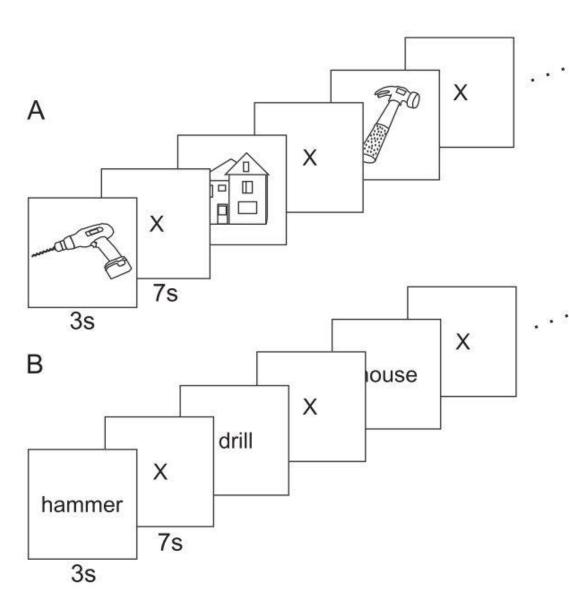
# Lab session 3: FMRI data preprocessing

Andrew Bauer 01/27/16

Session no.	Date (all Wednesday)	Topic/activity	Topic of quiz that day	Topic of lab write-up (assignment) due that day
1	13-Jan	Lab overview		
2	20-Jan	Brain anatomy		
3	27-Jan	Data preprocessing	Brain anatomy (no. 1)	
4	3-Feb	Set up GLM model	Functional brain anatomy (no. 2)	
5	10-Feb	Single-subject SPM contrasts	Data preprocessing and GLM model (no. 3)	Brain anatomy (no. 1)
6	17-Feb	Within-subject MVPA		Single-subject SPM contrasts (no. 2)
7	24-Feb	SIBR tour and review for mid-term exam		Within-subject MVPA (no. 3)
No lab	2-Mar	No lab (mid-term exam)		
No lab	9-Mar	No lab (spring break)		
8	16-Mar	Group-level SPM contrasts		
9	23-Mar	Between-subjects MVPA		Group-level SPM contrasts (no. 4)
10	30-Mar	Voxel-wise modeling		Between-subjects MVPA (no. 5)
11	6-Apr	Functional connectivity analysis (no assignment)		
12	13-Apr	Review for final exam		Voxel-wise modeling (no. 6)
No lab	20-Apr	No lab		
No lab	27-Apr	No lab (final exam)		

# Raw, raw data (k-space) **Reconstructed raw data** $p_{\text{uncorrected}}$ Data analysis & results Data preprocessing pipeline

# Introducing our dataset



(A) Mitchell et al. (2008): "Think of properties of depicted objects" (w/nouns underneath too)

(B) Just et al. (2010):

"Think of properties of referred-to objects" (nouns *only*)

We are analyzing set **B**("purer" brain activity due to conceptual thought, no pics)

### 1. Motion correction

 Ensures that brain activity of voxel i corresponds to the same volume of brain tissue throughout whole experiment

