# fMRI preprocessing and contrasts on SPM

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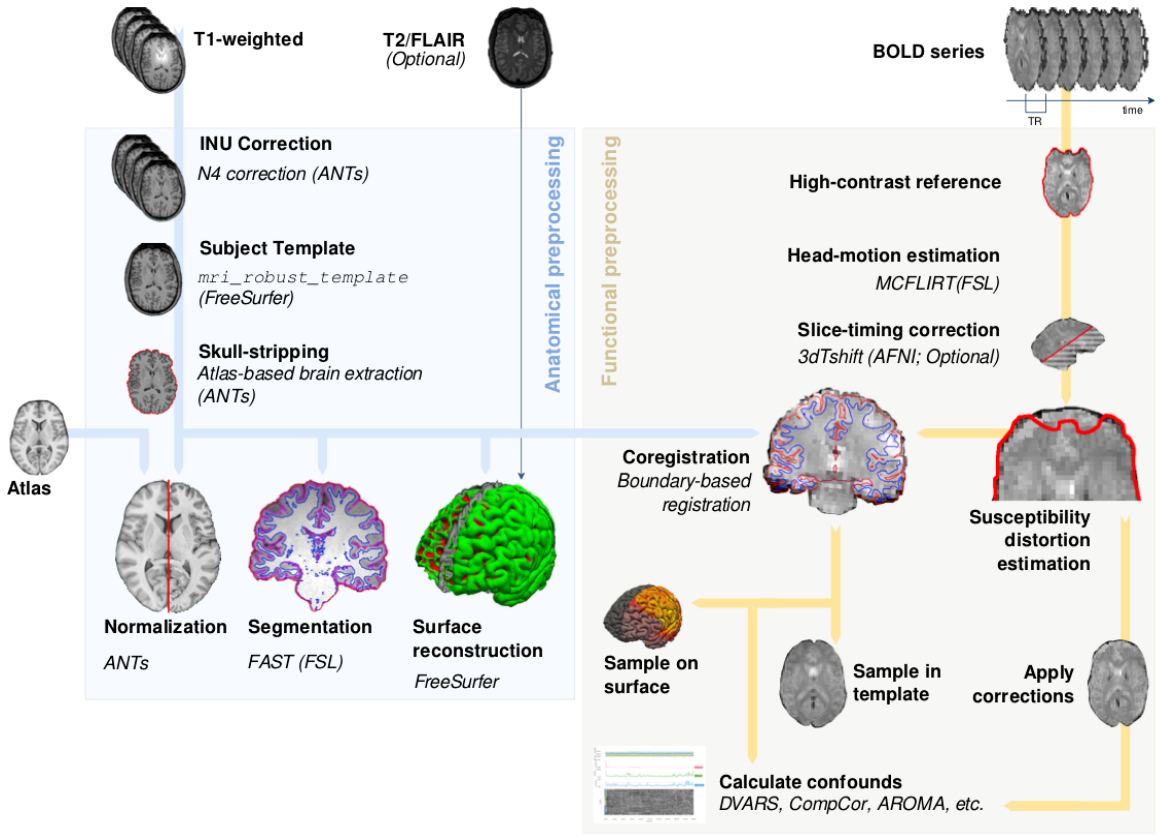
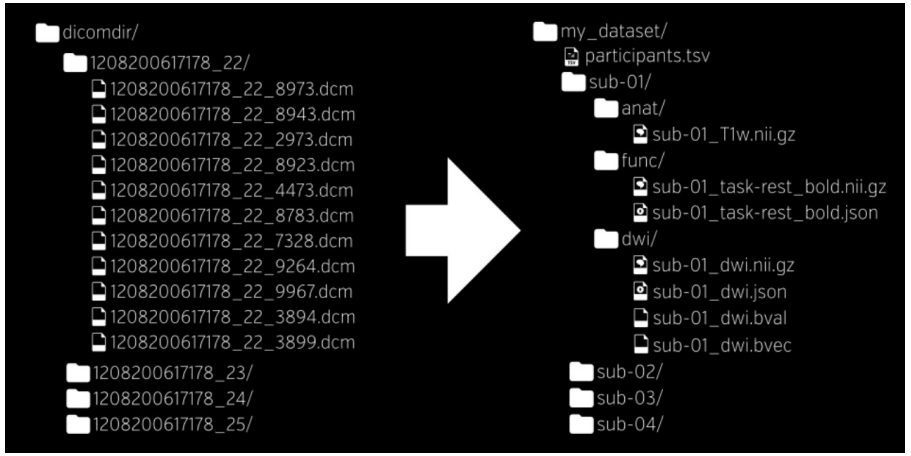
# Preprocessing on SPM

# fMRIPrep & BIDs format




BIDS
BRAIN IMAGING DATA STRUCTURE



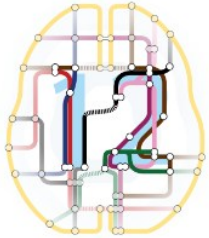

Recent, open standard, with protocol for organizing and describing imaging data

# DICOM, NifTI & SPM

- DICOM (Digital Imaging and Communications in Medicine, 1993)
  Current standard communication protocol used for the capture, storage and transmission of medical images and related data

- NifTI (Neuroimaging Informatics Technology Initiative, NIH, 2003)
  A comprehensive data format used by imaging software but without a communication protocol

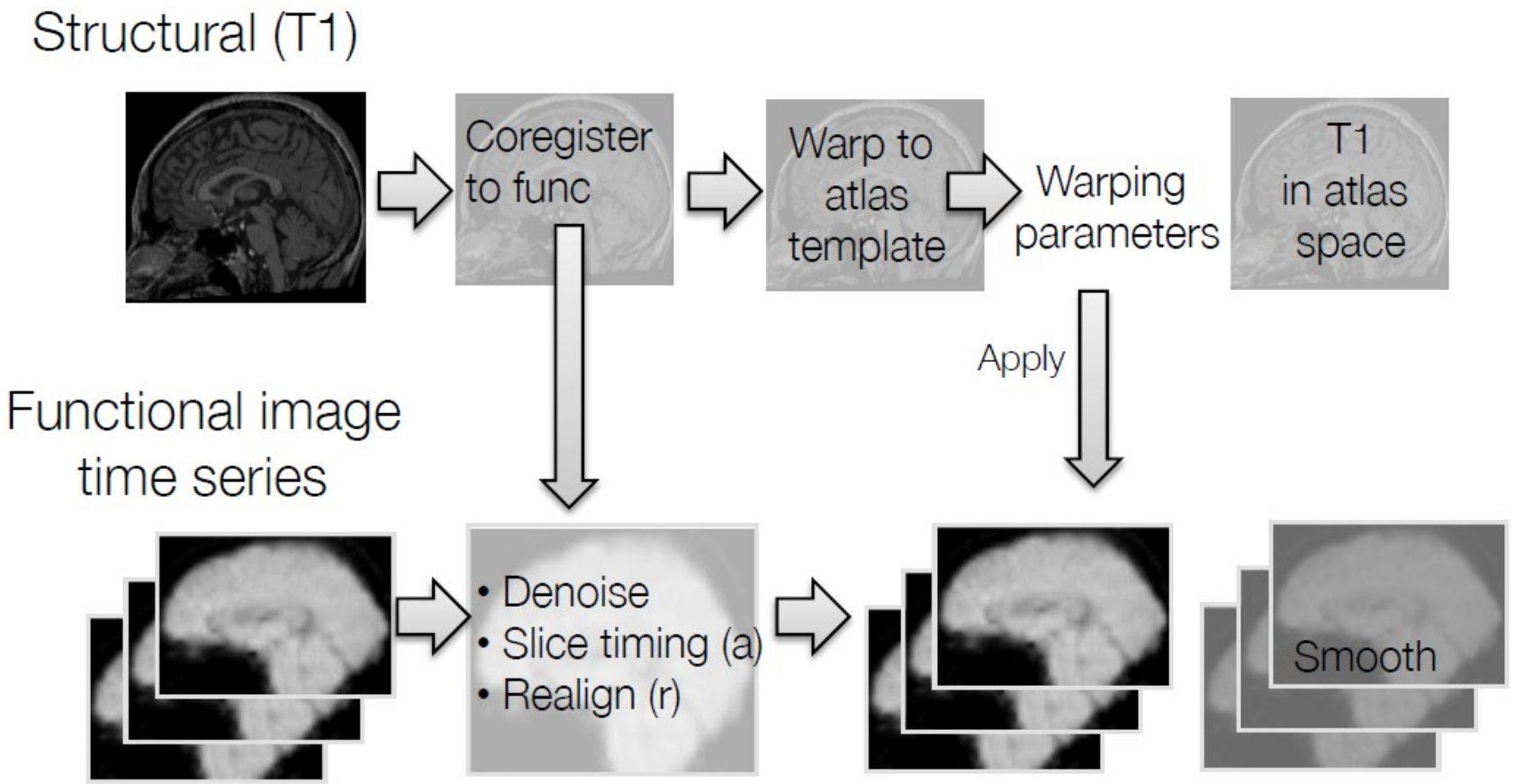
- SPM (Matlab, 1991)
  One of the software specialized in analyzing NifTI images



# Preprocessing: why is it needed?

- fMRI Returns a 3D array of voxels repeatedly sampled over time, with changes in activation in each voxel correlated with experimental task
- Key Assumptions:
  1) The voxels need to come from the same part of the brain
  2) All voxels must be acquired simultaneously
- Assumptions violated:
  1) Brain moves in the scanner
  2) The last slice is acquired TR seconds after the first slice
- Problem: These sources of variance lower the signal-to-noise ratio
- Solution: Preprocessing such as slice-timing correction (assumption 2), realignment of images (assumption 1), etc.

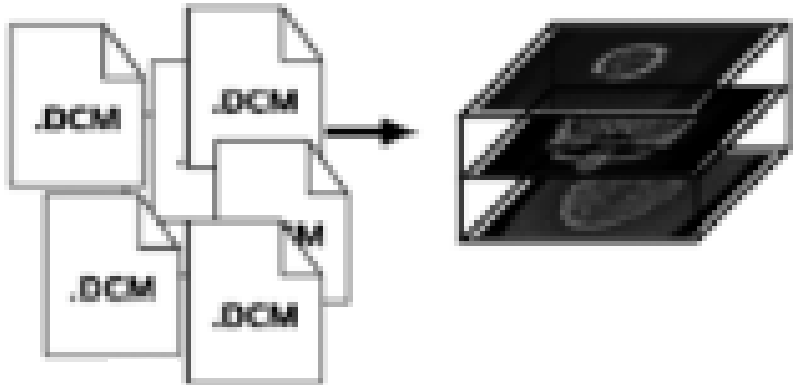
# Data processing pipeline




**Preprocessing**

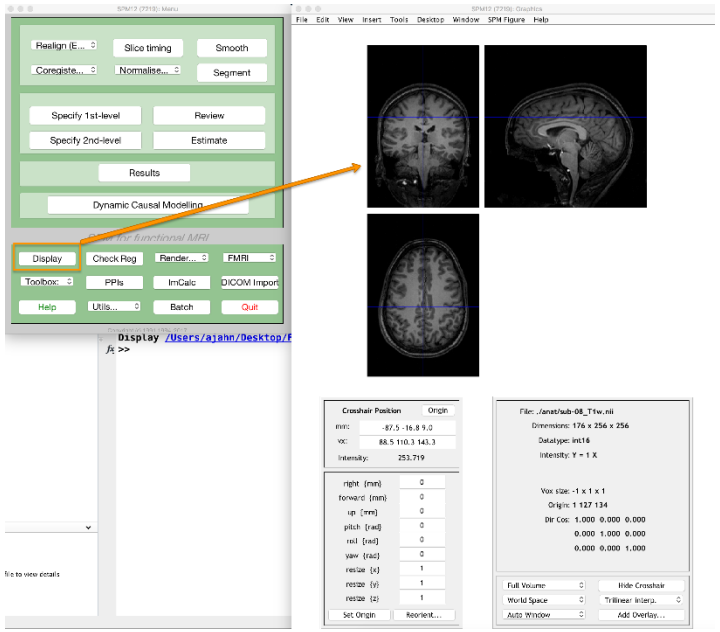
- **To minimize the influence of data acquisition and physiological artifacts**
- **To check statistical assumptions and transform the data to meet assumptions**
- **To standardize the locations of brain regions across subjects to achieve validity and sensitivity in group analysis.**

# Pipeline: 1. DICOM to NifTI

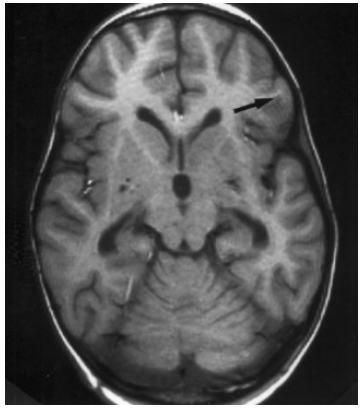


# Pipeline: 2. Visualization

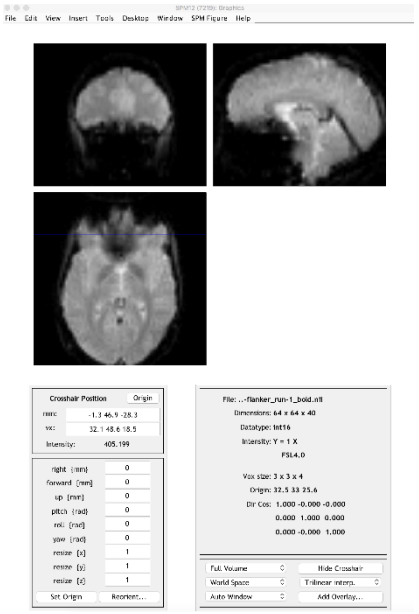
## Inspect anatomical images



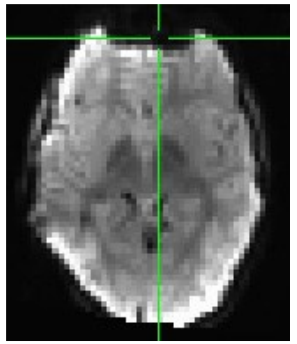

Look out for artifacts, such as ripples. They may be caused by subjects moving too much in the scanner

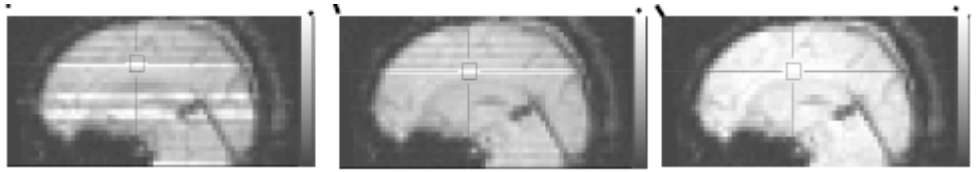


## Inspect functional images



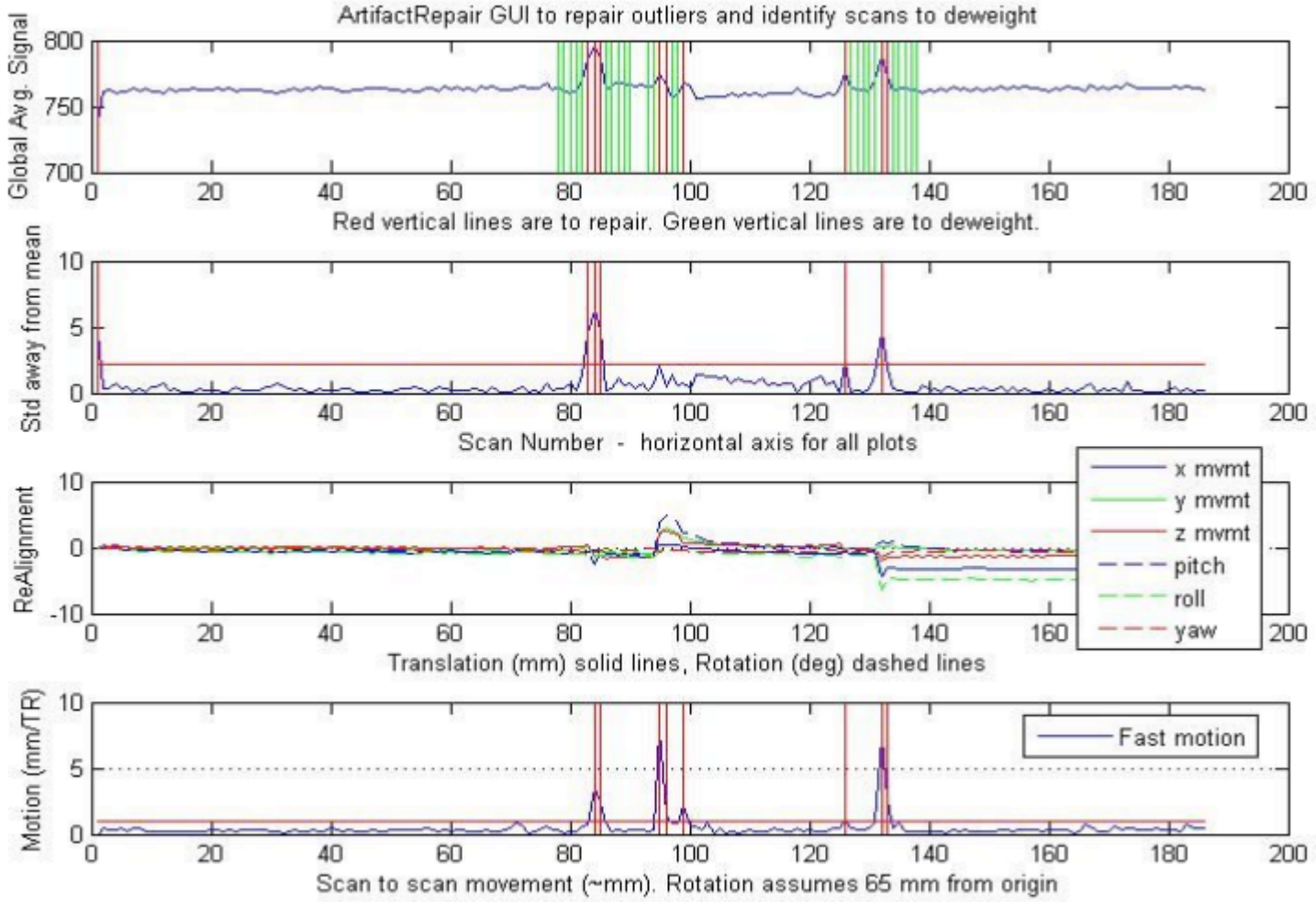
Look out for noise, transient artifacts, ghosting, dropouts, etc.





# Pipeline: 3. Artifact removal (optional)

## *Detection of Bad Volumes (art_global)*

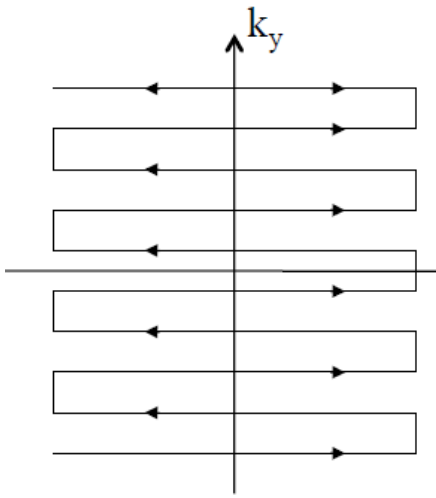


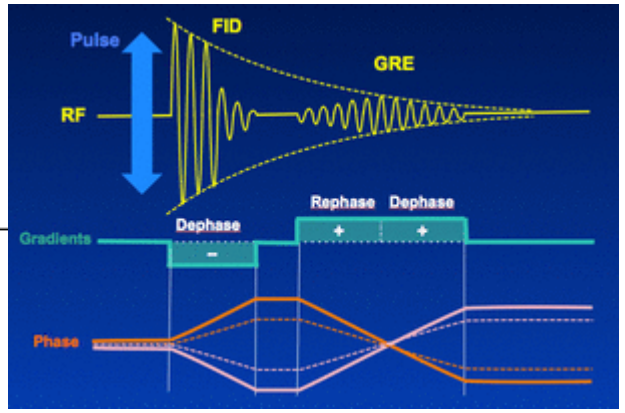

- Can also be done at the end of preprocessing
- Beware, previous versions included a script error that needed correction by-hand

https://cibsr.stanford.edu/content/dam/sm/cibsr/documents/tools/methods/artrepair-software/ArtRepairOverview.pdf

# Pipeline: 4. Field Map

fMRI data is usually acquired via Echo Planar Imaging (EPI) for rapid acquisition times. The sequence acquires large amounts of gradient echoes in one TR cycle by rapidly alternating frequencies.

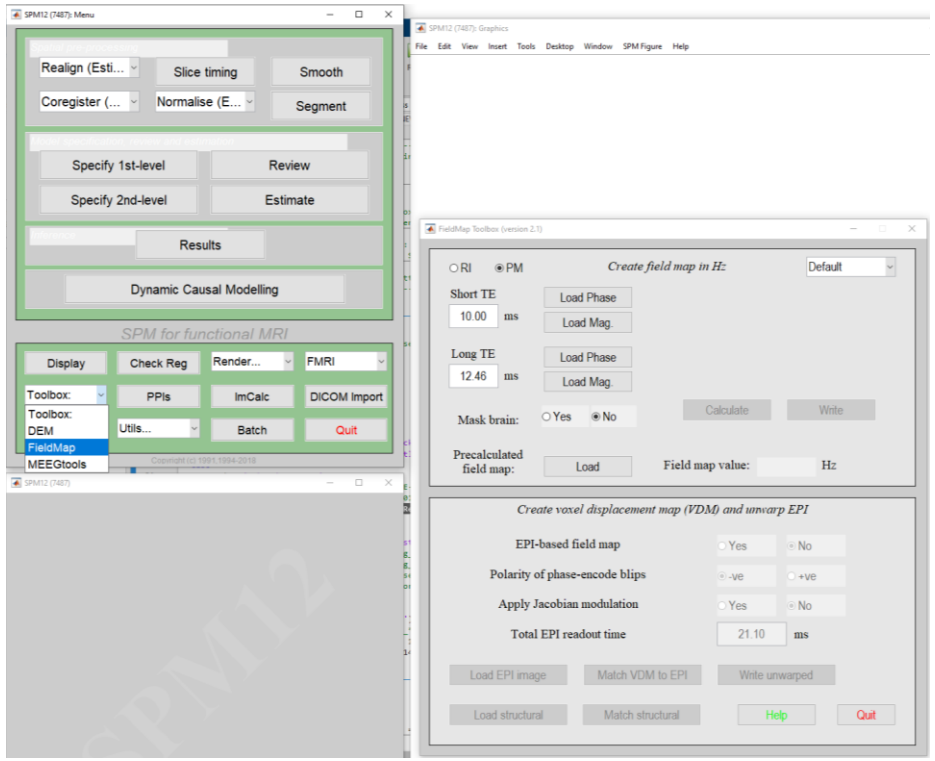



However, EPI is more sensitive to spatial disturbances (inhomogeneity) of the magnetic field, induced by ferromagnetic components of the magnet or the patient. The result is varying image quality + artifacts.

