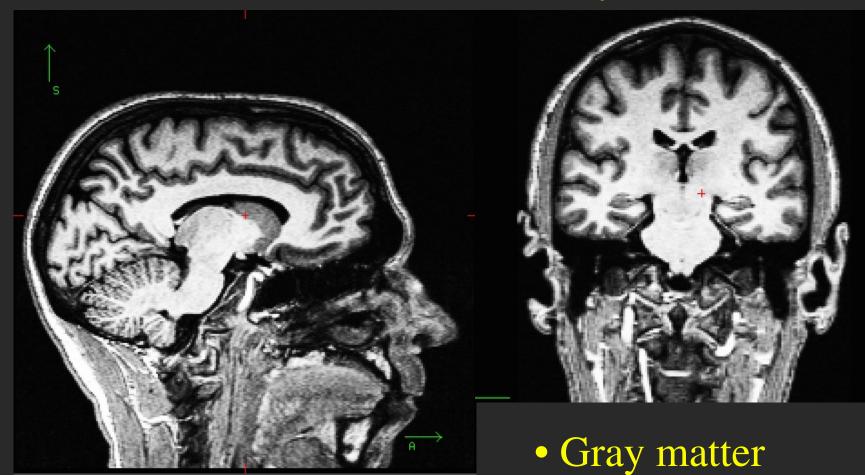
Basics of fMRI Analysis: Preprocessing, First Level Analysis, and Group Analysis



Overview

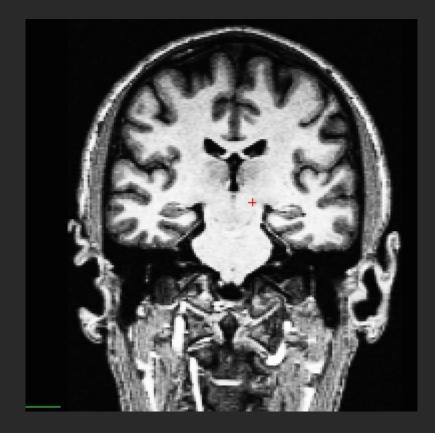
- Neuroanatomy 101 and fMRI Contrast Mechanism
- Preprocessing
- Hemodynamic Response
- "Univariate" GLM Analysis
- Hypothesis Testing
- Group Analysis (Random, Mixed, Fixed)

