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# SPM

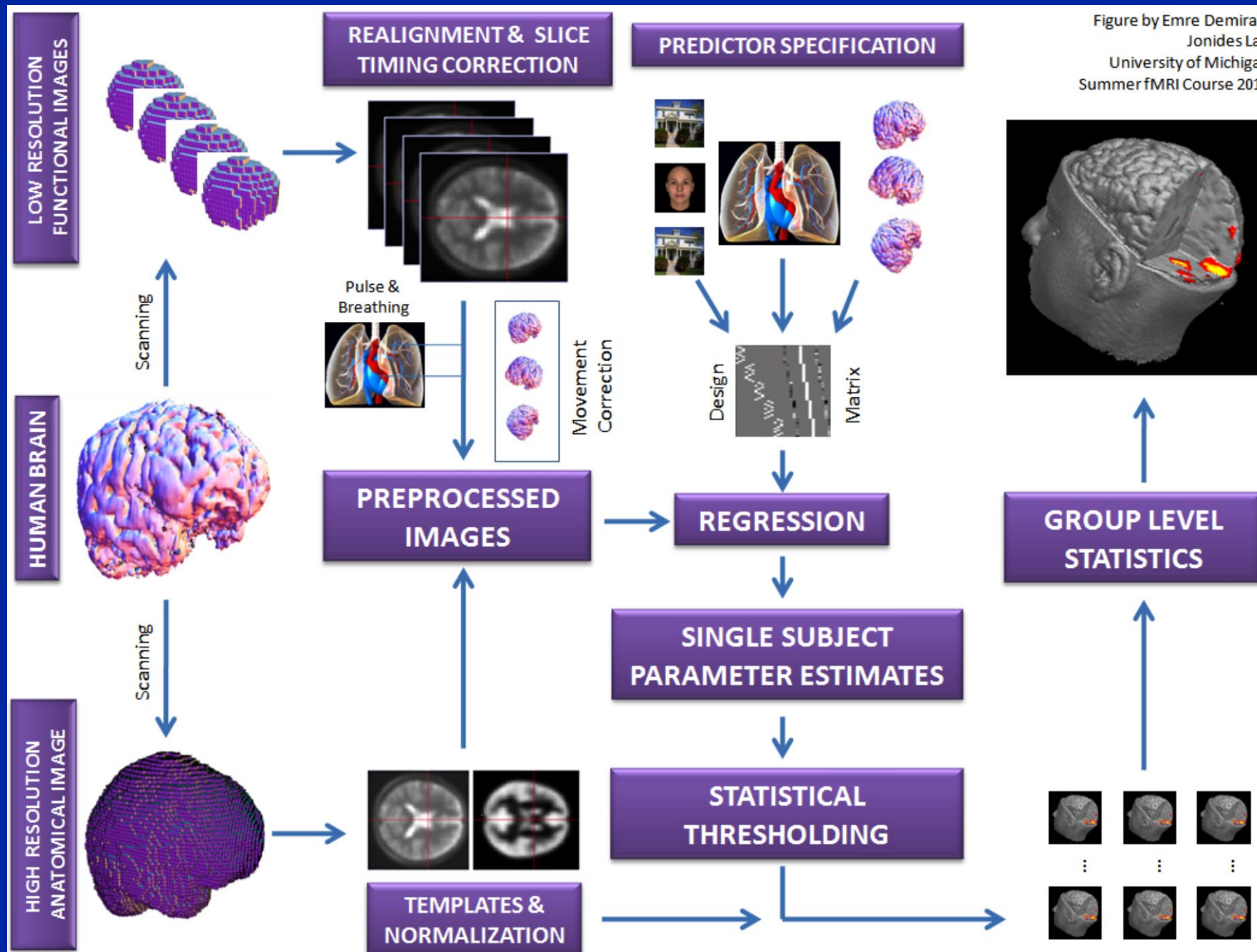
## Introduction

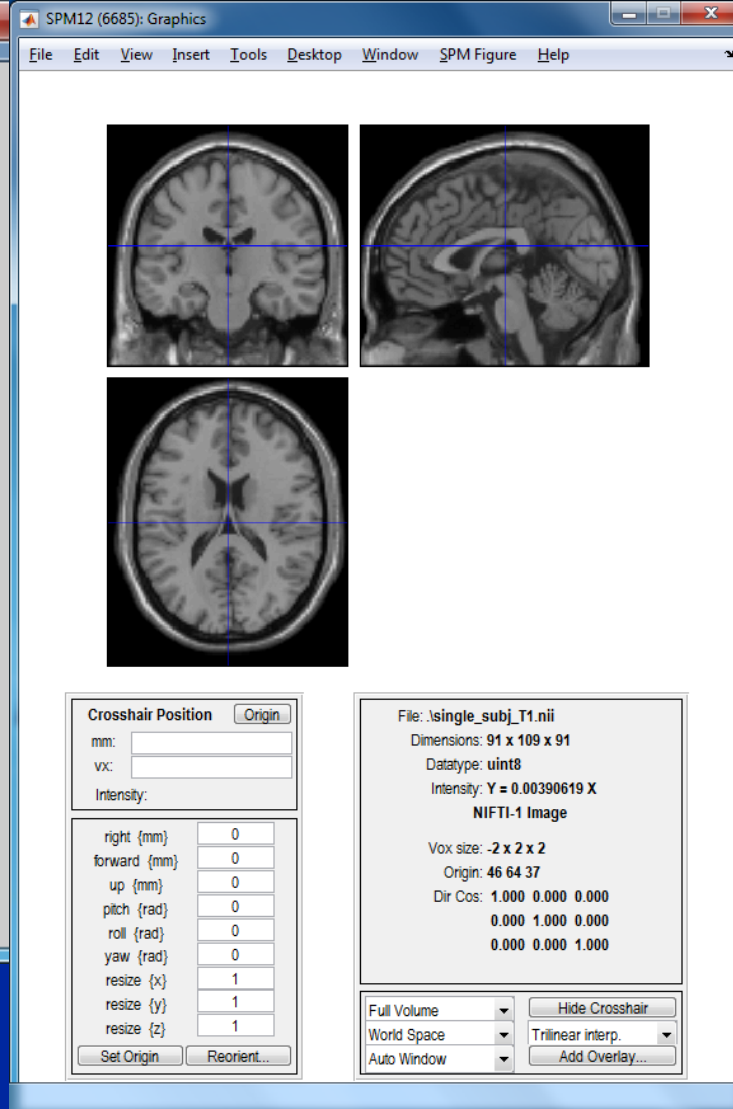
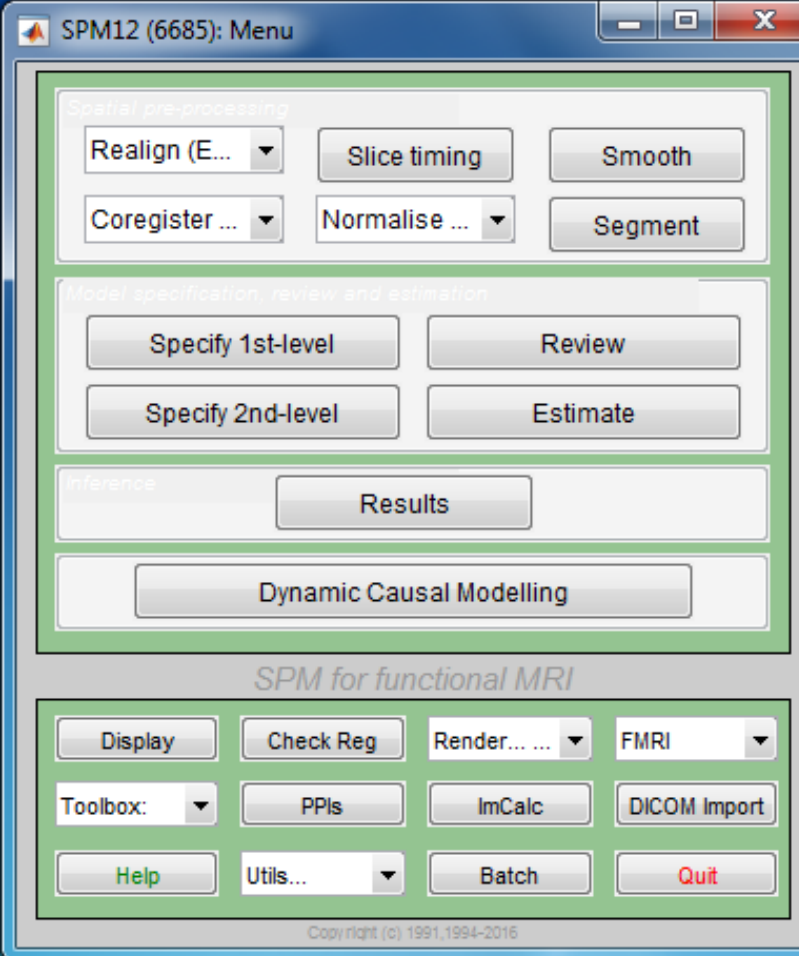
Scott Peltier