### 2. Slice-time correction

Brain slices are not collected simultaneously each image acquisition

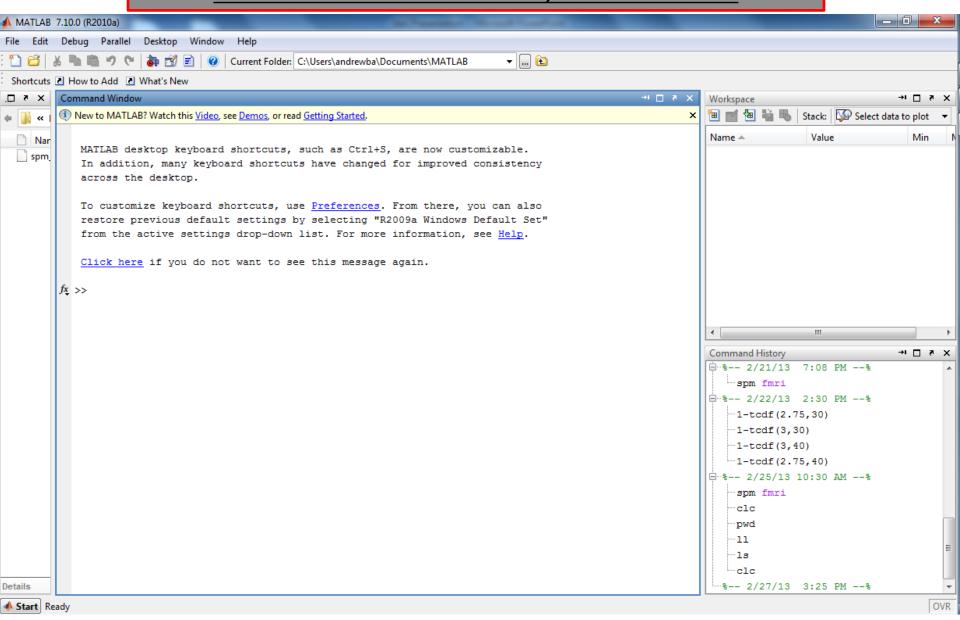
### 3. Spatial normalization

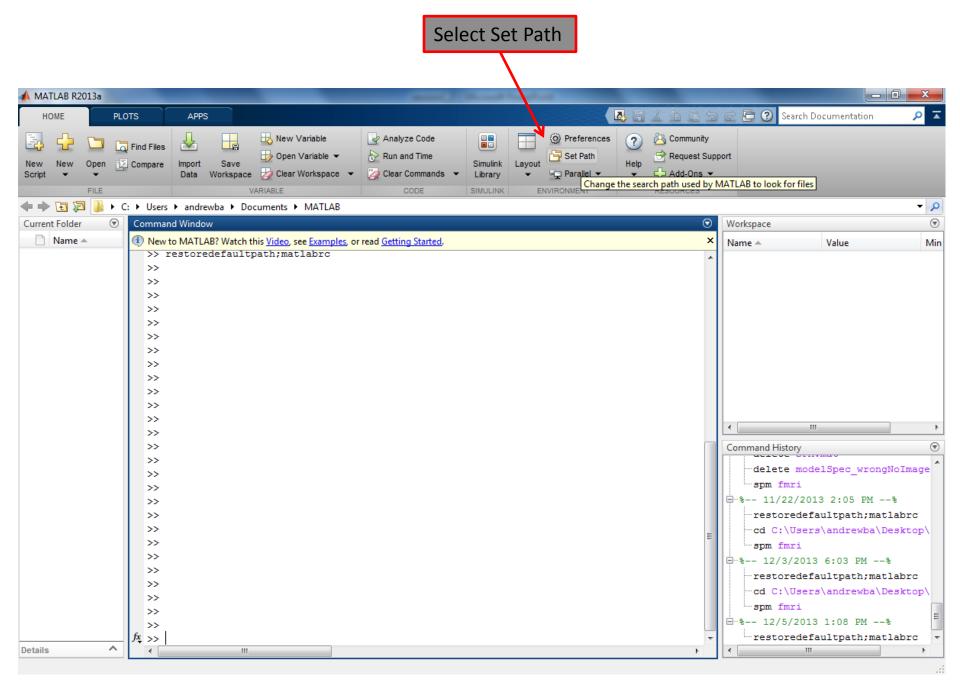
Morphs each subject's brain to a common/template brain

