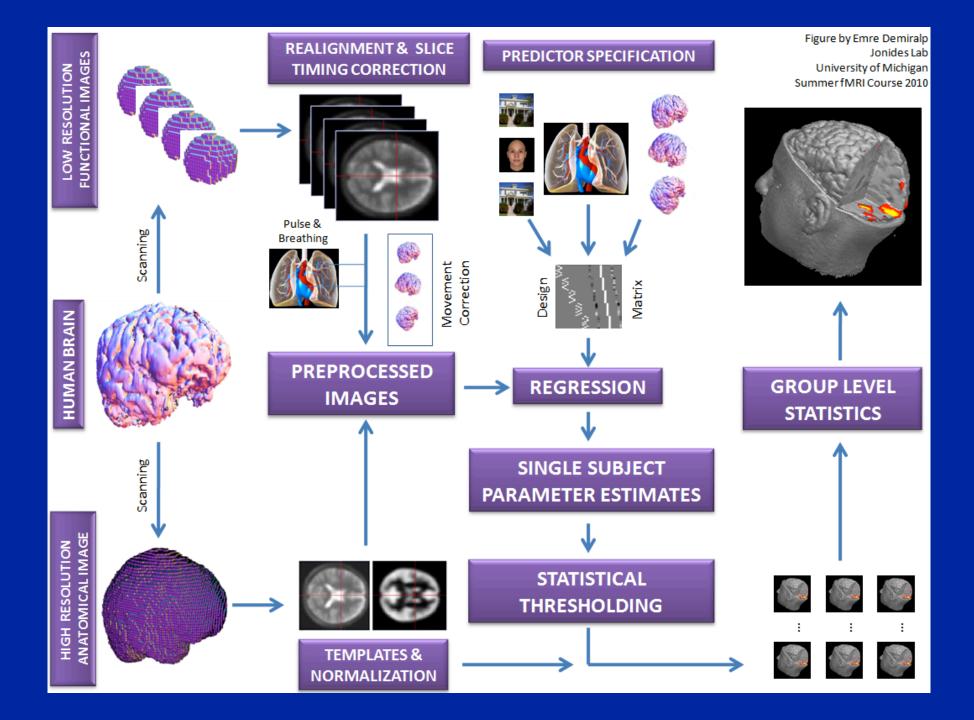
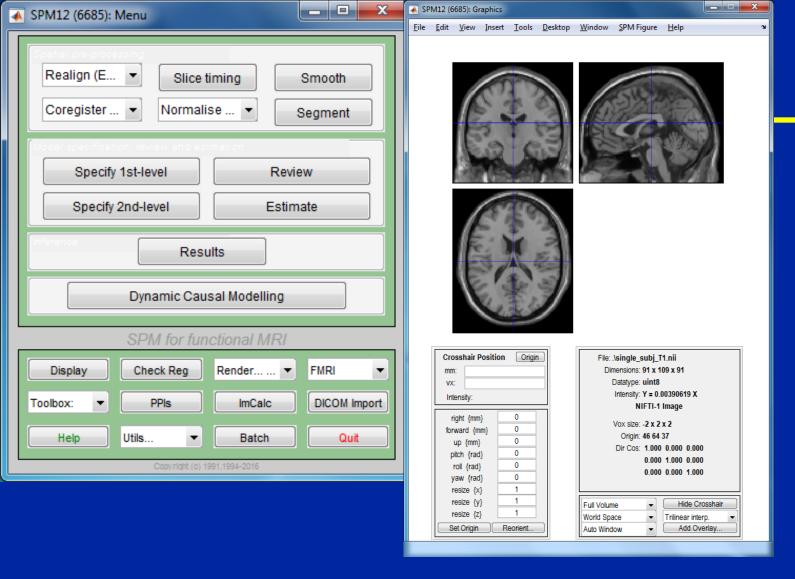
# SPM Introduction