A fieldmap is a measure of such deviations. We use the Fieldmap toolbox to address the difference between two echoes, and to correct the distortions. The file will be used later in the preprocessing.

More at FSL Course: EPI Distortion Correction and Registration: https://www.youtube.com/watch?v=DfGIZcEvQus



# fMRI parameters example

**Routine**

| | |
|---|---|
| Slice group | 1 |
| Slices | 52 |
| Dist. factor | 10 % |
| Position | L0.4 P3.6 H8.4 mm |
| Orientation | T > C-25.2 > S1.2 |
| Phase enc. dir. | P >> A |
| AutoAlign | Head > Brain |
| Phase oversampling | 0 % |
| FoV read | 210 mm |
| FoV phase | 100.0 % |
| Slice thickness | 2.40 mm |
| TR | 1600 ms |
| TE | 30.00 ms |
| Multi-band accel. factor | 2 |
| Filter | Prescan Normalize |
| Coil elements | HC1-7 |

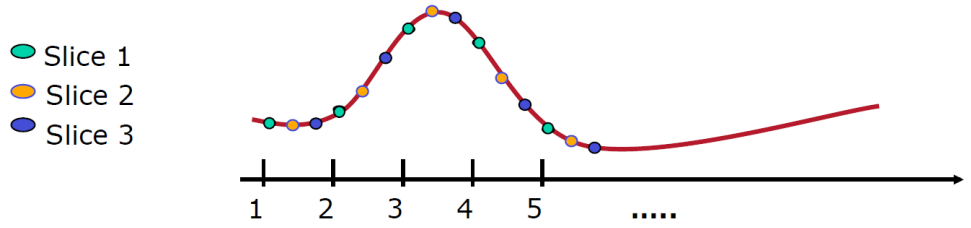
**Contrast - Common**

| | |
|---|---|
| TR | 1600 ms |
| TE | 30.00 ms |
| MTC | Off |
| Magn. preparation | None |
| Flip angle | 75 deg |
| Fat suppr. | Fat sat. |

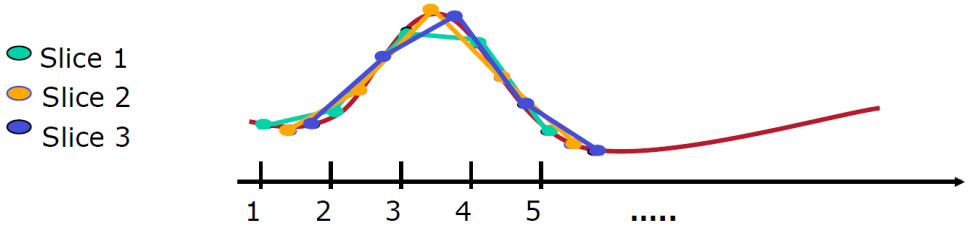
# Pipeline: 5. Slice timing

**Correcting assumption 2:**

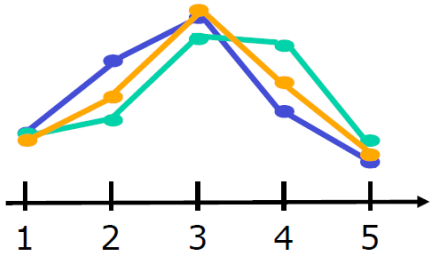
- We construct brain volumes by sampling multiple slices of the brain during each individual repetition time (TR)
- Each slice is sampled at a slightly different time points




• Slice time correction shifts each voxel's time series so that they all appear as sampled simultaneously.




Can be corrected using temporal interpolation.




## Temporal Interpolation

- Use information from nearby time points to estimate the amplitude of the MR signal at the onset of each TR

# Pipeline: 6. Registration (Realign & unwarp)

**Correcting assumption 1:**

- When analyzing the time series associated with a voxel, we assume it depicts the same region of the brain at every time point
- Movements such as head motion may make this assumption incorrect

We correct that by looking for the best possible alignment between an input image and some target image (i.e., registration):

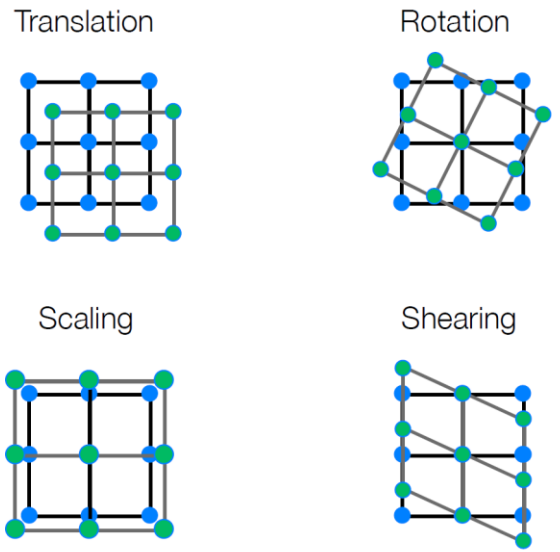
- We define a target image, usually defined the first or mean image in the fMRI time series
- The goal is to find the set of parameters which minimizes some cost function that assesses similarity between the image and the target
- To align the two images, one of them needs to be transformed via rigid body functions or non-linear functions

Realignment via linear transformations:

- Rigid body (6 DOF) – translation, rotation
- Similarity (7 DOF) – translation, rotation, global scaling
- Affine (12 DOF) – translation, rotation, scaling and Shearing

Unwarping:

Non-linear transformation to modify shape

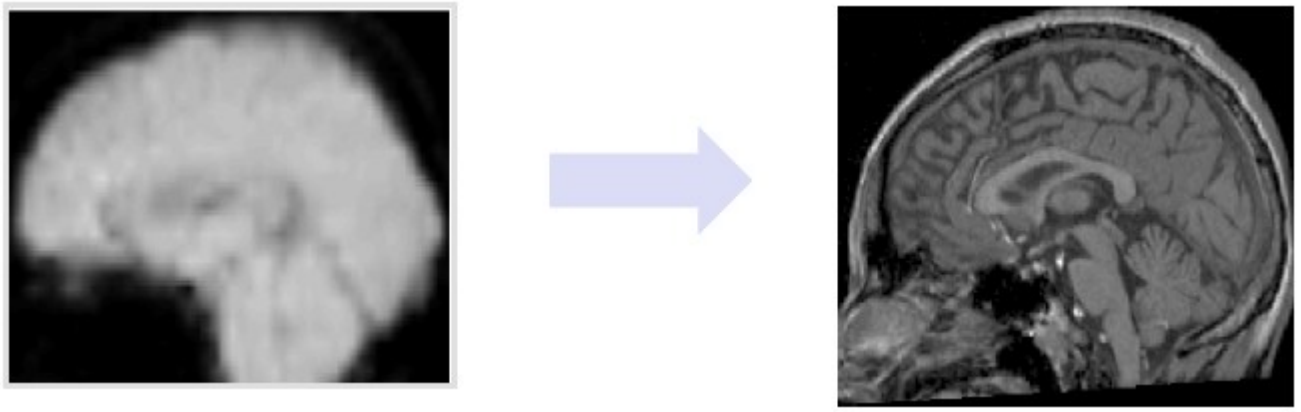


# Pipeline: 7. Coregistration

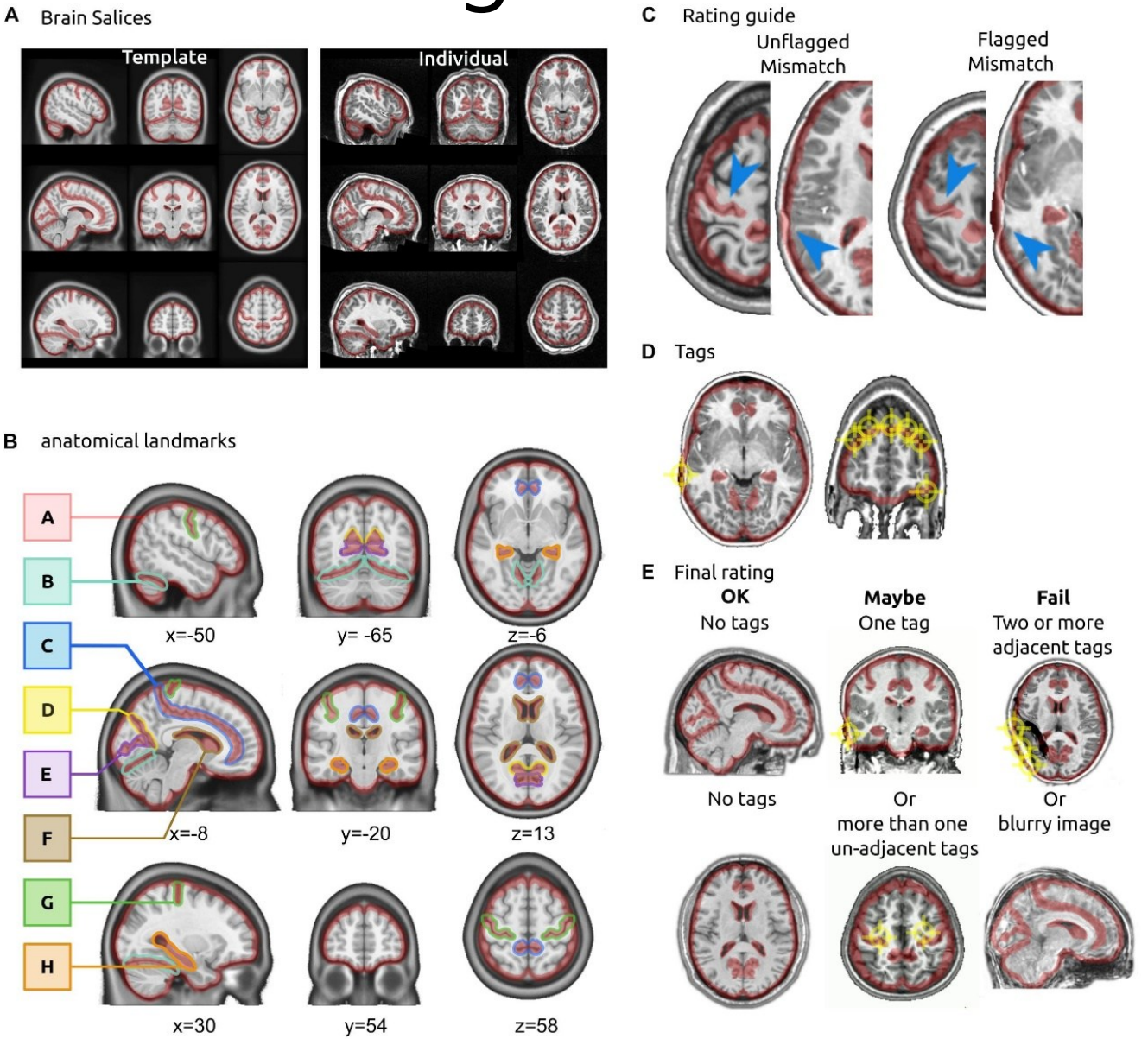
We coregister the functional images to the structural image:

– Allows one to visualize single-subject task activations overlaid on the individual's anatomical information

– Simplifies later transformation of the fMRI images to a standard coordinate system



# Pipeline: 8. Check registration and corrections



# Pipeline: 9. Segmentation (tissue probability maps)

The brain is composed of two main tissue types:

- Grey matter (containing high densities of unmyelinated neurons)
- White matter (containing high densities of myelinated neurons).

- The brain is also surrounded by cerebrospinal fluid (CSF), and large amounts of CSF are contained in internal spaces within the brain called ventricles.

Knowing which voxels belong to which tissue type can assist in the next steps of preprocessing (Normalizing the anatomical image, warping it to match a template in standardized space).

SPM has images of six tissue priors representing their best guess as to which voxel in standardized space belongs to which tissue type. Accurately mapping the tissues of our anatomical image to the tissues of the template will increase the accuracy of our registration.

Why six? Because the anatomical image also contains non-brain tissues:

- Soft tissue (e.g., dura mater)
- Skull
- All other tissues not captured by any of the above; usually air inside the sinuses and outside the brain, or abnormal tissue, such as tumors

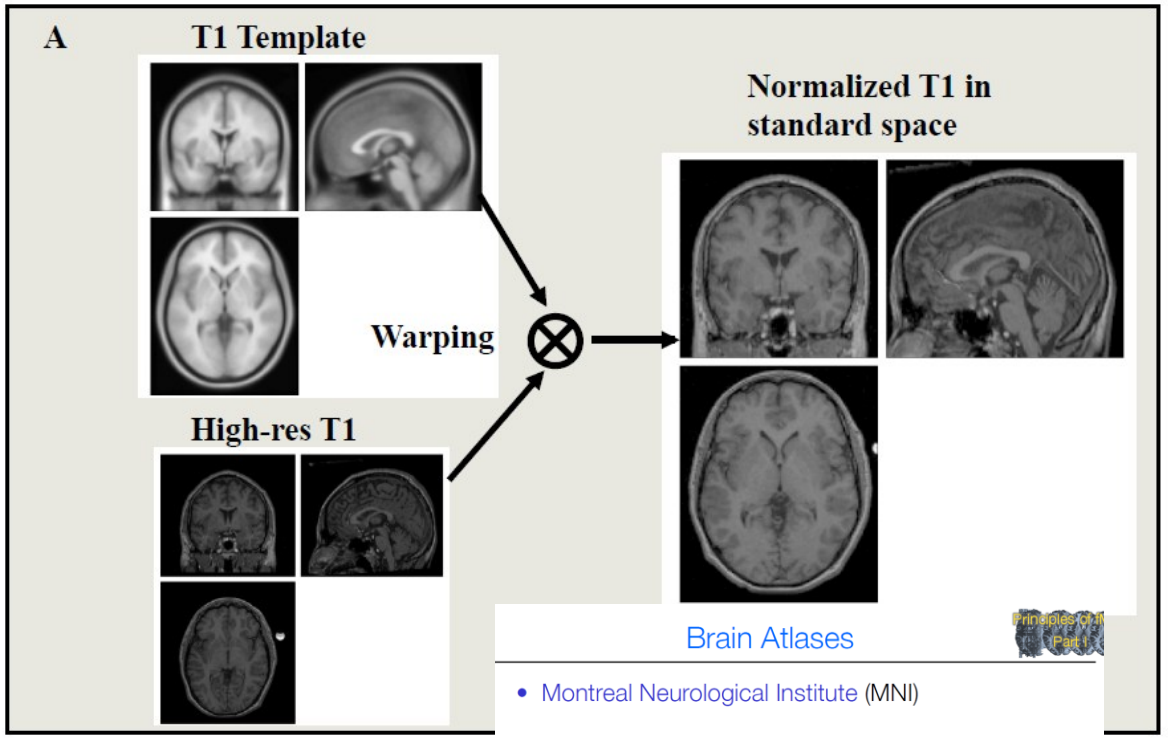
# Pipeline: 10. Normalization

• All brains are different. The brain size of two subjects can differ in size by up to 30%
• There may also be substantial variation in the shapes of the brain
• Normalization allows one to stretch, squeeze and warp each brain so that it is the same as some standard brain

PROS
• Spatial locations are consistent
• Results can be generalized to larger population
• Results can be compared across studies.
• Results can be averaged across subjects

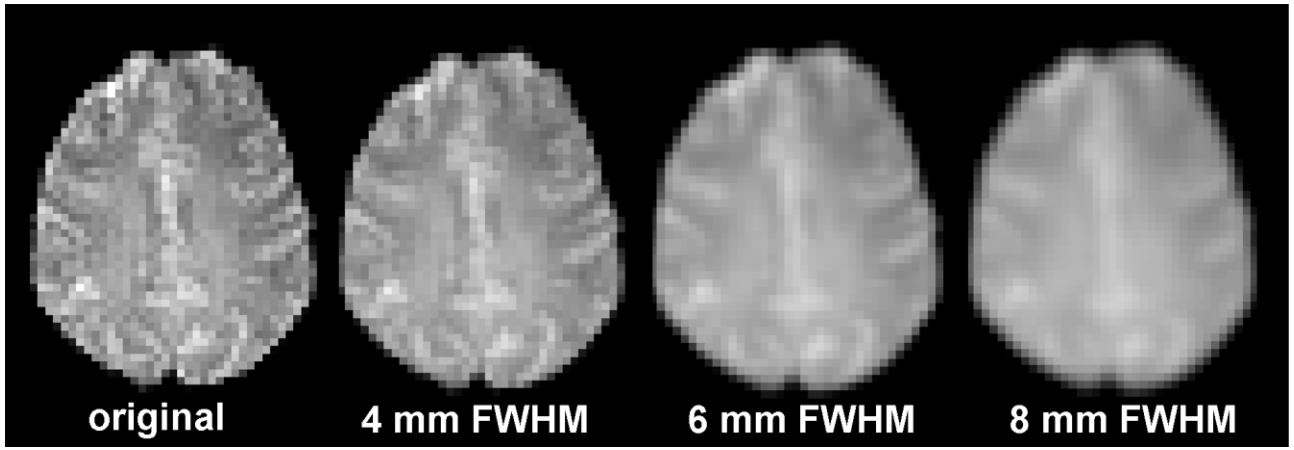
CONS
• Reduces spatial resolution
• Introduces potential errors

The structural MR image used in the coregistration procedure is warped onto a template image



# Pipeline: 11. Smoothing

Because spatial normalization across subjects is imperfect, activations in e.g., hippocampus will not line up perfectly in a group analysis.
Spatial smoothing consists in averaging over nearby voxels (e.g., 4mm, 10mm) so it is more likely that activations overlap and therefore are detected.




Smoothing consists in applying a Gaussian filter to voxels:

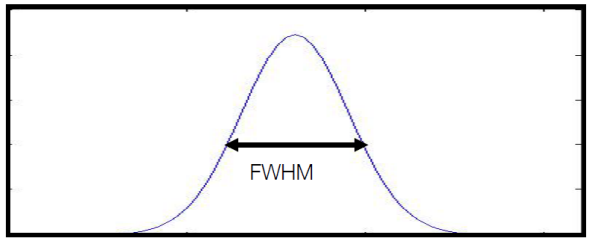
- We choose a kernel size for the Gaussian filter, called full width at half maximum (usually 3*voxel size)
- The data is averaged over the width of the FWHM.

PROS

- May overcome limitations in the normalization by blurring any residual anatomical differences
- can cancel out the noise and enhance the signal, increasing the signal-to-noise ratio (SNR)
- May increase the validity of the statistical analysis
- Required for Gaussian random fields

CONS

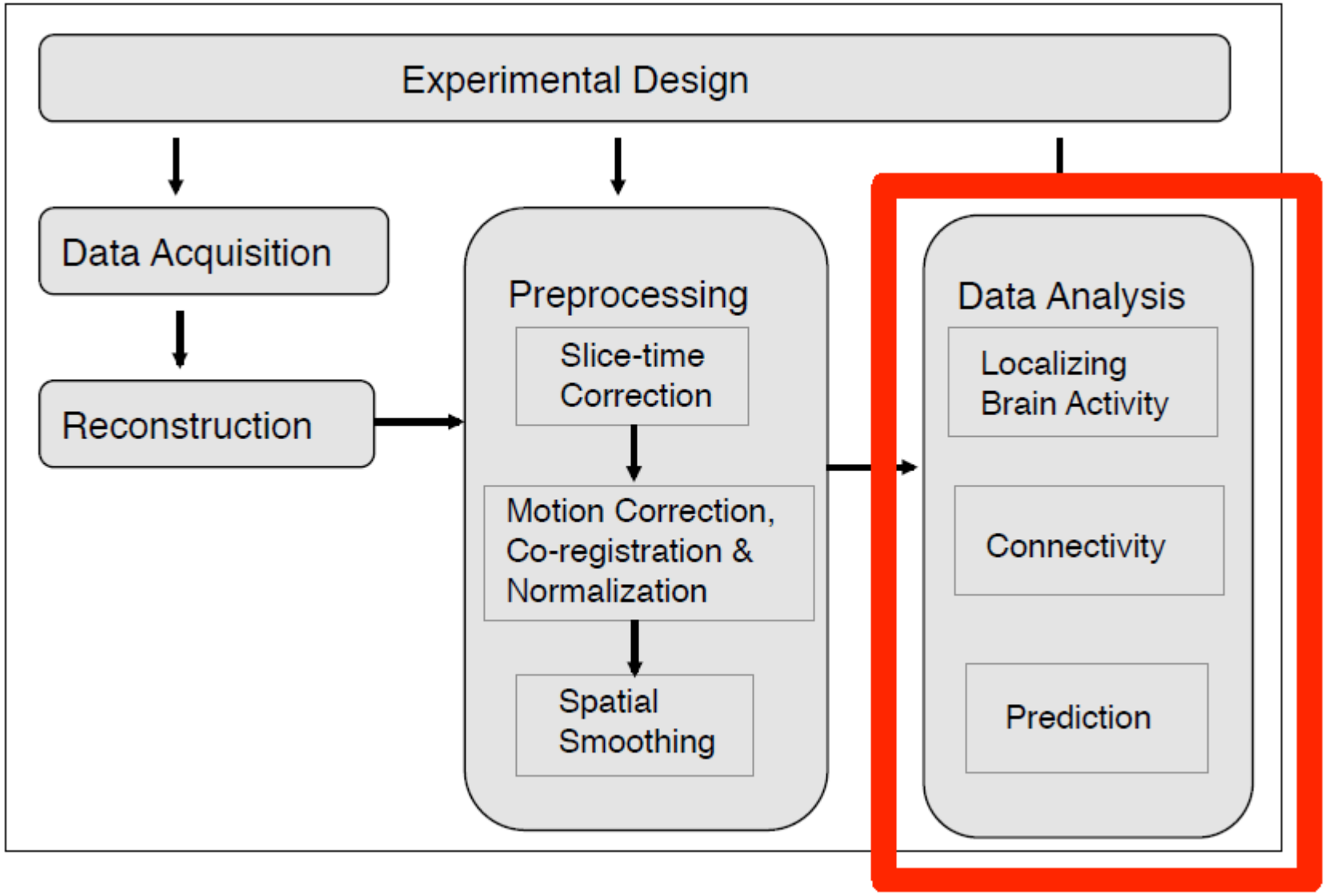
- The image resolution is reduced




$$\sigma = \frac{FWHM}{2\sqrt{2\ln(2)}}$$

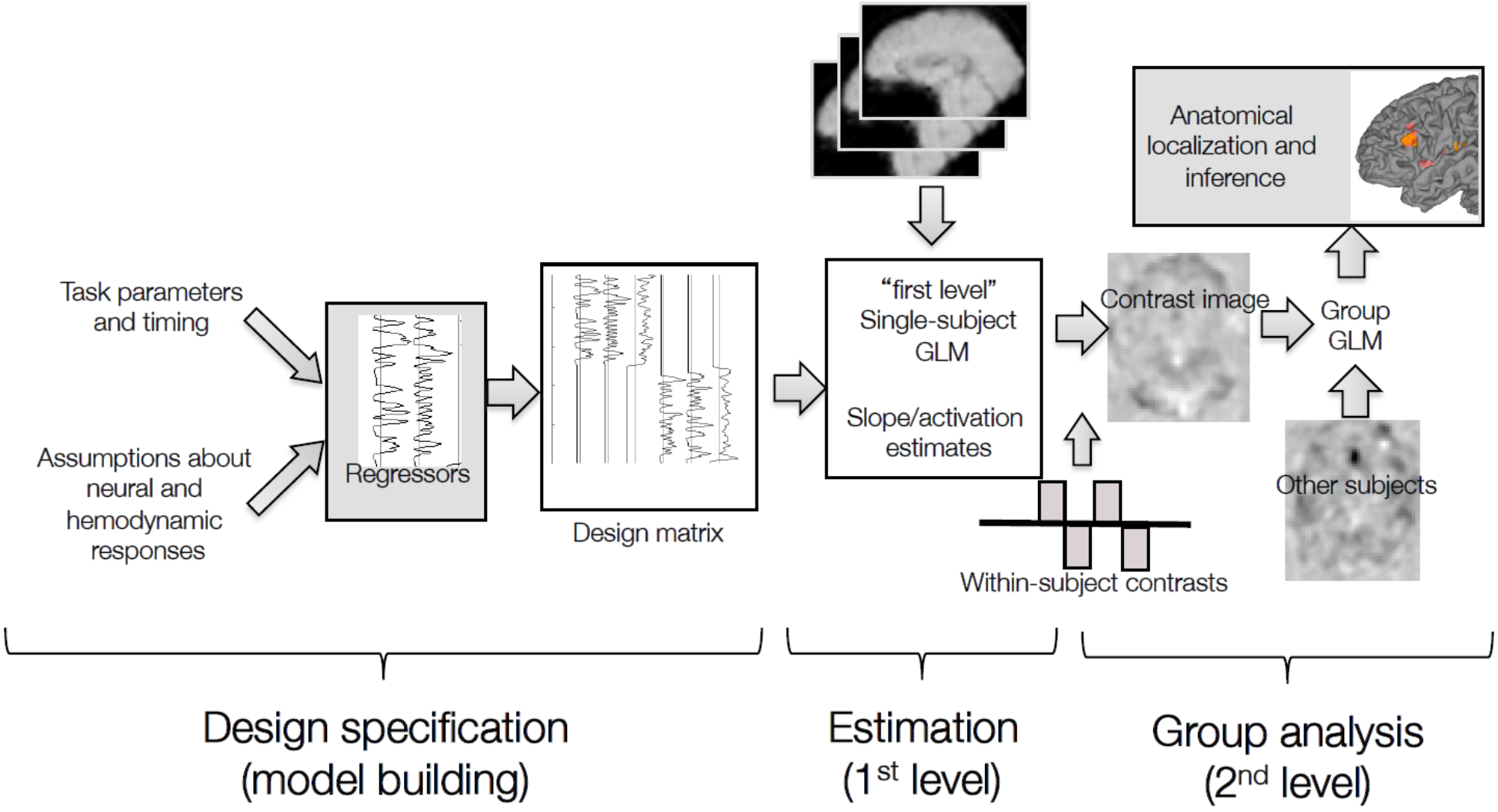
# Contrasts on SPM

# Statistical analyses




Sources: Martin Lindquist and Tor Wager – Principles of fMRI (discontinued)

