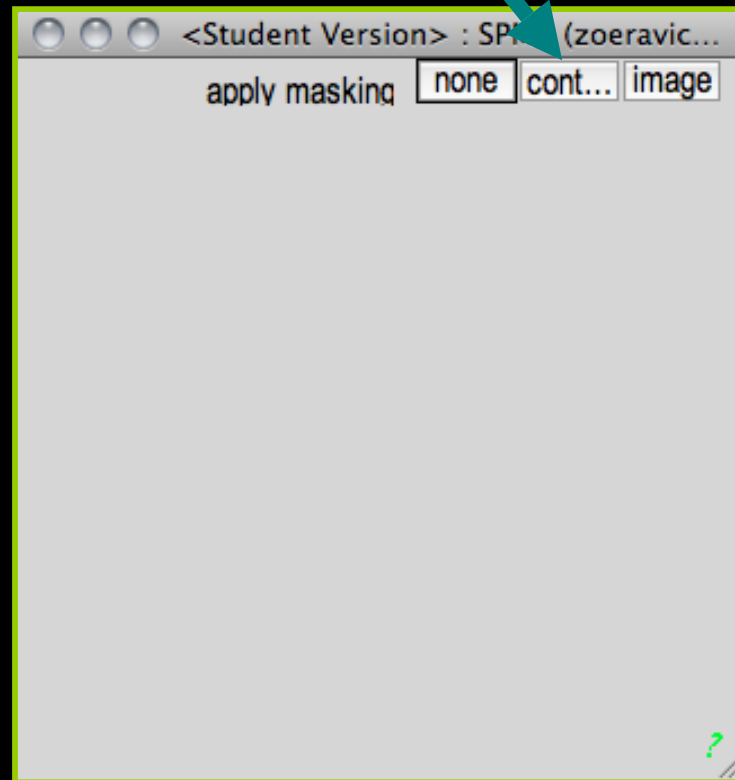
F-Contrasts



Step 13

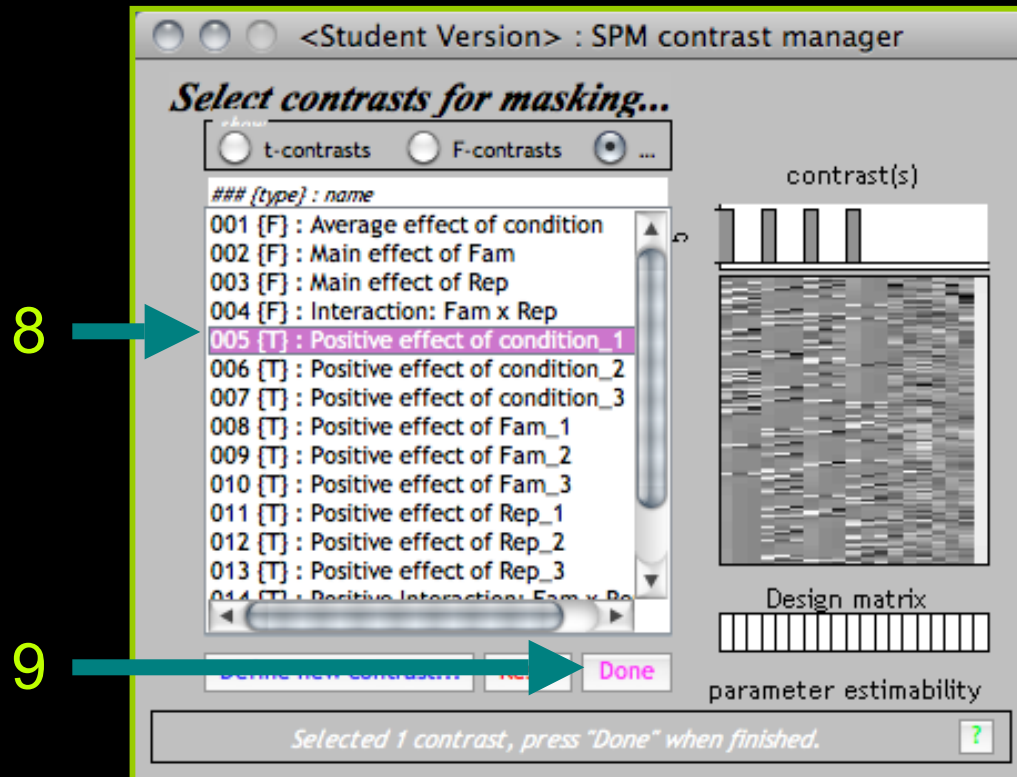
F-Contrasts

7



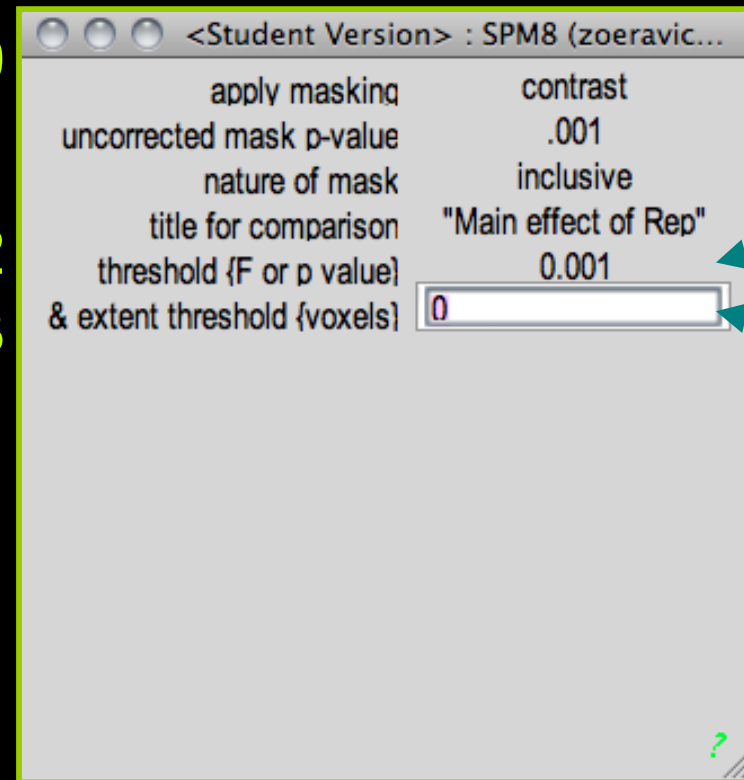
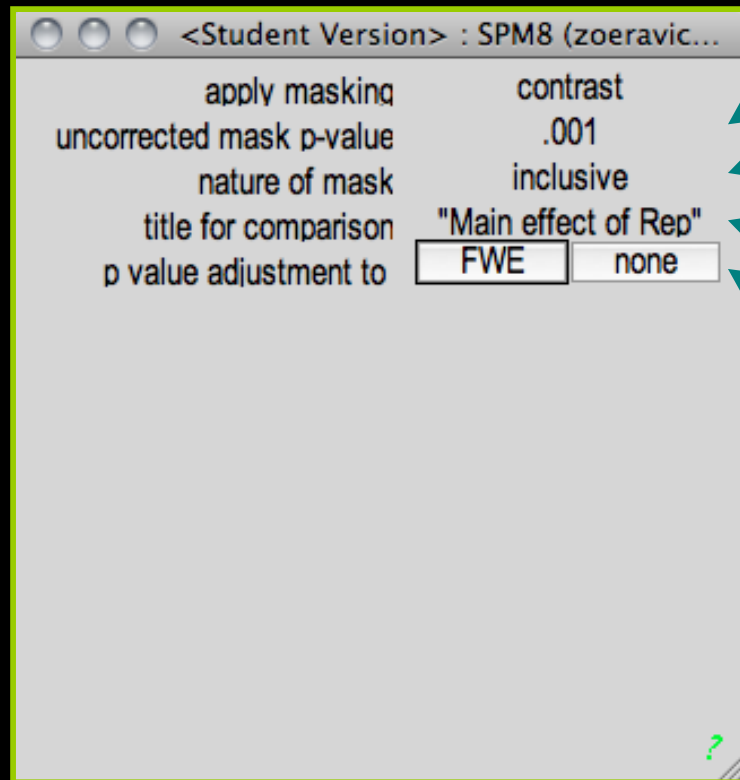
Step 13