Scott Peltier

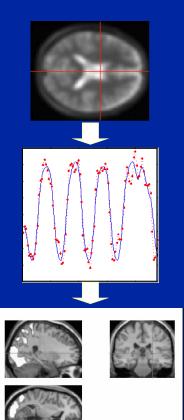
FMRI Laboratory University of Michigan







#### SPM!



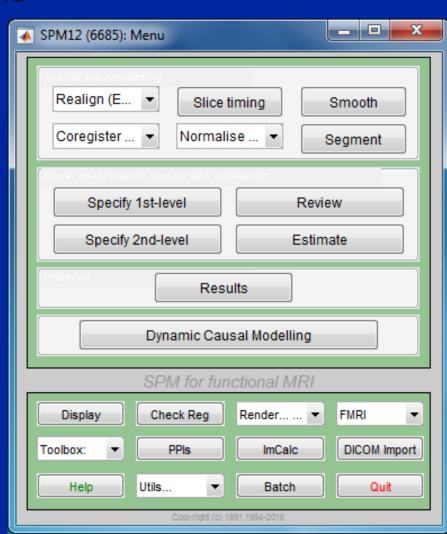
Software to perform computation, manipulation and display of imaging data

## SPM: Overview

Library of MATLAB and C functions

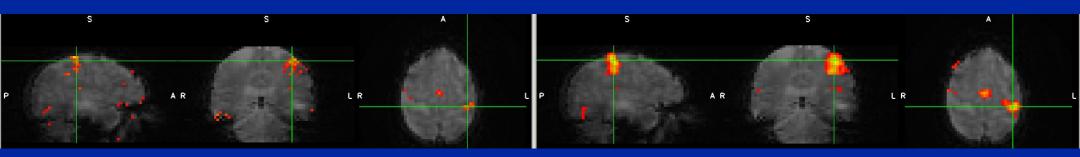
Graphical user interface

- Four main components:
  - Preprocessing
  - Model Specification & Fitting
  - Inference & Results Interrogation
  - Supplemental Tools



# Preprocessing

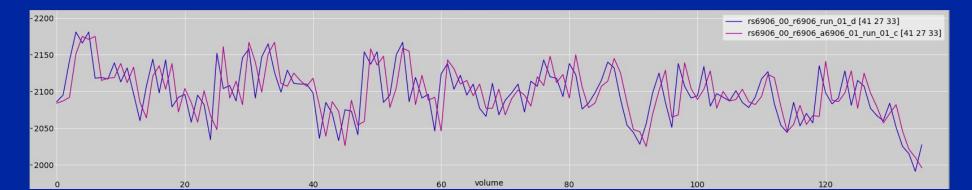
 Eliminate systematic variation before statistical modeling



Before t=5.89

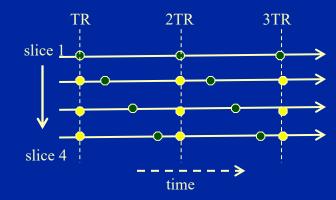
After t=10.04

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

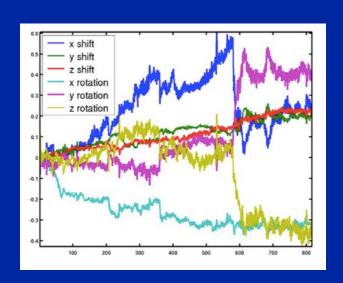


# SPM: Preprocessing

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



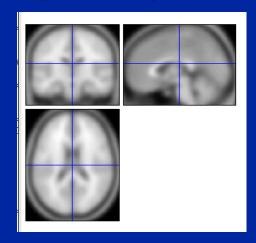
- "Realign"ment
  - Intrasubject registration
  - Motion correction
  - Done in UM stream