# GLM analysis process



# GLM

A standard GLM can be written:

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon} \qquad \boldsymbol{\varepsilon} \sim N(\mathbf{0}, \mathbf{V})$$

where

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} 1 & X_{11} & \cdots & X_{1p} \\ 1 & X_{21} & \cdots & X_{2p} \\ \vdots & \vdots & & \vdots \\ 1 & X_{n1} & \cdots & X_{np} \end{bmatrix} \times \begin{bmatrix} \beta_0 \\ \beta_1 \\ \vdots \\ \beta_p \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{bmatrix}$$

fMRI Data | Design matrix | Regression coefficients | Noise

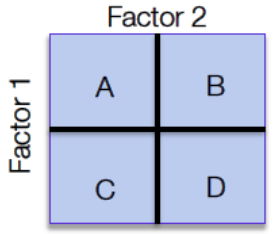
V is the covariance matrix whose format depends on the noise model.

- The matrices X and Y are assumed to be known, and the noise is assumed to be uncorrelated.
- Our goal is to find the value of $\boldsymbol{\beta}$ that minimizes:

$$(\mathbf{Y} - \mathbf{X}\beta)^T (\mathbf{Y} - \mathbf{X}\beta)$$

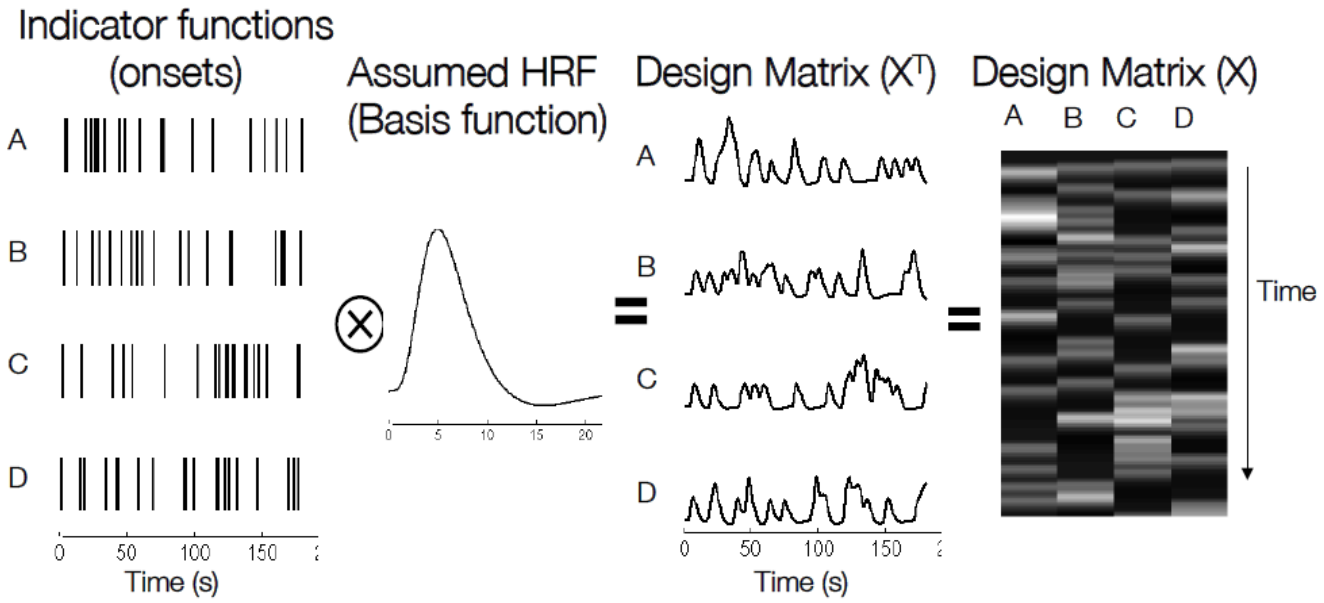
Sums of squared errors (SSE)

# Design specification




Example: Memory experiment
Four word types, grouped into two factors:

Factor 1: Visual vs. Auditory presentation (2 levels)
Factor 2: High vs. low imageability (2 levels)




Assumptions!

Assume neural activity function is correct

Assume HRF is correct

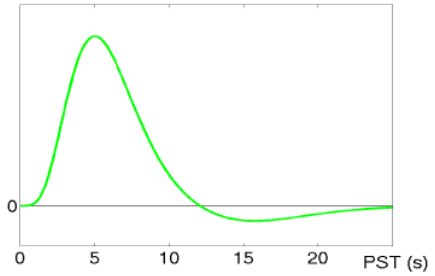
Assume LTI system

We will look at how to relax these later

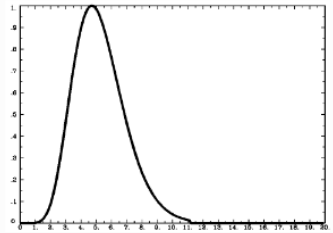
# Assumptions about HRF & onsets

- The BOLD signal follows a consistent shape, peaking around 6s then falling back to baseline over the next several seconds

- Often a fixed canonical HRF is used to model the response to neuronal activity
  - Linear combination of 2 gamma functions.
  - Optimal if correct.
  - If wrong, leads to bias and power loss.
    - Unlikely that the same HRF is valid for all voxels.
    - True response may be faster/slower
    - True response may have smaller/bigger undershoot




Single impulse onset (stimulus)



*The HRF generated by a single impulse stimulus. In this figure, the stimulus occurs at timepoint 0 on the x-axis.*

Boxcar onset (stimulus)

6s

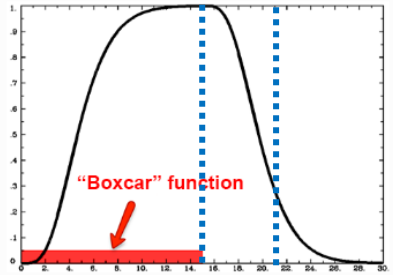
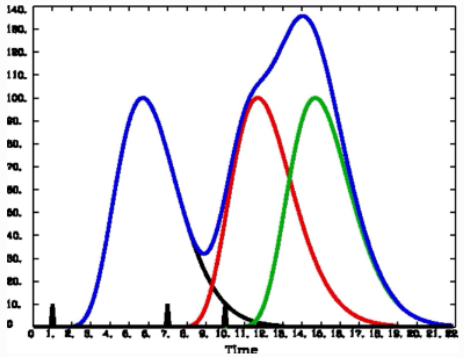



*Illustration of the HRF generated by a boxcar stimulus lasting for fifteen seconds. Note that the BOLD signal begins descending back to baseline around the fifteen-second mark.*

HRF overlap



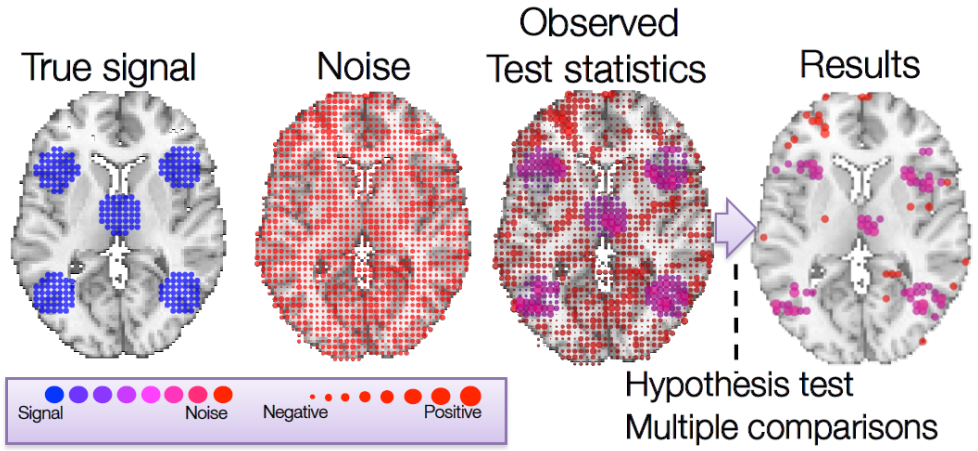

*Convolution of the HRFs for individual stimuli. The overall BOLD response (blue) is a moving average of the individual HRFs outlined in black, red, and green. The vertical black lines on the x-axis represent impulse stimuli. Figure created by Bob Cox of AFNI.*

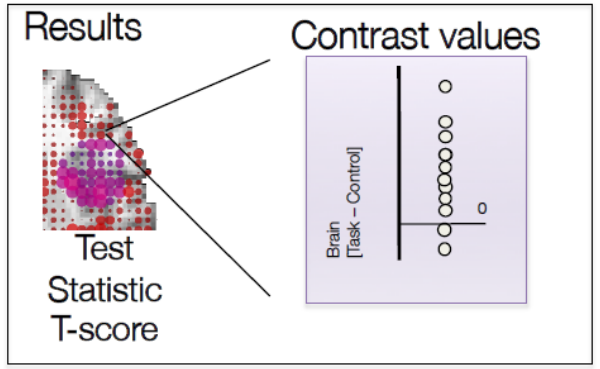
# Nuisance covariates

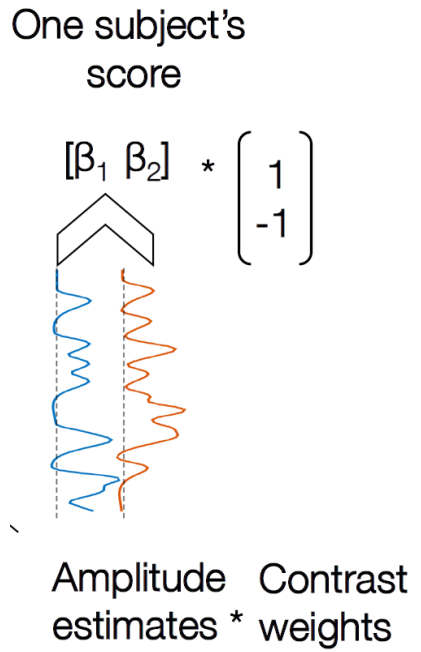
- Often model factors associated with known sources of variability, but that are not related to the experimental hypothesis, need to be included in the GLM.

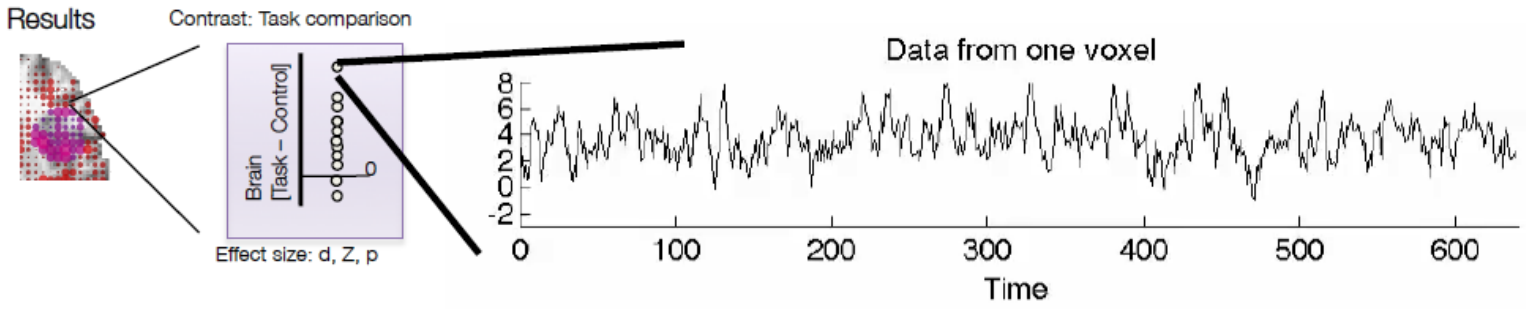
- Examples of possible 'nuisance regressors':
  - Signal drift
  - Physiological (e.g., respiration) artifacts
  - Head motion, e.g. six regressors comprising of three translations and three rotations.
    - Sometimes transformations of the six regressors also included.

# Estimation (single subject GLM)



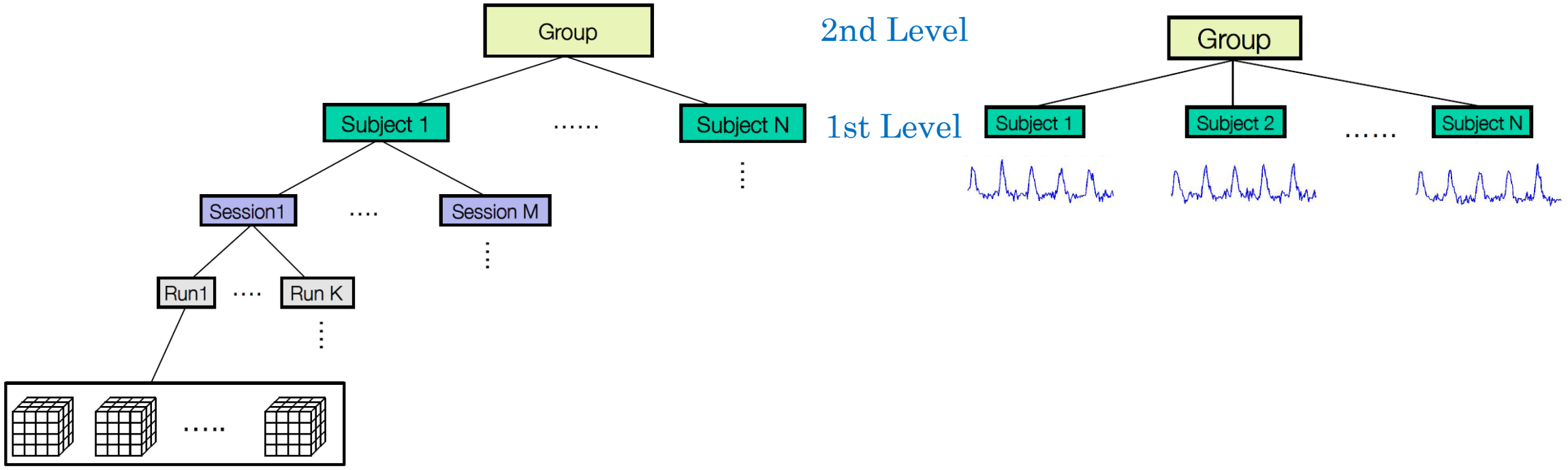



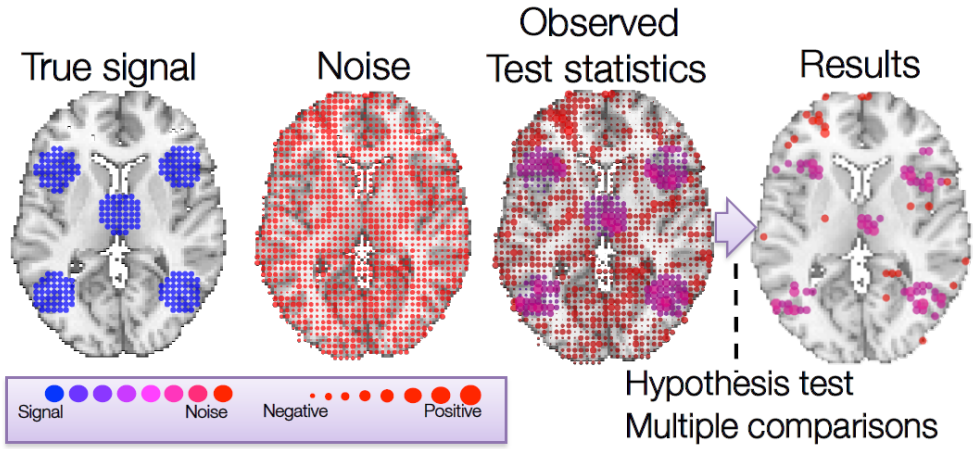



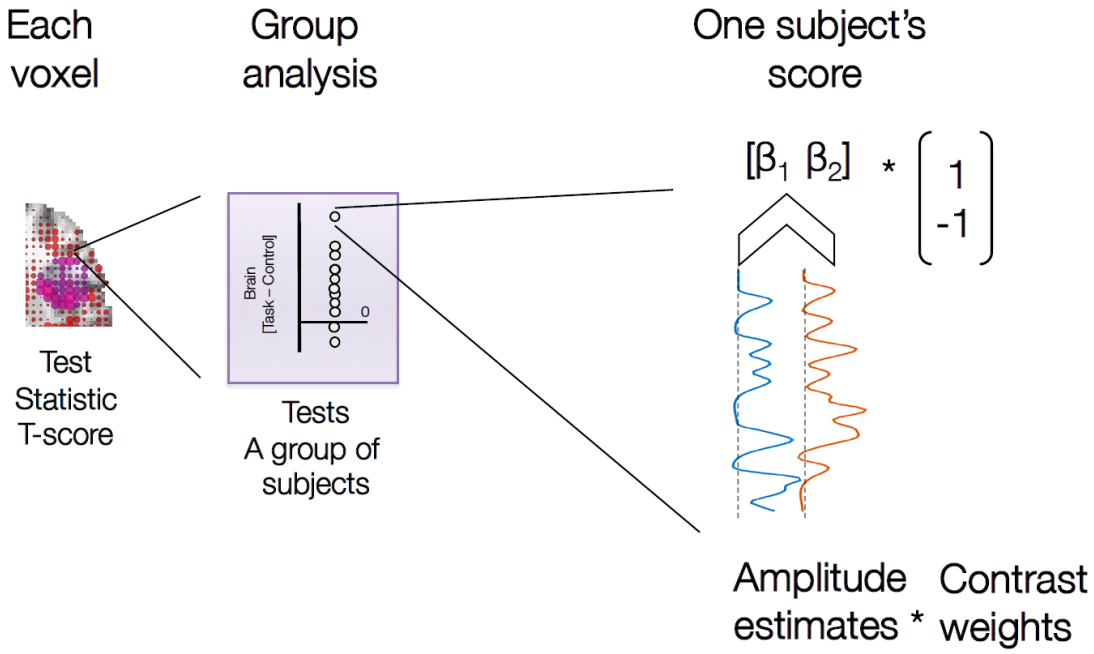
# Group analysis

Data is hierarchical in nature: lower-level observations nested within higher levels



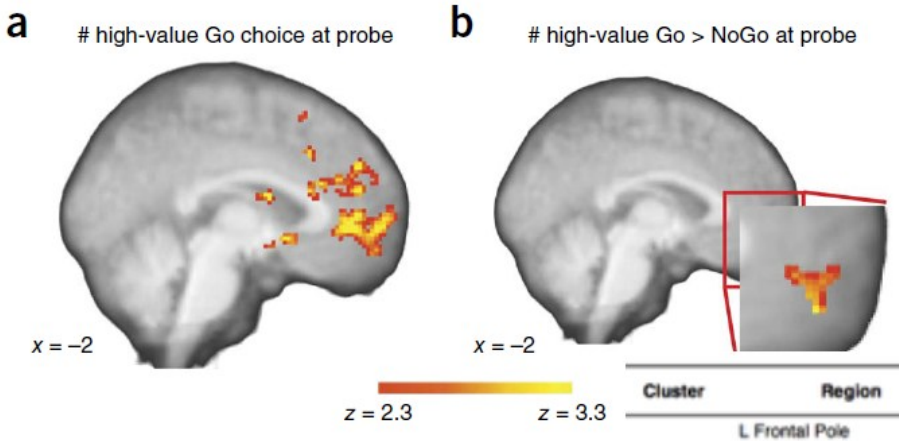
# Estimation (group GLM)