F-Contrasts



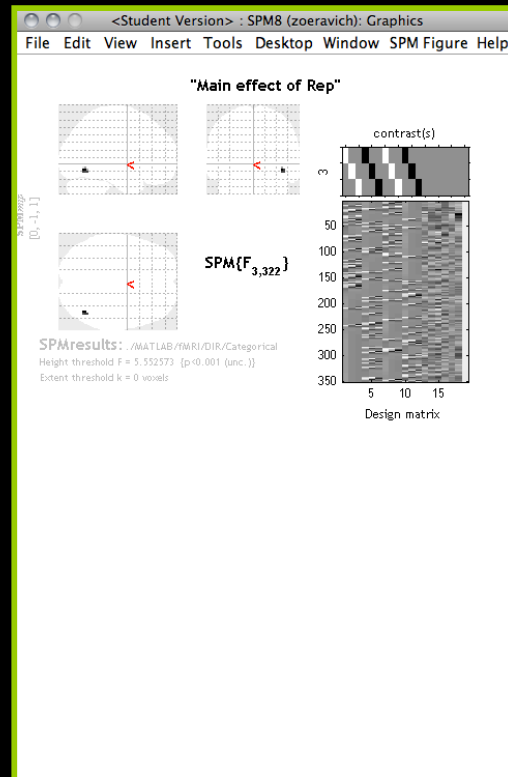
Step 13

F-Contrasts



Step 13

F-Contrasts



Step 13

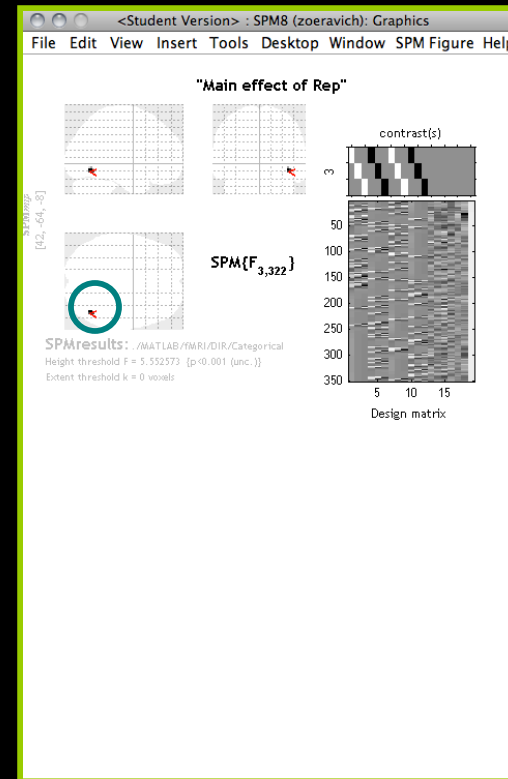
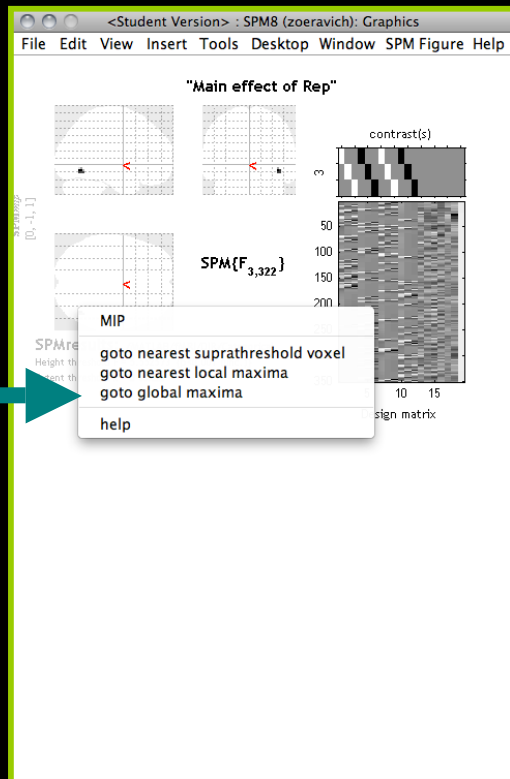
F-Contrasts (Optional)

- Right-click on the MIP and select “goto global maxima” (e.g., [42 -64 -8])
- Click the PLOT button
 - “Plot”; Click “Event-related responses”
 - “Which effect...”; Click “F1”
 - “Plot in terms of...”; Click “Fitted response and PSTH”