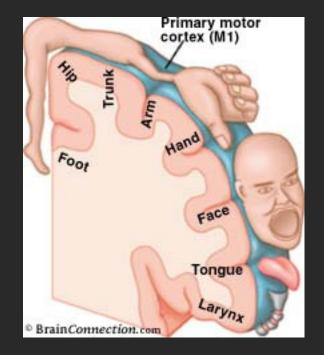
Neuroantomy



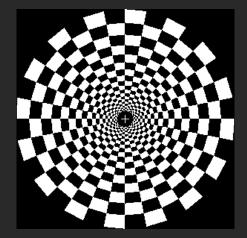
- White matter
- Cerebrospinal Fluid

Functional Anatomy/Brain Mapping



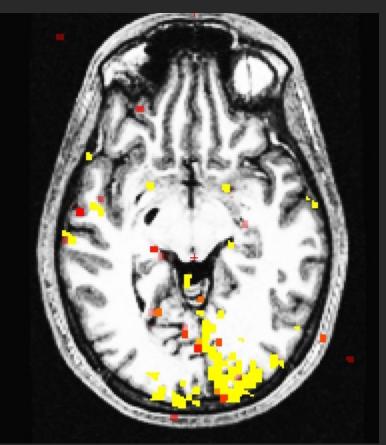


Visual Activation Paradigm



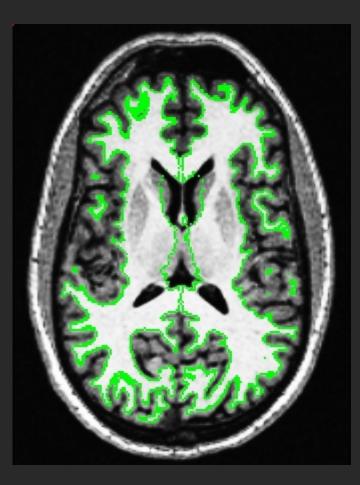
Flickering Checkerboard

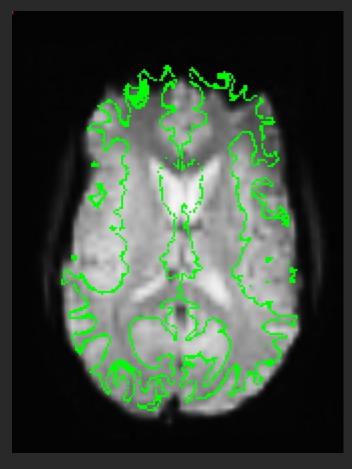
Visual, Auditory, Motor, Tactile, Pain, Perceptual, Recognition, Memory, Emotion, Reward/Punishment, Olfactory, Taste, Gastral, Gambling, Economic, Acupuncture, Meditation, The Pepsi Challenge, ...



- Scientific
- Clinical
- Pharmaceutical

Magnetic Resonance Imaging

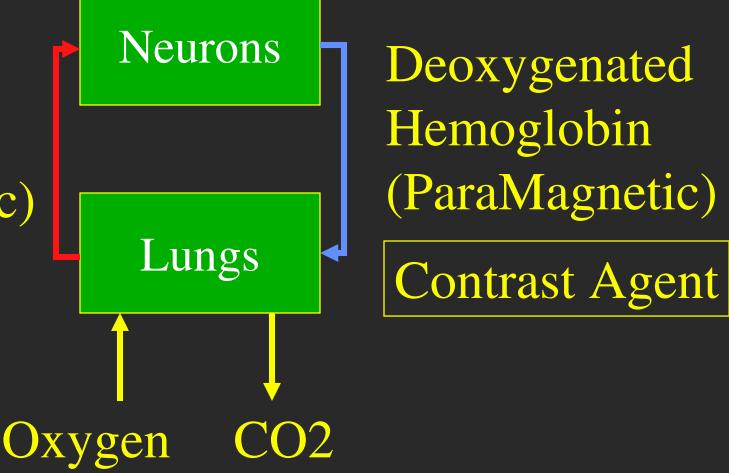




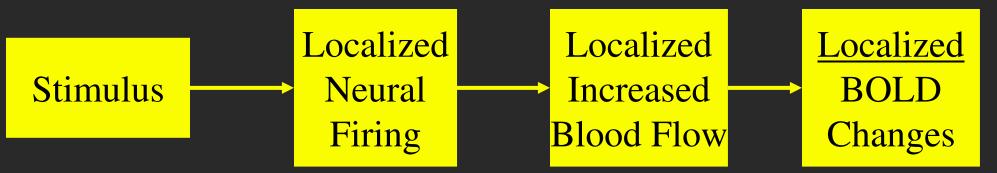
T1-weighted Contrast BOLD-weighted Contrast

Blood Oxygen Level Dependence (BOLD)

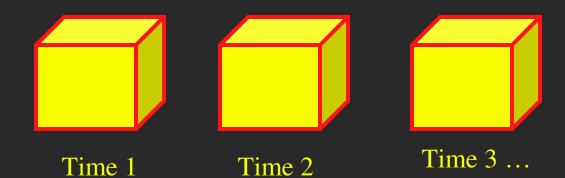
Oxygenated Hemoglobin (DiaMagnetic)



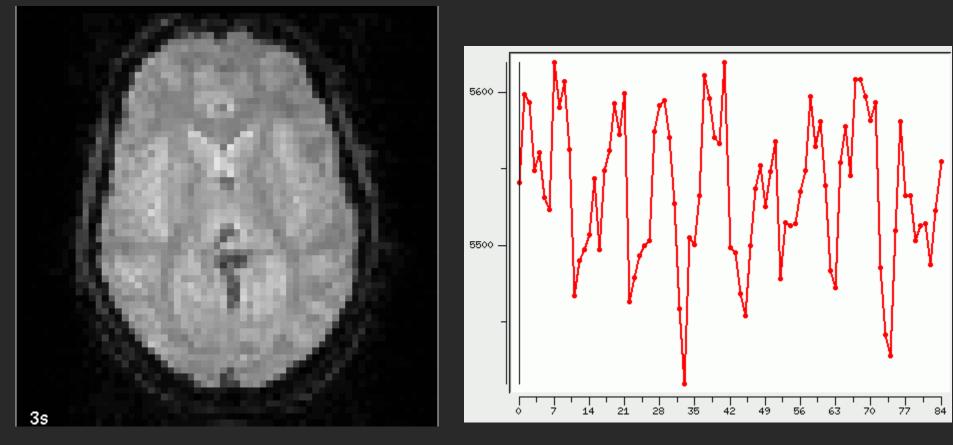




Sample BOLD response in 4D Space (3D) – voxels (64x64x35, 3x3x5mm^3, ~50,000) Time (1D) – time points (100, 2 sec) – Movie