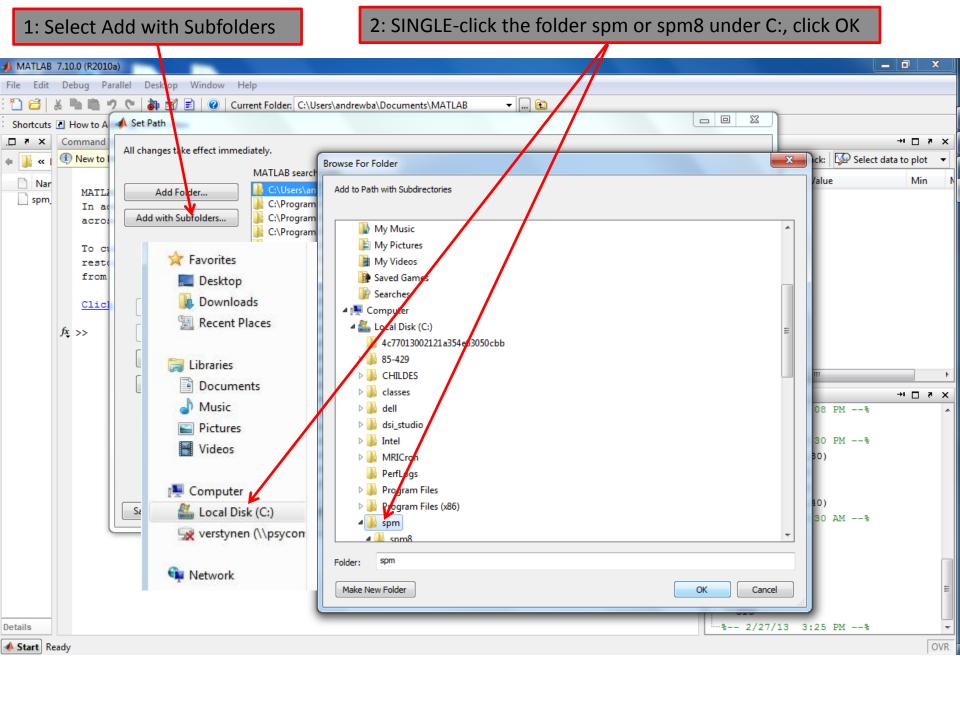
### 4. Smoothing

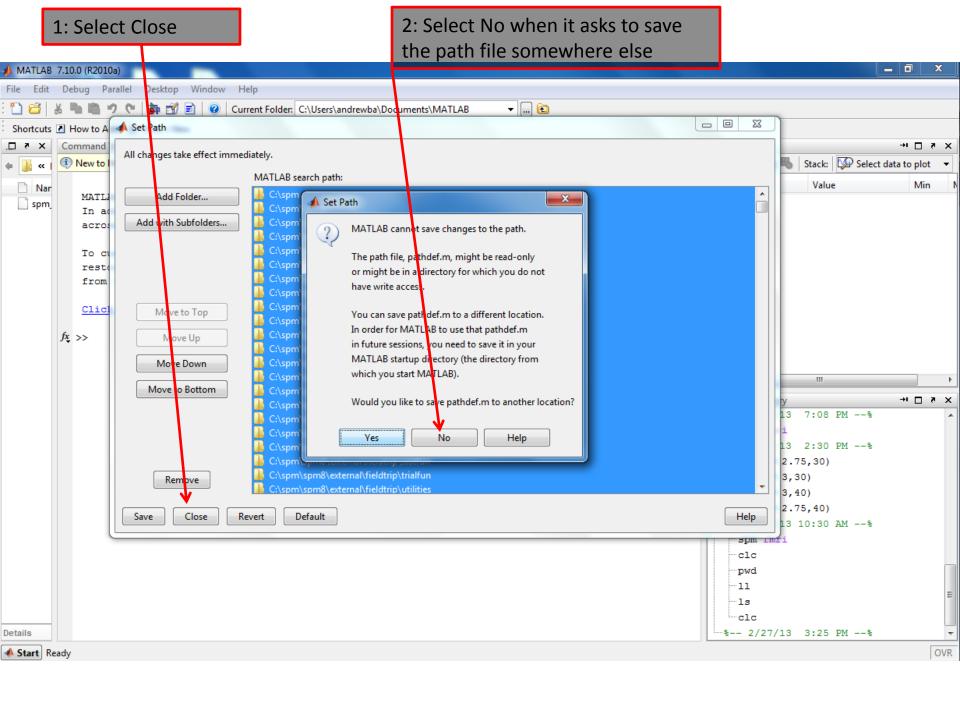
Reduces amount of noise per voxel by averaging over nearby voxels

# Start Matlab 2012b (on desktop, or type "matlab" in Start menu to find it) NOTE: You MUST select Matlab 2012b, do NOT select 2014b





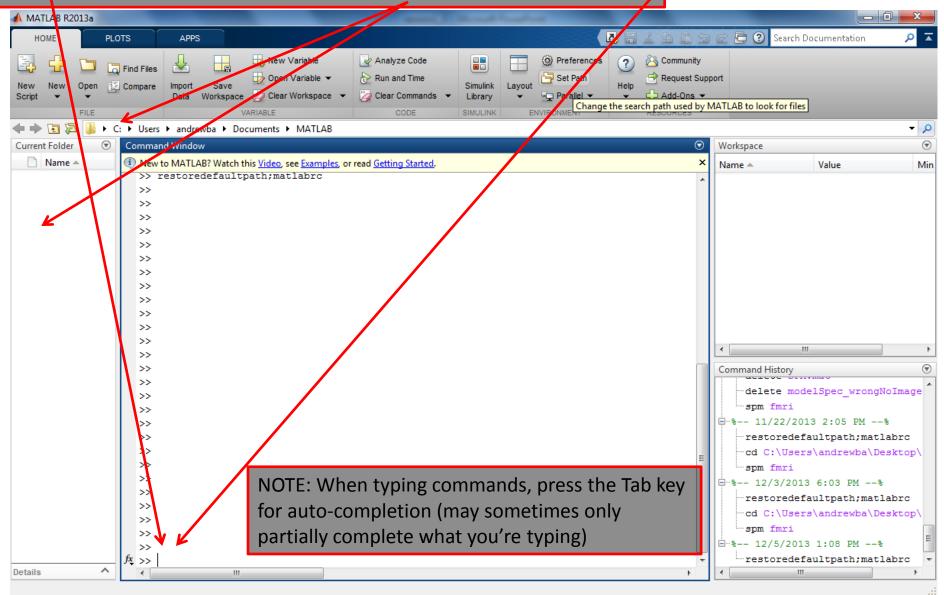


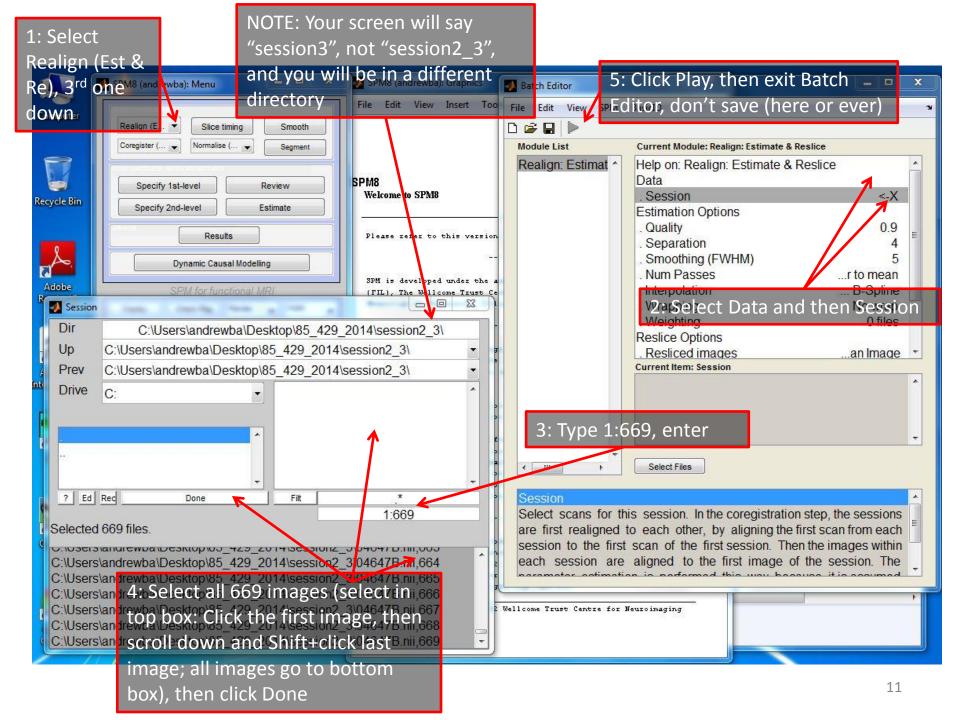


1: Go to the Matlab Command Window and type: cd C:/Users/Public/lab\_85\_429\_2016/session3

