

# Preprocessing

*What is it and why do we bother?*

*Some is adapted from Luiz's powerpoints!*

# What is the goal of fMRI studies?

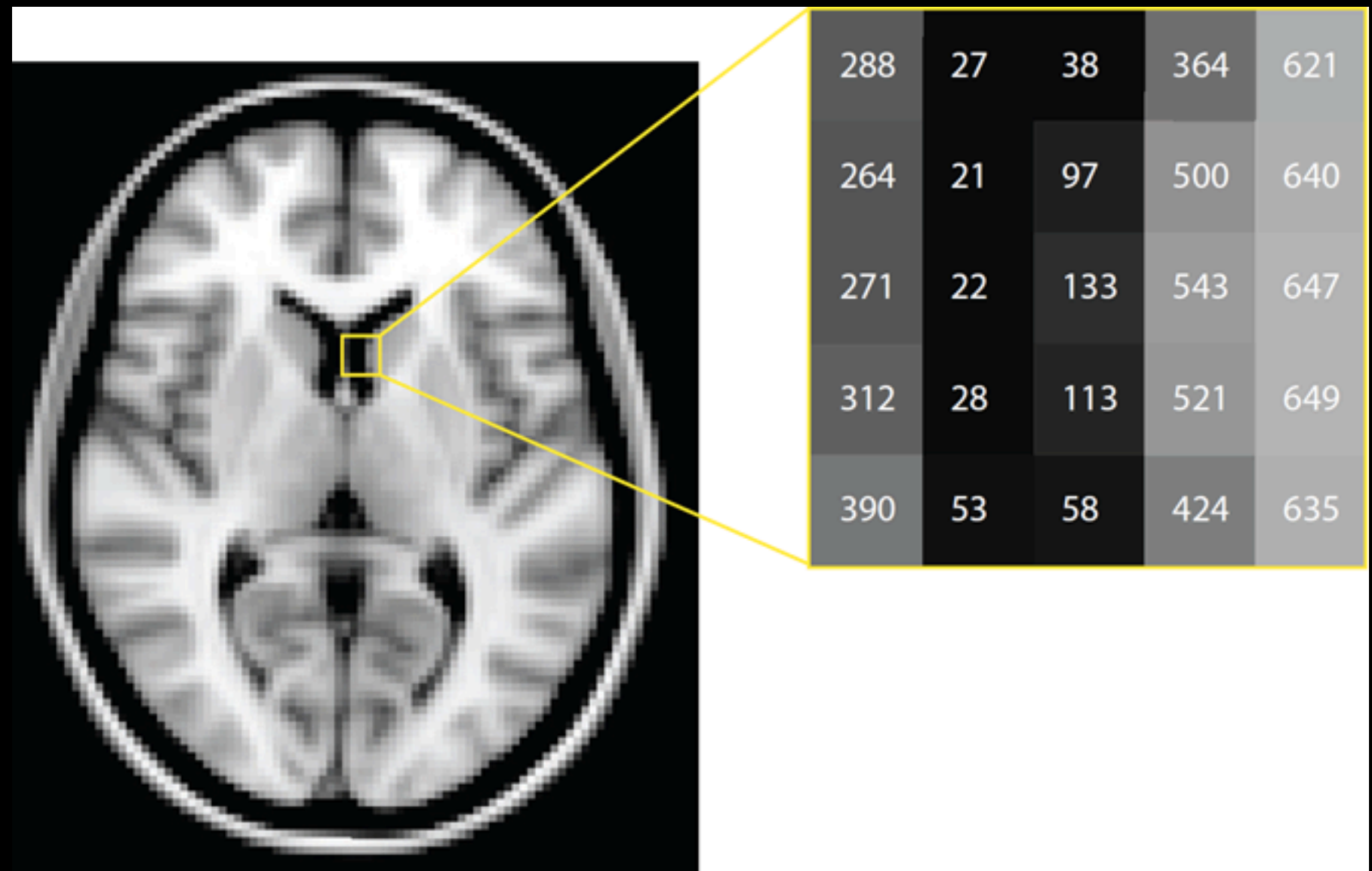
- Generally not to study individual differences, but to study effects in *groups* of people.