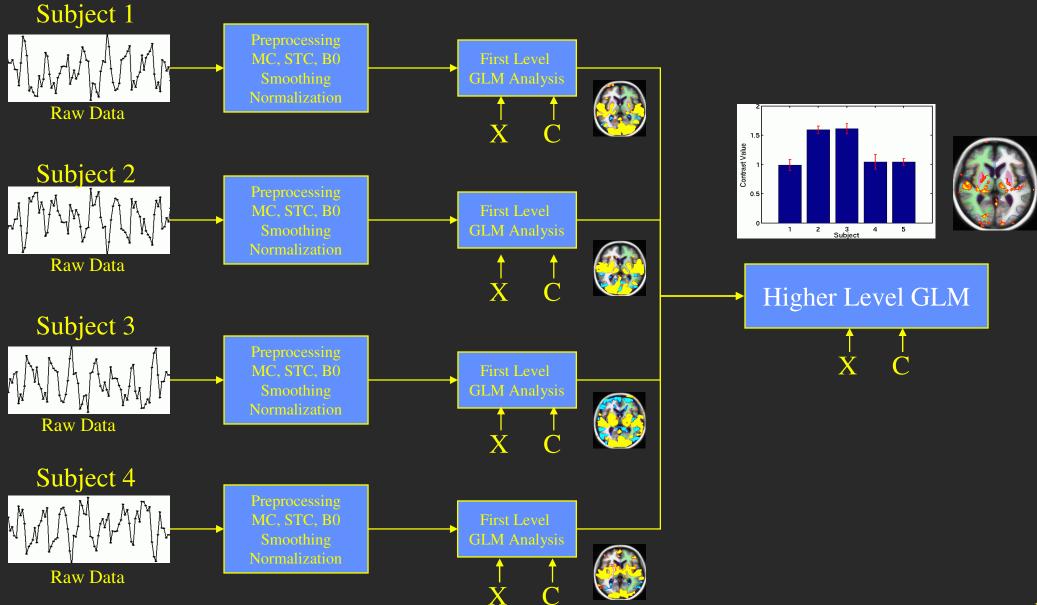






85x1

fMRI Analysis Overview



Preprocessing

• Assures that assumptions of the analysis are met

- Time course comes from a single location
- Uniformly spaced in time
- Spatial "smoothness"
- Analysis separating signal from noise

Preprocessing

- Start with a 4D data set
- 1. Motion Correction
- 2. Slice-Timing Correction
- 3. B0 Distortion Correction
- 4. Spatial Normalization
- 5. Spatial Smoothing
- End with a 4D data set
- Can be done in other orders
- Not everything is always done

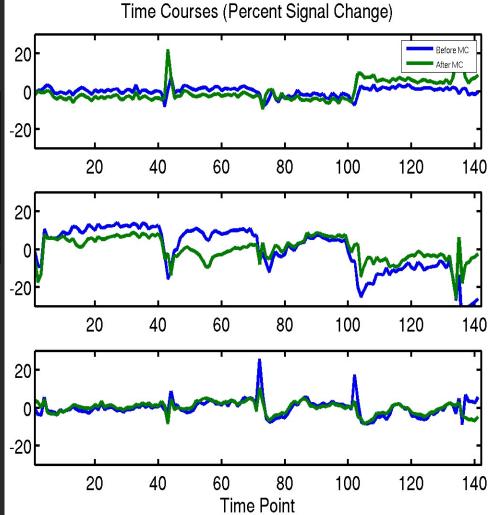
Motion

- Analysis assumes that time course represents a value from a single location
- Subjects move
- Shifts can cause noise, uncertainty
 - Edge of the brain and tissue boundaries