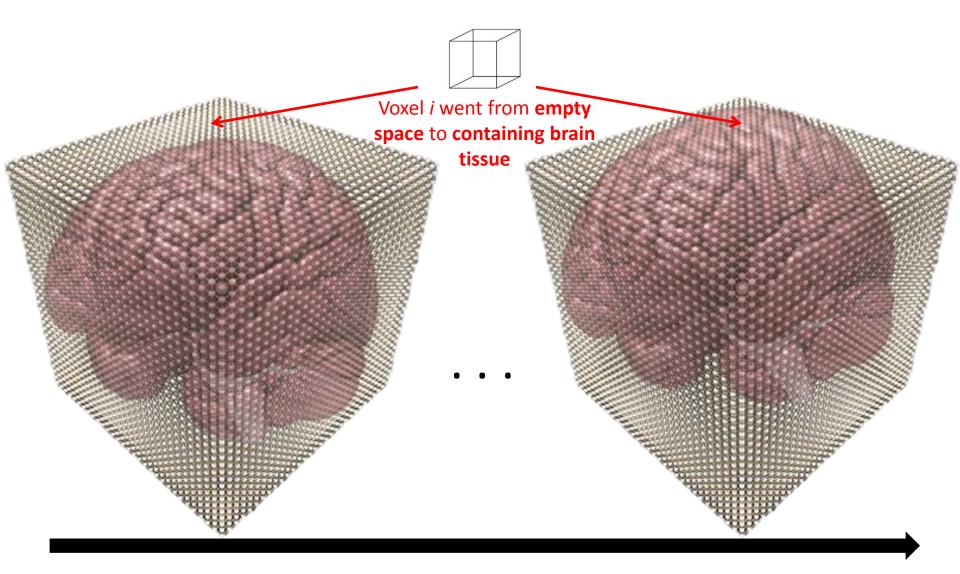
2: Then type: spm fmri

...(OR navigate there using the browser)





# Need to correct for head motion For example:



Time: t = 0 minutes

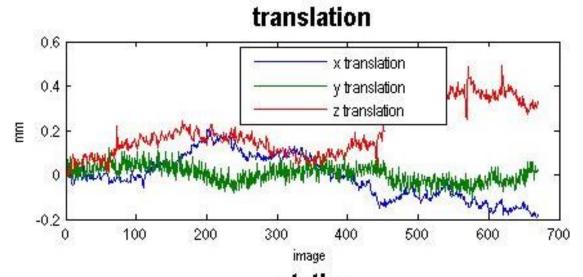
# Viewing head motion

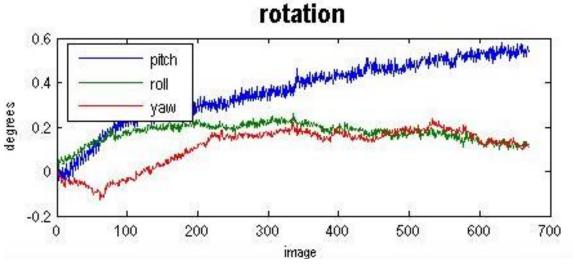
### Translation:

Deviation in space for each dimension

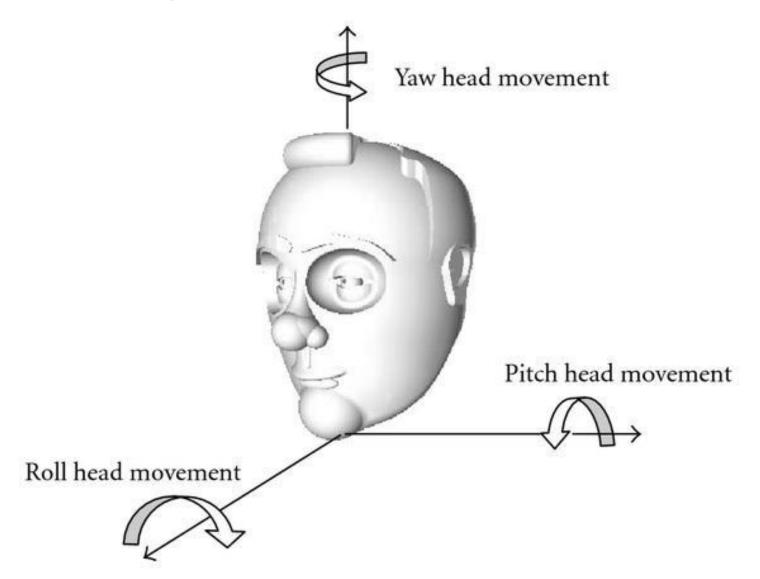


Deviation in angle/degree for each direction





# Spatial rotation terms



### 1. Motion correction

 Ensures that brain activity of voxel i corresponds to the same volume of brain tissue throughout whole experiment

### 2. Slice-time correction

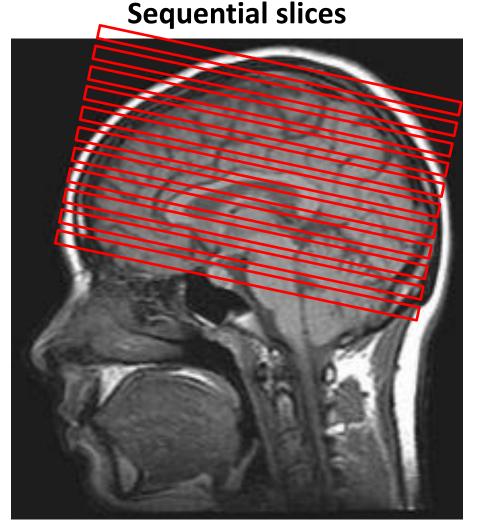
Brain slices are not collected simultaneously each image acquisition