- If all brains are different shapes, how can we relate what happens in your brain to what is happening in my brain?
  - *Not to mention brains will not be in the exact same space when they are scanned!*
- What do we have to do to make brain data across individuals comparable?

# What is a brain image?

- “A graphical representation of a matrix” AKA a grid of voxels



# Preprocessing: a brief overview (don't stress about it too much)

There are six steps we take to prepare brain data for analysis. These are all meant to improve the signal of the data and eliminate extraneous things that will make our lives difficult.

1. Slice timing correction
2. Motion correction
3. Distortion correction
4. Coregistration
5. Normalization
6. Temporal and spatial filtering

# Slice Timing Correction

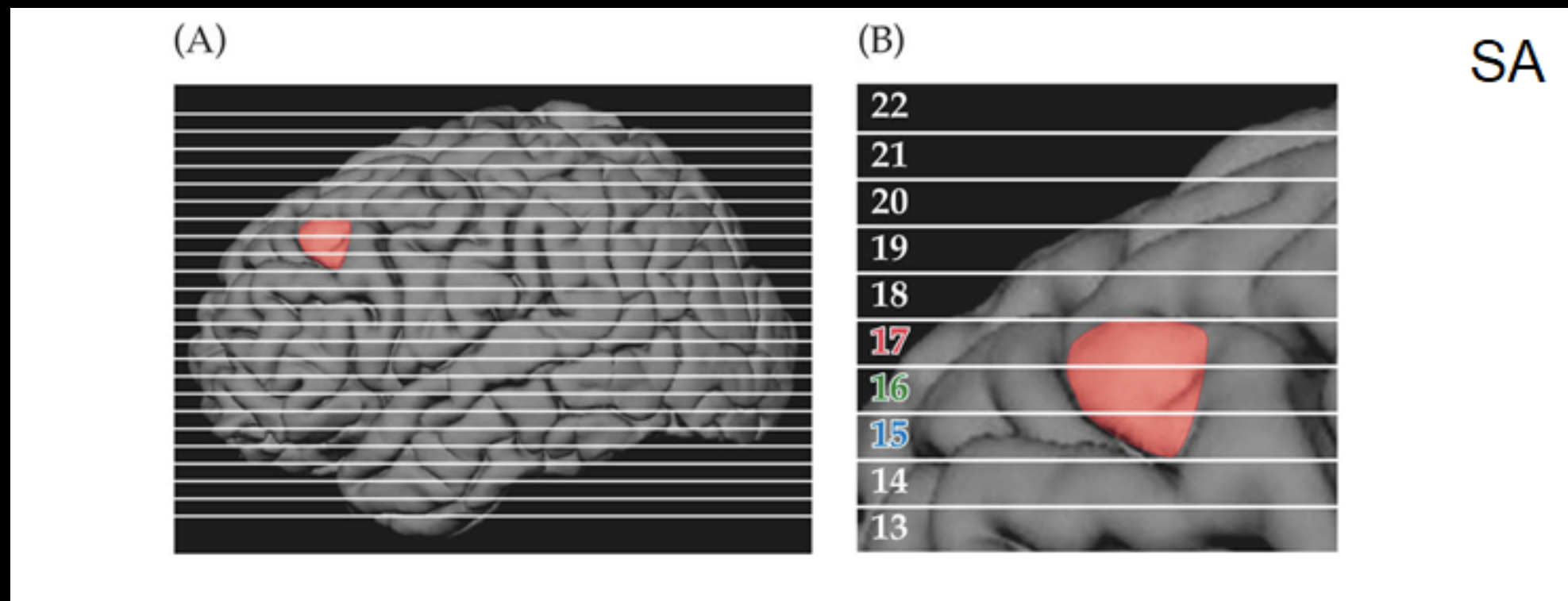
- fMRI data are acquired one slice at a time, typically 20-30 slices within 3 seconds!
- These slices are taken in an interleaved fashion
  - eg, odd slices are taken on first pass, evens on the way back
  - This means each slice is taken at a different time point