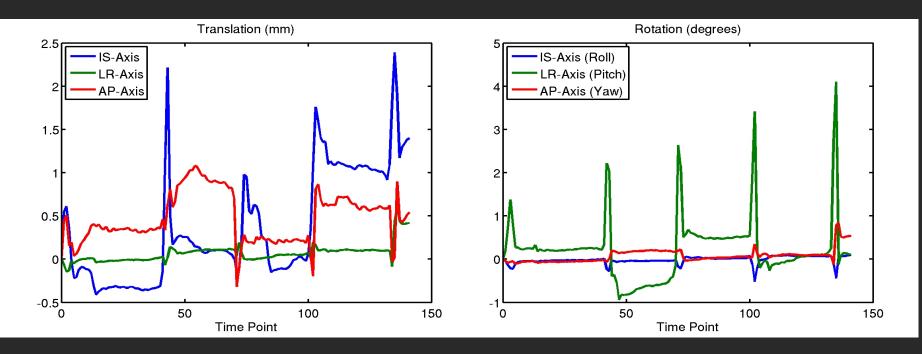
Motion and Motion Correction



Motion correction reduces motionNot perfect

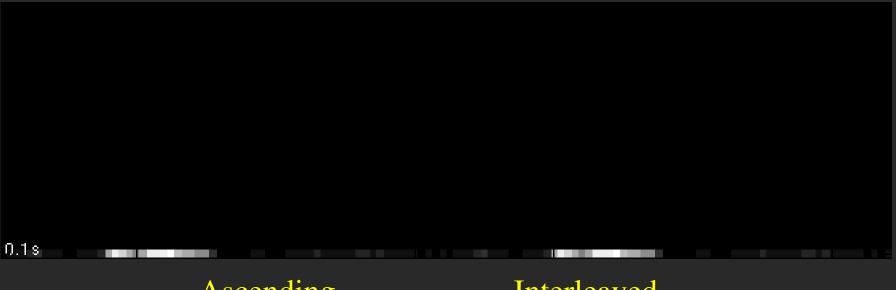


Motion Correction



- Motion correction parameters
- Six for each time point
- Sometimes used as nuisance regressors
- How much motion is too much?





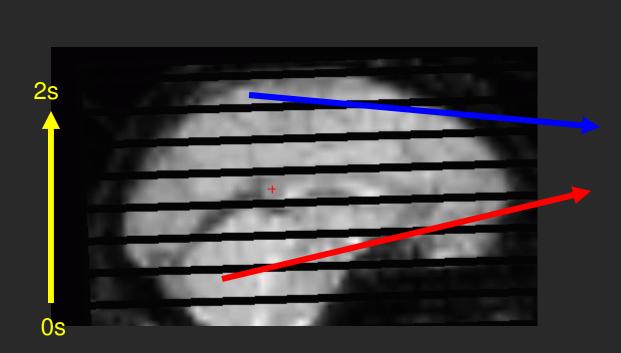
Ascending

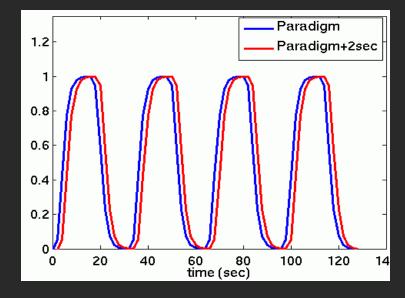
Interleaved

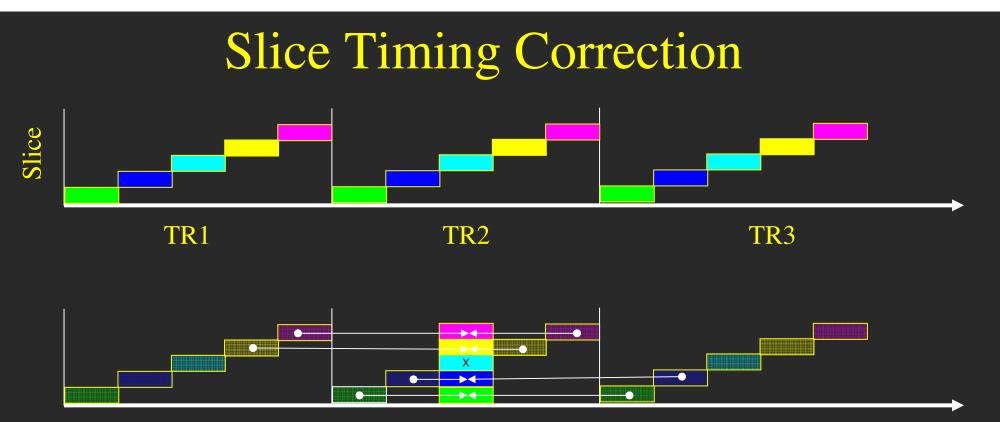
- Volume not acquired all at one time
- Acquired slice-by-slice
- Each slice has a different delay