Step 13

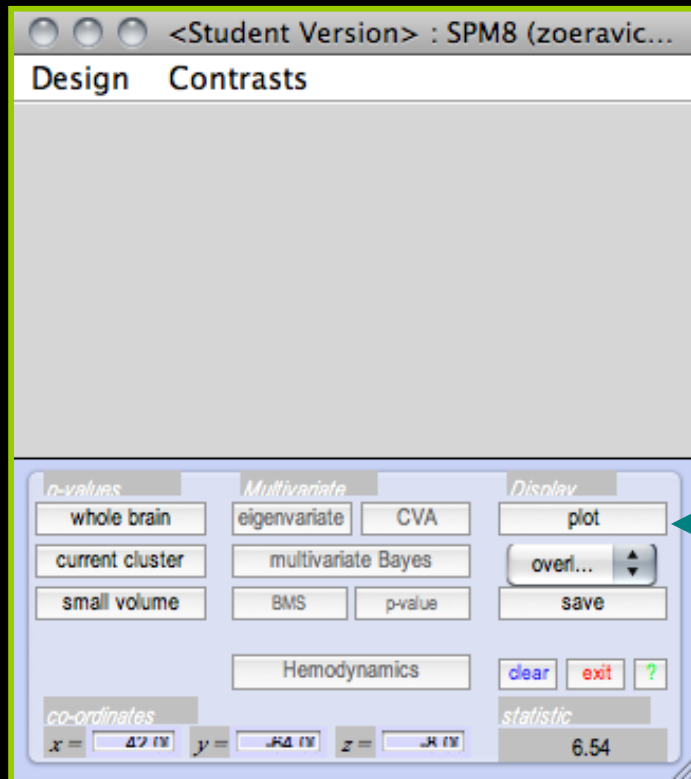
F-Contrasts (Optional)

16

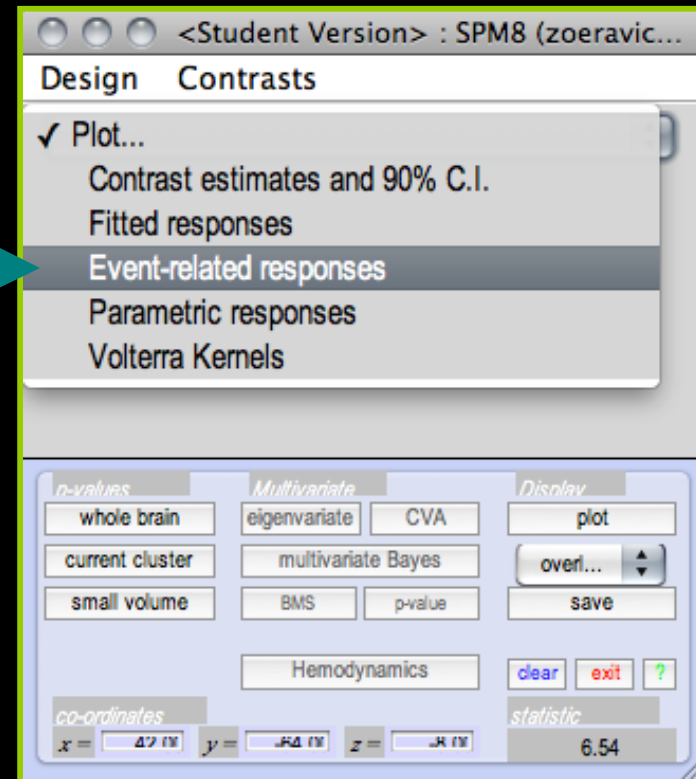


Step 13

F-Contrasts (Optional)



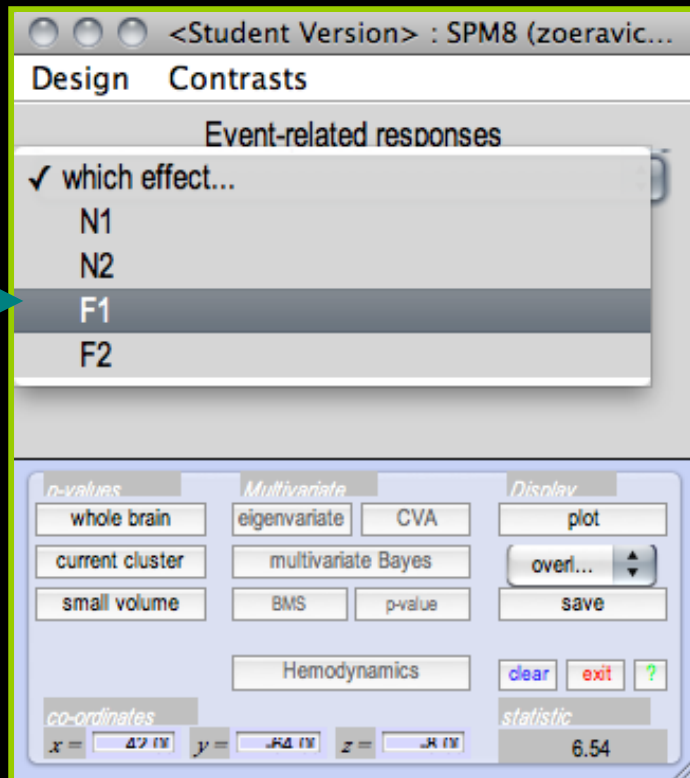
18 →



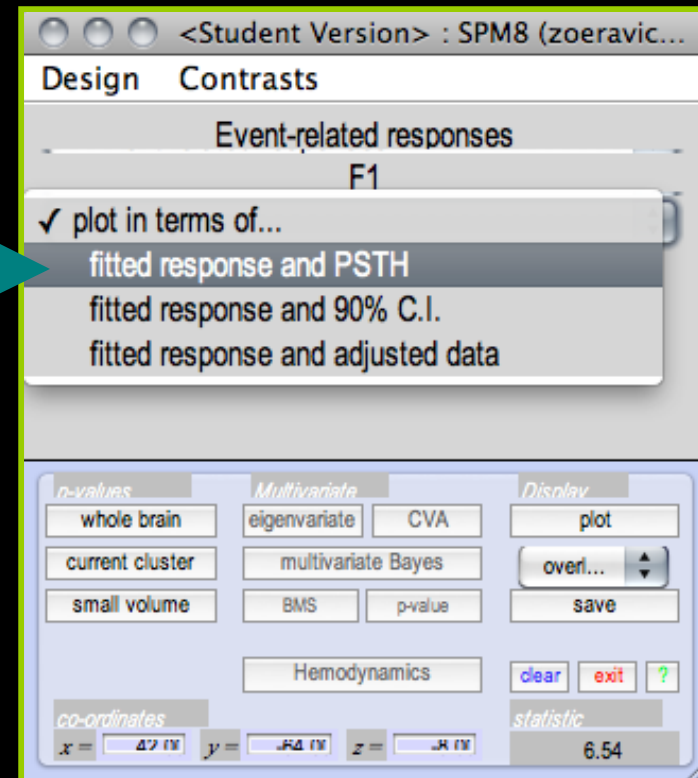
Step 13

F-Contrasts (Optional)