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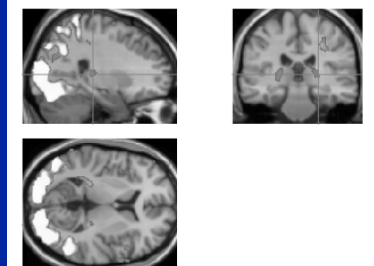
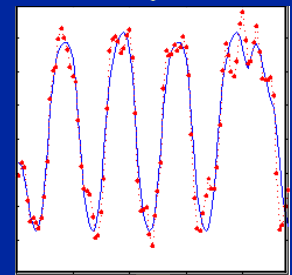
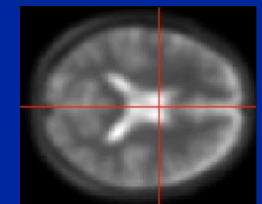
FMRI Laboratory  
University of Michigan







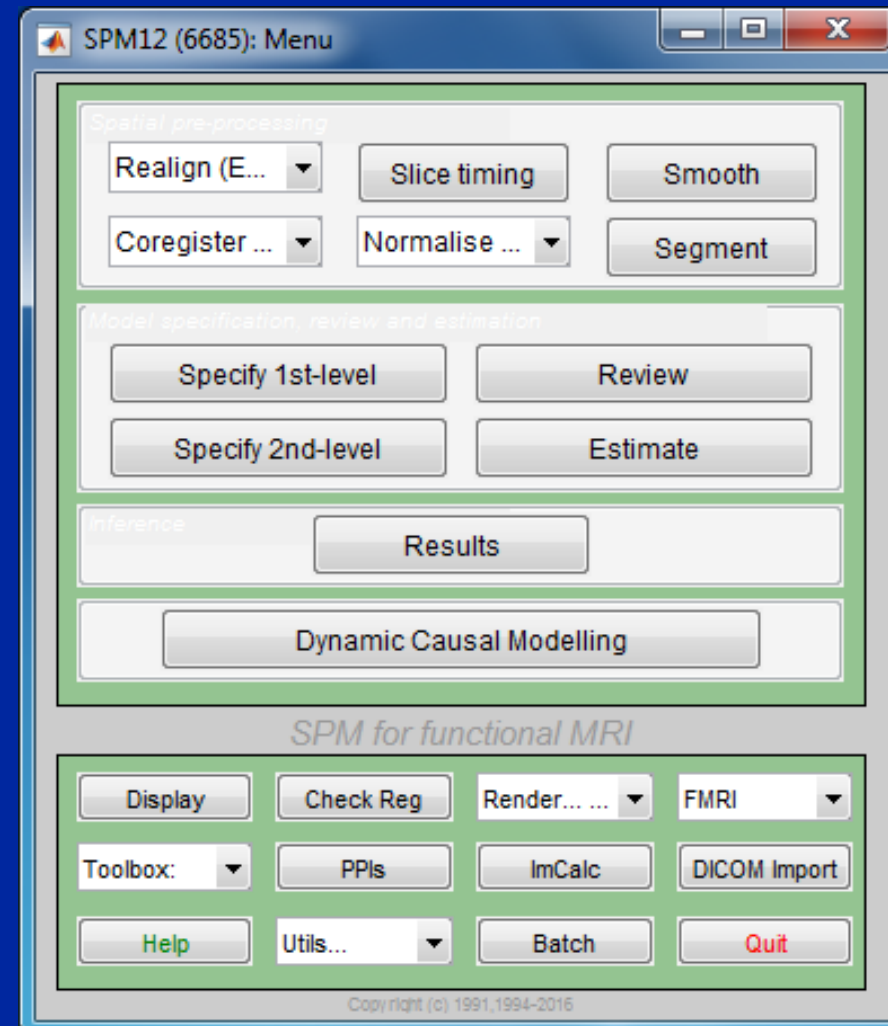
# SPM!



Software to perform computation,  
manipulation and display of imaging data

# SPM : Overview

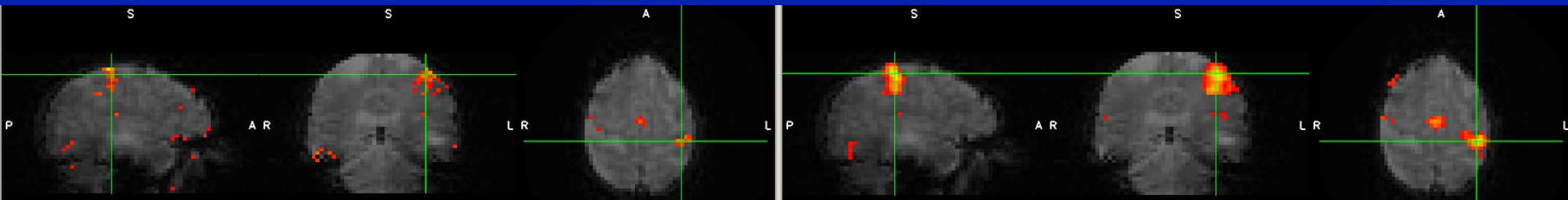
- Library of MATLAB and C functions
- Graphical user interface
- Four main components:
  - Preprocessing
  - Model Specification & Fitting
  - Inference & Results Interrogation
  - Supplemental Tools





# Preprocessing

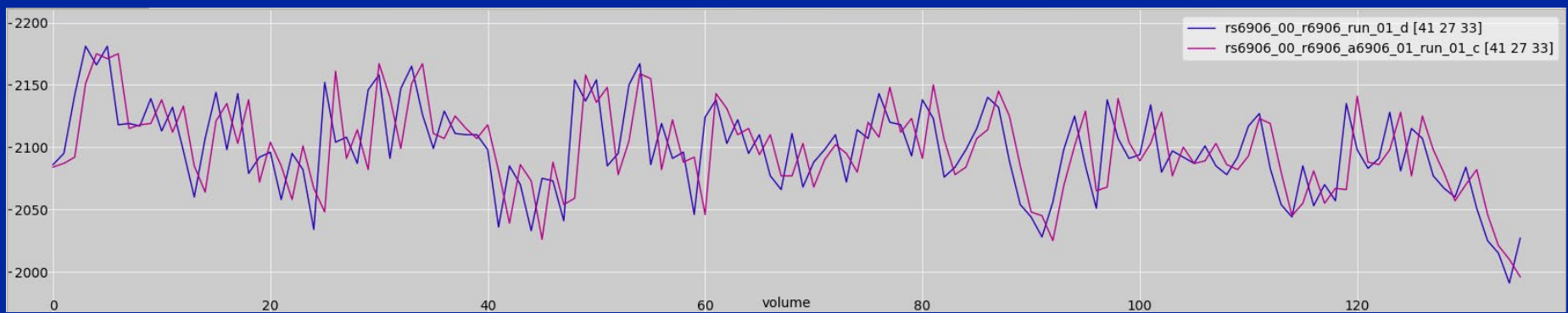
- Eliminate systematic variation before statistical modeling



Before  
t=5.89

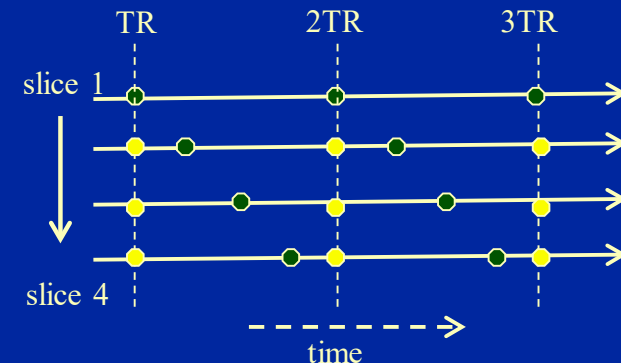
Processed with slice-timing correction, motion correction,  
and smoothed with 5mm isotropic kernel.