# Guidelines: reporting contrasts & tables

Source: Russell Poldrack – Reporting fMRI data

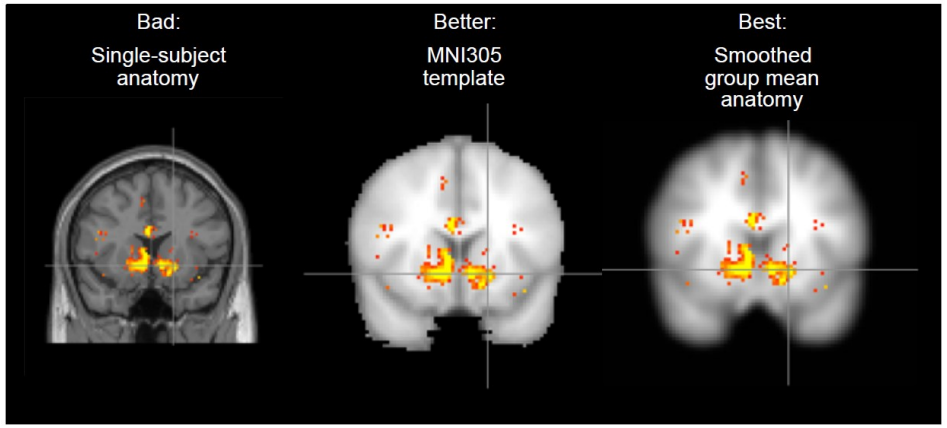



| Cluster | Region | Number of voxels in region | Cluster size | x | y | z | Peak z stat |
|---|---|---|---|---|---|---|---|
| | L Frontal Pole | 398 | | | | | |
| | L Paracingulate Gyrus | 241 | | | | | |
| | R Paracingulate Gyrus | 214 | | | | | |
| | R Anrterior Cingulate Gyrus | 197 | | | | | |
| 1 | R Frontal Pole | 171 | 1820 | 8 | 40 | 0 | 3.9 |
| | L Anterior Cingulate Gyrus | 156 | | | | | |
| | L Superior Frontal Gyrus | 76 | | | | | |
| | R Superior Frontal Gyrus | 44 | | | | | |
| | L Frontal Medial Cortex | 27 | | | | | |
| | L Caudate | 61 | | | | | |
| 2 | R Caudate | 48 | 397 | 8 | -2 | 16 | 4.23 |
| | R Thalamus | 14 | | | | | |
| | L Accumbens | 26 | | | | | |
| | R Subcallosal Cortex | 25 | | | | | |
| 3 | L Putamen | 22 | 266 | -6 | 2 | -12 | 3.62 |
| | L Pallidum | 19 | | | | | |
| | L Subcallosal Cortex | 13 | | | | | |
| | L Paracingulate Gyrus | 81 | | | | | |
| | R Paracingulate Gyrus | 71 | | | | | |
| 4 | L Superior Frontal Gyrus | 26 | 241 | -8 | 10 | 46 | 3.6 |
| | L Supplementary Motor Cortex | 11 | | | | | |

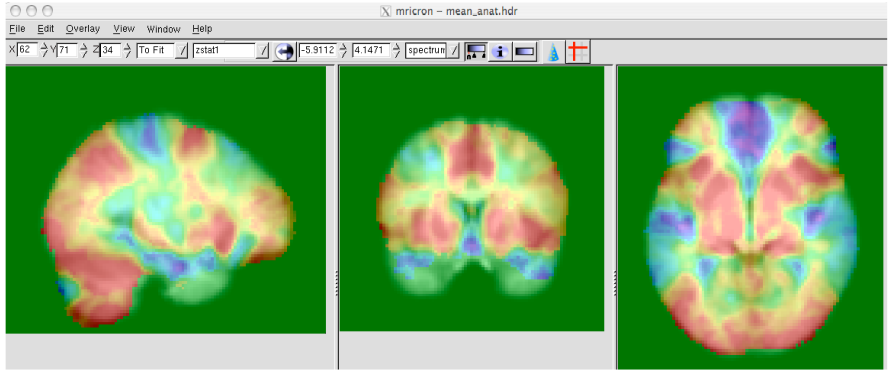
Schonberg et al., 2014

# Guidelines: reporting contrasts & tables

- Use a background image that accurately reflects the anatomy and any applied smoothing




Using full color maps to visualize statistical maps




Better use probabilistic anatomical maps, not Talairach&Tournoux + Brodmann areas
MNI recommended (152S)

## Labeling activation

**Table 3**
**Coordinates of Clusters of Activation Showing Significantly Different Activity in Comparisons Between Concept-Learning Tasks**

| Region | *k* | *x* | *y* | *z* | BA |
|---|---|---|---|---|---|
| | | Implicit > Verbal | | | |
| Left occipital | 308 | −40 | −90 | 2 | 18 |
| | | −46 | −78 | −2 | 19 |
| | | −32 | −88 | −12 | 18,19 |
| | | Verbal > Implicit | | | |
| Medial prefrontal | 392 | −8 | 56 | −2 | 10 |
| | | 6 | 44 | −10 | 10, 11 |
| | | −6 | 38 | −8 | 32 |
| | | Novel–Implicit > Verbal | | | |
| Left occipital | 1,180 | −38 | −86 | 8 | 19 |
| | | −40 | −76 | −2 | 18 |
| | | −26 | −86 | −8 | 18 |
| Right occipital | 249 | 36 | −88 | 0 | 18 |
| | | 44 | −72 | −6 | 19 |
| | | 48 | −64 | −4 | 19 |
| | | Verbal > Novel–Implicit | | | |
| No significant clusters of activation | | | | | |
| | | Novel–Implicit > Implicit | | | |
| No significant clusters of activation | | | | | |
| | | Implicit > Novel–Implicit | | | |
| No significant clusters of activation | | | | | |

Note—All clusters reached an uncorrected significance level of $p = .01$ and an extent threshold of 20 voxels. For each cluster, coordinates are given for the maximally activated voxel and up to two local maxima. *k*, number of voxels in cluster; BA, Brodmann's areas; *x*, *y*, *z*, MNI coordinates.

# Guidelines: using ROI analysis

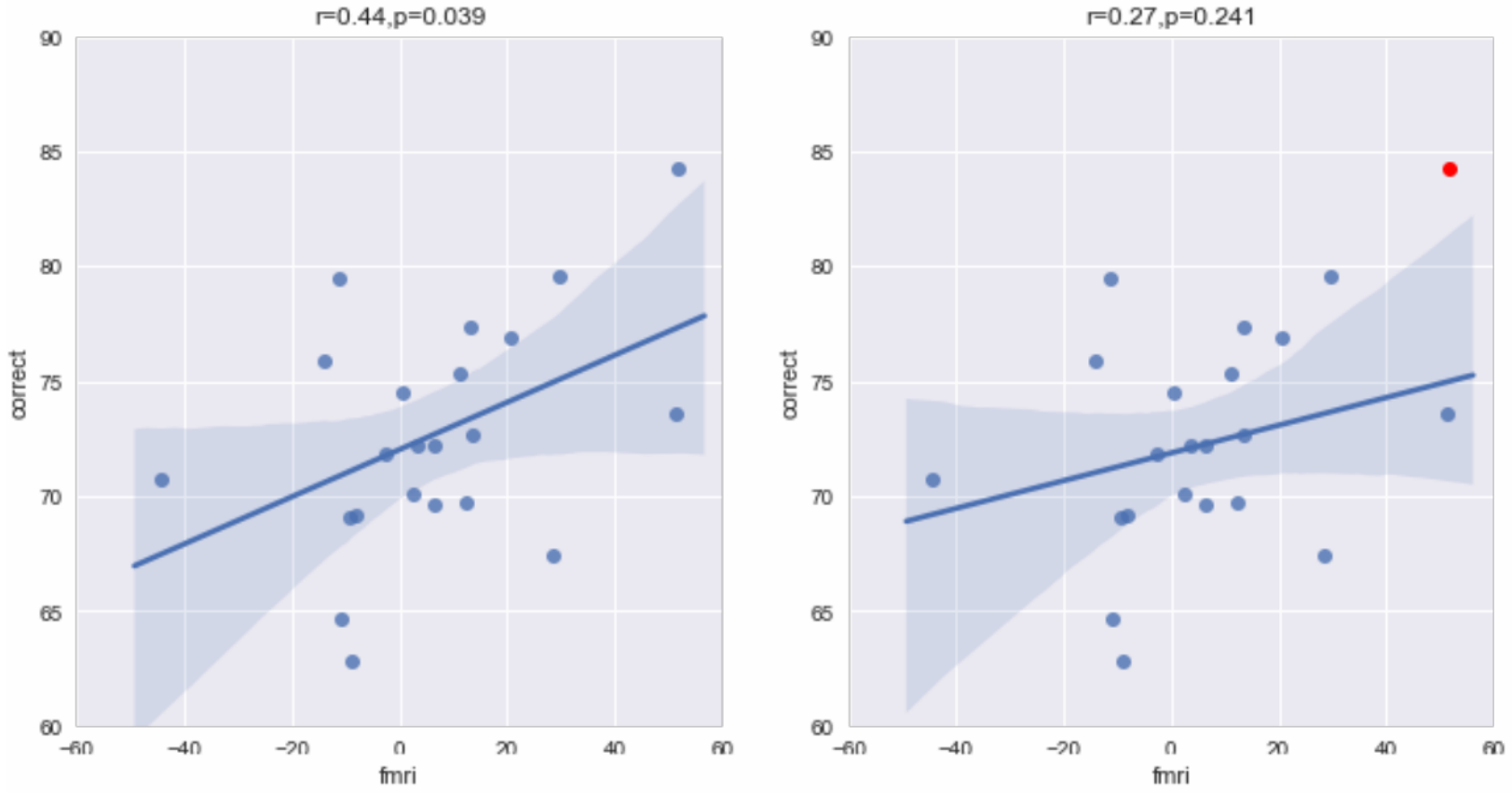
- Characterize/explore signal
- Limit correction for multiple comparisons
- Examine functionally characterized Regions
- With complex designs, it is often difficult to tell what is going on simply by looking at maps
- Plotting signal from ROIs can be Enlightening
- Control for multiple tests over the whole brain can be highly conservative
- Limiting the number of tests (voxels) can increase power
  - Only when you have a pre-existing anatomical hypothesis
  - Can't do this based on the results of another analysis of the same data!

## Example

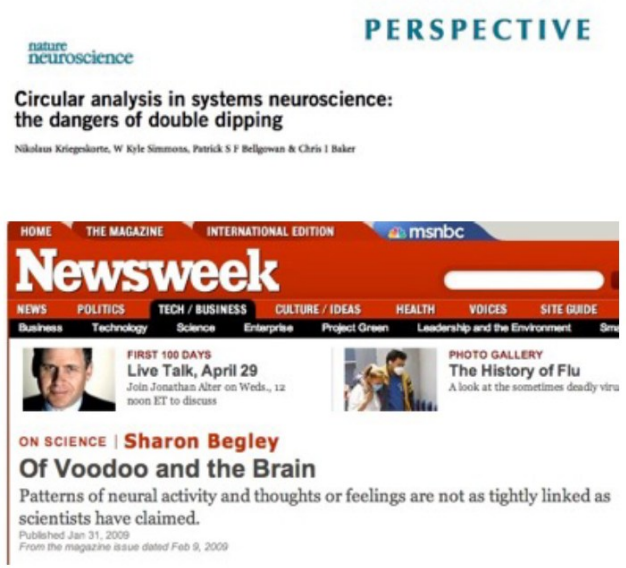
- P<.001, whole brain (2410 resells [smoothed voxels])
  - Cluster with 41 voxels: • P=0.465
- P<.001, small volume correction for 10mm radius sphere (5.7 resels)
  - Same cluster: p=.002

# Guidelines: detecting outliers

- Plotting data from ROIs can also help identify outliers or influential observations



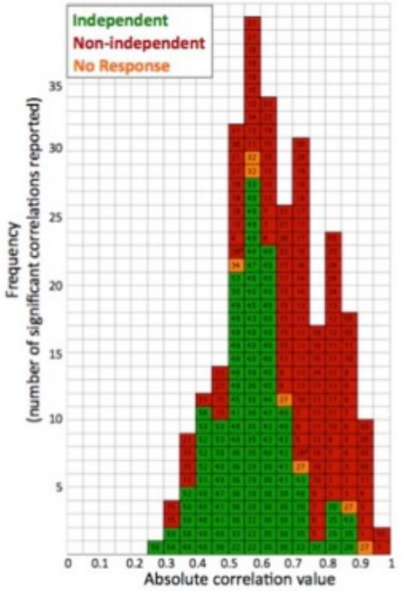
# Guidelines: bias and circularity





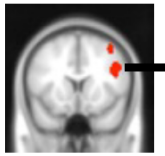
- Independent:
  - ROI determined independently from the data being analyzed
- Non-independent:
  - ROI determined from the same data being analyzed

- Correlations are substantially higher for non-independent analyses



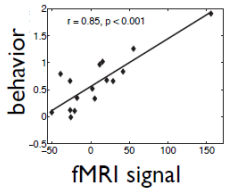

Vul et al., 2009

Run whole-brain analysis



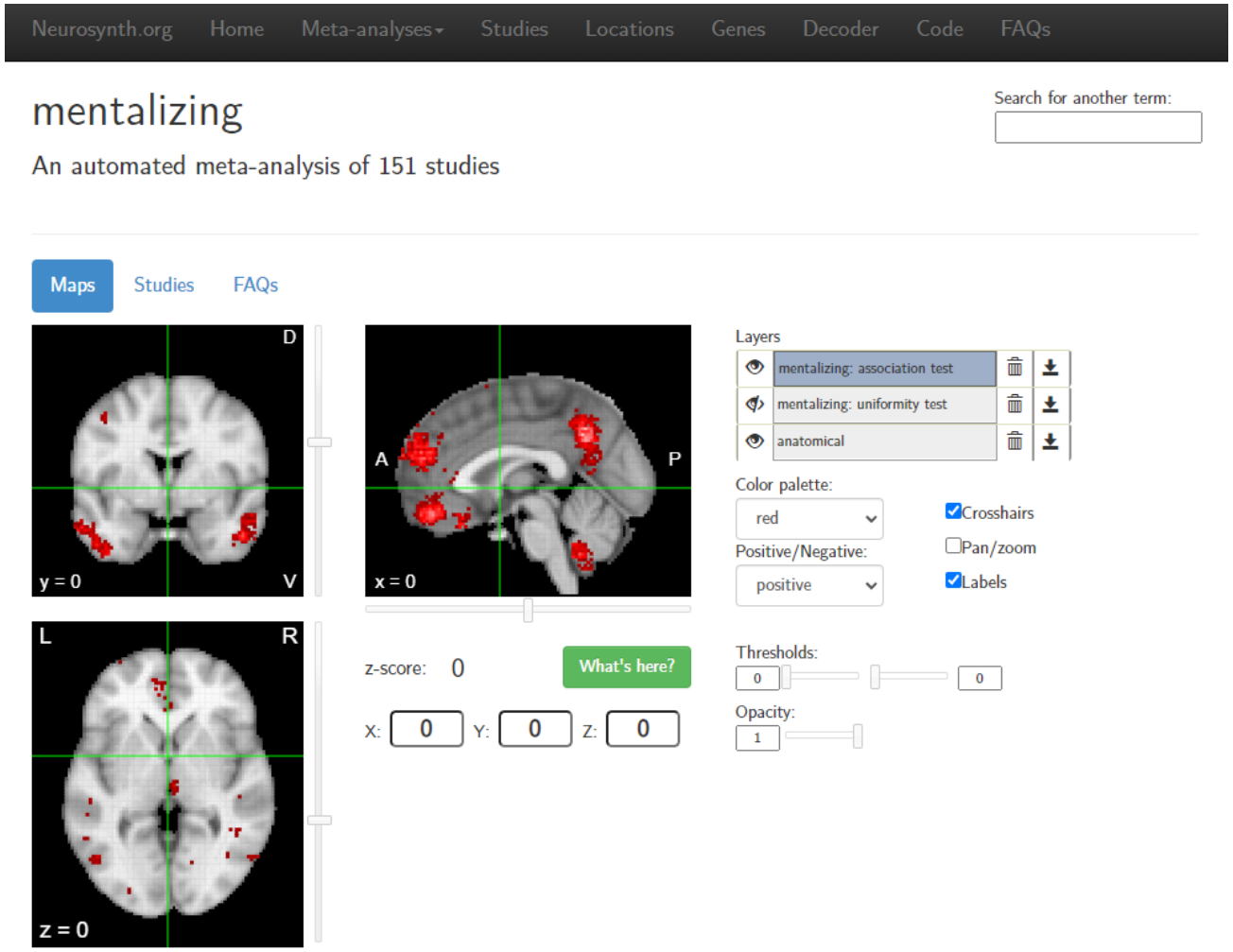
Extract signal from significant voxel/cluster

Perform statistics on extracted data




Of course it's strongly correlated!

# Guidelines: Using neurosynth.org to obtain a priori ROIs



# Guidelines: transparent reporting of methods

**Table 2.** Simple Solution to the Problem of False-Positive Publications

Requirements for authors

1. Authors must decide the rule for terminating data collection before data collection begins and report this rule in the article.
2. Authors must collect at least 20 observations per cell or else provide a compelling cost-of-data-collection justification.
3. Authors must list all variables collected in a study.
4. Authors must report all experimental conditions, including failed manipulations.
5. If observations are eliminated, authors must also report what the statistical results are if those observations are included.
6. If an analysis includes a covariate, authors must report the statistical results of the analysis without the covariate.

-Simmons et al., 2011, Psychological Science

# Guidelines: more publications

- Poldrack, R. A., Baker, C. I., Durnez, J., Gorgolewski, K. J., Matthews, P. M., Munafò, M. R., ... & Yarkoni, T. (2017). Scanning the horizon: towards transparent and reproducible neuroimaging research. *Nature reviews neuroscience*, *18*(2), 115-126.
- Nichols, T. E., Das, S., Eickhoff, S. B., Evans, A. C., Glatard, T., Hanke, M., ... & Yeo, B. T. (2017). Best practices in data analysis and sharing in neuroimaging using MRI. *Nature neuroscience*, *20*(3), 299-303.
- Devlin, J. T., & Poldrack, R. A. (2007). In praise of tedious anatomy. *Neuroimage*, *37*(4), 1033-1041.
- Poldrack, R. A., & Mumford, J. A. (2009). Independence in ROI analysis: where is the voodoo?. *Social cognitive and affective neuroscience*, *4*(2), 208-213.
- Vul, E., Harris, C., Winkielman, P., & Pashler, H. (2009). Puzzlingly high correlations in fMRI studies of emotion, personality, and social cognition. *Perspectives on psychological science*, *4*(3), 274-290.
- Etc.

# Toolboxes, softwares and platforms

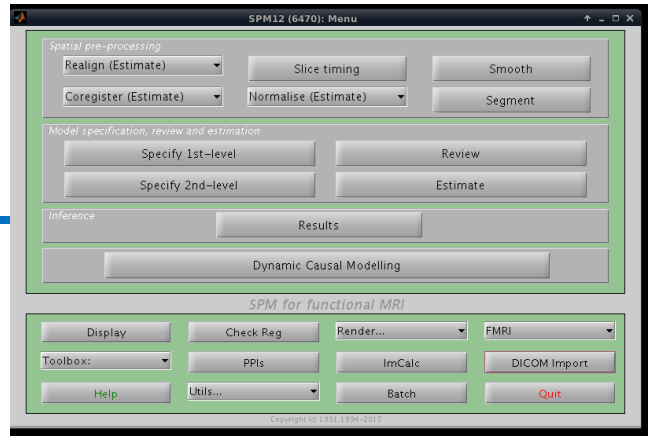
Toolboxes
- ARTrepair: repairs scans with artifacts (e.g., head movements)
- AAL1: automated anatomical parellation of T1 volumes (provided by the MNI)
- AAL2: alternative parcellation of the OFC
- AAL3: alternative parcellation of the anterior cingulate, thalamus and some brain nuclei
- CONN: connectivity toolbox that loads .SPM designs
- MarsBaR: fo regions of interest (ROIs)

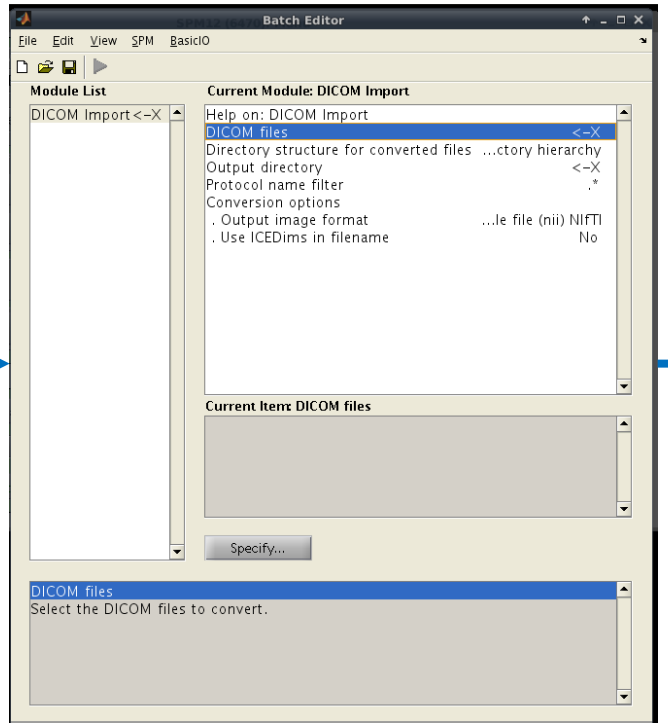
Softwares
- Mango: visualizer
- MRIcrogl: visualizer that supports scripting; better for publications
- BrainNetViewer: visualizer for connectivity; can save movies
- RFXplot: data visualisation for 2nd level analyses
- WFU_PickAtlas: generation of ROI masks based on the Talairach Daemon database (Brodmann area, Lobar, Hemisphere, Anatomic Label and Tissue type)
- Xjview: rendering software; loads .SPM; functions for ROI selection, pValue slider, multiple images display, common area analysis, etc.