19 →

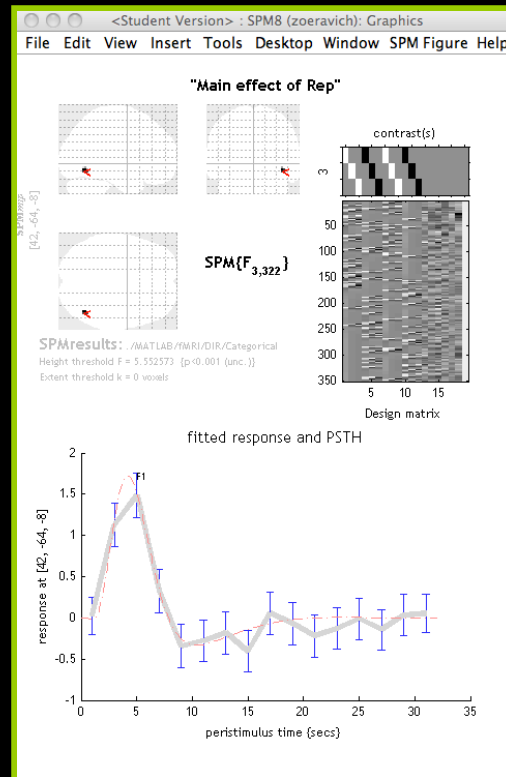


20 →



Step 13

F-Contrasts (Optional)



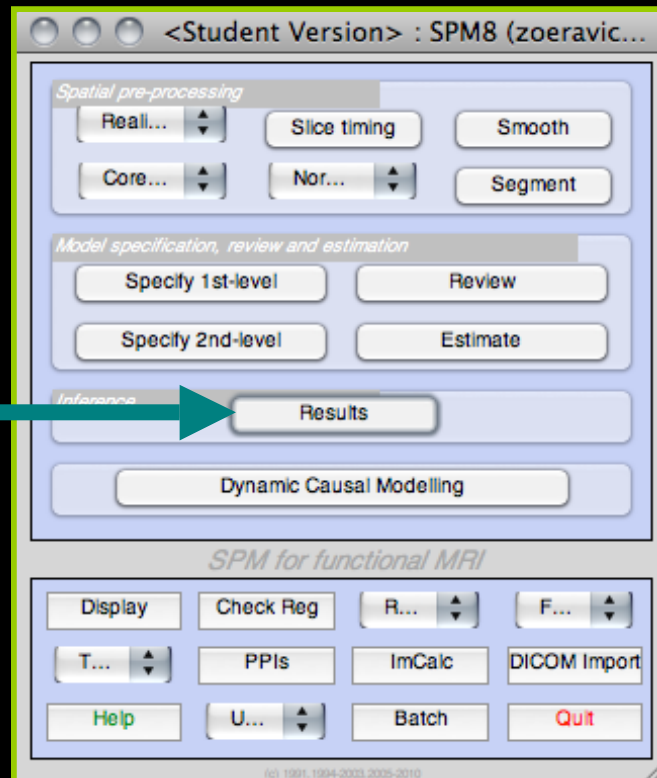
Step 14

Testing Effects of Movement

- Press the RESULTS button
 - Select the SPM.mat file saved in the DIR/categorical directory
 - Specify “F-contrast” in the Contrast Manager and “Movement-related effects” in the “Contrasts weight matrix” window
 - Submit and select the contrast
 - “Mask with other contrast?”; Click “No”
 - “Title for comparison?”; Accept the default
 - “Corrected height threshold”; Select “FWE”
 - “Corrected p value”; Accept the default value, “0.05”