After  
t=10.04

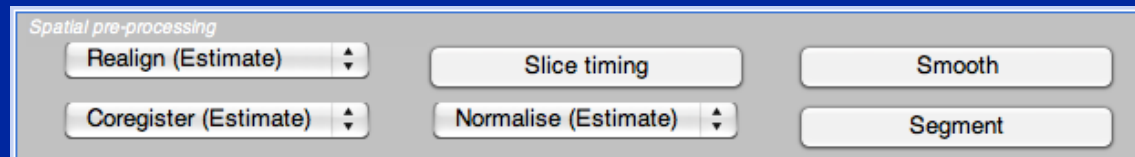
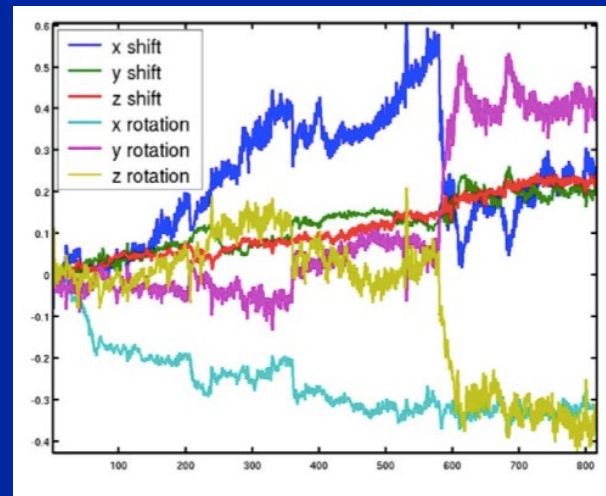


# SPM: Preprocessing

- Slice timing
  - Adjust for variable acquisition time over slices
  - In UM processing stream, this is already done

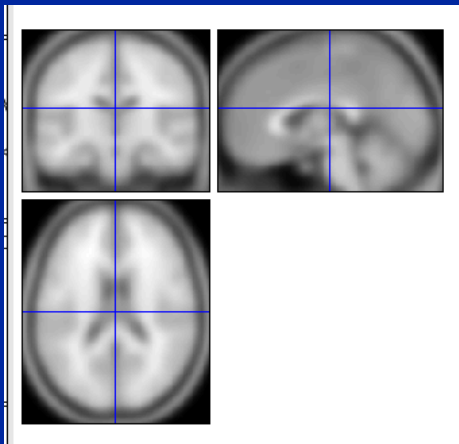


- “Realign”ment
  - Intrasubject registration
  - Motion correction
  - Done in UM stream



# SPM: Preprocessing

- “Coregister”ation
  - Intrasubject, intermodality registration
  - Registration of MR images with different TR/TE
- Spatial “Normalize”ation
  - Intersubject registration
  - Register subject anatomy to atlas space



SPM  
T1 template  
MNI space

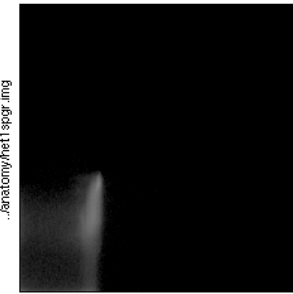
## Normalised Mutual Information Coregistration

$X1 = 1.093^{\circ}X - 0.011^{\circ}Y - 0.008^{\circ}Z - 10.591$

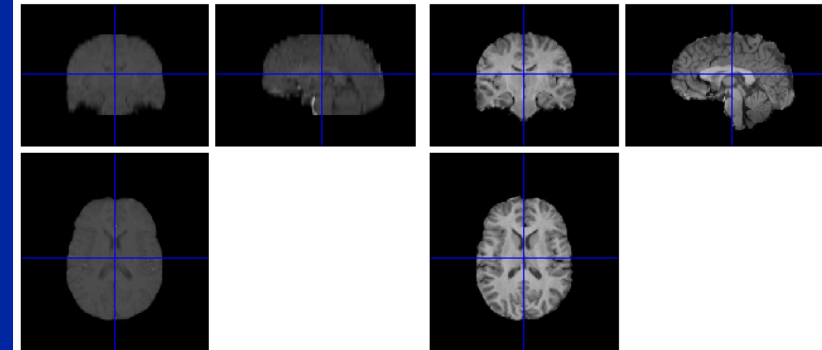
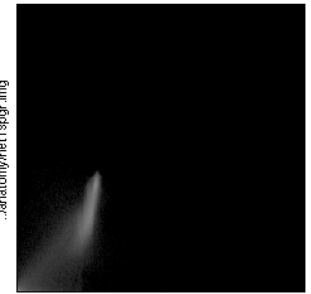
$Y1 = 0.010^{\circ}X + 1.086^{\circ}Y - 0.190^{\circ}Z + 8.054$

$Z1 = 0.001^{\circ}X + 0.020^{\circ}Y + 0.298^{\circ}Z - 7.243$

Original Joint Histogram



Final Joint Histogram



## Spatial pre-processing

Realign (Estimate)

Slice timing

Smooth

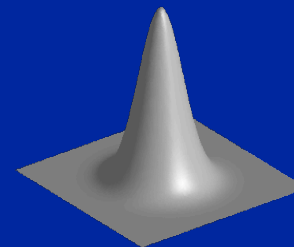
Coregister (Estimate)

Normalise (Estimate)

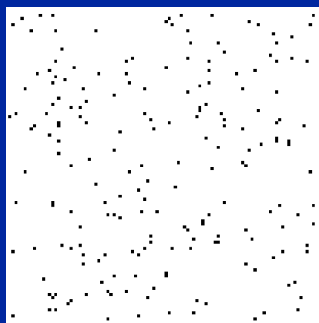
Segment

# SPM: Preprocessing

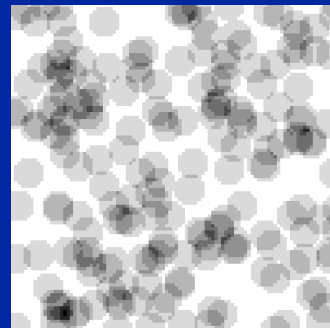
- Spatial “Smooth”ing
  - Blur data into submission...
    - To satisfy random field theory assumptions
    - For intersubject analyses



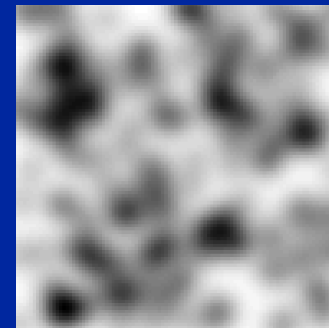
**Before  
convolution**



**Convolved  
w/ circle**

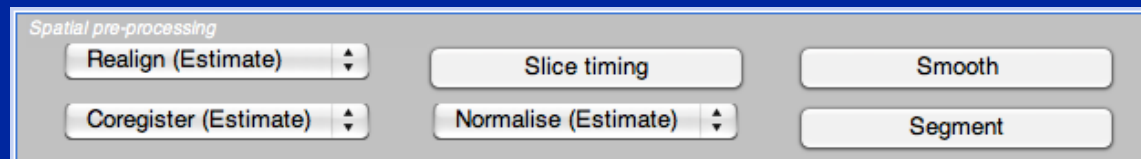


**Convolved  
w/ Gaussian**



Adapted from SPM course slides

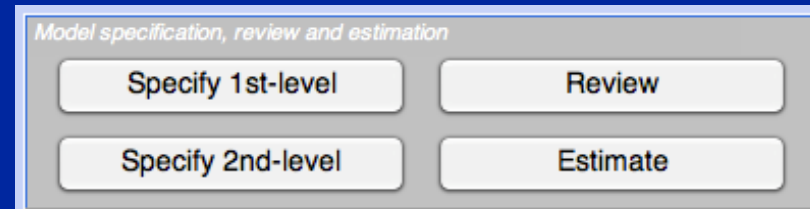
- “Segment”ation into GM/WM/CSF
  - Useful for structural studies