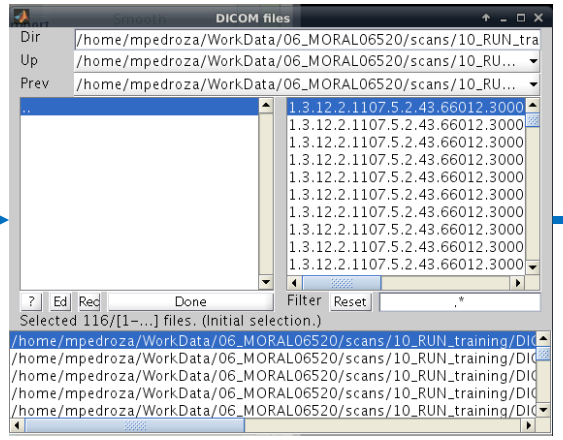
Platforms
- Neurosynth.org: platform for large-scale, automated synthesis of fMRI data
- OpenNeuro.org: platform for open-source validating and sharing BIDS-compliant data
- andysbrainbook.readthedocs.io: comprehensive tutorials for brain data analyses, paired with https://www.andysbrainblog.com/

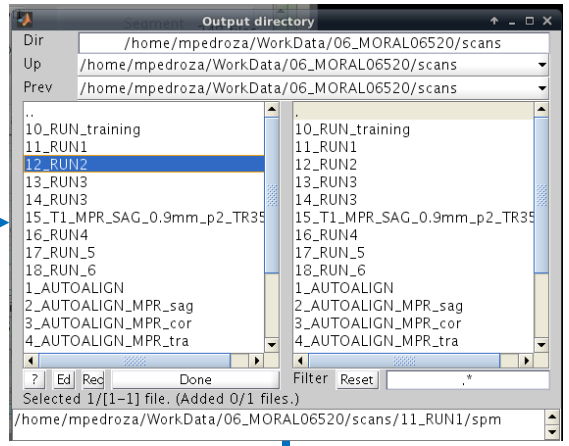
# Preprocessing on SPM – practical work

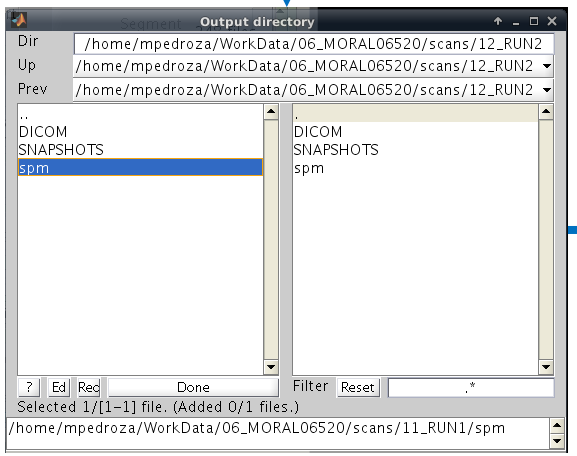
# Pipeline: 1. DICOM to NifTI

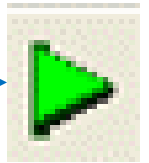


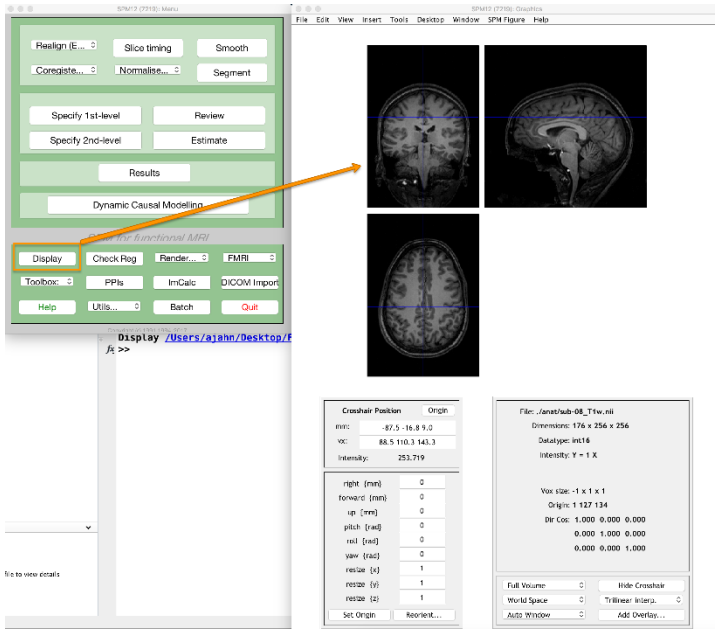



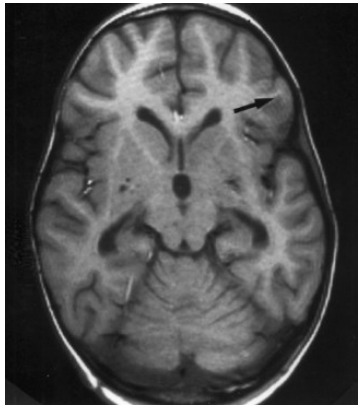



# Pipeline: 2. Visualization

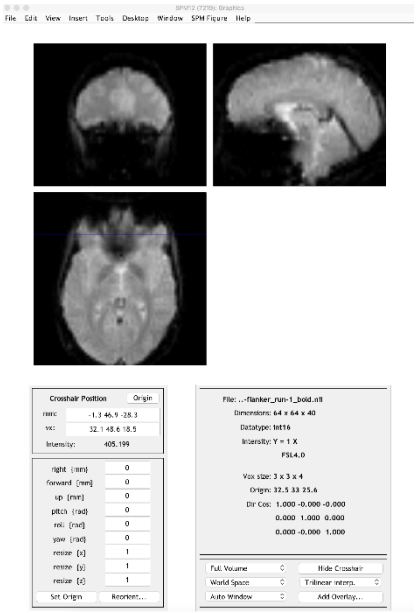
## Inspect anatomical images




Look out for artifacts, such as ripples. They may be caused by subjects moving too much in the scanner

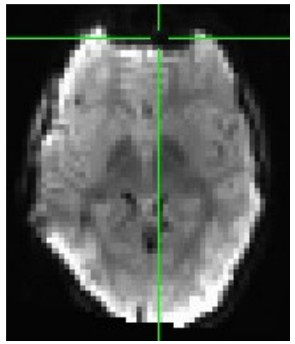


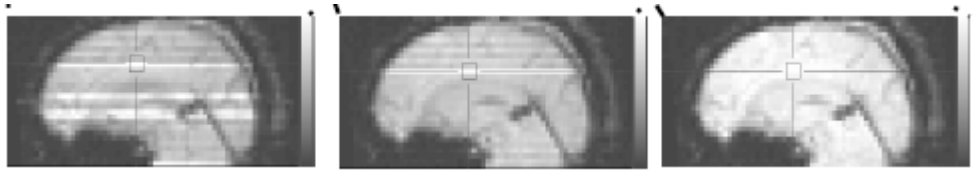
## Inspect functional images






Look out for noise, transient artiacts, ghosting, dropouts, etc.

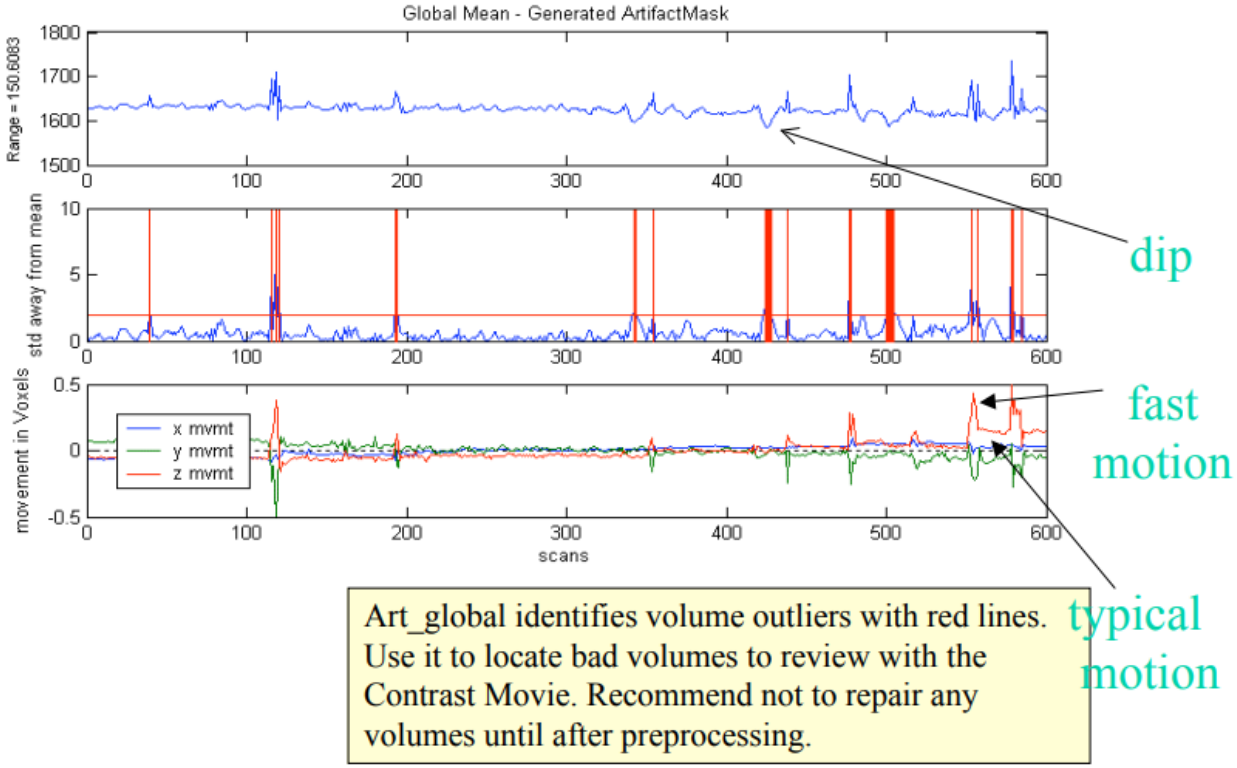




# Pipeline: 3. Artifact removal (optional)

Can also be done at the end of preprocessing

## *Detection of Bad Volumes (art_global)*



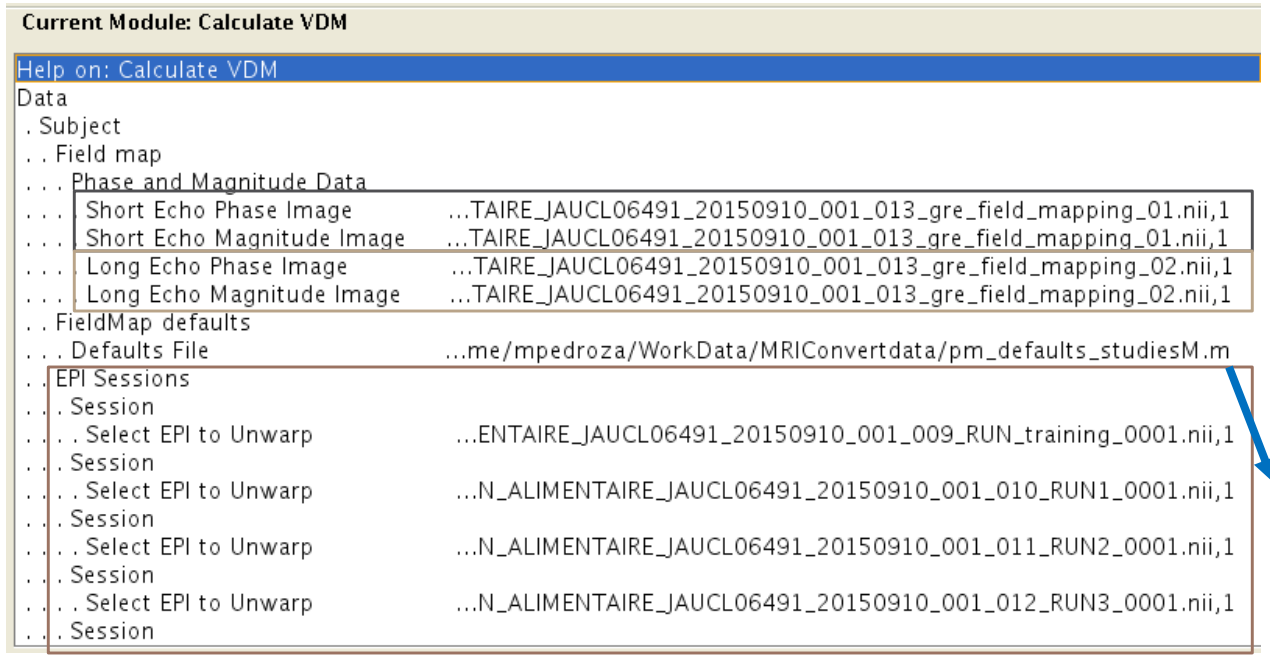

Art_global identifies volume outliers with red lines. Use it to locate bad volumes to review with the Contrast Movie. Recommend not to repair any volumes until after preprocessing.

Beware, previous versions included a script error that needed correction by-hand. Unfortunately, we forgot what was the error specifically

https://cibsr.stanford.edu/content/dam/sm/cibsr/documents/tools/methods/artrepair-software/ArtRepairOverview.pdf

# Pipeline: 4. Field Map

(Calculate Voxel Displacement Maps VDM), 7 steps

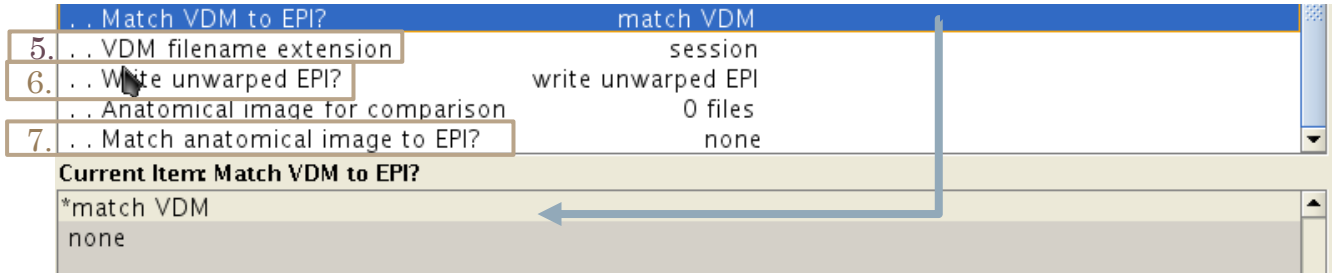



1. Same fieldmap file with the “01” suffix; located at the first fieldmap folder of each participant (gre_fieldmap_mapping…..)

2. Same fieldmap file with the “02” suffix; located at the first fieldmap folder of each participant (gre_fieldmap_mapping…..)

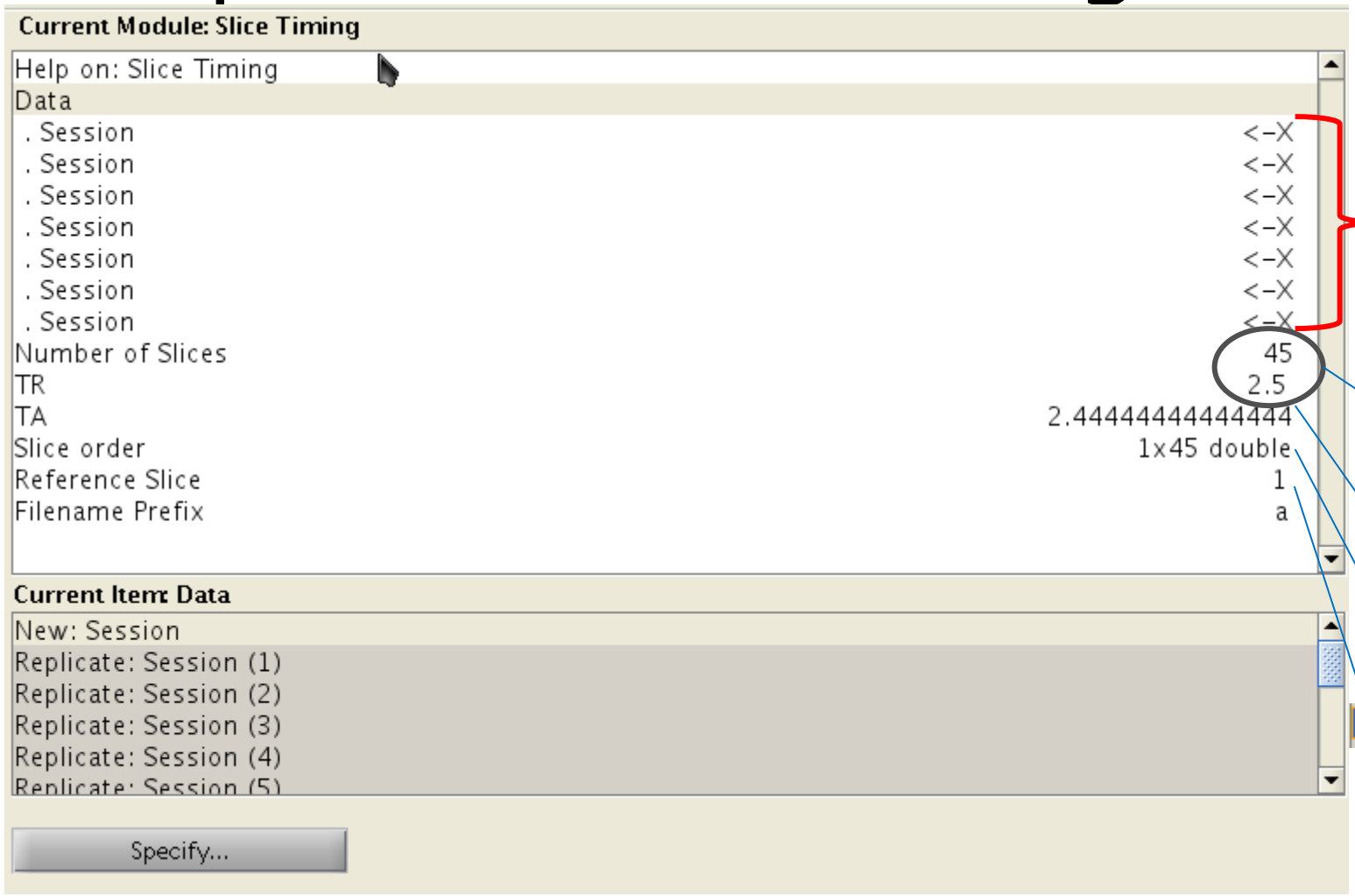
3. File pm_defaults_studiesM.m

4. Choose the **first image** from **each session** of the participant




Keep in mind the order of sessions and use them consistently throughout the rest of the preprocessing steps.

# Pipeline: 5. Slice timing




Keep in mind the order of sessions and use them consistently throughout the rest of the preprocessing steps.

For each participant and each functional session (run 1-6), select the corresponding .nii files

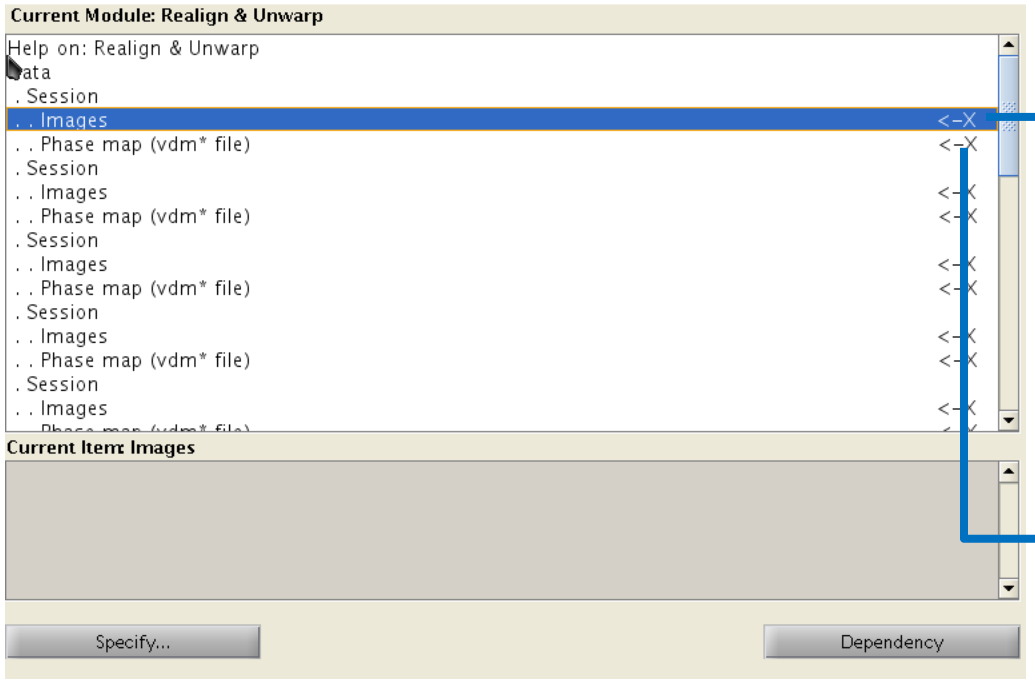
These parameters were established in collaboration with Primage tech team.

TA=TR-(TR/nslices)


Type in the dialog box:
[1:2:45 2:2:45]

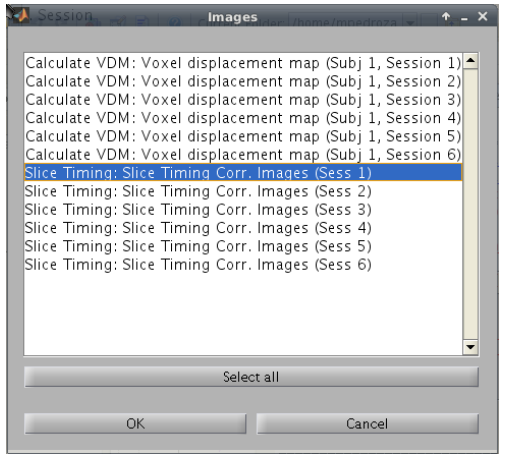
Specify : 1

# Pipeline: 6. Registration (Realign & unwarp)



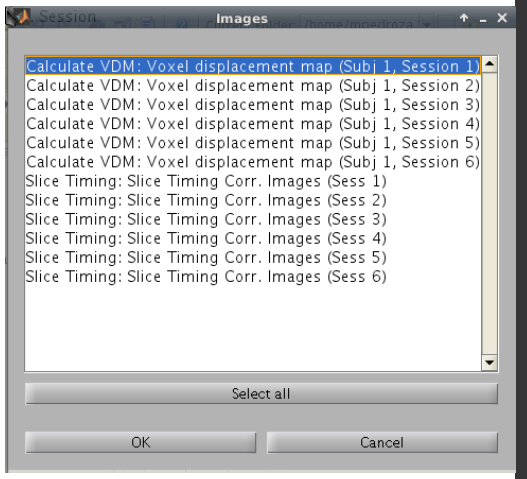


1. Use the dependency button to specify the file corresponding to each sessions (“a” suffix images ).




2. Use the dependency button to specify the file corresponding to each session

Phase map

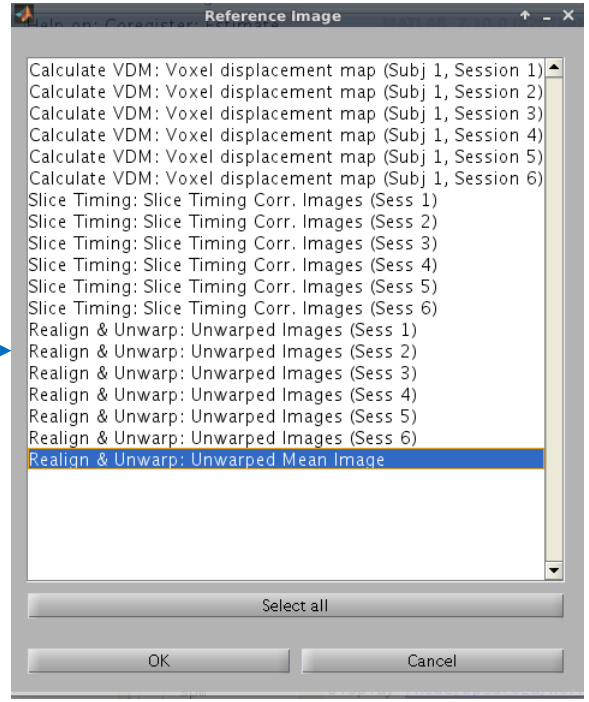


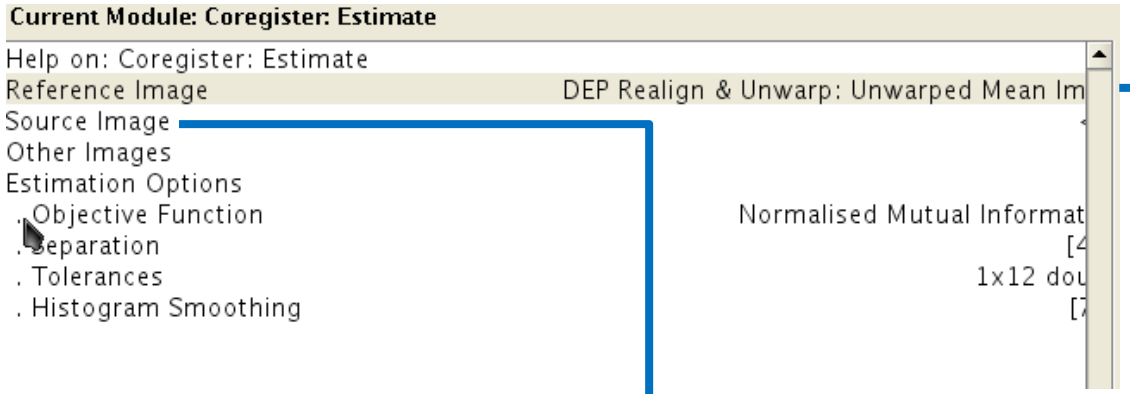

3. Do not modify the rest of parameters
Verify that file prefix is “u”

Mind the numbering of sessions: they are serial according to spm and not the original numbers