# Slice Timing Correction II

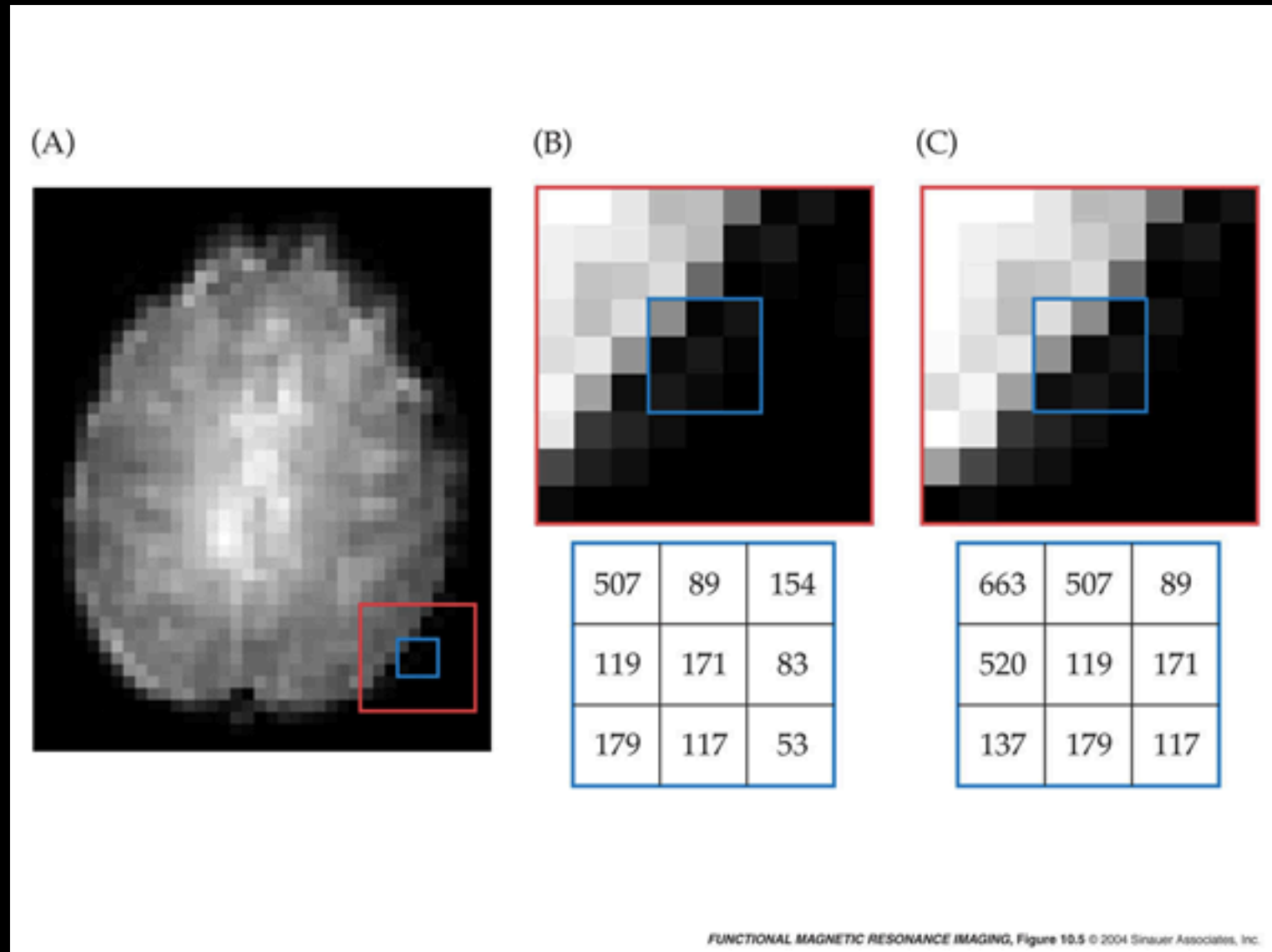
- Given what we know about the hemodynamic response, could this be an issue?