# SPM: Model Specification

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- “Specify 1st-level”
  - Specify the design, creating SPM.mat
- “Specify 2nd-level”
  - T-tests (One or two sample, paired)
  - Regression
- “Review”
  - Examine correlation of predictors
  - Power spectrum of experimental effects
- “Estimate”
  - Fit a specified model  
based on a SPM.mat file





# SPM: Inference

- “Results” button
- First brings up “Contrast Manager”
  - Can define single (t)
    - or sets (F) of contrasts
- Then displays MIP
  - MIP = Maximum Intensity Projection
  - Glass Brain
  - Can “surf” by dragging cursor

File Edit View Insert Tools Desktop Window SPM Figure Help

## WhyFaceWhyHand\_-\_HowFaceHowHand - All Sessions

SPMmap  
[30, -82, -35]

SPM{T<sub>285</sub>}

contrast(s)

Design matrix

**SPMresults:** .\sub03\results\precooked\2x2  
 Height threshold T = 3.119073 (p<0.001 (unc.))  
 Extent threshold k = 15 voxels

**Statistics: p-values adjusted for search volume**

set-level		cluster-level				peak-level					mm mm mm		
p	c	p <sub>FWE-cor</sub>	q <sub>FDR-cor</sub>	k <sub>E</sub>	p <sub>uncor</sub>	p <sub>FWE-cor</sub>	q <sub>FDR-cor</sub>	T	(Z)	p <sub>uncor</sub>	mm	mm	mm
0.000	15	0.000	0.000	985	0.000	0.000	0.000	9.87	Inf	0.000	30	-82	-35
						0.000	0.000	8.66	Inf	0.000	15	-88	-38
						0.000	0.000	6.75	6.50	0.000	-33	-82	-35
		0.000	0.000	8757	0.000	0.000	0.000	9.26	Inf	0.000	-9	71	10
						0.000	0.000	9.18	Inf	0.000	-54	-58	28
						0.000	0.000	9.18	Inf	0.000	-54	17	-11
		0.000	0.000	1719	0.000	0.000	0.000	7.64	7.28	0.000	-3	-49	22
						0.000	0.000	7.23	6.92	0.000	-3	-67	43
						0.000	0.000	7.04	6.75	0.000	-6	-55	37
		0.000	0.000	383	0.000	0.000	0.000	6.96	6.68	0.000	51	-64	46
						0.000	0.000	6.37	6.16	0.000	54	-61	34
						0.065	0.011	4.75	4.66	0.000	36	-58	40
		0.000	0.000	239	0.000	0.011	0.002	5.18	5.06	0.000	-9	11	10
						0.145	0.023	4.53	4.45	0.000	-3	-13	10
						0.244	0.039	4.38	4.30	0.000	15	11	16
		0.040	0.015	57	0.003	0.016	0.003	5.10	4.99	0.000	60	-46	-2
		0.170	0.049	36	0.015	0.096	0.015	4.65	4.56	0.000	3	20	-29
		0.056	0.019	52	0.005	0.290	0.046	4.32	4.25	0.000	6	-52	-41
						0.921	0.258	3.71	3.67	0.000	-3	-55	-47
		0.000	0.000	180	0.000	0.311	0.049	4.30	4.23	0.000	30	-25	64
						0.353	0.056	4.25	4.18	0.000	24	-31	64
		0.551	0.151	19	0.064	0.394	0.060	4.21	4.15	0.000	-18	-103	-11

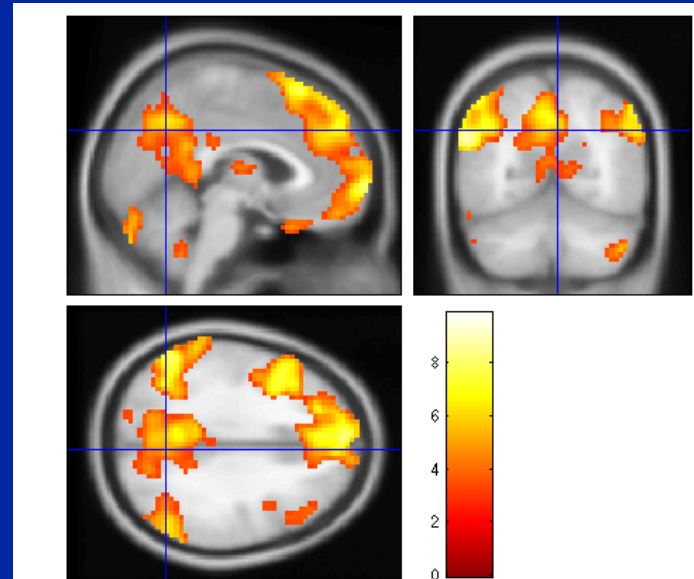
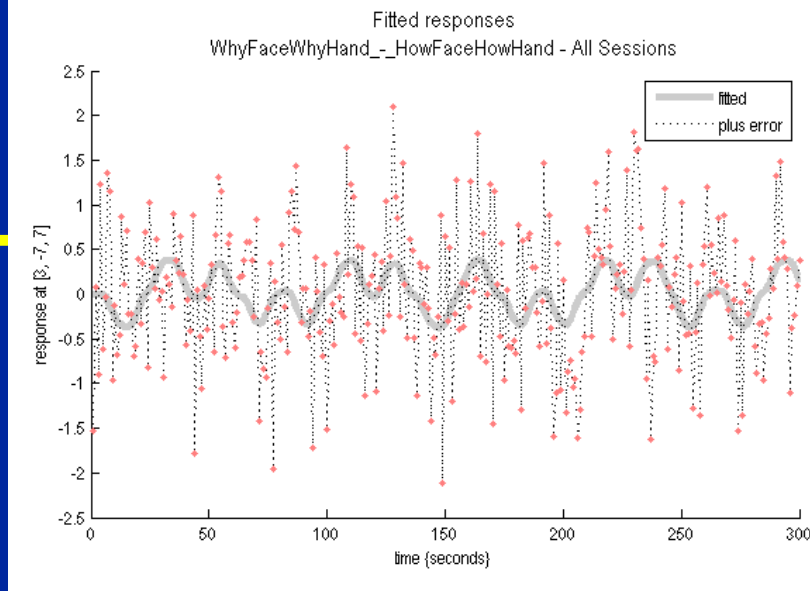
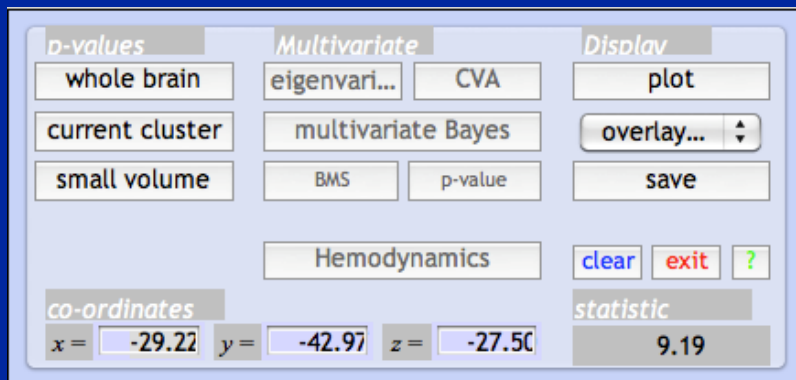
table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 3.12, p = 0.001 (1.000)  
 Extent threshold: k = 15 voxels, p = 0.095 (0.698)  
 Expected voxels per cluster, <k> = 5.537  
 Expected number of clusters, <c> = 1.20  
 FWEp: 4.819, FDRp: 4.298, FWEc: 57, FDRc: 36

Degrees of freedom = [1.0, 285.0]  
 FWHM = 11.4 11.1 10.2 mm mm mm; 3.8 3.7 3.4 (voxels)  
 Volume: 1700352 = 62976 voxels = 1180.1 resels  
 Voxel size: 3.0 3.0 3.0 mm mm mm; (resel = 47.92 voxels)  
 Page 1