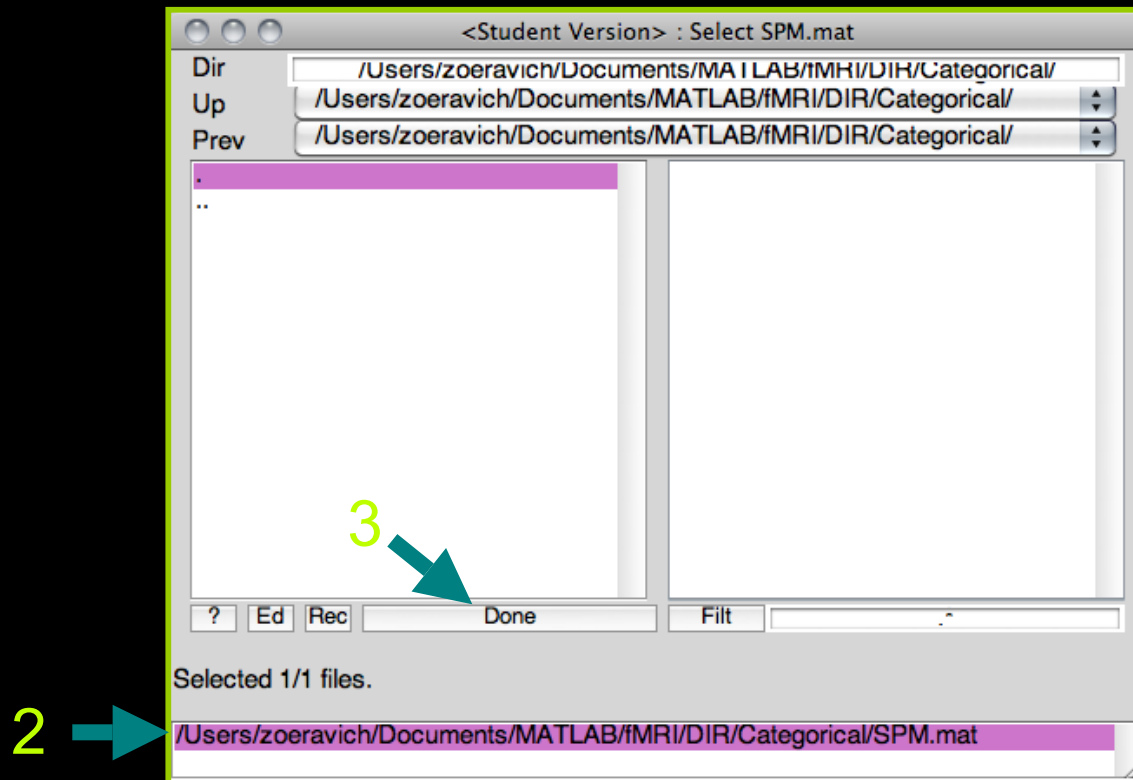
Step 14

Testing Effects of Movement



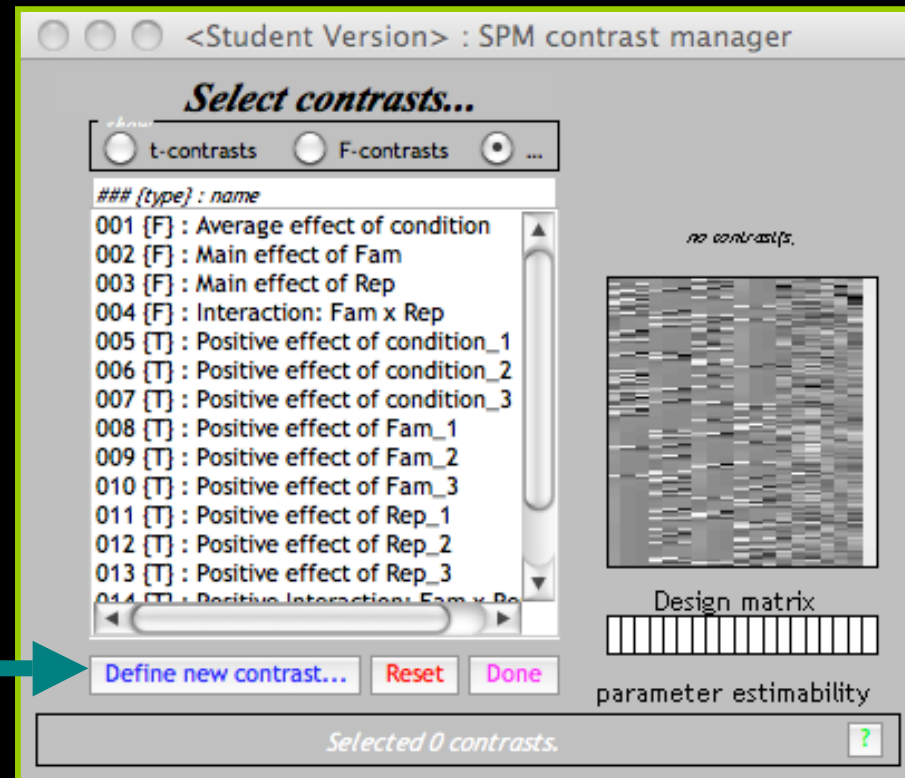
Step 14

Testing Effects of Movement



Step 14

Testing Effects of Movement



Step 14

Testing Effects of Movement

5 → **define contrast...** dialog, name field: `Movement-related effects`

6 → **define contrast...** dialog, contrast field: `1 17 14`

7 → **define contrast...** dialog, OK button

8 → **Select contrasts...** dialog, list item: `017 [F] : Movement-related effects`

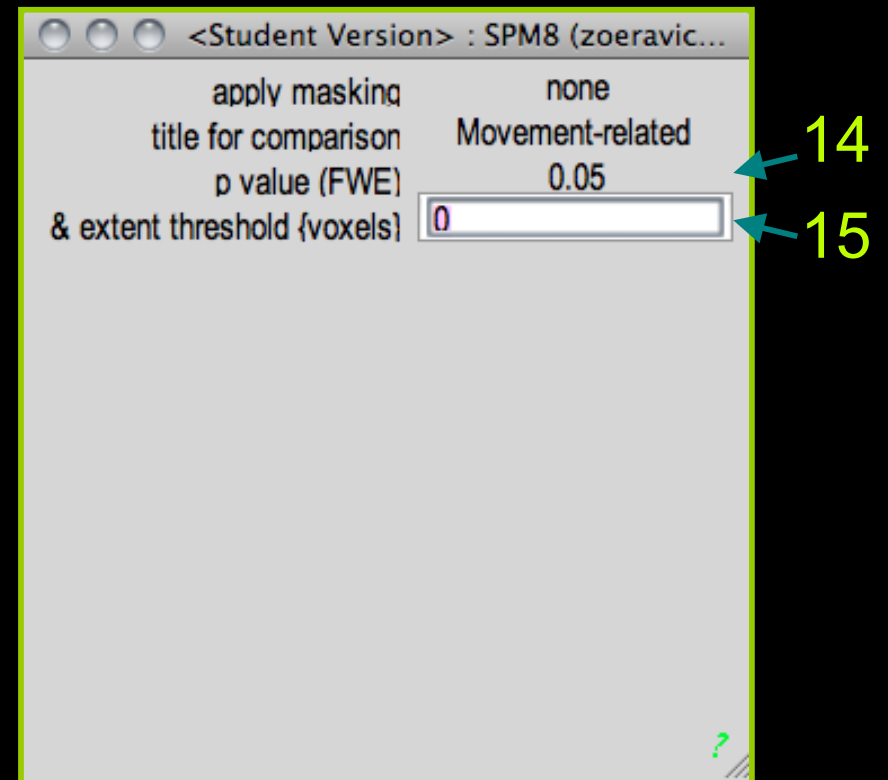
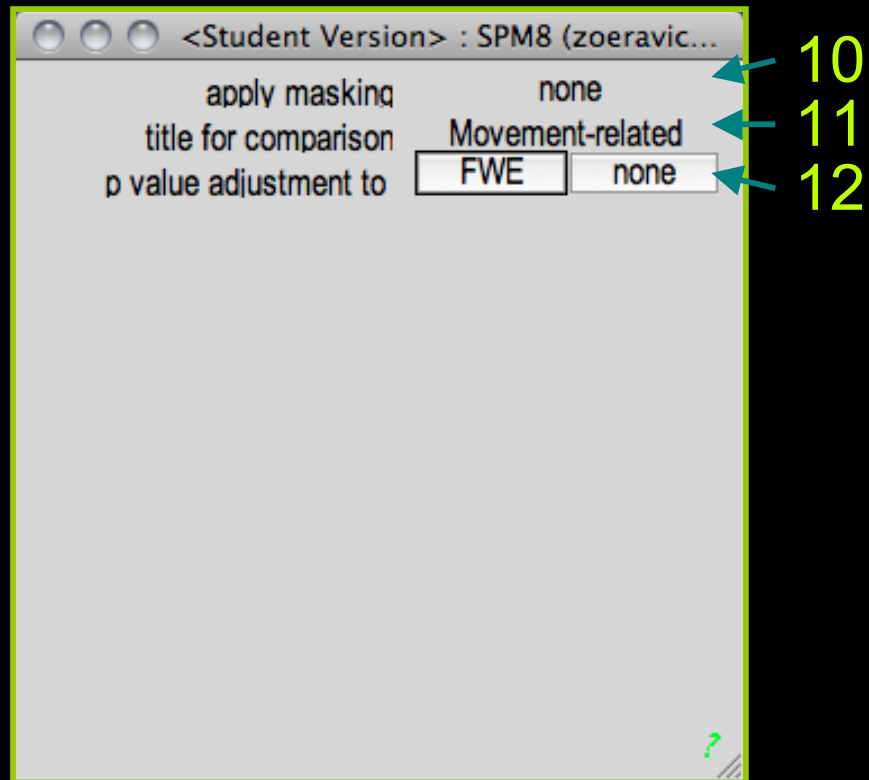
9 → **Select contrasts...** dialog, Done button