- 



# Head Motion

- Scanners have no way of knowing the exact position of the brain.
- When a participant moves, each voxel's data will come from multiple brain areas!
- We tend to use short runs to avoid motion related to fatigue



# Correcting for head motion

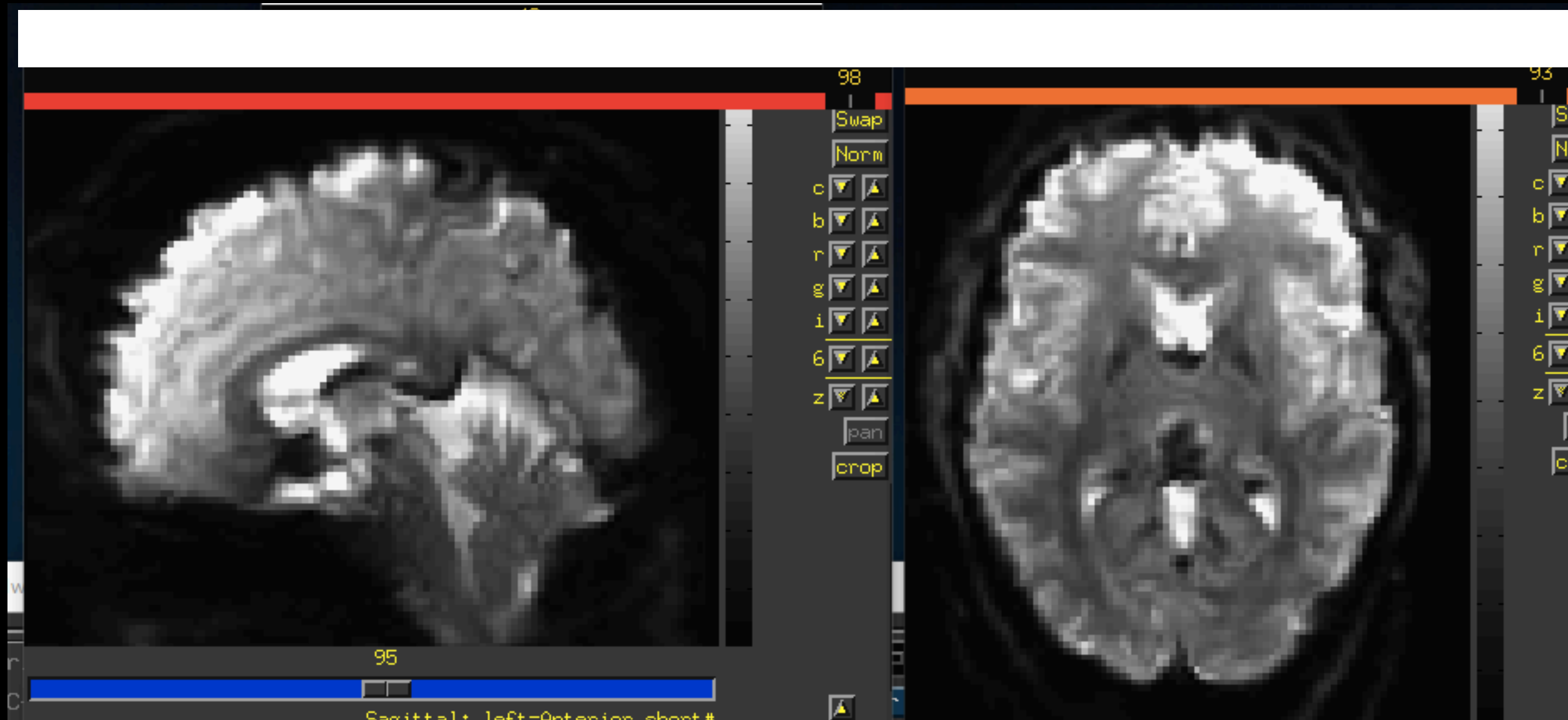
- We can try to adjust each image so that the brain is in the same position in every image using **Coregistration**.
  - This aligns all images to a single reference volume — generally the first, middle or last image of the time series.



# Correcting for head motion

## II

- We also use registration and transformation.
  - Registration: determine the 6 parameters that describe the **rigid body transformation** between each image and the reference image.
    - 3 translations (x-, y-, and z- axis)
    - 3 rotations (x-y, x-z, and y-z planes)
      - Also called “Pitch”, “Yaw”, and “Roll”
  - **Transformation:** resampling each image according to registration parameters
- This process is never perfect! It's always easiest to try to avoid a lot of motion to begin with.