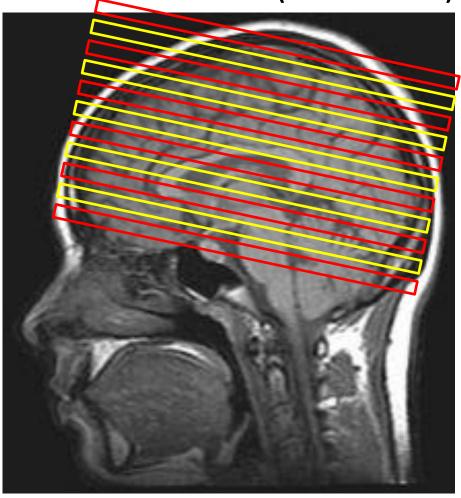
## How do we acquire one whole picture of the brain?

- Read individual "slices" and put them together
- Typical acquisition time (TR) of reading slices over the whole brain is 1 sec
- TR depends on voxel size & amount of brain coverage

... or Interleaved slices

(same duration)





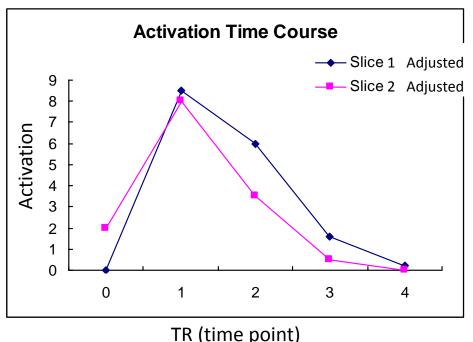
### Adjust slice activation to correct for slice asynchrony

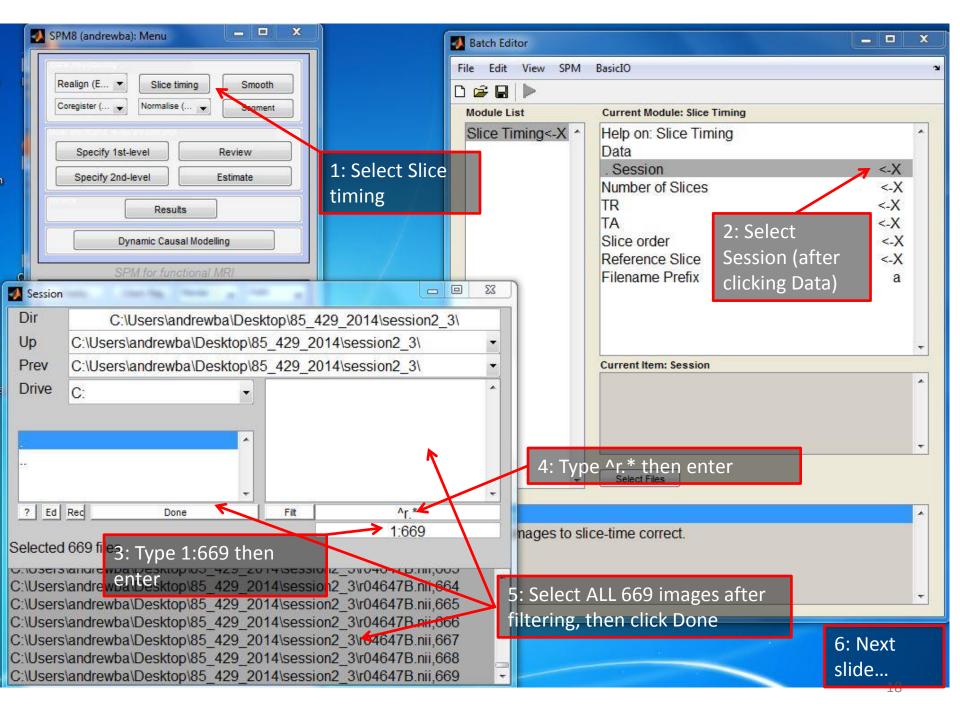
- Notice that Slice 2 activation appears to peak earlier, and to decrease earlier
  - Why? Slice 2 is acquired after Slice 1; Slice 2's activation waveform at TR = 0 is really at around TR = 0 plus that extra delay time, during which its activation has increased a bit
- The solution is temporal interpolation: Estimates new slice activations for each TR;
   makes slices more synchronous (can be more accurate for Interleaved slice-reading)