Effect of Slice Delay on Time Course

- Volume = 30 slices
- TR = 2 sec
- Time for each slice = 2/30 = 66.7 ms

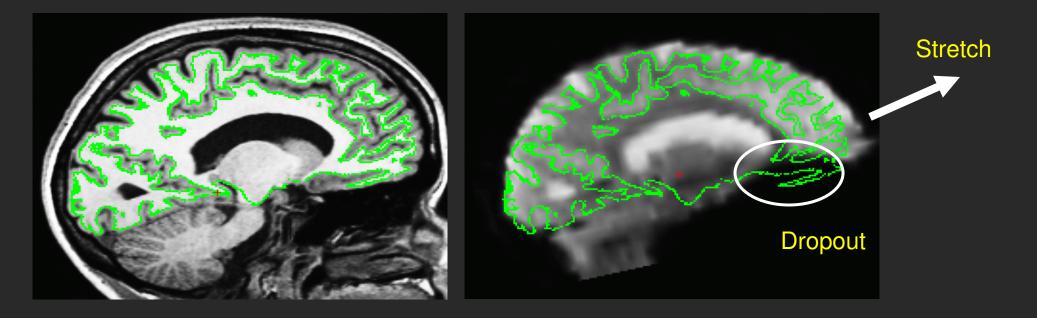






- Temporal interpolation of adjacent time points
- Usually sinc interpolation
- Each slice gets a different interpolation
- Some slices might not have any interpolation
- Can also be done in the GLM
- You must know the slice order!

B0 Distortion



- Metric (stretching or compressing)
- Intensity Dropout
- A result of a long readout needed to get an entire slice in a single shot.
- Caused by B0 Inhomogeneity

B0 Map

Magnitude

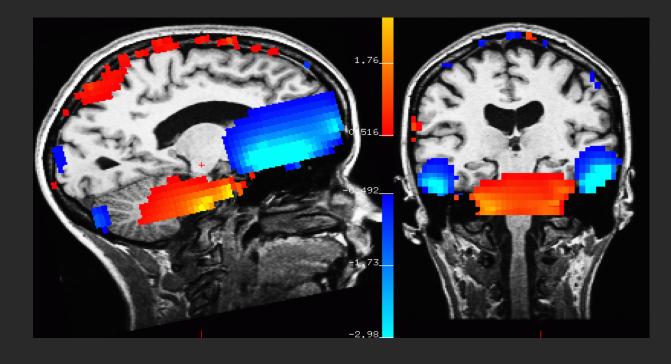
Phase

Echo 1 TE1

Echo 2 TE2

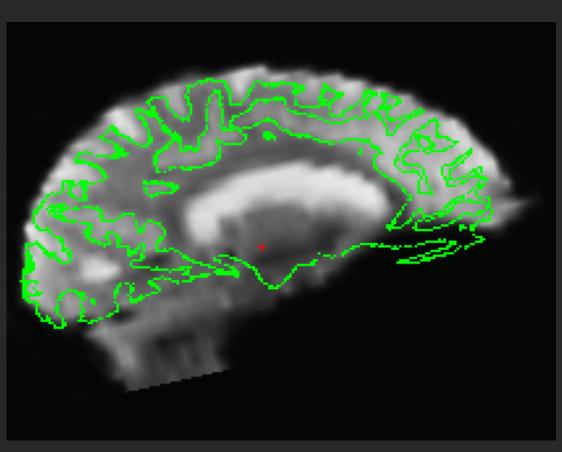


Voxel Shift Map



- Units are voxels (3.5mm)
- Shift is in-plane
- Blue = $P \rightarrow A$, Red $A \rightarrow P$
- Regions affected near air/tissue boundaries
 - sinuses