# Pipeline: 7. Coregistration

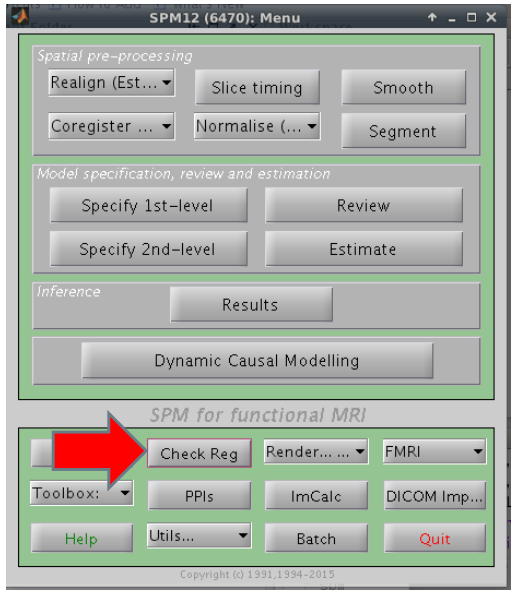

1. Reference image: click on dependency button and select : Unwraped Mean Image

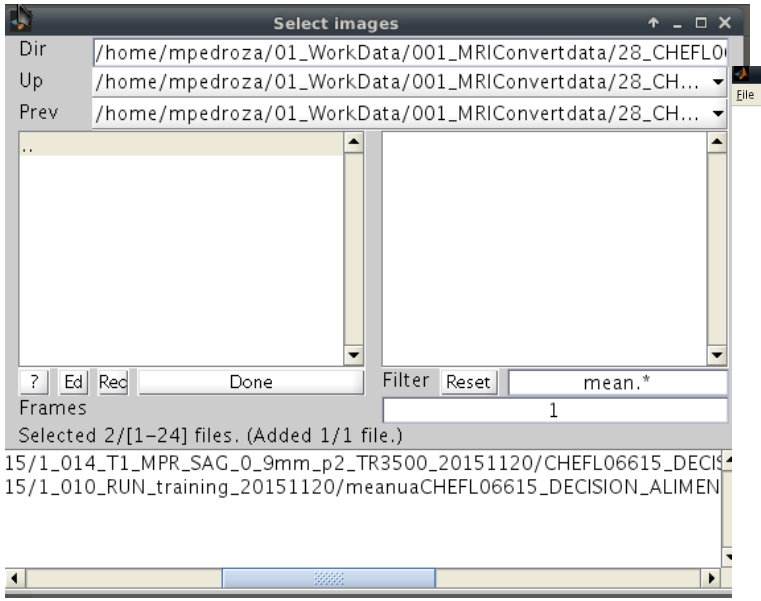


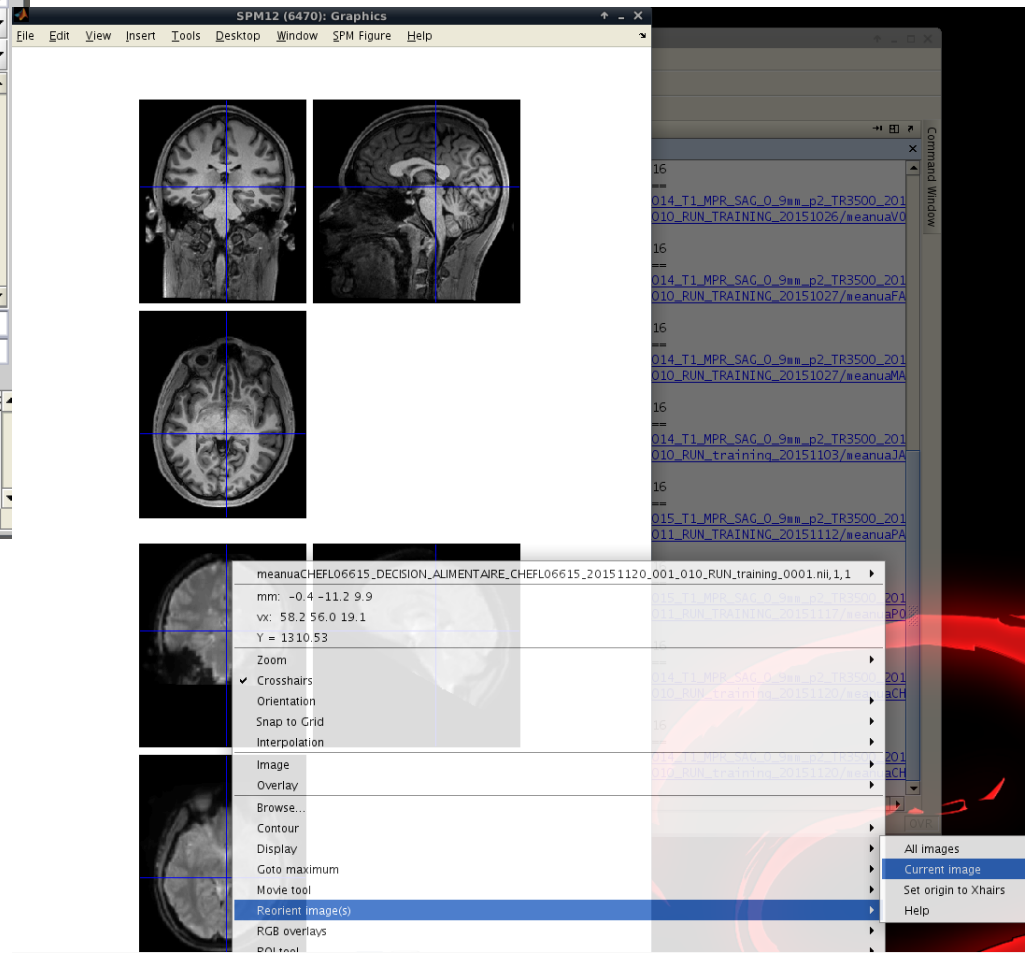




2. Specify the T1 anatomical scan (T1_MPR_SAG….Folder)

# Pipeline: 8. Check registration and movement corrections



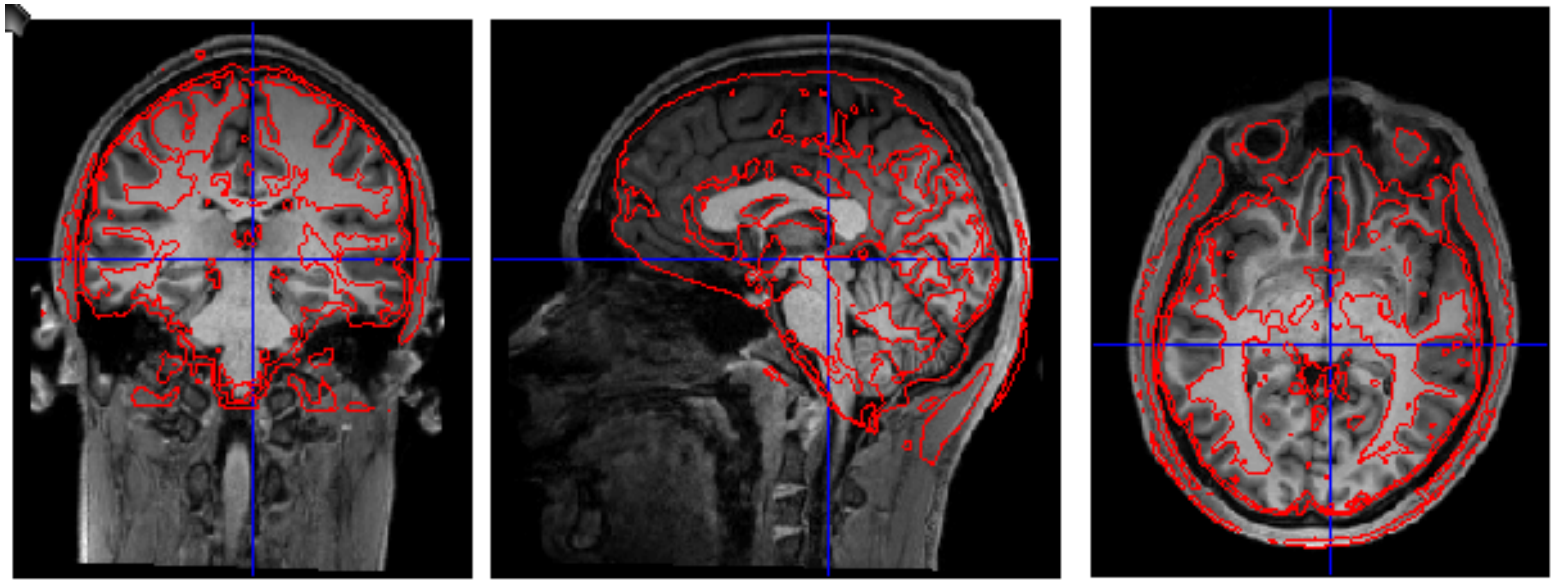




1. Select T1 anatomical image
2. Type: mean at the filter (right box) and select the mean image located at the folder containing the first run from the experiment.
3. Click Done

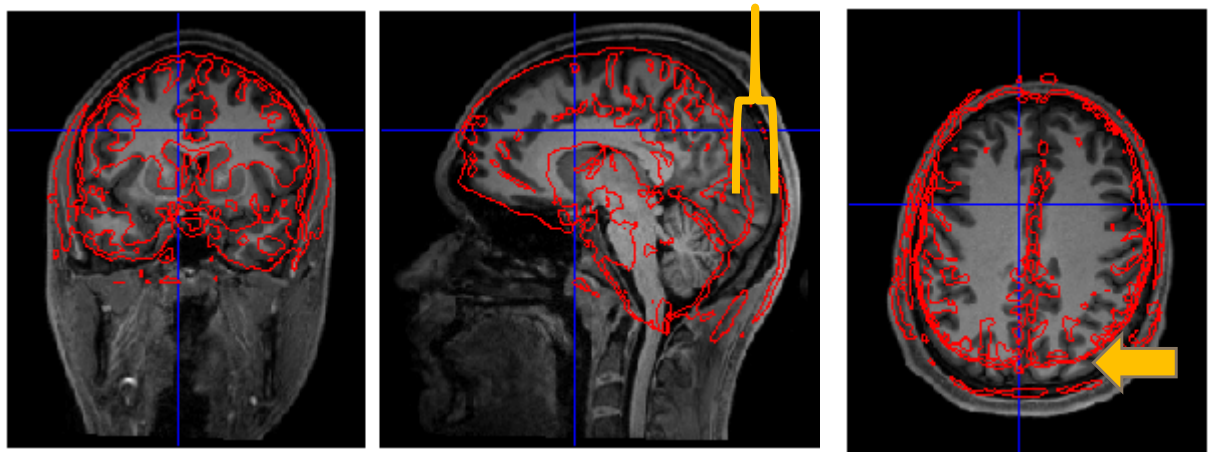
Using the mouse to navigate, move around the brain volume and:

1. Verify that red lines (corresponding to the functional images) follow closely the brain perimeter.

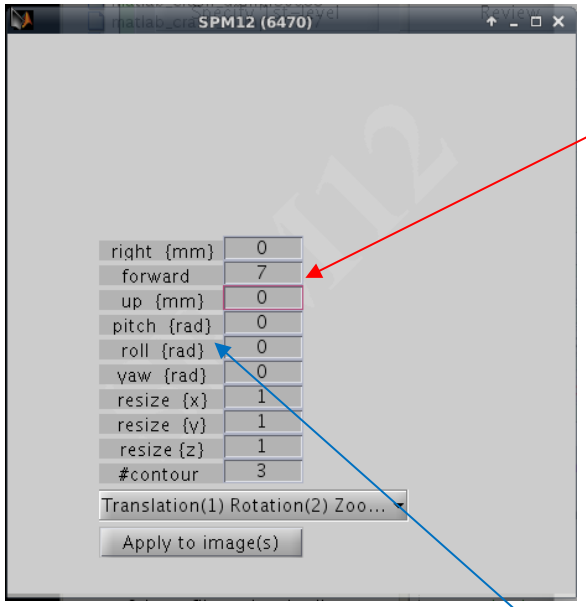
2. Verify anatomical features: i.e. ventricules, white and grey matter, cerebellum, etc.



Check for mismatchs as shown below (http://imaging.mrc-cbu.cam.ac.uk/meg/RepositioningMRIs)



Mismatches may need to correct the alignment **of the functional (EPI) image** run by run.



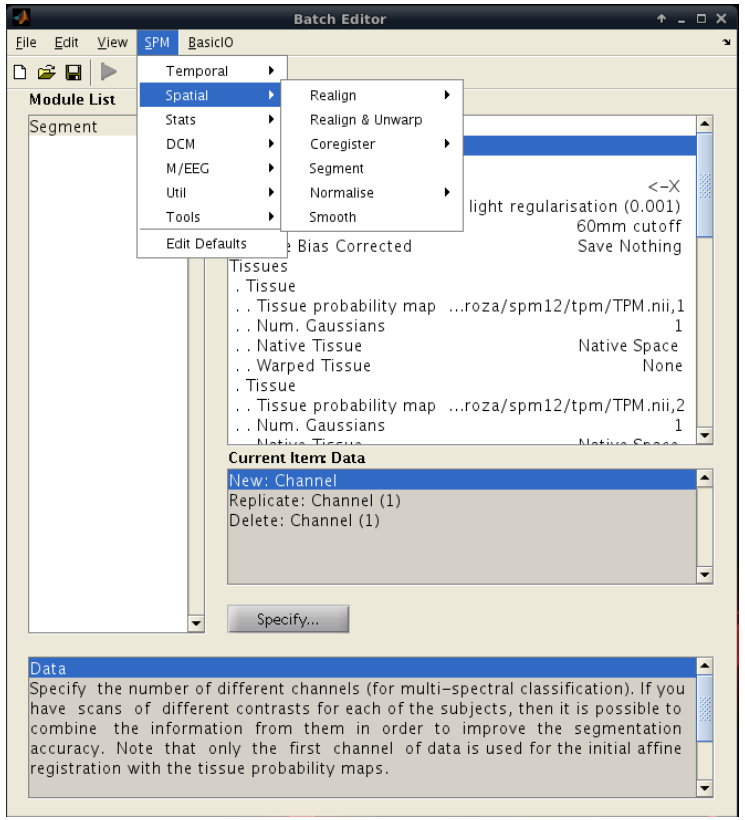

Using the manual alignment toolbox, adjust the images trying with different distances along the 3 axis.
Check the corrections at the Graphics window and once image is correctly fitted, click on the button Apply to image(s)

In the file selection box,
Select all (^) "ua" prefix images
And click DONE

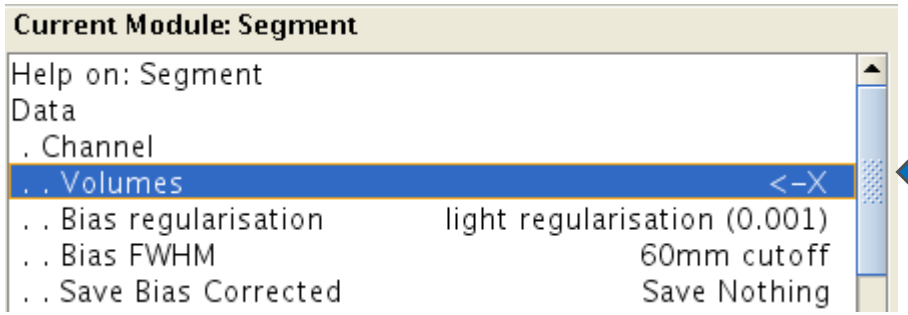
Watch out radian units: use values < 0; i.e., 0.01

Launch again the check reg from the SPM menu and check that corrections were correctly applied to **all runs**. Use one functional image with "ua" prefix from one run and overlay on top of T1

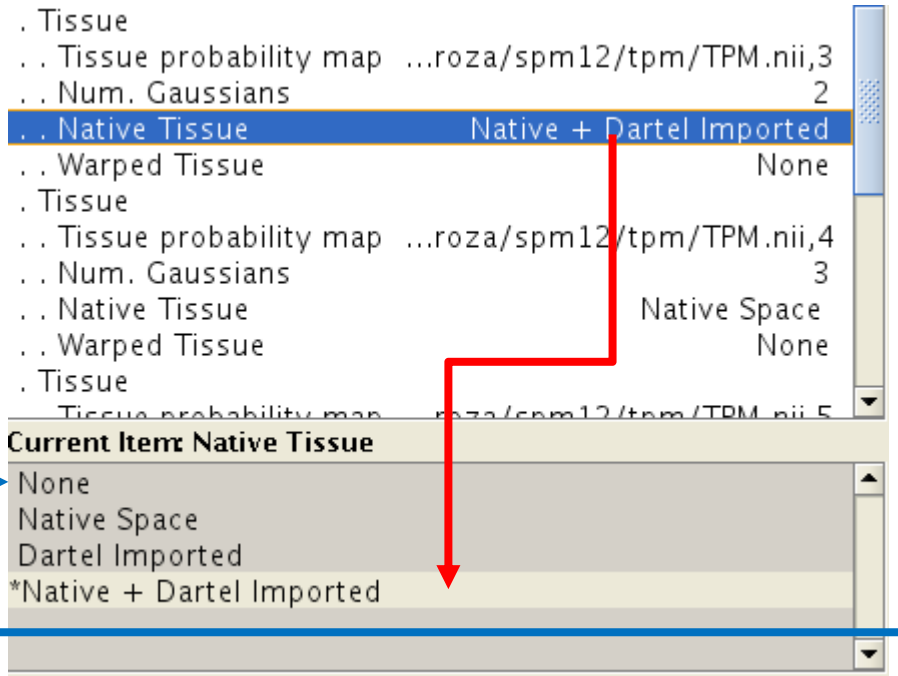
# Pipeline: 9. Segmentation




Use a batch with all participants so that all segmentation is done before doing DARTEL

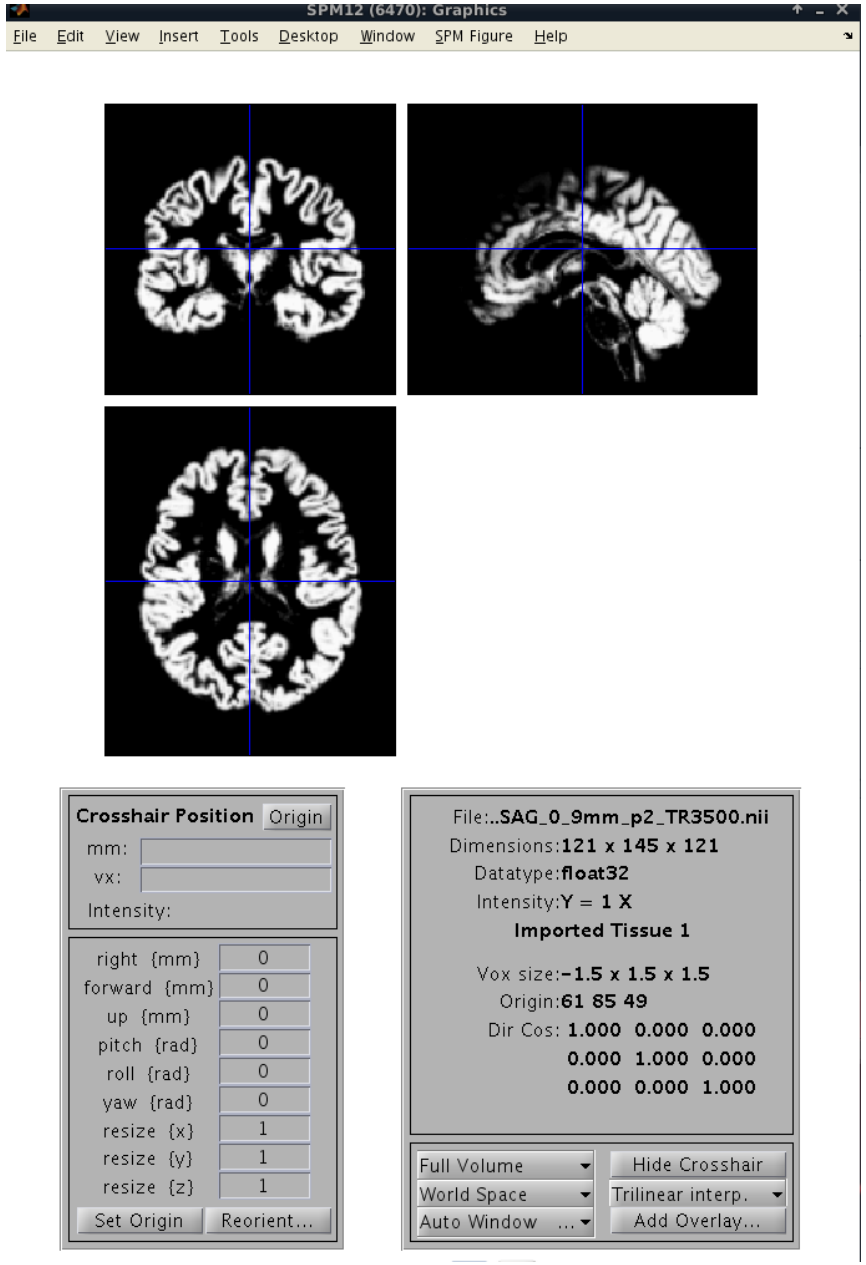



T1 image




For tissue 1 to 3: Click on Native tissue and select Native+ Dartel imported from the current box items below.