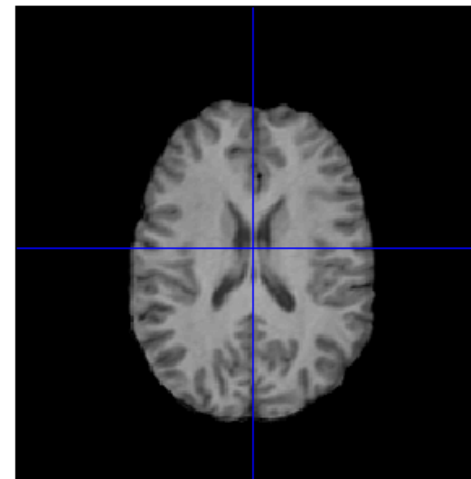
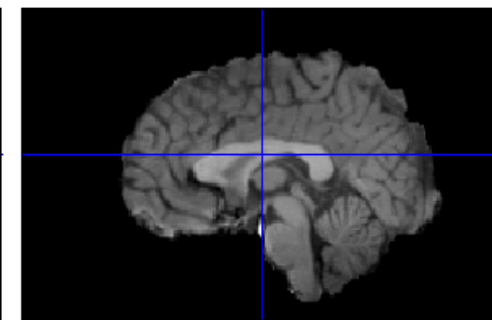
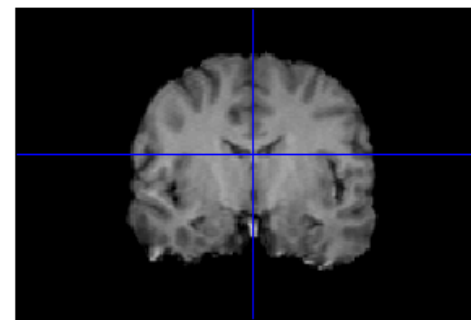
# SPM: Inference

- Interactive window
  - p-values
    - Corrected for whole brain or subregion
  - Plotting of time courses
  - “Overlays”
    - Superimpose results on other images
  - Current location and value



# SPM: Miscellaneous Tools

- “Display”
  - Displays image with orthogonal sections
  - Check intensity values
  - Change origin
  - Change world space
    - i.e. Apply rotations/translations



Crosshair Position

mm:	0.8 -2.5 4.5
vx:	129.4 125.9 56.5
Intensity:	534.268

right {mm}	0
foward {mm}	0
up {mm}	0
pitch {rad}	0
roll {rad}	0
yaw {rad}	0
resize {x}	1
resize {y}	1
resize {z}	1

Reorient images... Reset...

File: **..8ak/anatomy/het1spgr.img**

Dimensions: **256 x 256 x 106**

Datatype: **int16**

Intensity: **Y = 1 X**

**FSL3.2beta**

Vox size: **0.94 x 0.94 x 1.5**

Origin: **128 128 53.5**

Dir Cos: **1.000 0.000 0.000**  
**0.000 1.000 0.000**  
**0.000 0.000 1.000**

Full Volume	Hide Crosshairs
World Space	NN interp
Auto Window	Add Blobs

SPM for functional MRI

Display

Check Reg

Ren... ▾

FMRI ▾

Tool... ▾

PPIs

ImCalc

DICOM Import

Help

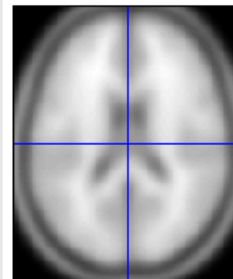
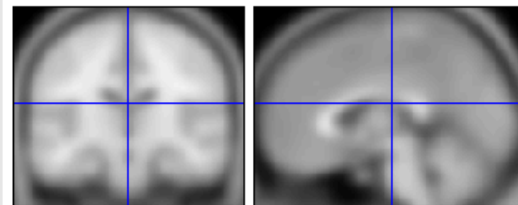
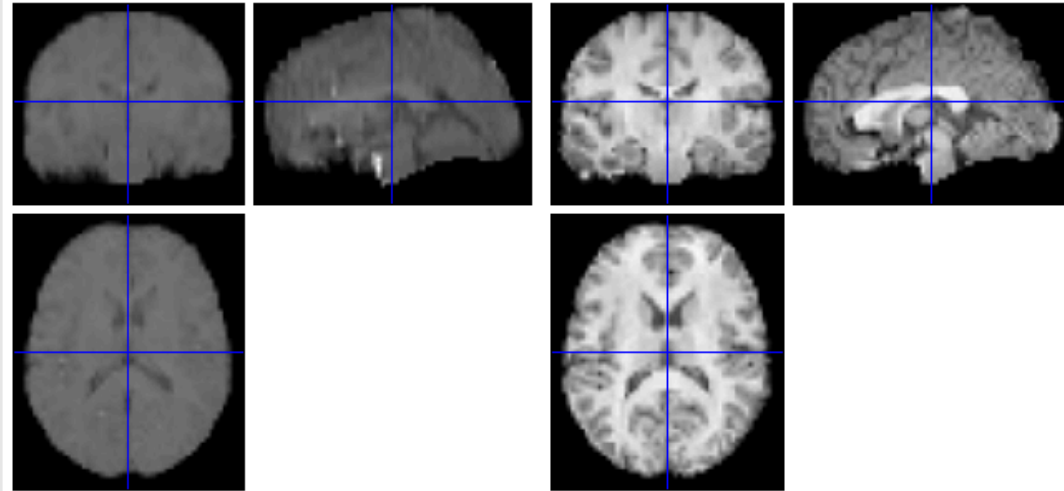
Utils.... ▾

Batch

Quit

# SPM: Miscellaneous Tools

- “Check Reg”
  - Display multiple images
  - Essential tool for assessing alignment of images
  - All images are displayed in the space of the first image