name defined, contrast defined

Selected 1 contrast, press "Done" when finished.

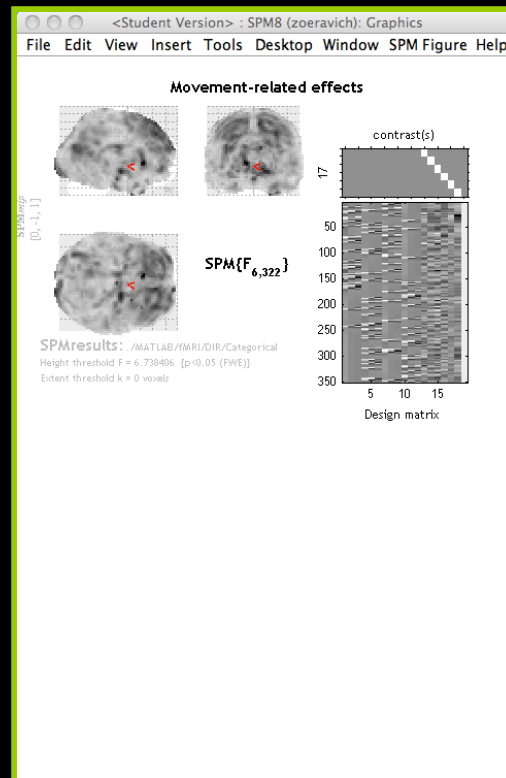
Step 14

Testing Effects of Movement



Step 14

Testing Effects of Movement



Step 14

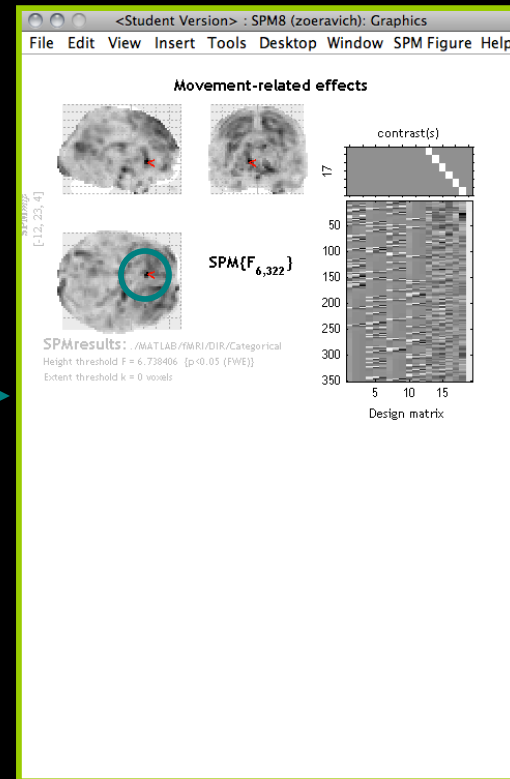
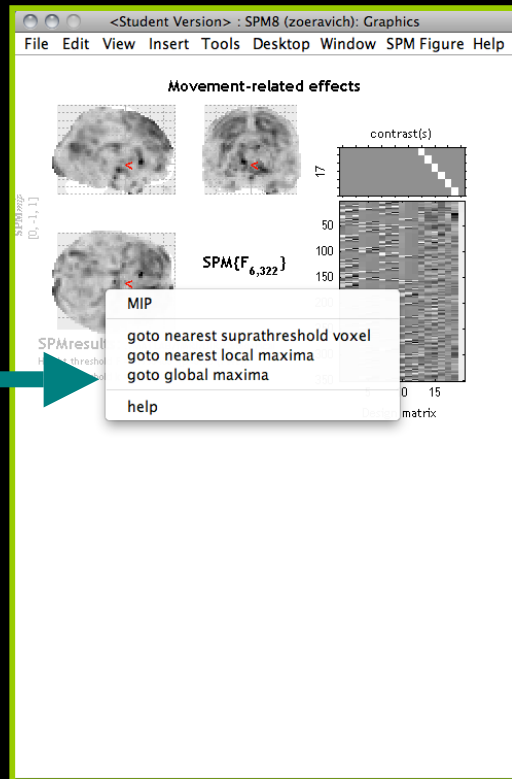
Testing Effects of Movement (Optional)

- Press the RESULTS button
 - Select the SPM.mat file saved in the DIR/categorical directory
 - Specify “F-contrast” in the Contrast Manager and “Movement-related effects” in the “Contrasts weight matrix” window
 - Submit and select the contrast
 - “Mask with other contrast?”; Click “No”
 - “Title for comparison?”; Accept the default
 - “Corrected height threshold”; Select “FWE”
 - “Corrected p value”; Accept the default value, “0.05”