B0 Distortion Correction



- Can only fix metric distortion
- Dropout is lost forever

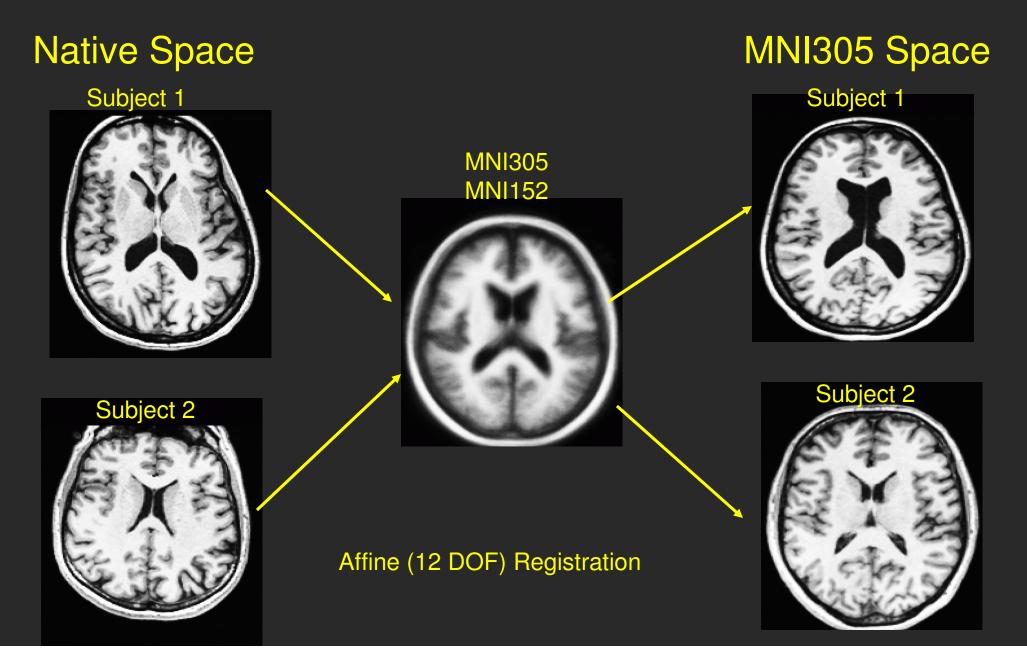
B0 Distortion Correction

- Can only fix metric distortion
- Dropout is lost forever
- Interpolation
- Need:
 - "Echo spacing" readout time
 - Phase encode direction
- More important for surface than for volume
- Important when combining from different scanners

Spatial Normalization

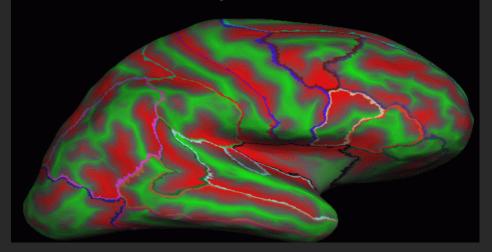
- Transform volume into another volume
 - Re-slicing, re-gridding
- New volume is an "atlas" space
- Align brains of different subjects so that a given voxel represents the "same" location.
- Similar to motion correction
- Preparation for comparing across subjects
- Volume-based
- Surface-based
- Combined Volume-surface-based (CVS)

Spatial Normalization: Volume

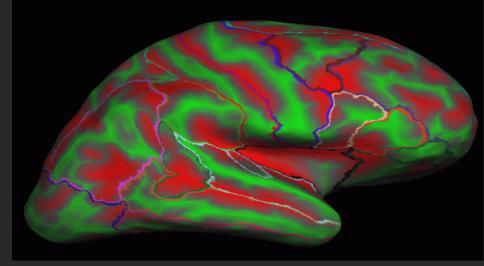


Spatial Normalization: Surface

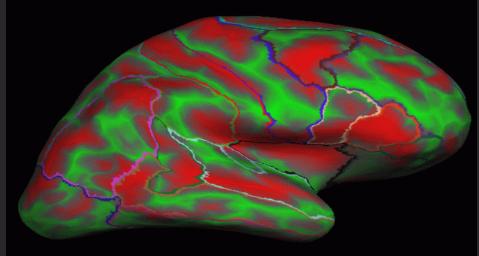
Subject 1



Subject 2 (After)



Subject 2 (Before)