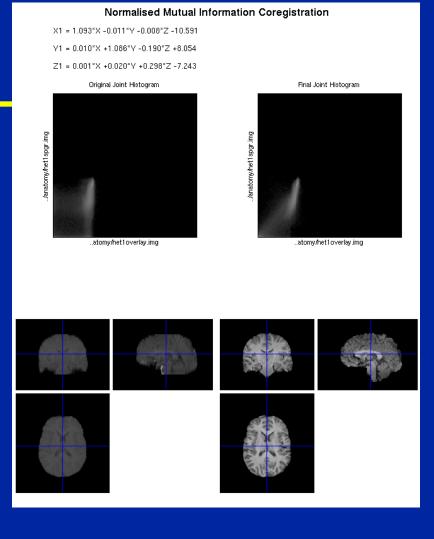
Spatial pre-processing		
Realign (Estimate) 💠	Slice timing	Smooth
Coregister (Estimate) 💠	Normalise (Estimate) 💠	Segment

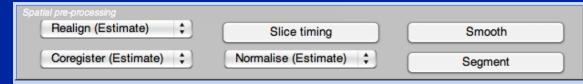
## **SPM: Preprocessing**

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



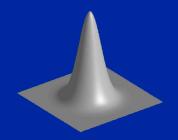
SPM T1 template MNI space



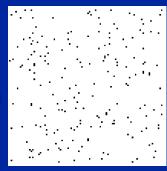


# SPM: Preprocessing

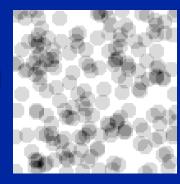
- Spatial "Smooth"ing
  - Blur data into submission...
    - To satisfy random field theory assumptions
    - For intersubject analyses



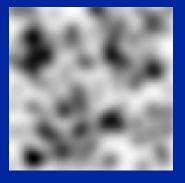
Before convolution



Convolved w/ circle

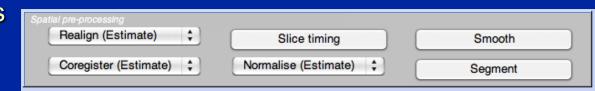


Convolved w/ Gaussian



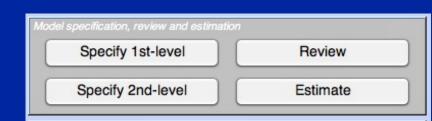
Adapted from SPM course slides

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



# SPM: Model Specification

- "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



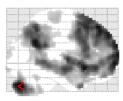
## **SPM: Inference**

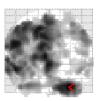
- "Results" button
- First brings up "Contrast Manager" Can define single (t) or sets (F) of contrasts
- Then displays MIP
  - MIP = Maximum Intensity Projection
  - Glass Brain
  - Can "surf" by dragging cursor

Results

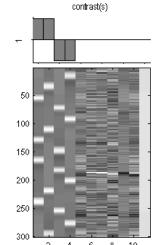
#### View Insert Tools Desktop Window SPM Figure Help

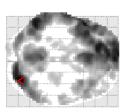
#### WhyFaceWhyHand - HowFaceHowHand - All Sessions