For the rest of tissues (4 to 6): Select None




Segmentation output are 3 images with the "RC" prefix which will be saved at the T1 folder.

rc1*.nii files = grey matter
rc2*.nii files = white matter
rc3*.nii files = CSF

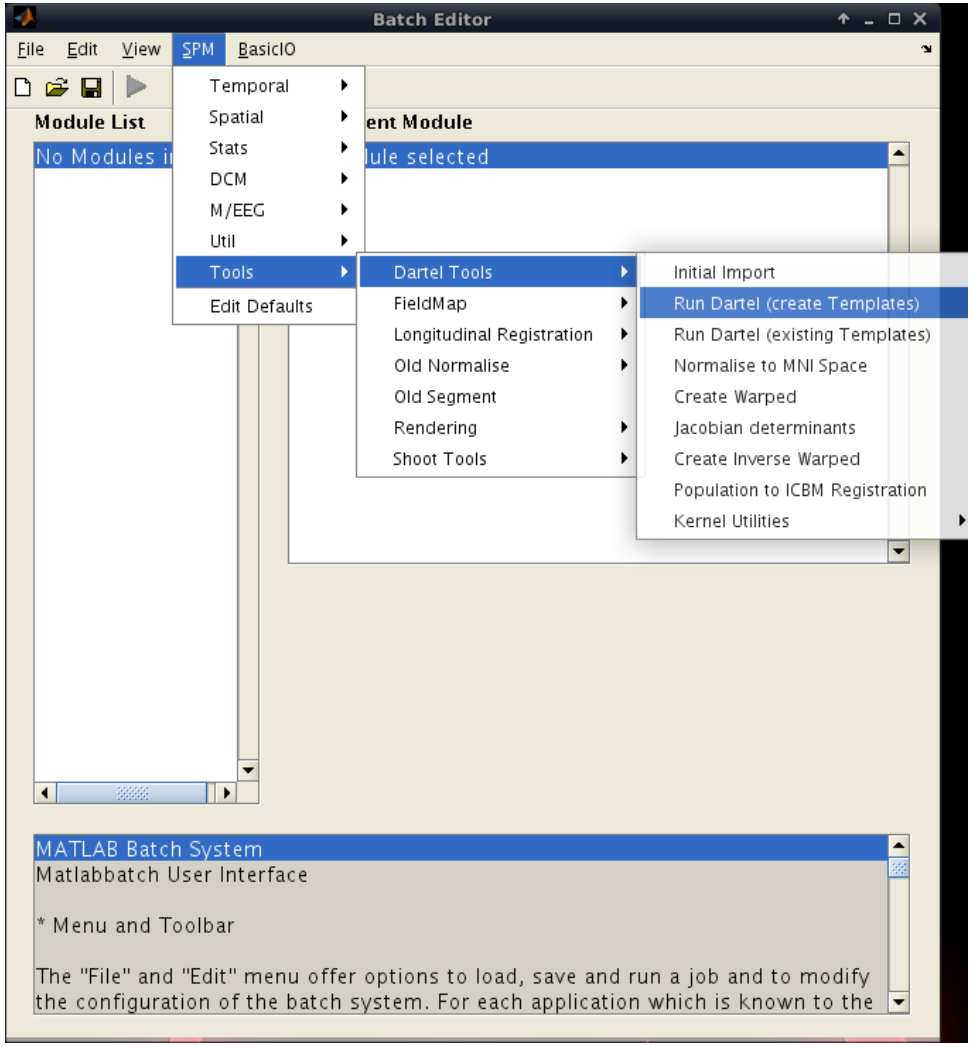
Images will be saved at the T1 folder

**Output:**

**rc1*.nii file**
**rc2*.nii file**
**rc3*.nii file**

**For each participant**

# Pipeline: 10 & 11. Normalization (DARTEL + MNI Space normalization + Smoothing)

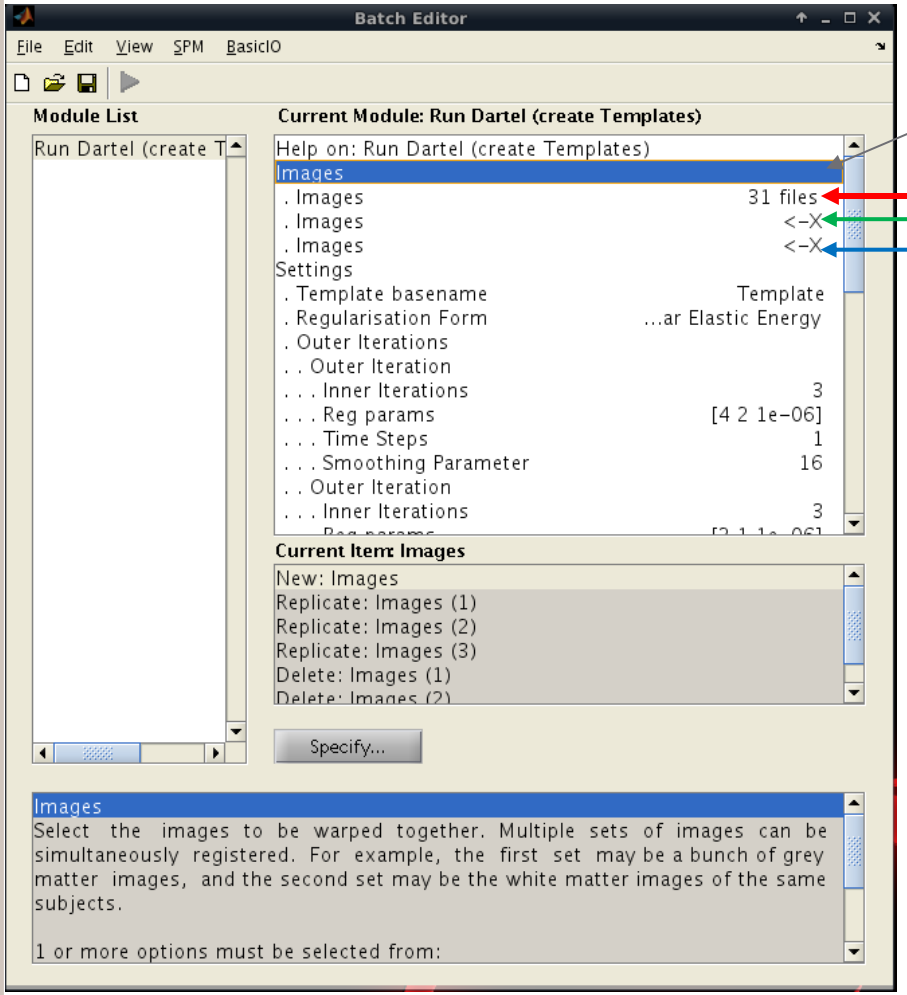



The Diffeomorphic Anatomical Registration Through Exponentiated Lie Algebra (DARTEL, Ashburner 2007) Toolbox is a high dimensional warping process that increases the registration between individuals, which results in improved localization and increased sensitivity in analyses.

Run DARTEL (create a template)

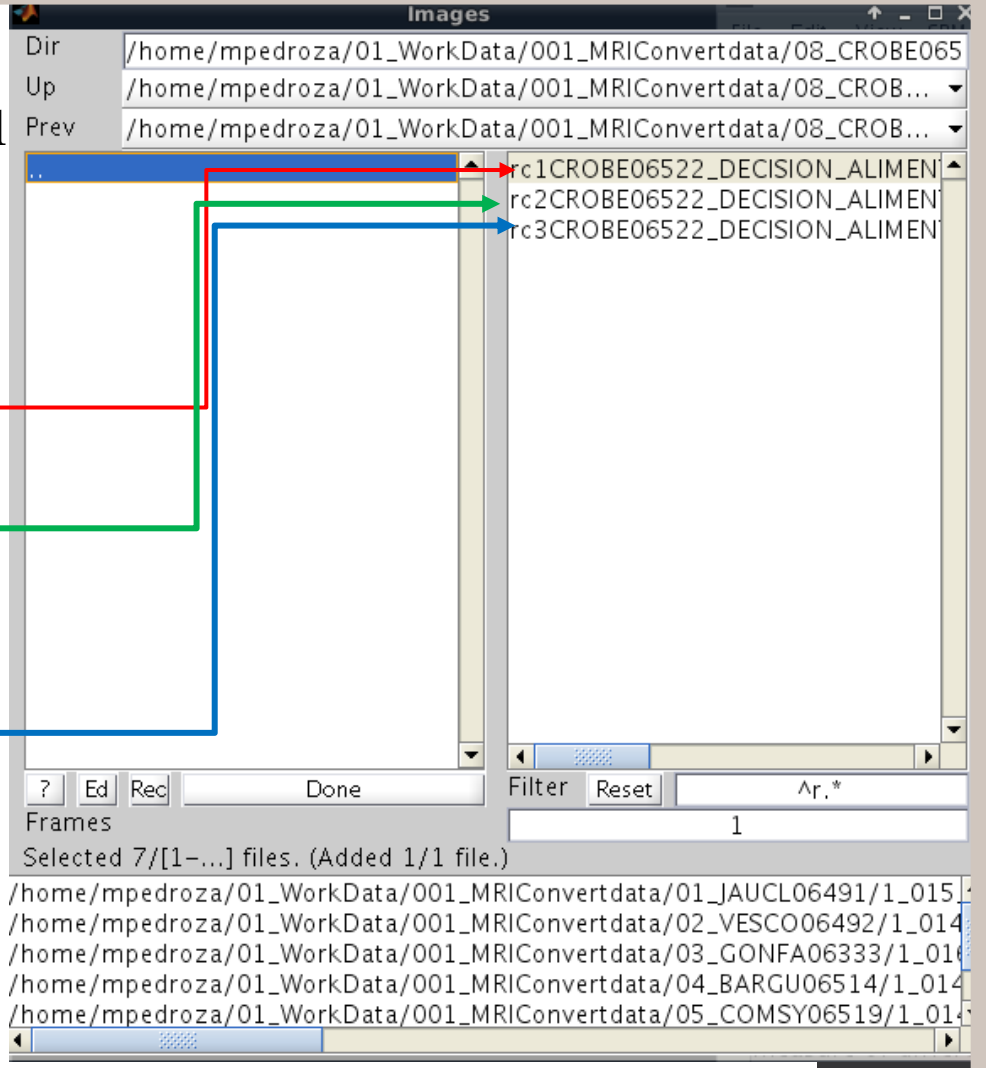
Needs all segmentation rc files and batch 1 processes to be ready before launching!

**The whole procedure takes (in the order of) about a week of processing time for 400 subjects**



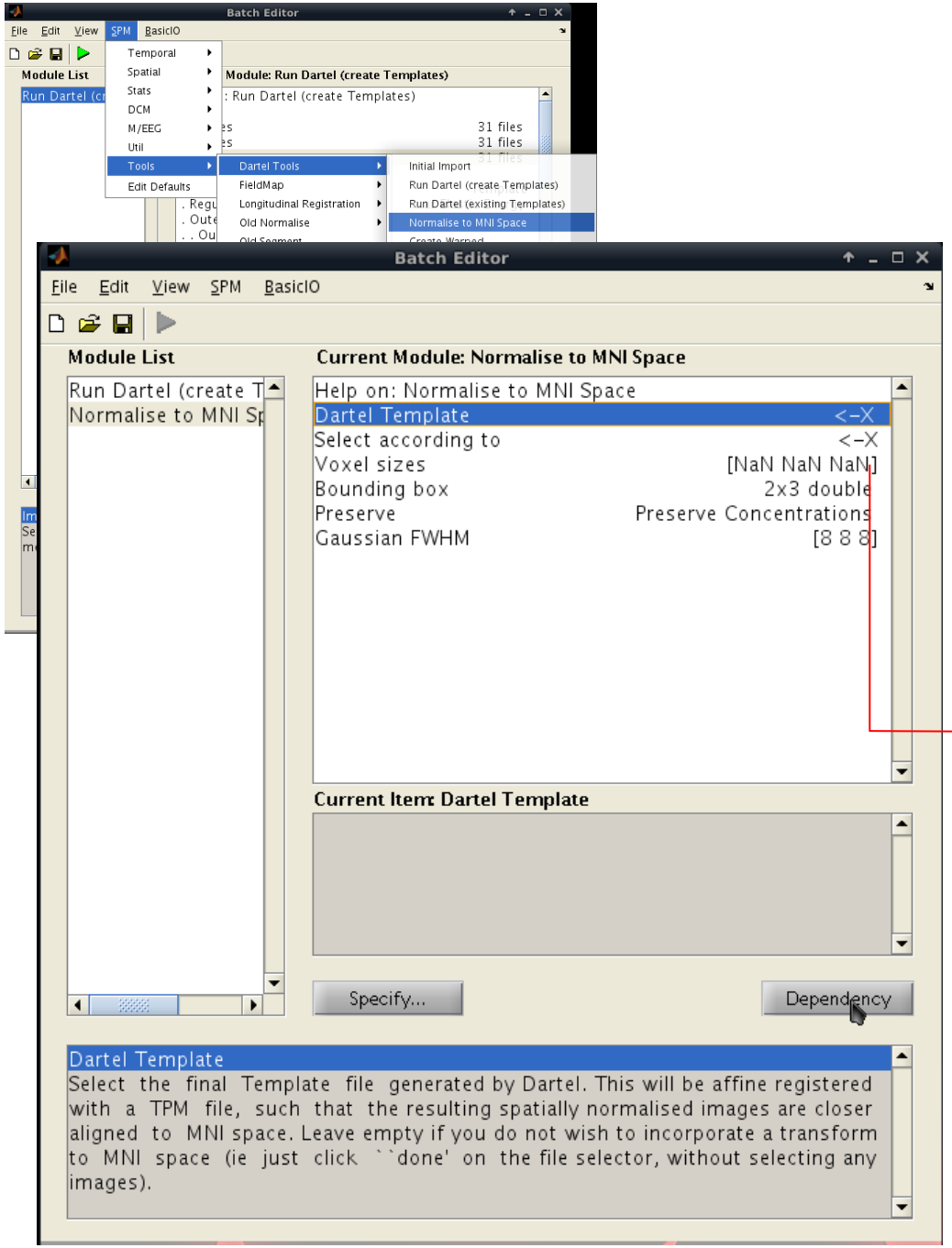

Click at the images field and create 3 fields for each image

1. First field will correspond to rc1 images from all subjects
2. Second field will correspond to rc2 images from all subjects
3. Third field will correspond to rc3 images from all subjects

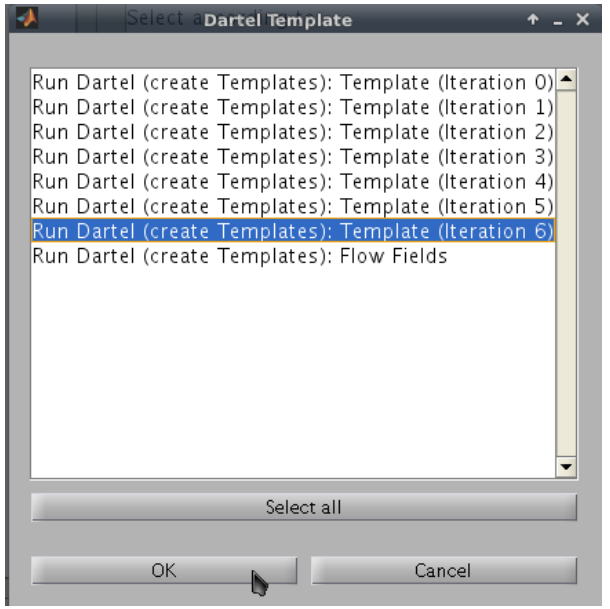



KEEP THE SAME ORDER WHILE ADDING FILES!
The first rc1*.nii is assumed to correspond with the first rc2*.nii **from the same subject**, the second with the second, and so on..

The template for all-participants will be saved at the T1 folder of the first participant: **Output = u_rc1*.nii file aka "flow fields"**





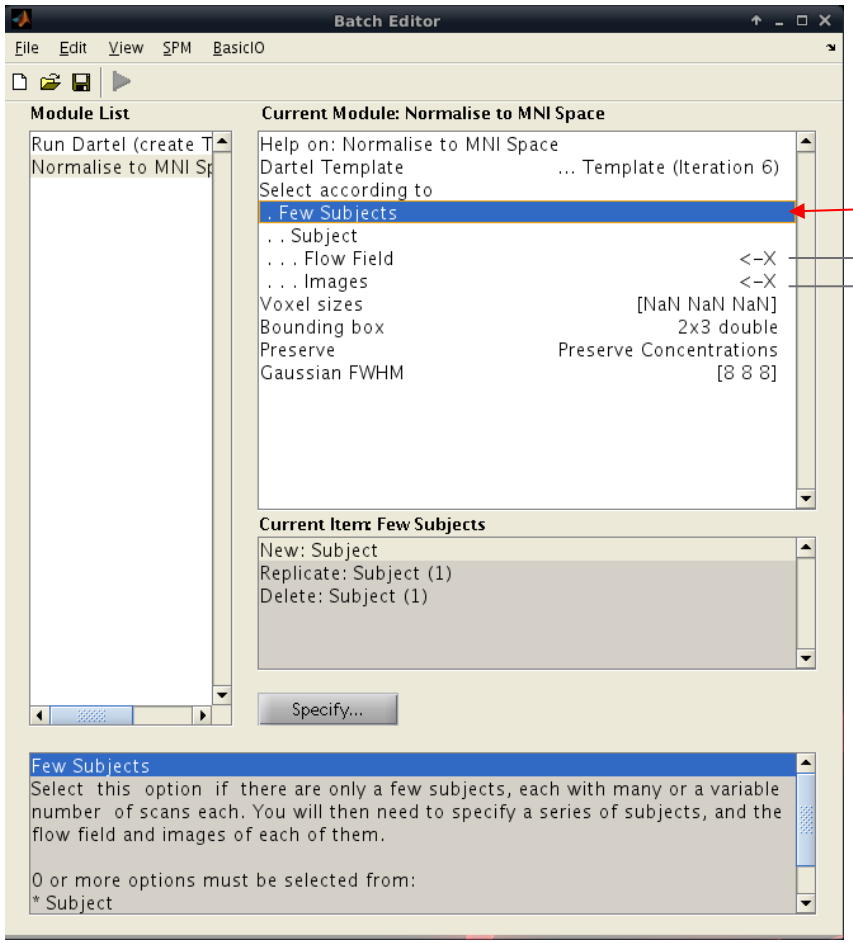




Using dependency button, specify the last of the series of templates that was created by RunDartel (create Template). This is usually called **Template_6.nii**
**The file is usually located at the T1 folder from first participant from the DARTEL template batch.**

For fMRI analyses, Select according to : **Few Subjects**

This will display new fields for adding files (see next slide)



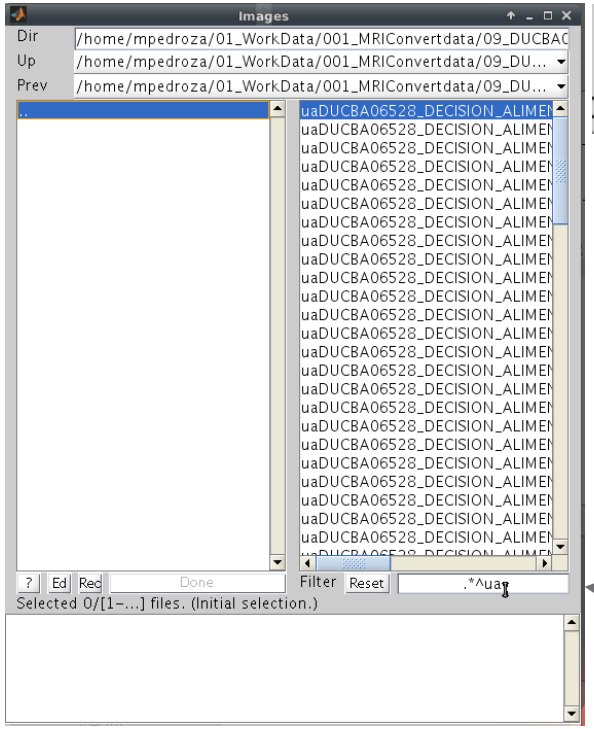

Add as many subjects as needed and then :

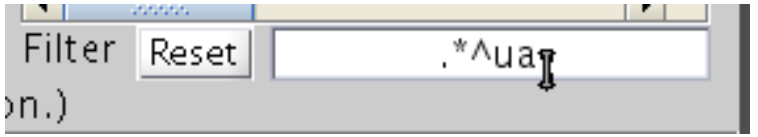
Dependency

**Flow Field**: specify the u_rc1* image of the subject (T1 folder)

**Images**: add all the ua functional images (type in the filter .*^ua) from all runs (*training* to 6)

There is no need to separate by run



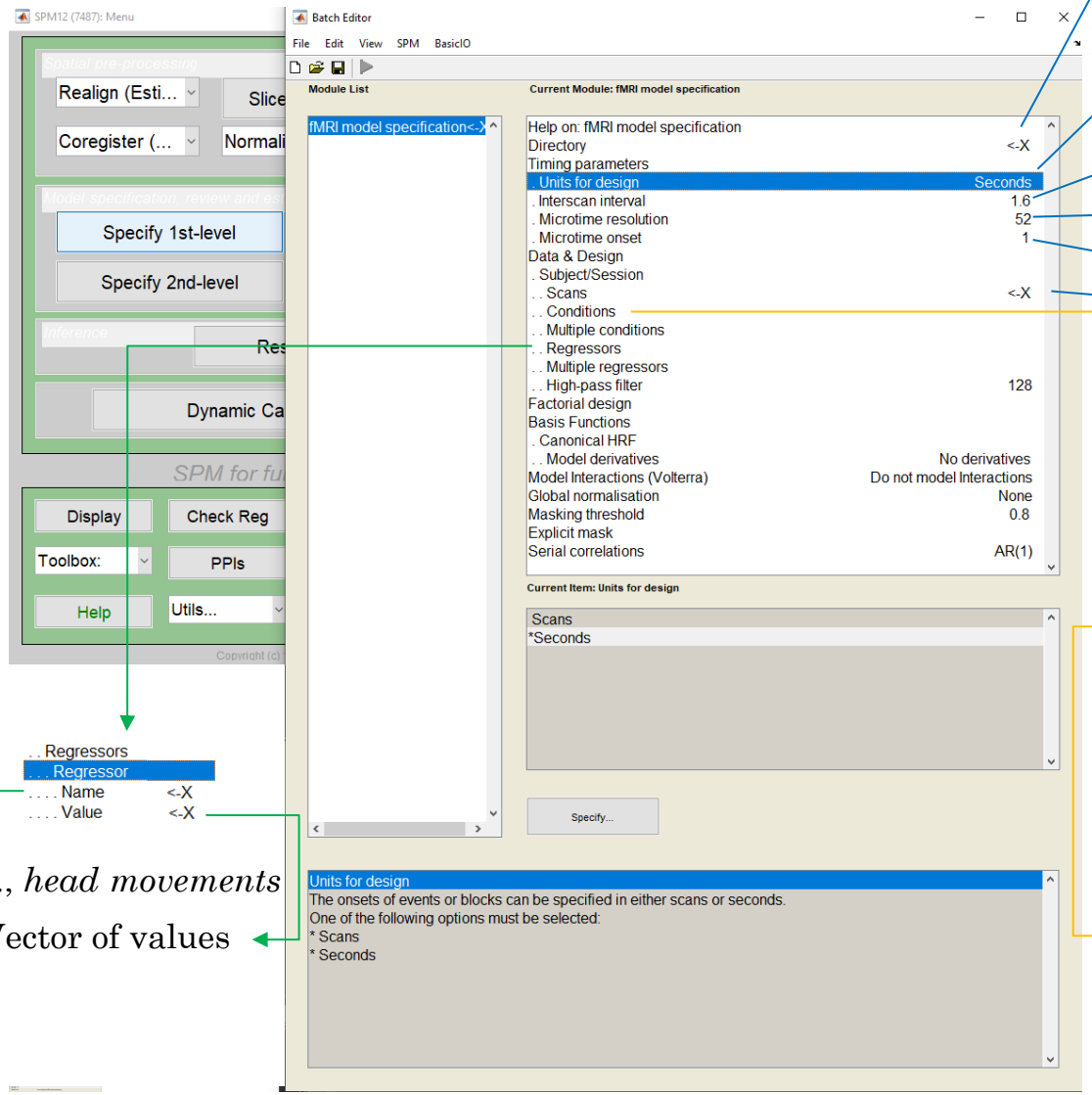




Hit  to run

**Output = smwc1*.nii files Stored folderwise for each participant**

# Contrasts on SPM - practical work

# Design specification: single-subject




Output directory

Following the fMRI machine settings chosen for the experiment

TR (repetition time)