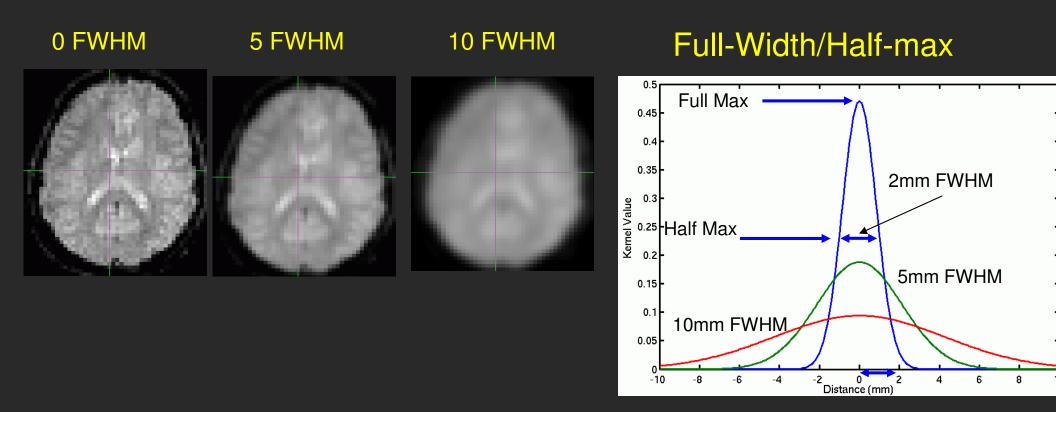
- Shift, Rotate, Stretch
- High dimensional (~500k)
- Preserve metric properties
- Take variance into account
- Common space for group analysis (like Talairach)

Spatial Smoothing

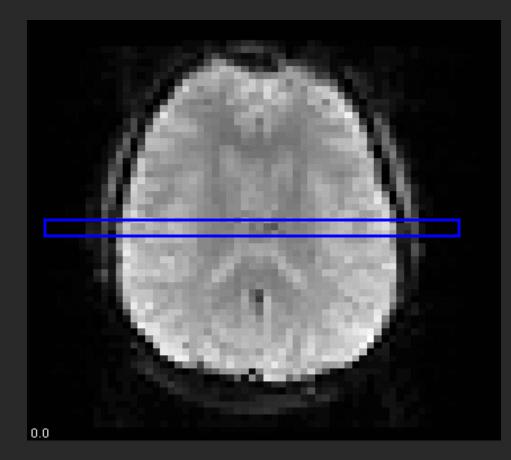
- Replace voxel value with a weighted average of nearby voxels (spatial convolution)
- Weighting is usually Gaussian
- 3D (volume)
- 2D (surface)
- Do after all interpolation, before computing a standard deviation
- Similarity to interpolation
- Improve SNR
- Improve Intersubject registration
- Can have a dramatic effect on your results

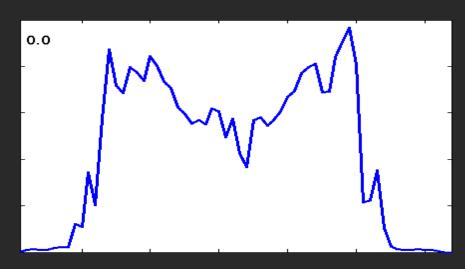
Spatial Smoothing

- Spatially convolve image with Gaussian kernel.
- Kernel sums to 1
- Full-Width/Half-max: FWHM = $\sigma/sqrt(log(256))$
- σ = standard deviation of the Gaussian