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





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

#### Statistics: n-values adjusted for search volume

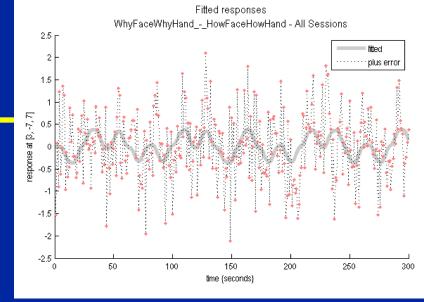
set-level		cluster-level			peak-level					papa i	mm mr		
р	С	р FIME-corr	Ø <sub>FDR-corr</sub>	k <sub>E</sub>	рипсоп	P <sub>FU∕E-corr</sub>	∉ FDR-coπ	T	(Z_)	Рипсоп	mm	11111 1111	п
0.000 15	0.000	0.000	985	0.000	0.000	0.000	9.87	Inf	0.000	30	-82	-3	
						0.000	0.000	8.66	Inf	0.000	15	-88	-:
						0.000	0.000	6.75	6.50	0.000	-33	-82	-:
		0.000	0.000	8757	0.000	0.000	0.000	9.26	Inf	0.000	-9	71	
						0.000	0.000	9.18	Inf	0.000	-54	-58	:
						0.000	0.000	9.18	Inf	0.000	-54	17	
		0.000	0.000	1719	0.000	0.000	0.000	7.64	7.28	0.000	-3	-49	:
						0.000	0.000	7.23	5.92	0.000	-3	-67	
						0.000	0.000	7.04	6.75	0.000	-6	-55	
		0.000	0.000	383	0.000	0.000	0.000	6.96	6.68	0.000	51	-64	
						0.000	0.000	6.37	6.16	0.000	54	-61	
						0.055	0.011	4.75	4.66	0.000	35	-58	
		0.000	0.000	239	0.000	0.011	0.002	5.18	5.06	0.000	-9	11	
						0.145	0.023	4.53	4.45	0.000	-3	-13	
						0.244	0.039	4.38	4.30	0.000	15	11	
		0.040	0.015	57	0.003	0.016	0.003	5.10	4.99	0.000	60	-46	
		0.170	0.049	36	0.015	0.096	0.015	4.65	4.56	0.000	3	20	-
		0.056	0.019	52	0.005	0.290	0.046	4.32	4.25	0.000	6	-52	
						0.921	0.258	3.71	3.67	0.000	-3	-55	-
		0.000	0.000	180	0.000	0.311	0.049	4.30	4.23	0.000	30	-25	
						0.353	0.056	4.25	4.18	0.000	24	-31	
		0.551	0.151	19	0.064	0.394	0.060	4.21	4.15	0.000	-18	-103	-:
				table sho	ws 3 local n	naxima more t	han 8.0mm a	apart –					

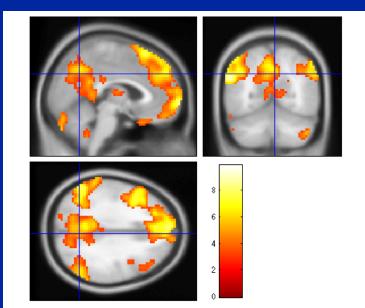
Height threshold: T = 3.12, p = 0.001 (1.000) Extent threshold: k = 15 voxels, p = 0.095 (0.698)Expected voxels per cluster, <k> = 5.537 Expected number of clusters, <c> = 1.20 FWEp: 4.819, FDRp: 4.298, FWEc: 57, FDRc: 36 Degrees of freedom = [1.0, 285.0] FWHM = 11.4 11.1 10.2 mm mm mm; 3.8 3.7 3.4 {voxels} 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
    - Correced for whole brain or subregion
  - Plotting of time courses
  - "Overlays"
    - Superimpose results on other images
  - Current location and value



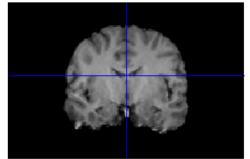


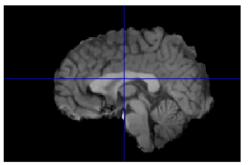


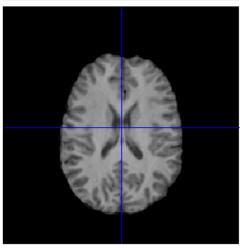
#### **SPM: Miscellaneous Tools**

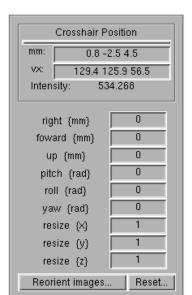
- "Display"
  - Displays image with orthogonal sections
  - Check intensity values
  - Change origin
  - Change world space
    - i.e. Apply rotations/translations