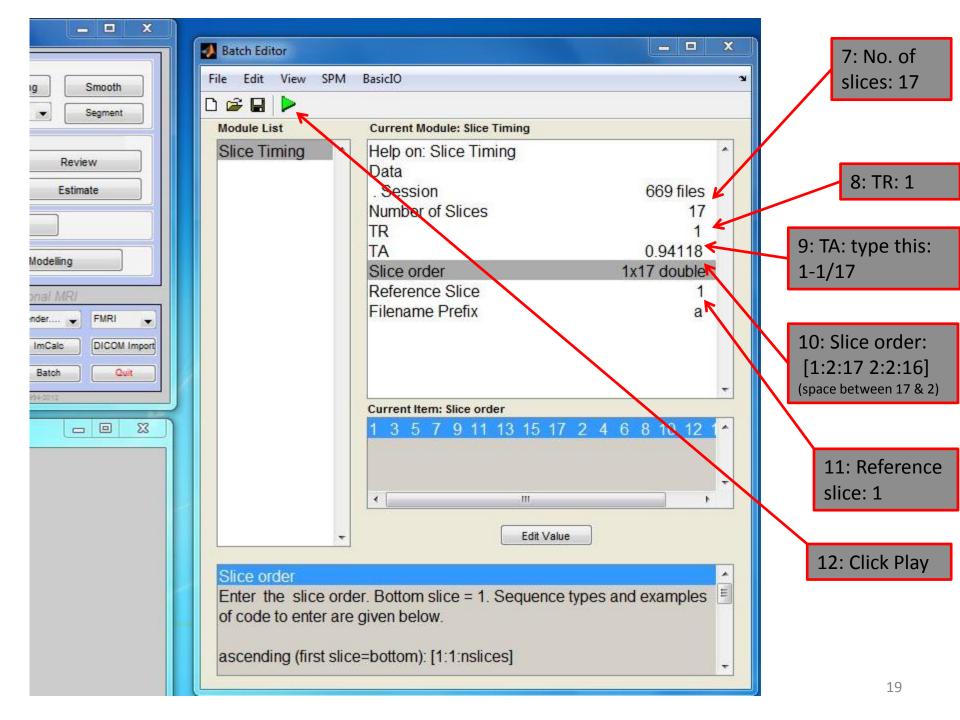
### **Before slice-time correction**

# Activation Time Course Slice 1 Slice 2 On the state of the state of

#### After slice-time correction







### 1. Motion correction

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### 3. Spatial normalization

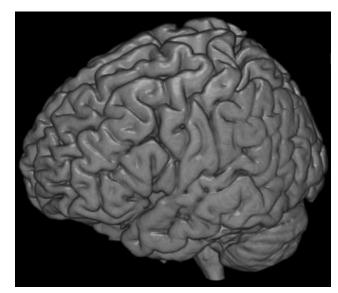
Morphs each subject's brain to a common/template brain

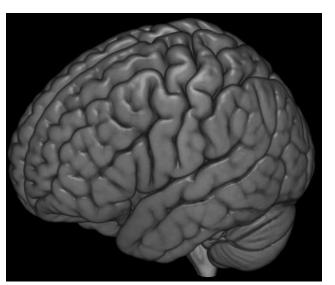
# Spatial normalization

Morph an individual's brain to a common template to examine activation in the same voxels across subjects

We are using the Montreal Neurological Institute (MNI) template, which is the average of 152 brains

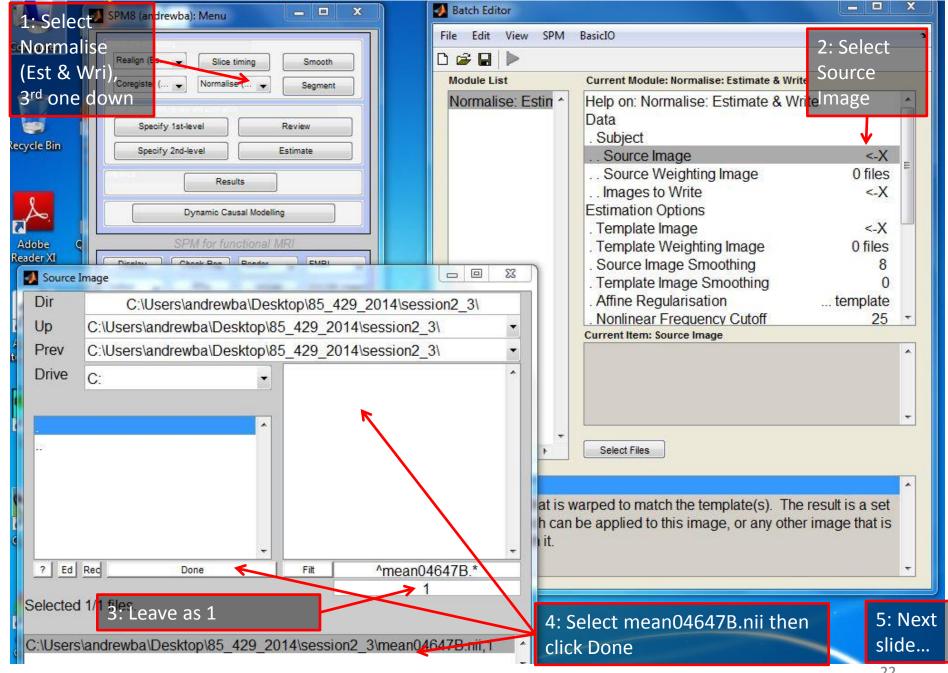
(Too perfect-looking to be an actual brain...) →