- Just an example of distortions head motion can cause even AFTER preprocessing

# Coregistration of Functional and Structural Images

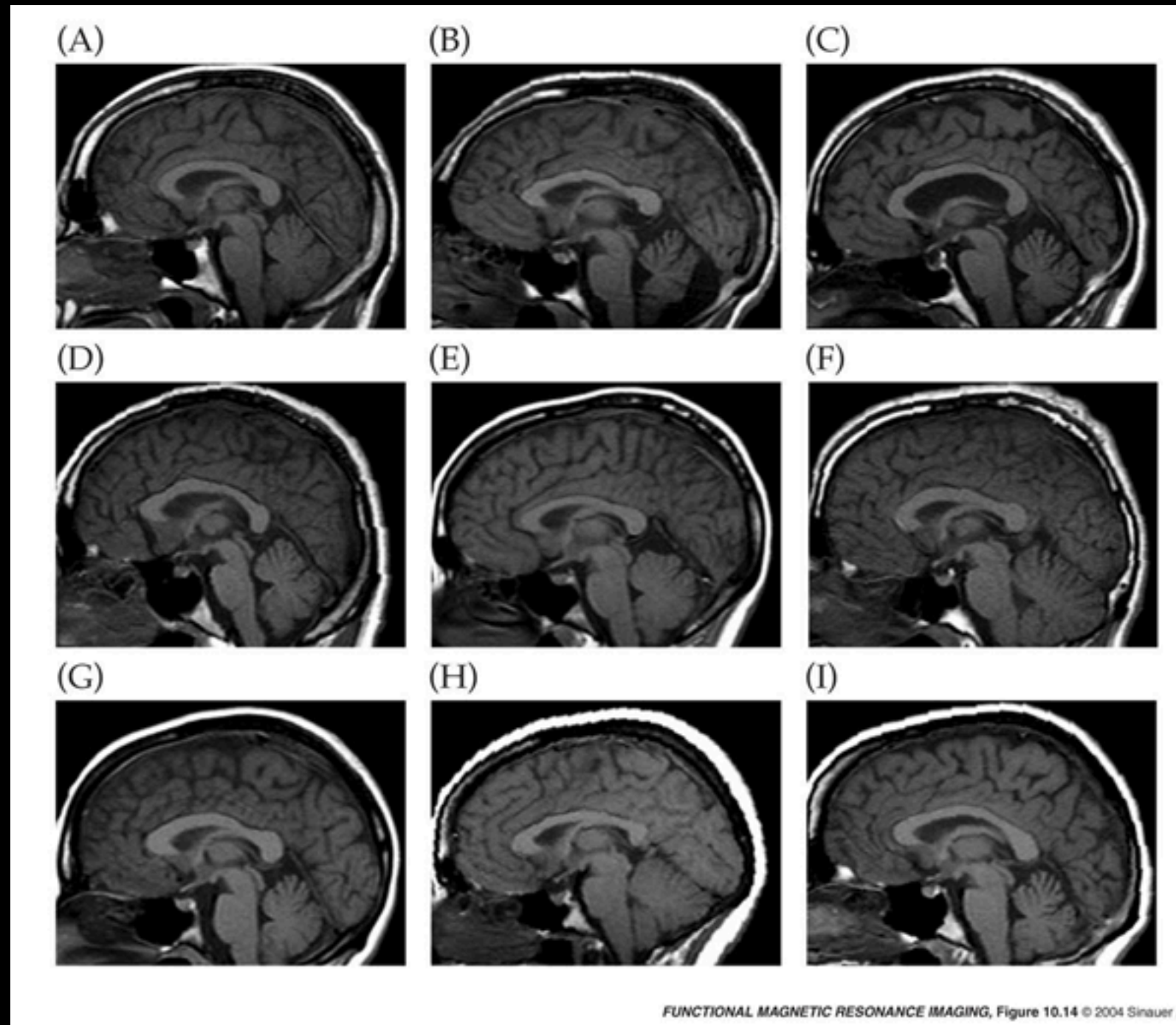
- While at the scanner, we take high resolution structural images to get a good sense of brain shape and structure. Structural images do not record any temporal (data over time) information, so it does not matter if it is slow. **These are MRI images.**
  - *This is why the T1 image takes 6 minutes to create.*
- Our functional images (data take during experiment) are generally very low quality because we are trying to get as many as we can to avoid gaps in our data. **These are *functional* MRI images.**
  - *Remember, one full brain scan happens every 3 seconds or so!*

# Coregistration of Functional and Structural Images

- While structural and functional images are roughly aligned with each other if obtained during the same scanning session, things like movement require them to be **coregistered** through rigid-body transformation

# Spatial normalization

Back to the issue of brains being different...