SPM for functional MRI

Display

Check Reg

Ren... ▾

FMRI ▾

Tool... ▾

PPIs

ImCalc

DICOM Import

Help

Utils.... ▾

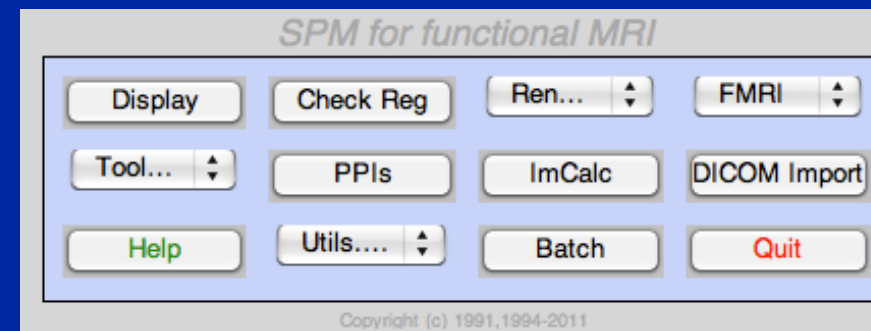
Batch

Quit

# SPM: Miscellaneous Tools

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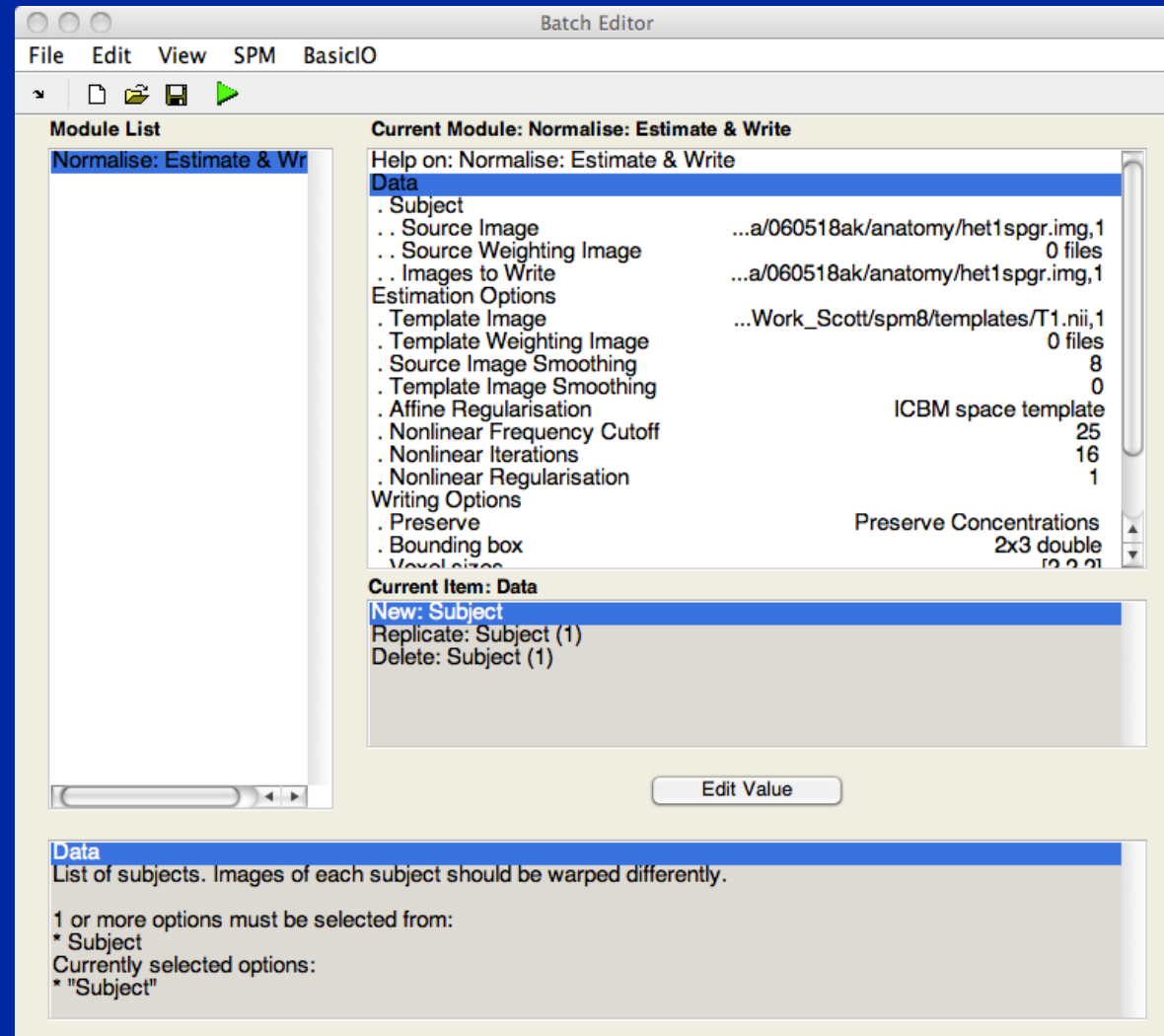
- “ImCalc”
  - Image calculator
  - Give one or more images, perform MATLAB arithmetic and write out result
- “Utils”
  - Change directory
    - Results are written to current directory!
  - Delete files, etc.





# SPM12 Batch Editor

- Allows jobs to be saved, re-loaded, changed
- Helps remove “Oops!” factor
- Multiple steps can be loaded, run at once



# SPM: Perspective

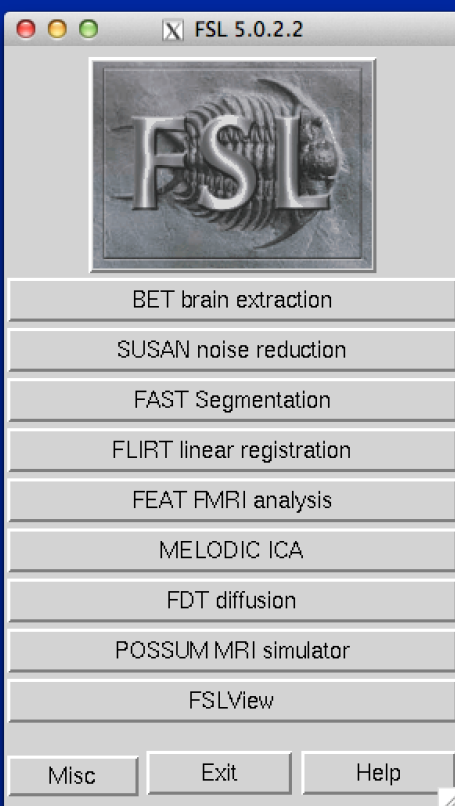
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- SPM tries to be a single solution for all fMRI processing and analysis, but there can be no such thing!
  - FMRI is a rapidly evolving field where each dataset has huge number of observations!
- Don't let SPM be a black box!
- Understand what each component does
- Understand how to get at the data
  - e.g. using 'Display', 'Check Reg'

# Resources

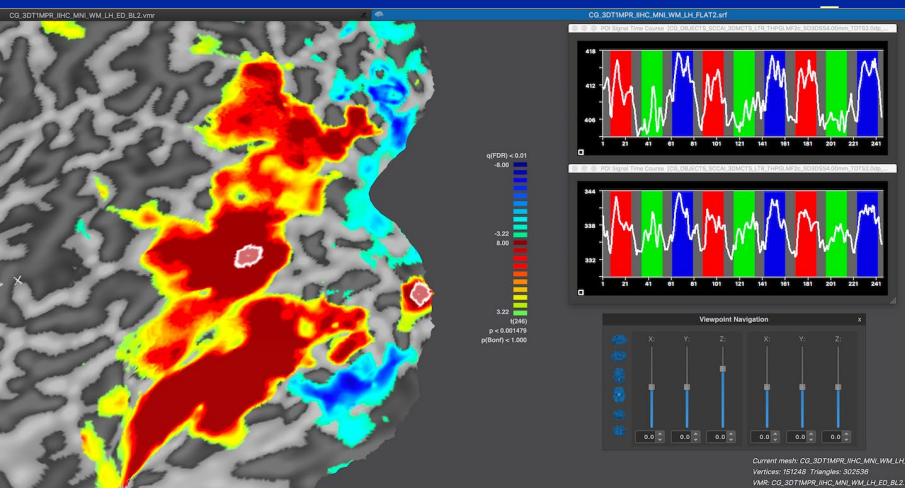
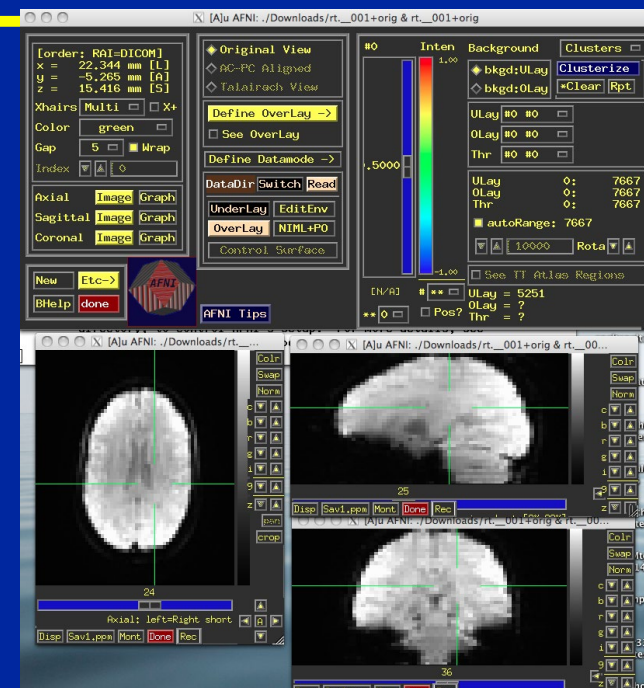
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- **SPMweb site:** <http://www.fil.ion.ucl.ac.uk/spm/>
  - Introduction to SPM
  - SPM code download: SPM12 (also older versions)
  - Documentation & Bibliography
  - SPM course videos
  - Example data sets
  - SPM extensions
  - SPM email discussion list
- **Other software packages can complement SPM**
  - MRICron: <https://people.cas.sc.edu/rorden/mricron/index.html>
  - Quick and easy to read, display, and convert image data