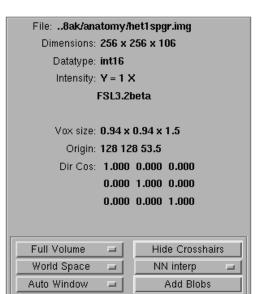






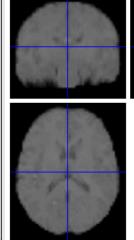


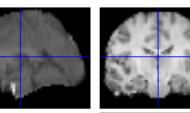


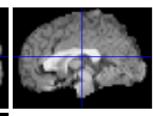


#### **SPM: Miscellaneous Tools**

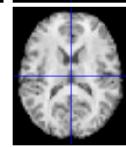
- "Check Reg"
  - Display multiple images
  - Essential tool for assessing alignment of images
  - All images are displayed in the space of the first image

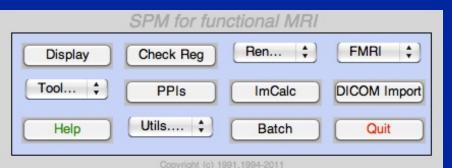


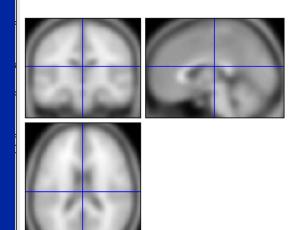












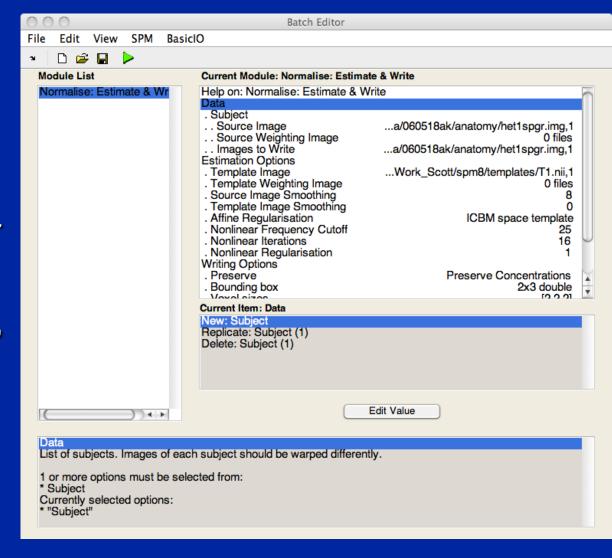
## SPM: Miscellaneous Tools

- "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

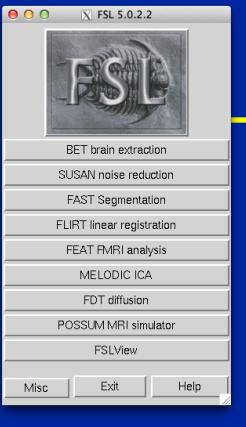


# SPM: Perspective

- 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

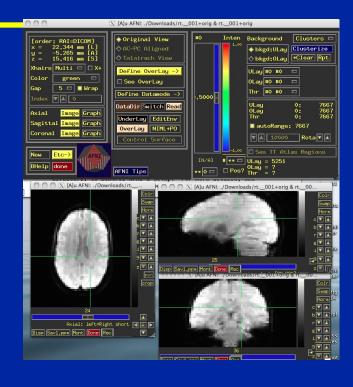
- SPMweb site: http://www.fil.ion.ucl.ac.uk/spm/
  - Introduction to SPM
  - SPM code download: SPM12 (also older versions)
  - Documentation & Bibliography
  - SPM course videos
  - Example data sets
  - SPM extensions
  - SPM email discussion list
- Other software packages can complement SPM
  - MRIcron: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