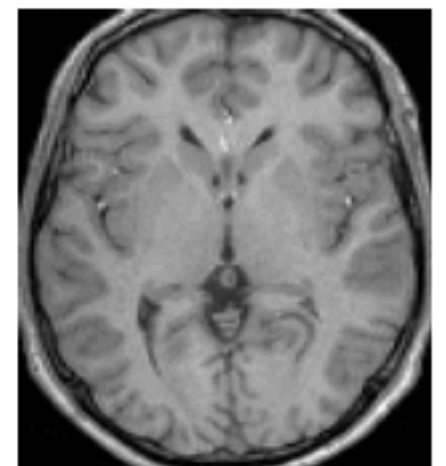
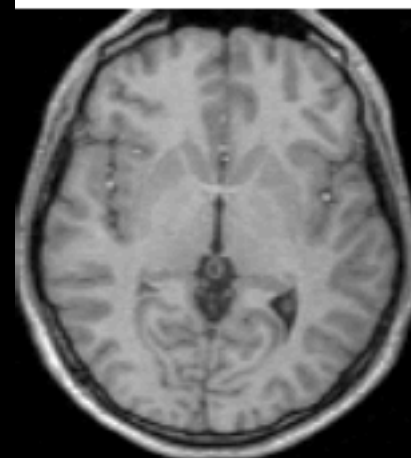
# Standard Space

- We typically transform brain data to fit a template brain, often referred to as **standard space** or **stereotactic space**.
- These days, it's often to fit the coordinate space developed by the Montreal Neurological Institute based on a large number of scans — referred to as **MNI space**.
- Once brains are transformed to fit into MNI space, we are able to compare regions across brains.

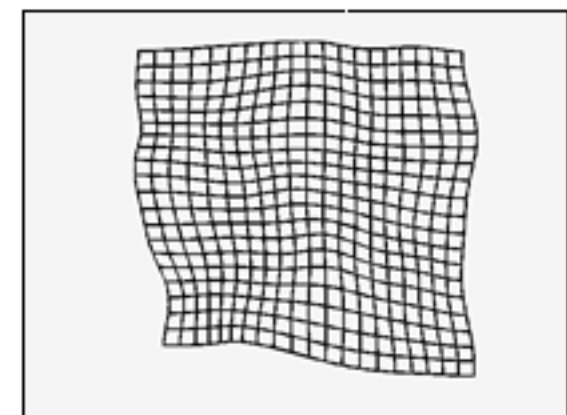
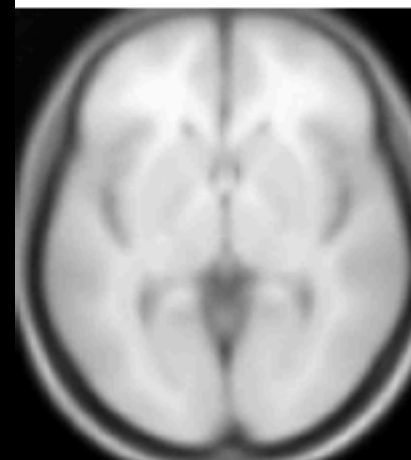
# Standard Space

We compensate for differences in brains by translating, rotating, stretching, and warping each brain to fit into a **standard space**.

- This process is not perfect, of course. But it allows us to generalize results to populations, provides a common coordinate space for reporting, and allows us to average across participants.