Step 14

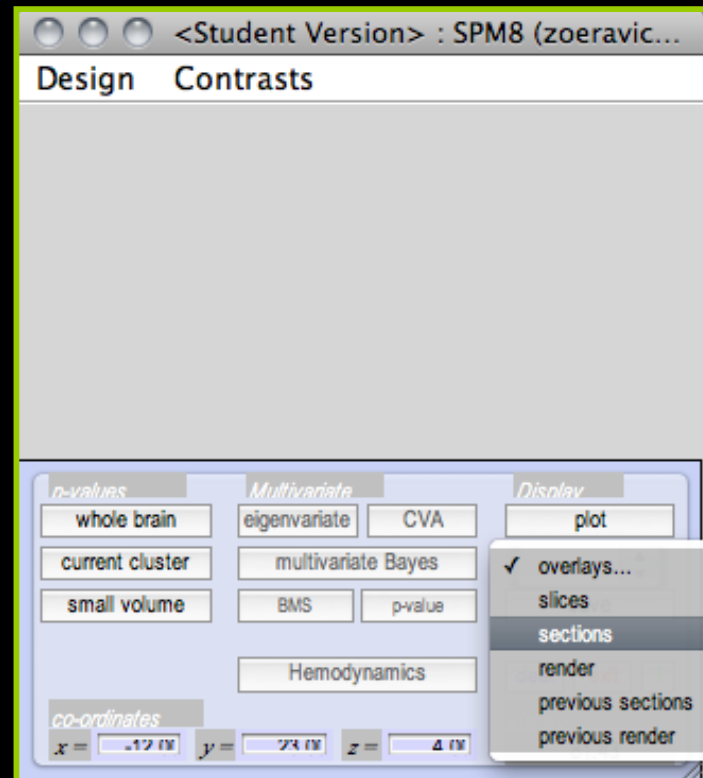
Testing Effects of Movement (Optional)

16



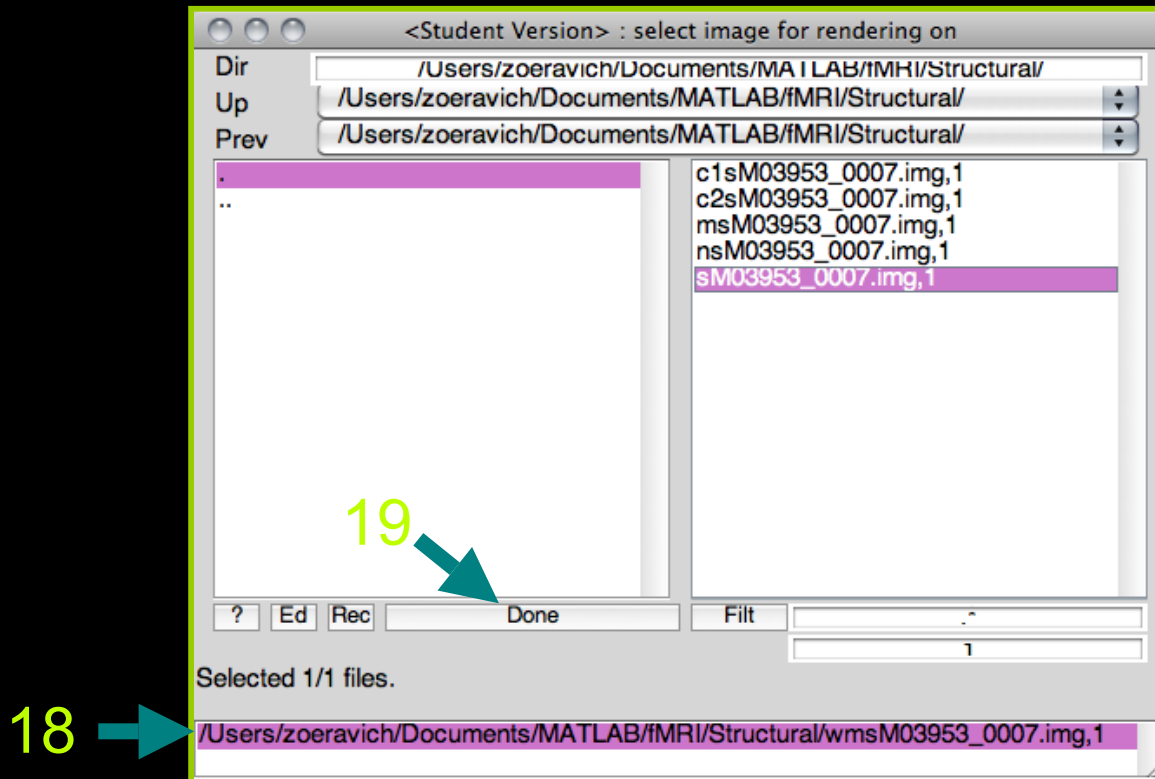
Step 14

Testing Effects of Movement (Optional)



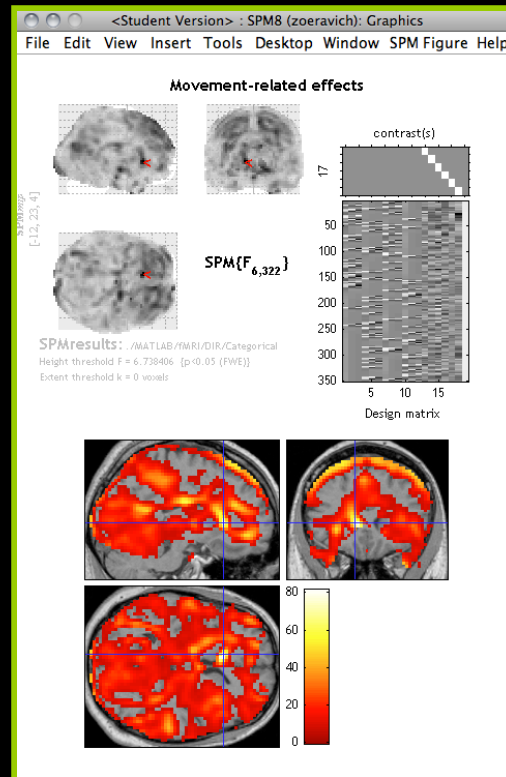
Step 14

Testing Effects of Movement (Optional)

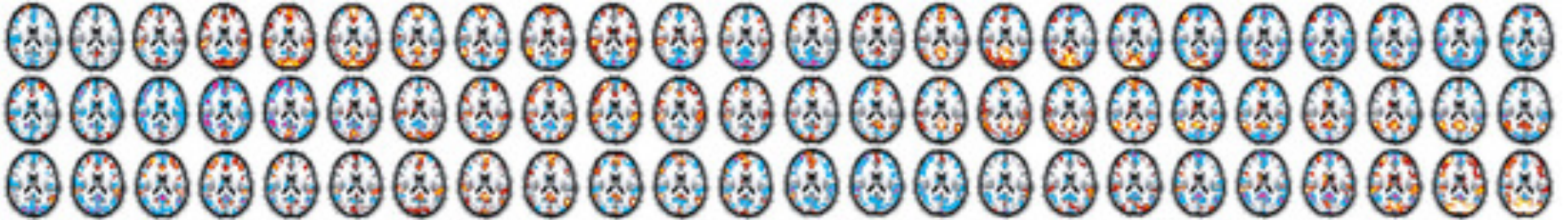


Step 14

Testing Effects of Movement (Optional)