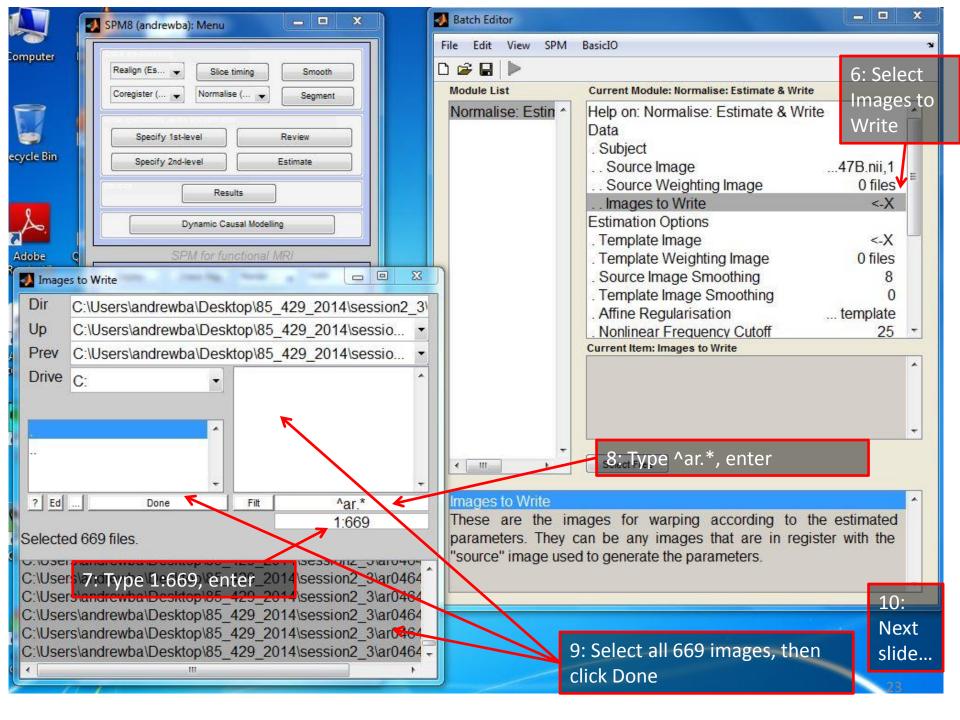


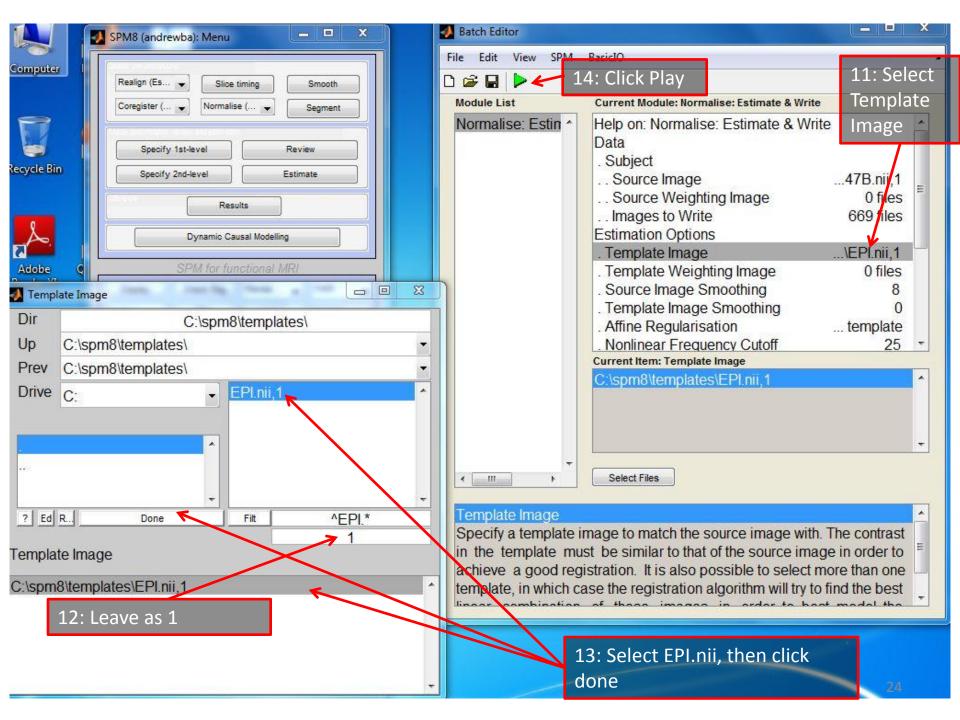


A person's real brain









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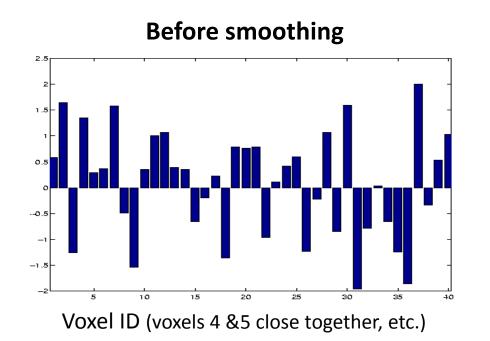
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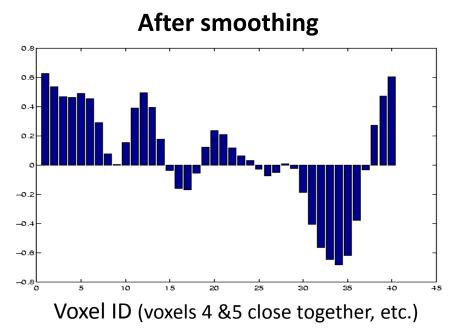
### 4. Smoothing