Spatial Normalisation



# Spatial filtering

- fMRI data are often smoothed/blurred in space
- This makes each voxel's data a result of applying a "weighted region of interest"
- While this seems counterintuitive, smoothing increases our signal to noise ratio because noise from one voxel cancels out another voxel's



# Signal to Noise

# What is in an MR signal?

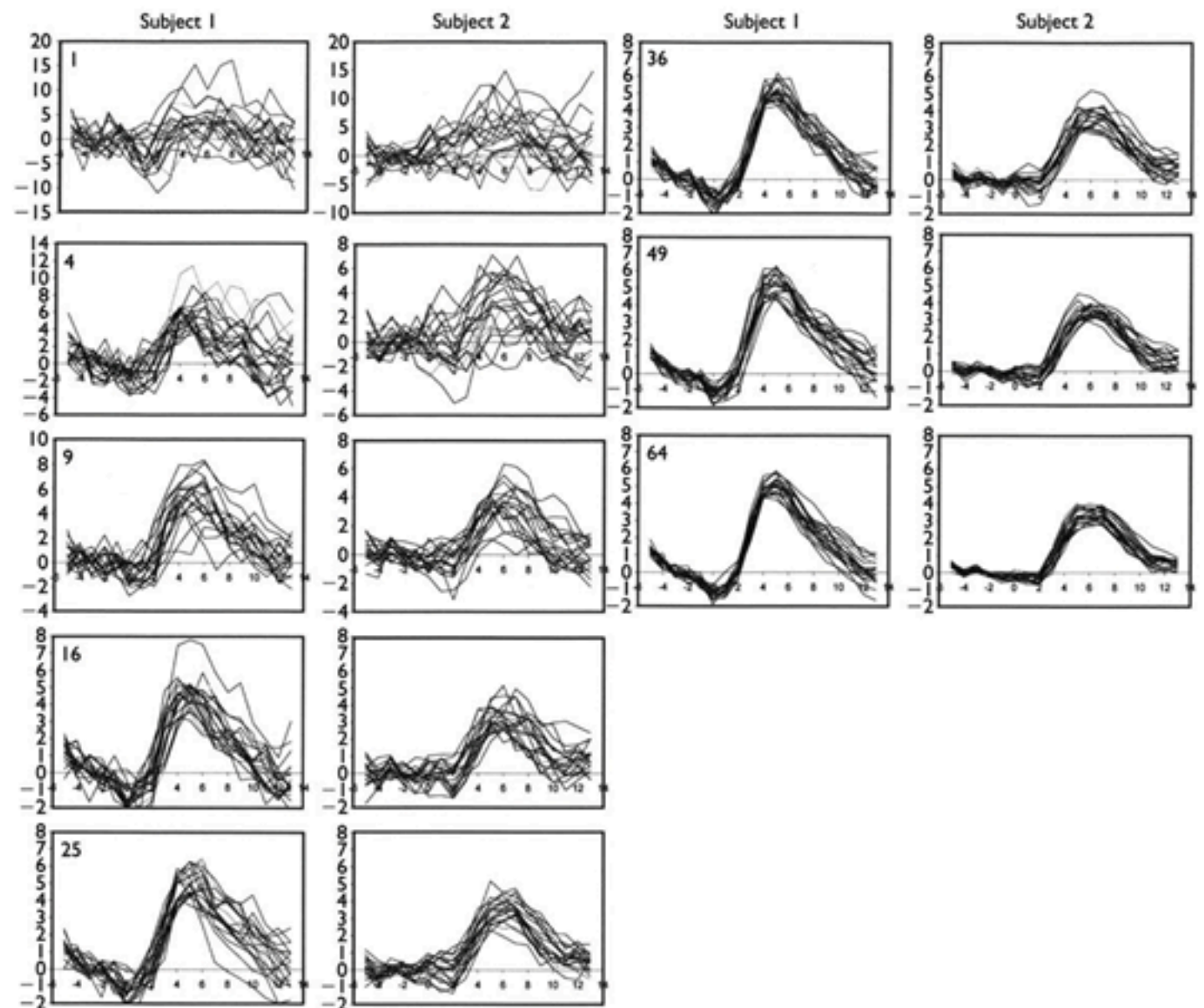
Changes in:

- Head motion
- Heart rate
- Respiration
- Scanner temperature
- Subject temperature
- Any other source of noise you can think of!

*Oh yeah, the BOLD signal change... That's only about 0.5-1% of the signal change*

# To increase SNR we average!

- This is why we want as many repetitions of trial types as possible and as many participants as possible!
- We are able to average the signal, allowing noise to “cancel” itself out as much as possible.



# General Linear Model (GLM)

AKA regression analysis

- Any phenomenon is impacted by multiple factors
- We use GLM to attempt to explain as much variance in a signal as possible.