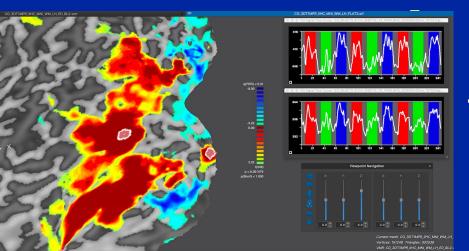


#### **Alternatives**

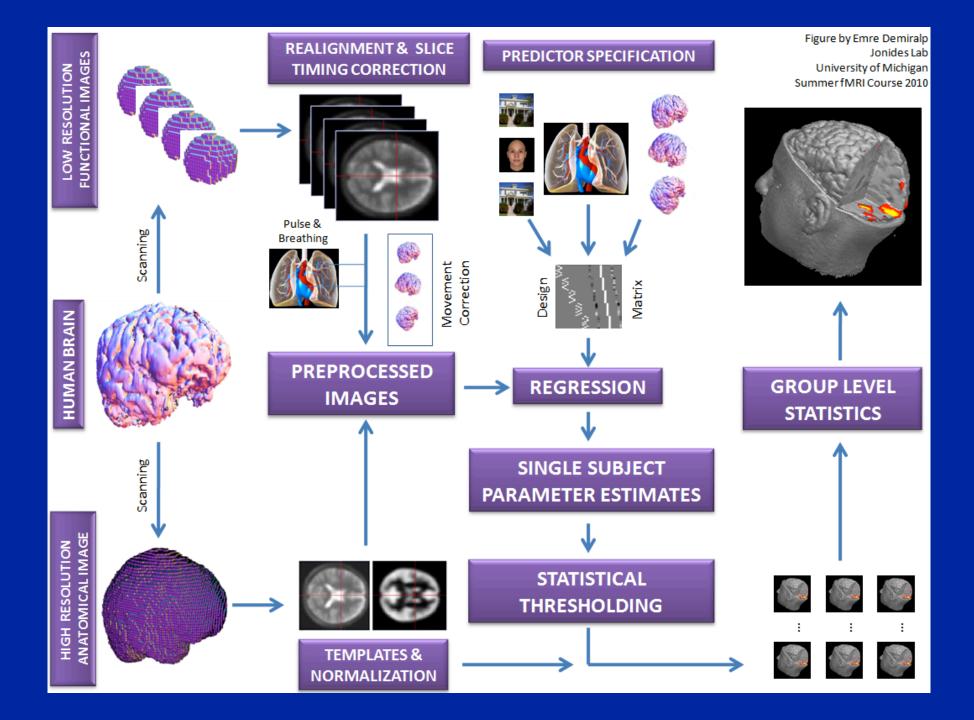
- FSL: http://www.fmrib.ox.ac.uk/fsl
  - Open source
  - Comprehensive tools for FMRI and DTI, has nice ICA analysis tool (MELODIC)
  - Free

- AFNI: http://afni.nimh.nih.gov
  - Open source
  - Active community, multiple plugins





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



# SPM Spatial Transformations

# Imaging data formats

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

Historical

Current

#### 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

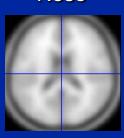
# Is Left Right?

- Two conventions for viewing images
  - Neurological
    - On the screen, Left is Left side of subject
    - As if standing behind the head of the patient
  - Radiological
    - On the screen, Left is Right side of subject
    - As if standing at the foot of the patient

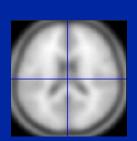
Standard in clinical radiology is, um, radiological

- 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

Nose



R



R

# Coregister & realignment

- 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

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

**Functional Space** 

Functional images raprun\_01.nii

Low-res anatomy t1overlay.nii

Reference

High-res anatomy t1spgr.nii

Source

**MNI Atlas Space** 

Template image T1.nii scalped\_avg152T1.nii Coregister button

Sets new world space in NIFTI header

Determined from: Rigid body, M.I. registration of high-res to low-res anatomy

# After Coregistration

**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**

**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



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

Functional Space

rap\_run' s

y\_\*.nii

MNI Atlas Space

wrap\_run's



beta's con's spmT's

All functional data transformed into atlas space

Intrasubject analysis result

con images ready for group analysis (already in atlas space)

#### 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