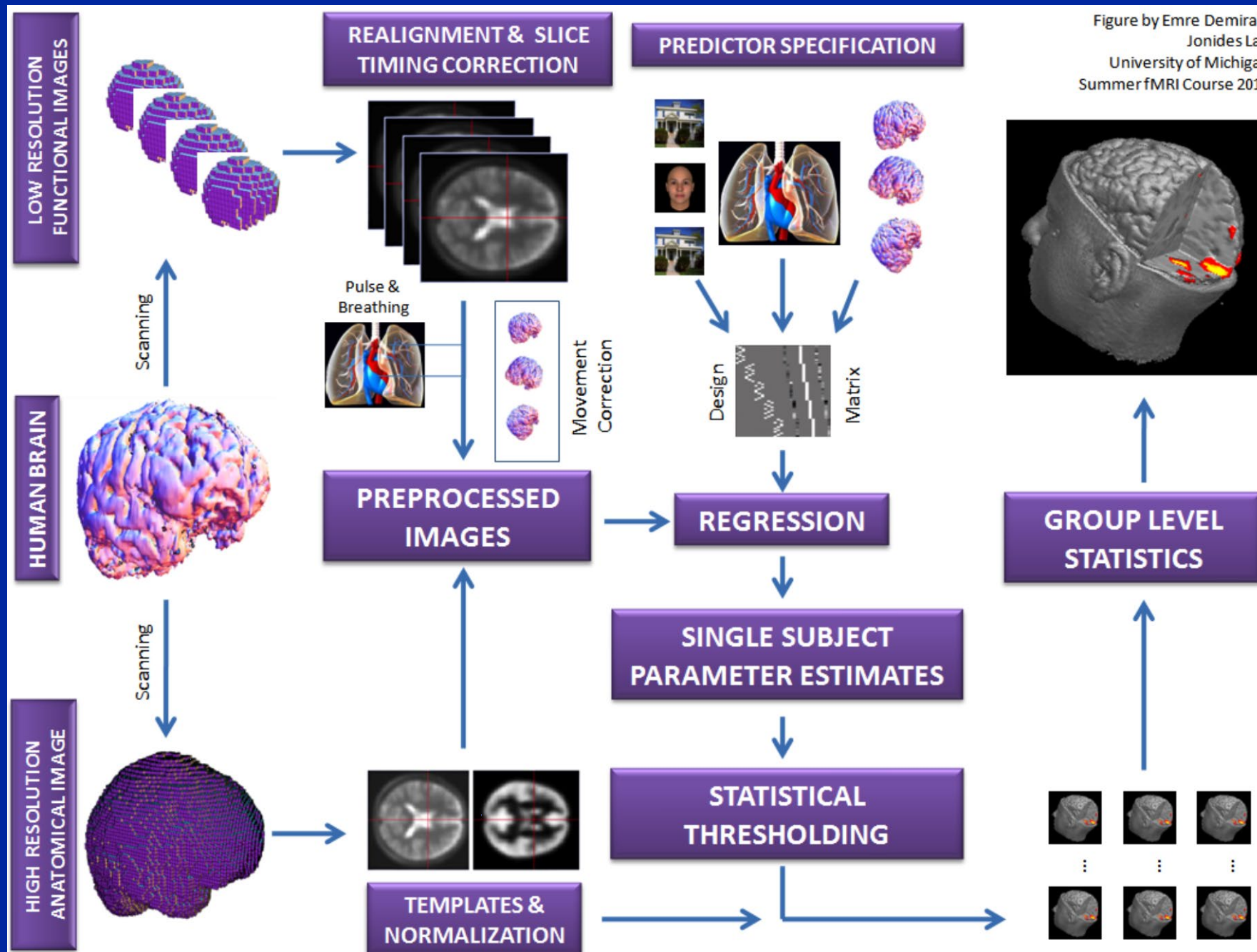


# Alternatives

- **FSL:** <http://www.fmrib.ox.ac.uk/fsl>
  - Open source
  - Comprehensive tools for FMRI and DTI, has nice ICA analysis tool (MELODIC)
  - Free
- **AFNI:** <http://afni.nimh.nih.gov>
  - Open source
  - Active community, multiple plugins



- **BrainVoyager:** <http://www.brainvoyager.com>
  - Excellent visualization
  - Closed source, ~\$7k





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# SPM

## Spatial Transformations

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# Imaging data formats

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- Analyze format

- .img Raw, binary data; 3D or 4D
- .hdr Small binary header
  - Image dimension
  - Voxel size

Historical

- NIFTI format

- .img + .hdr
- Like Analyze, but different .hdr definition
- .nii *Single file!* Header and Image file concatenated
- World space transformation coded in NIFTI header

Current

# Is Left Right?

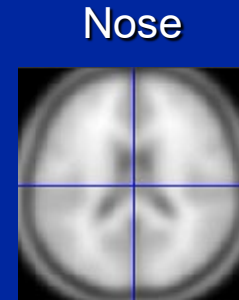
---

- Two conventions for viewing images

- Neurological

- On the screen, Left is Left side of subject
- As if standing behind the head of the patient

L

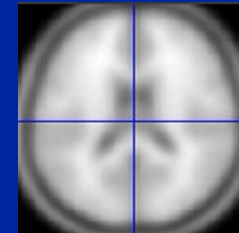


R

- Radiological

- On the screen, Left is Right side of subject
- As if standing at the foot of the patient

R



L

- Standard in clinical radiology is, um, radiological
- SPM always uses Neurological convention
  - Default for Analyze set by defaults.analyze.flip in spm defaults.m
    - flip = 0 ,Neuro., flip = 1 ,Rad.
    - NIFTI images *allegedly* have no ambiguity about left & right

# Coregister & realignment

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- Coregistration & Realignment are rigid body transformations
  - Subject's head doesn't change size or warp between scans
  - Well, actually...
- Each requires a “Reference” and a “Source”
  - Reference: Fixed image
  - Source: Image that is transformed
- SPM modifies the header of the *object* image
  - Unless you explicitly ask it to, it doesn't write out a new image
  - Saves lots of disk space!

# Voxel space vs. world space

- Voxel Space
  - Just the original image
  - No reorientations or flips
- World Space
  - Space defined by transformation from voxel to mm matrix  $M$ 
    - Let  $v$  be a voxel location indexed from  $(1,1,1)$
    - Then  $w=M*[v;1]$  is that location in world space, in mm
    - Can represent rotations, translations and flips