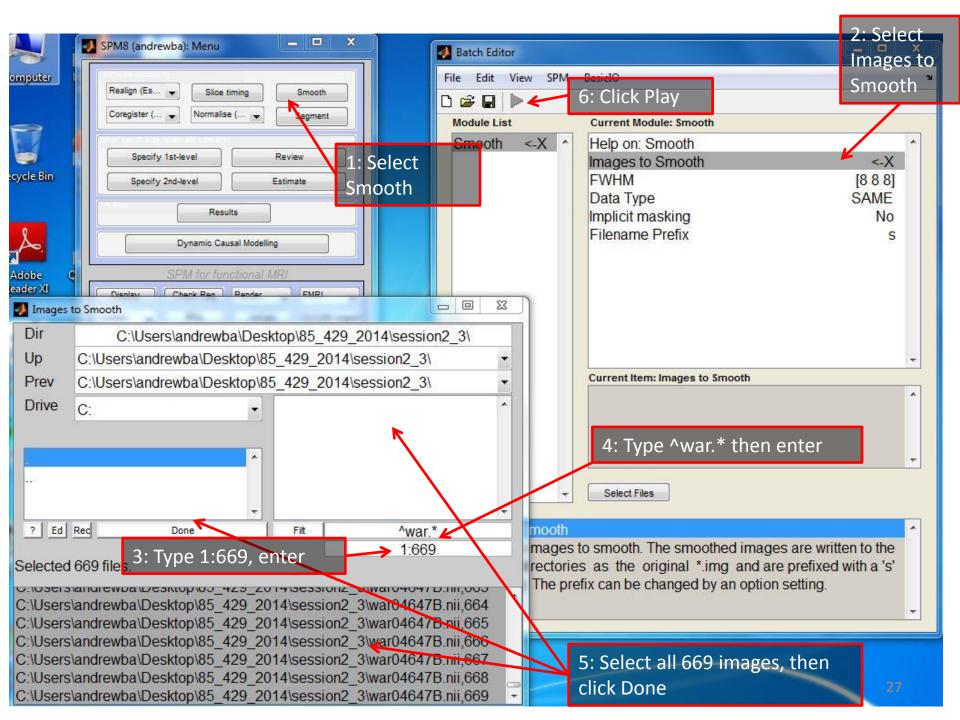
Reduces amount of noise per voxel by averaging over nearby voxels

# **Smoothing**

- Assumes (reasonably) that adjacent voxels contain neurons that have same or very similar functions
- Averages signals of neighboring voxels to filter out "noise" and boost "real" activation







# Final notes about data preprocessing

 Although some preprocessing always necessary, all steps can result in *loss* of data

- Smoothing (previous slide) is vulnerable to this
  - Lose small fluctuations in data that might be real
    - Some techniques can address this problem (later in lab)

- Another vulnerable step is spatial normalization
  - Lose individual quirks of a person's data

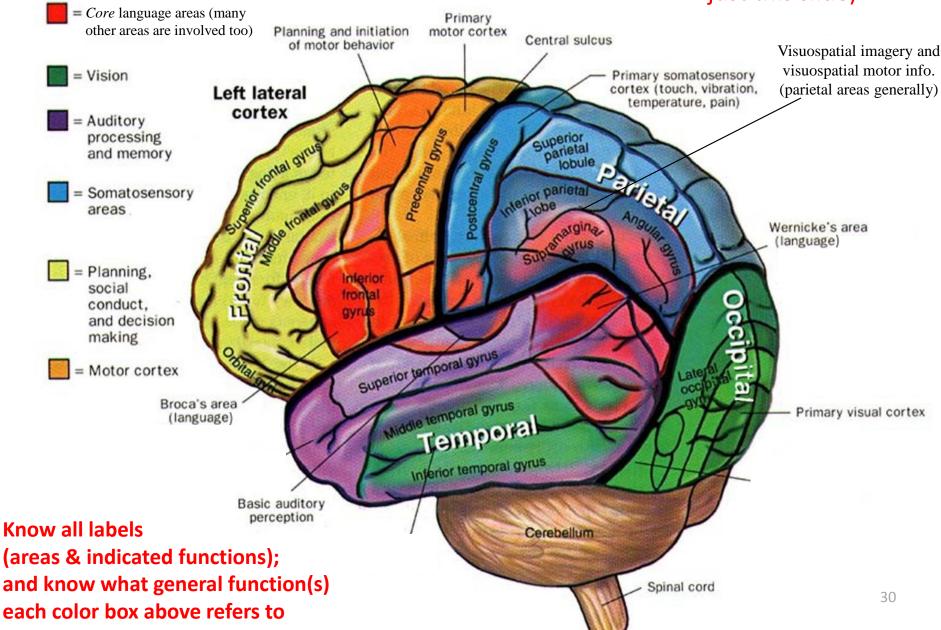
# Final notes about data preprocessing

 All steps can also result in artificial creation of seemingly real data

- Again, smoothing is vulnerable to this
  - If one voxel's activation level is high due to error/random chance, then averaging it in with other voxels will spread this error to other voxels, leading to a false cluster of activation

## General functional neuroanatomy (Quiz no. 2

just this slide)



## References

Just, M. A., Cherkassky, V. L., Aryal, S., & Mitchell, T. M. (2010). A neurosemantic theory of concrete noun representation based on the underlying brain codes. *PLoS One*, *5*(1), e8622. doi:10.1371/journal.pone.0008622

Mitchell, T. M., Shinkareva, S. V, Carlson, A., Chang, K. M., Malave, V. L., Mason, R. A, & Just, M. A. (2008). Predicting human brain activity associated with the meanings of nouns. *Science* (New York, N.Y.), 320(5880), 1191–5. doi:10.1126/science.1152876