t: number of time-bins per scan

t0: reference time-bin

Select the subject's preprocessed scans (affix: vswuaf)

e.g., *control*

Vector of onset **times**

Vector of duration for each onset:
stick function: duration=0
boxcar=real number

e.g., *head movements*

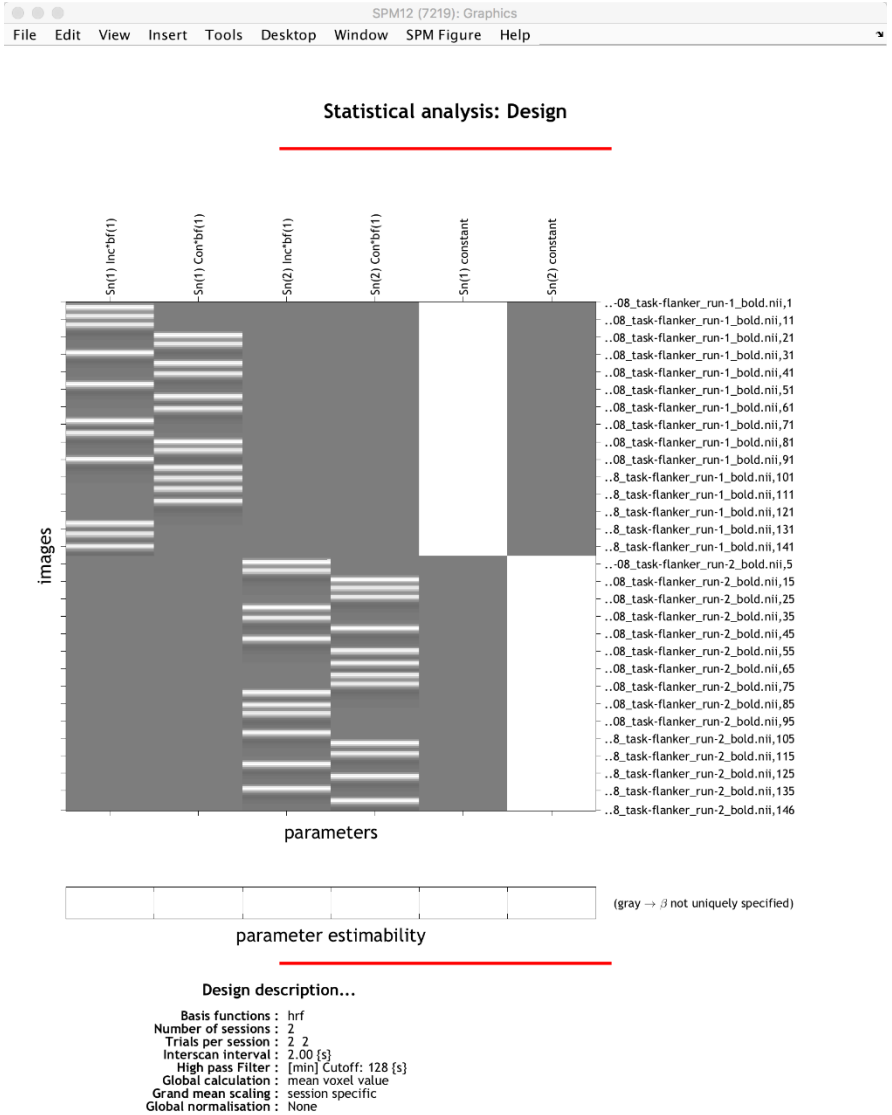
Vector of values

# Design output: single-subject

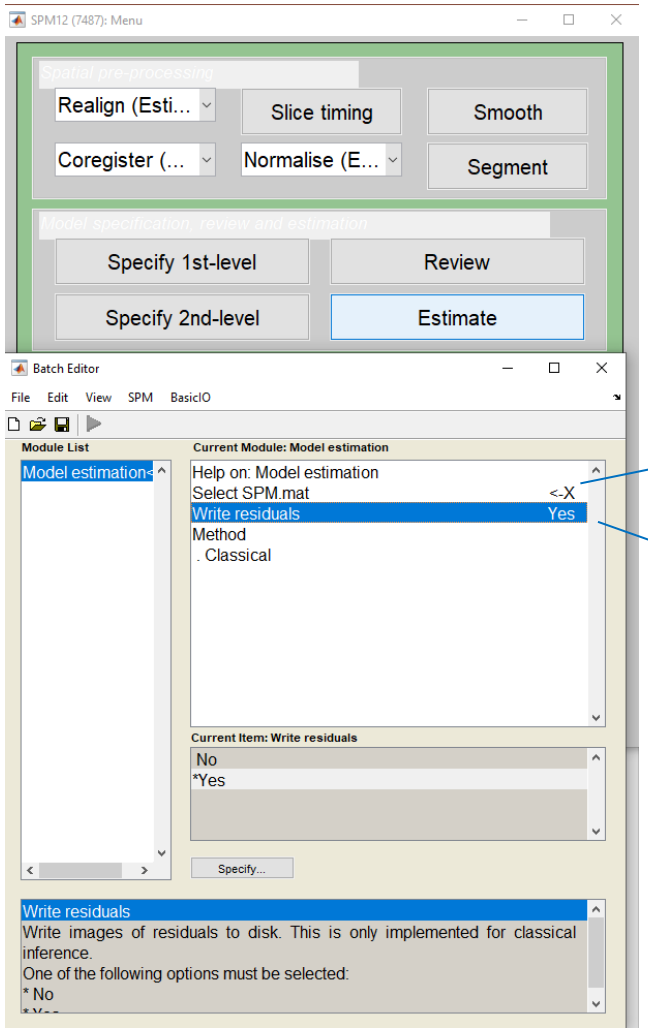
- Sn(1): time series for session 1
- Sn(2): time series for session 2

- Inc: time series for condition with incongruent stimuli
- Con: time series for condition congruent stimuli

- Constant: baseline regressors that capture the mean signal for each session



# Estimating the model: single-subject

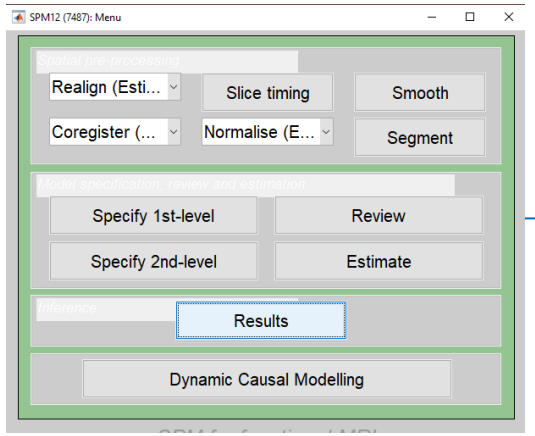


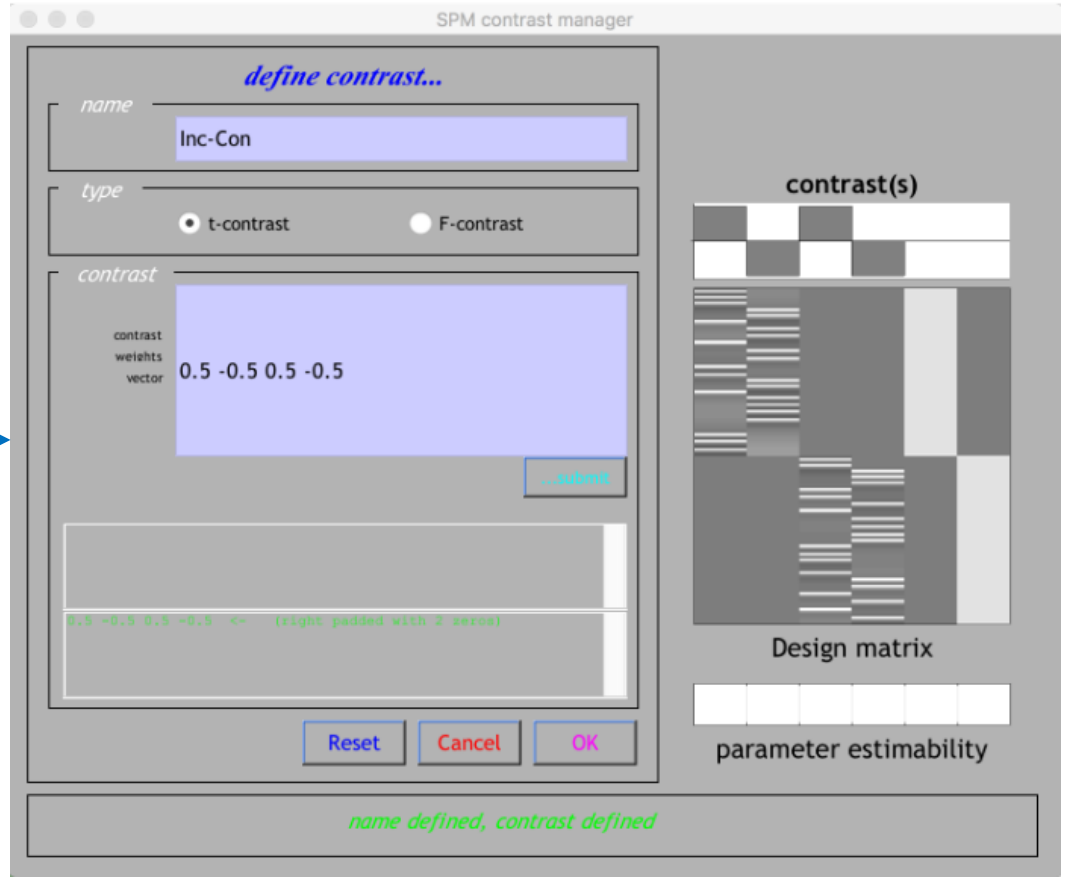

Select the SPM.mat for our specified design

Select Yes

# Contrasts specification: single-subject

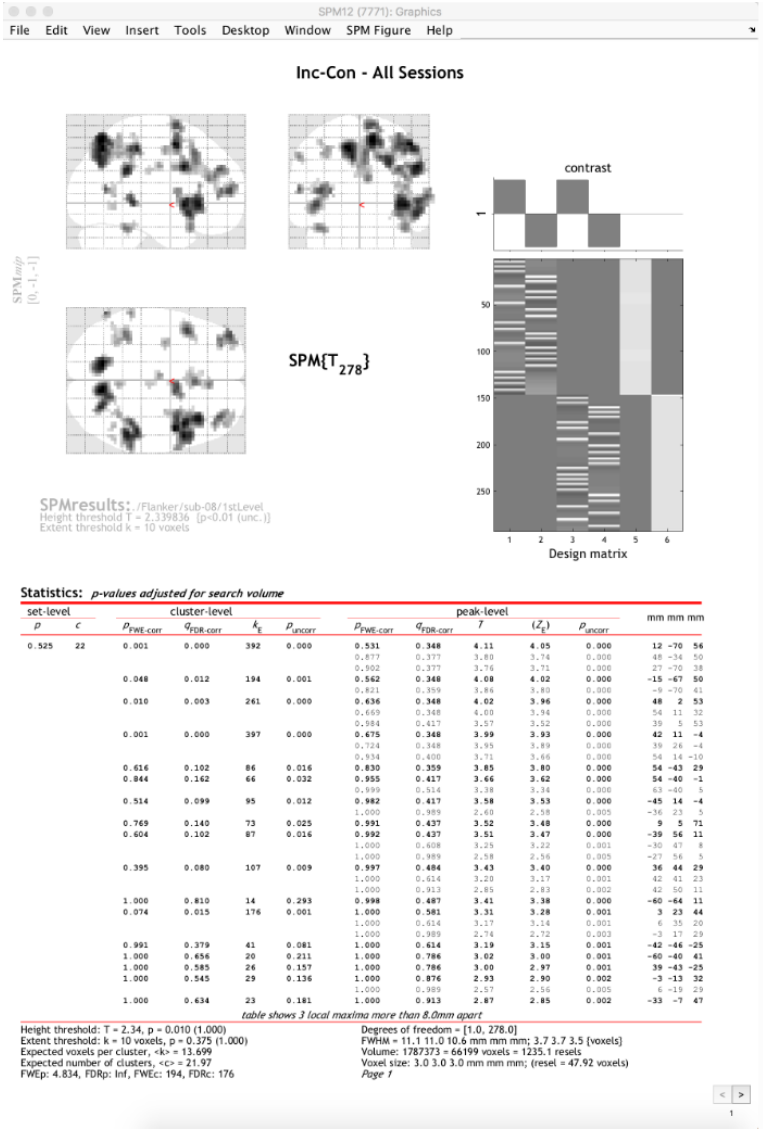
t-test
incongruent (Session1&Session2) > congruent(Session1&Session2)

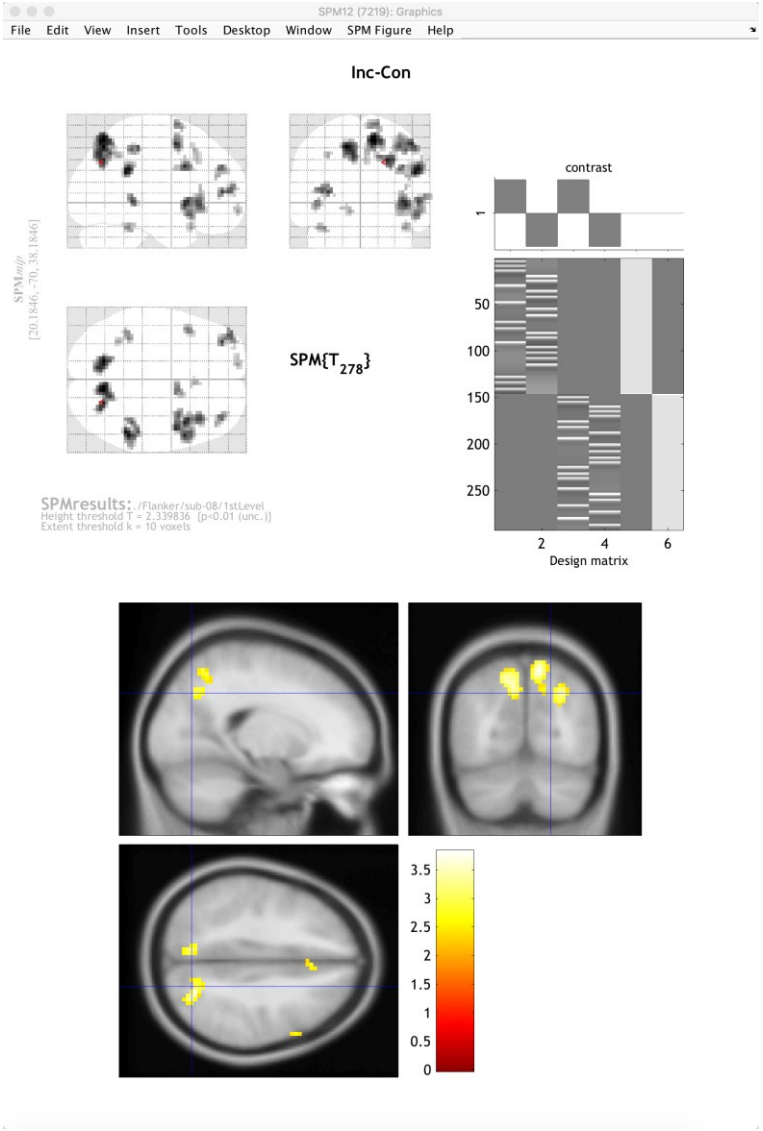


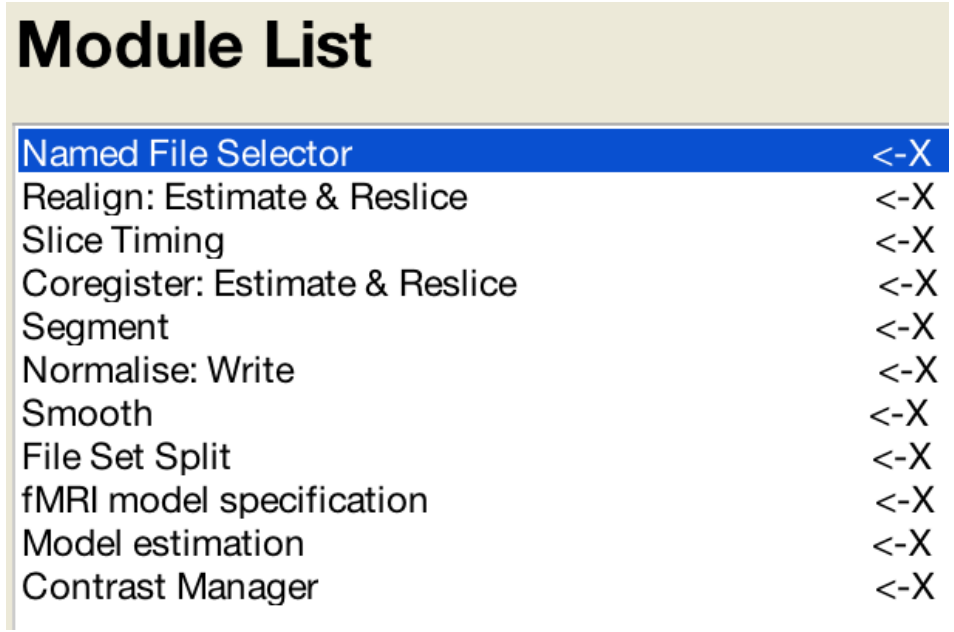
# Output: single-subject

results -> overlays -> sections
-> spm12/canonical -> avg152



# Scripting: single-subject



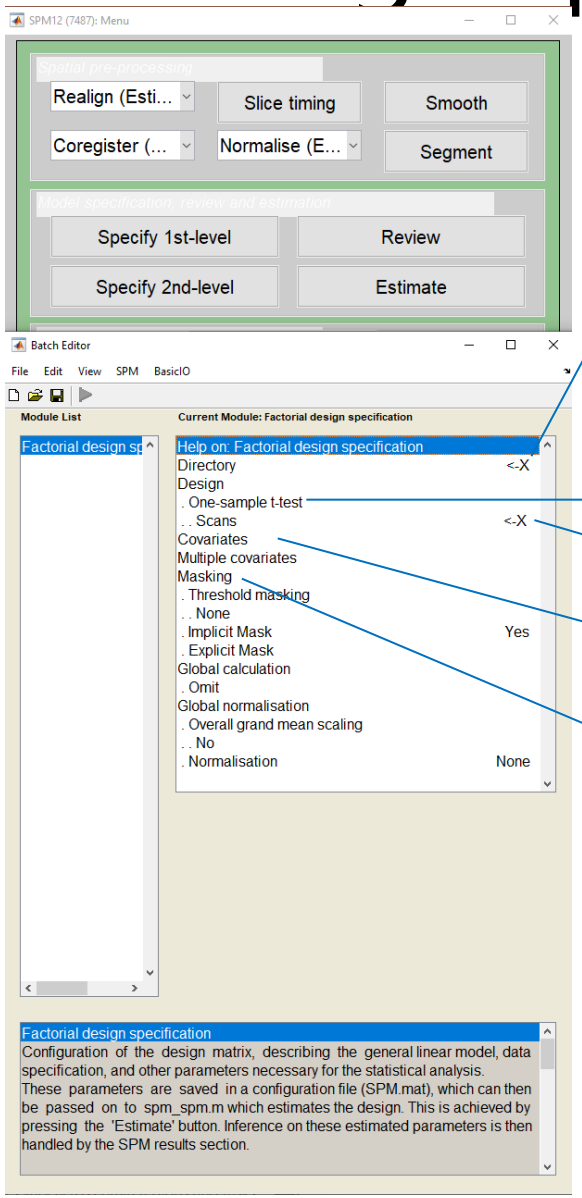

The Batch module we have just created is specific to 1 subject. If you clicked on the green Go button, it would run all of the preprocessing and model estimation steps in one go. With a few adjustments, however, we can adapt this module to all of the other subjects in our study.

First, we need to save the modules into a Matlab script. Click on File -> Save Batch and Script, and label the file RunPreproc_1stLevel. Save it to the directory that contains all of your subjects. This will create a Matlab script file that you can open in the Matlab window.

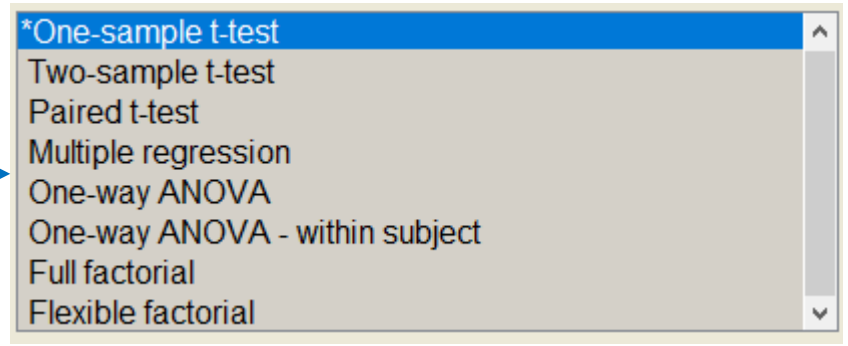
From the Matlab terminal, navigate to the directory which contains the RunPreproc_1stLevel.m script, and type

open RunPreproc_1stLevel_job.m
To adapt this file so that it can analyze any subject, we will need to store in a variable the different subject numbers and place the existing code in a for-loop which will run over a set of numbers indicating each subject in the study.

# Design specification: group-level




Output directory



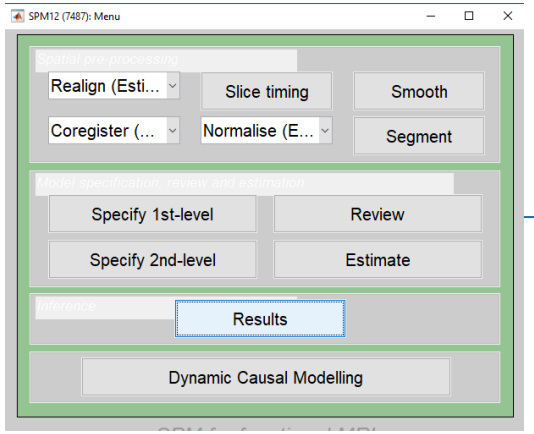

Contrasts con_*.nii for all subjects

e.g., *age*

According to a voxel value:
Explicit mask = exclusively includes voxels with that value;
Implicit mask = excludes voxel with that value

# Contrasts specification: group-level

Group-level t-test
incongruent (Session1&Session2) > congruent(Session1&Session2)





apply masking -> none
p value adjustment to control -> none
threshold {T or p value} -> 0.001
& extent threshold {voxels} -> 20

This will threshold the image to only show clusters that are composed of individual voxels each passing a threshold of 0.001.