# Data Fresh from fMRI Lab

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## Functional Space

**Functional images**  
raprun\_01.nii

**Low-res anatomy**  
t1overlay.nii

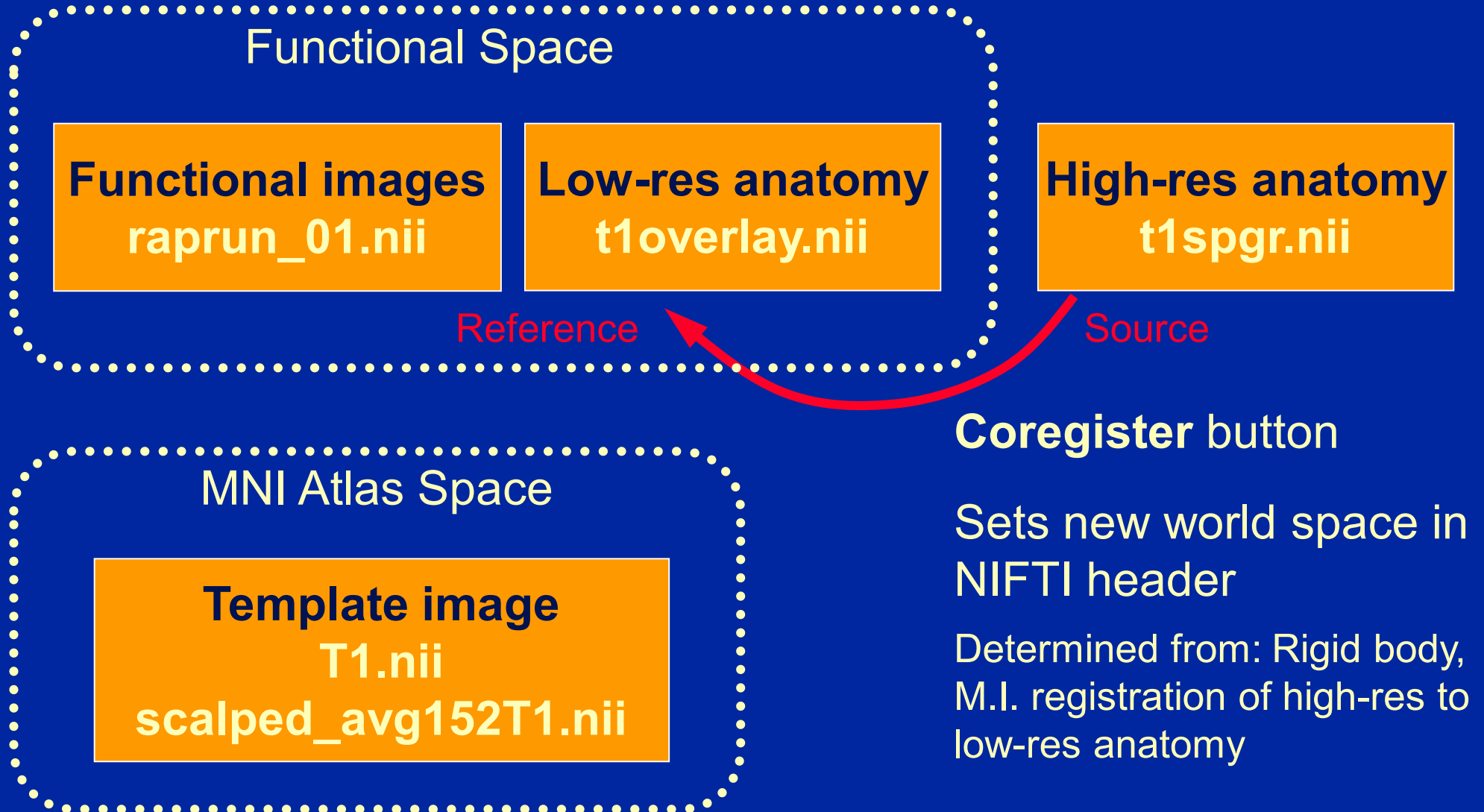
**High-res anatomy**  
t1spgr.nii

## MNI Atlas Space

**Template image**  
T1.nii  
scalped\_avg152T1.nii

# Coregistration

---



# After Coregistration

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## Functional Space

**Functional images**  
raprun\_01.nii

**Low-res anatomy**  
t1overlay.nii

**High-res anatomy**  
t1spgr.nii  
(NIFTI header)

## MNI Atlas Space

**Template image**  
T1.nii  
scalped\_avg152T1.nii

# Spatial Normalization

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## Functional Space

**Functional images**  
raprun\_01.nii

**Low-res anatomy**  
t1overlay.nii

**High-res anatomy**  
t1spgr.nii  
(NIFTI header)

## MNI Atlas Space

**Template image**  
T1.nii  
scalped\_avg152T1.nii

**Normalize** button

Creates **y\_\*.nii** file

Determined from:

Deformation fields calculated  
using segmented images

# Spatial Normalisation

---

## Functional Space

**Functional images**  
raprun\_01.nii

**Low-res anatomy**  
t1overlay.nii

**High-res anatomy**  
t1spgr.nii  
(NIFTI header)

## MNI Atlas Space

**Template image**  
T1.nii  
scalped\_avg152T1.nii

**y\_\*.nii**

file maps *any*

Functional Space image to MNI  
space!

# After “Writing Normalized”

---

## Functional Space

**Functional images**  
raprun\_01.nii

**Low-res anatomy**  
t1overlay.nii

**High-res anatomy**  
t1spgr.nii  
(NIFTI header)

## MNI Atlas Space

**Template image**  
T1.nii  
scalped\_avg152T1.nii

**Normalized images**  
wt1spgr.nii  
wraprun\_01.nii

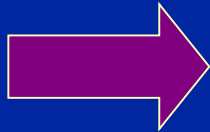


# Group Analysis: Strategy 1

## Only transform contrast img's

### Functional Space

rap\_run's



beta's  
con's  
spmT's

Intrasubject  
analysis result

y\_\*.nii

### MNI Atlas Space

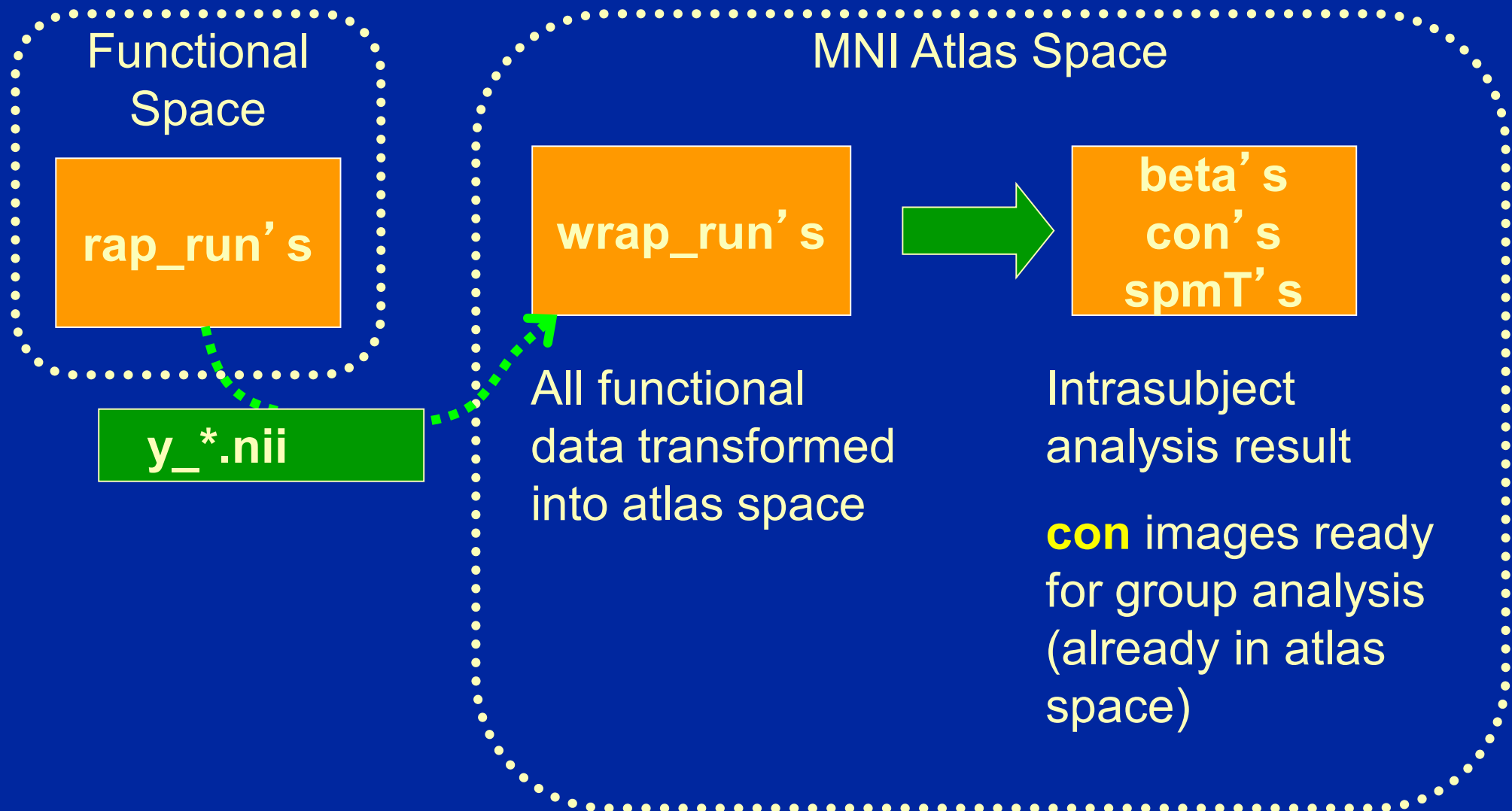
wcon's

Intrasubject analysis contrast images,  
transformed into atlas space (w/ **\_sn.mat**),  
ready for group analysis

# Group Analysis: Strategy 2

## Transform all functionals

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# Normalization recommendations

- If not doing segmented normalization, with ‘scalped’ brains use ‘scalped’ template
  - Scalped template **scalped\_avg152T1.nii**
  - *Should* give best results
    - We don’t care about scalp alignment!
- Make sure WM equal in brightness
  - T1’s can have inhomogeneity artifact, where center of volume is brighter
  - Should apply homogeneity correction (bias correction)
  - UM: make sure to use (e)**ht1spgr**, (e)**ht1overlay**