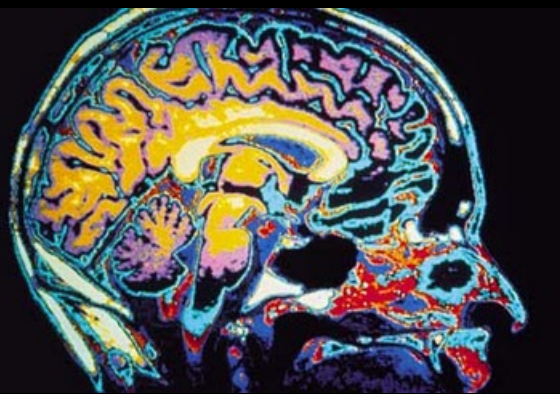


fMRI Second-Level Data Analysis



fMRI Data Files

- **M2i** (Using contrast images from an “informed” basis set, consisting of the canonical HRF and its two partial derivatives with respect to time (onset latency) and dispersion)
 - 12 (subjects) x 3 (basis functions) con*.imgs from the first level model using the informed basis (M1i)



Create an “Informed” subdirectory

Step 1

One-Way ANOVA (Part 1)

- Press the SPECIFY 2ND-LEVEL button
 - In “Factorial design specification”, highlight “Design” and then choose “Full Factorial”
 - Under “Factors” create a single “New Factor”
 - “Factor”; Type in “Basis”
 - “Levels”; Type “3”
 - Highlight “Independence” and select “No”
 - Highlight “Specify cells” and create 3 new cells
 - “Levels”; Enter “1”, “2”, and “3” consecutively
 - Enter the canonical contrast images under scans (0003 to 0014, 0015 to 0026, and 0027 to 0038, respectively)

Step 1

One-Way ANOVA (Part 2)

- Highlight “Directory”, then select “Specify files”, and choose the subdirectory “informed” to place the design matrix in
- Save the job files as DIR/informed.mat
- Press the “Run” button
- Press the ESTIMATE button to estimate the parameters of the model
 - Select the SPM.mat file just created
 - Press the “Run” button

Step 2

Nonsphericity

- Go to “Review” → “Design” → “Explore” → “Covariance Structure” to show the estimated covariance matrix
 - **SPM.xVi.Vi{1}** (variance of the canonical derivative)
 - **SPM.xVi.Vi{2}** (variance of the temporal derivative)
 - **SPM.xVi.Vi{3}** (variance of the dispersion derivative)
 - **SPM.xVi.Vi{4}** (covariance between canonical and temporal derivative)
 - **SPM.xVi.Vi{5}** (covariance between canonical and dispersion derivative)
 - **SPM.xVi.Vi{6}** (covariance between temporal and dispersion derivatives)

Step 3

Informed Results (Part 1)

- Press the RESULTS button
 - Select the SPM.mat file
 - Press “Define new contrast” and select “F”
 - “Contrast”; Type “eye(3)”
 - “Name”; Enter “Faces vs. Baseline: Informed”
 - Press the “Submit” button and then press OK
 - Press the “Done” button
 - “Mask with other contrast(s)?”; Click “No”
 - “Title for comparison?”; Type “Faces vs Baseline: Informed”
 - “p value adjustment to control”; Click “FWE”
 - “Family-wise p-value”; Type “0.05”
 - “Extent threshold {voxels}”; Accept the default value, “0”

Step 3

Informed Results (Part 2)

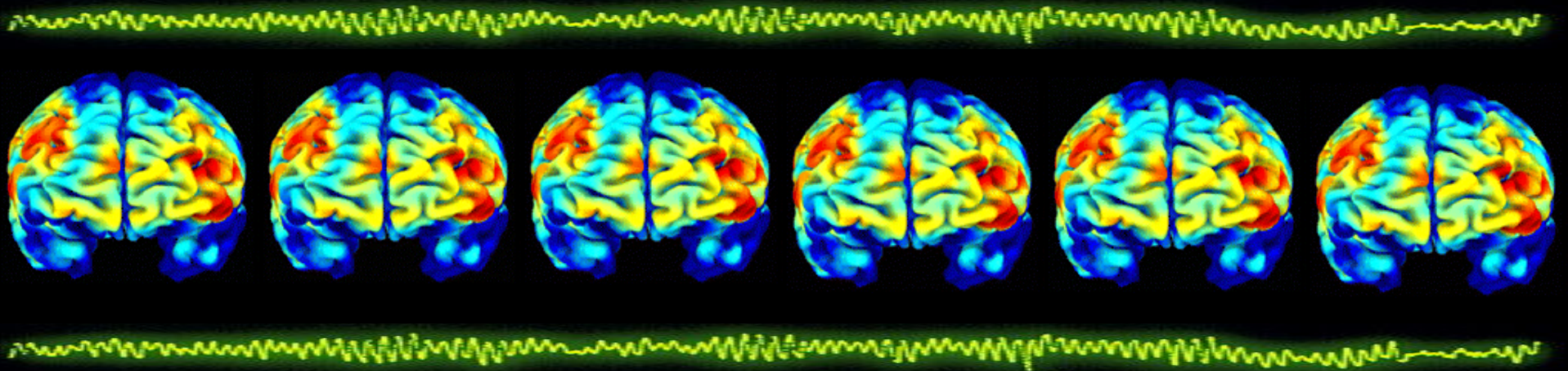
- Right click on the MIP and select “goto global maxima”
 - Press “plot”, select “Contrast estimates and 90% C.I.”, and then select the “Faces vs Baseline: Informed” contrast
 - Compare the size of the first, second, and third bars to the error bars in order to accurately determine the contributions of the different basis functions

Step 4

T- and F-Contrasts

- Press the RESULTS button
 - Select the SPM.mat file
 - Press “Define new contrast” and select “T”
 - “Contrast”; Type “eye(3)”
 - “Name”; Enter “Faces vs. Baseline: Informed”
 - Press the “Submit” button and then press OK
 - Press the “Done” button
 - “Mask with other contrast(s)?”; Click “No”
 - “Title for comparison?”; Type “Faces vs Baseline: Informed”
 - “p value adjustment to control”; Click “FWE”
 - “Family-wise p-value”; Type “0.05”
 - “Extent threshold {voxels}”; Accept the default value, “0”

Congratulations!



You Successfully Processed
and Explored SPM's fMRI
Dataset!