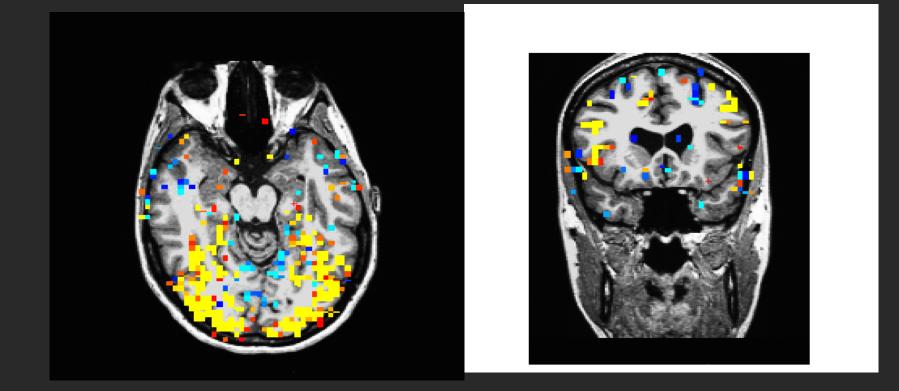


Spatial Smoothing



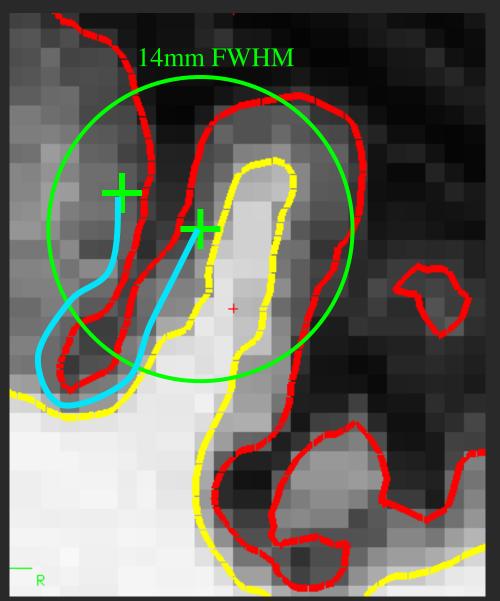


Effect of Smoothing on Activation



- Working memory paradigm
- FWHM: 0, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20

Volume- vs Surface-based Smoothing



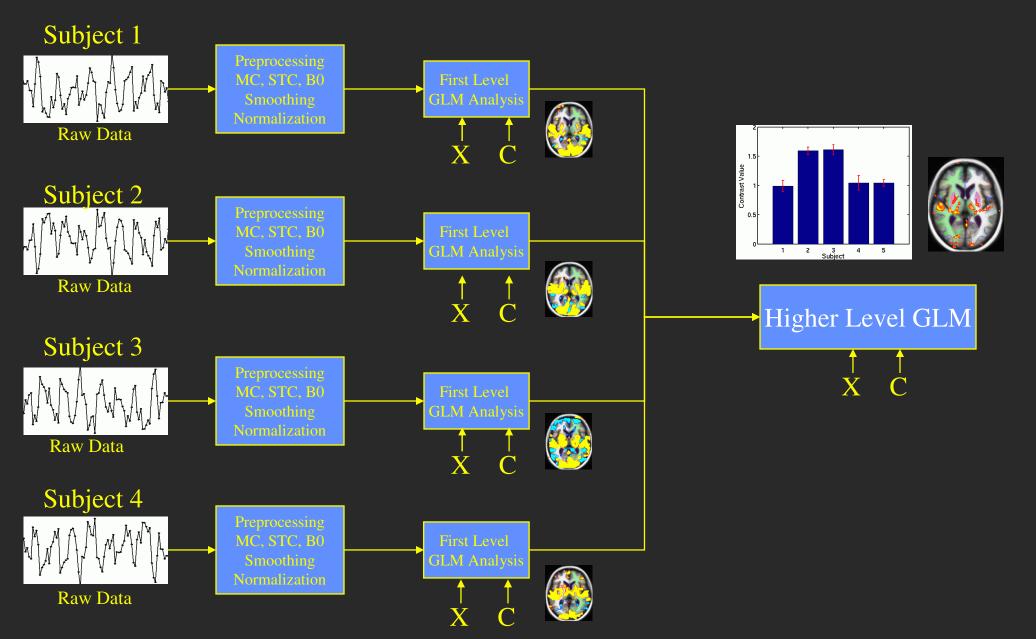
- 5 mm apart in 3D
- 25 mm apart on surface
- Averaging with other tissue types (WM, CSF)
- Averaging with other functional areas

Preprocessing

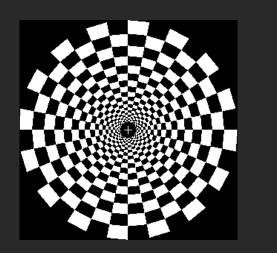
- Start with a 4D data set
- 1. Motion Correction Interpolation
- 2. Slice-Timing Correction
- 3. B0 Distortion Correction Interpolation
- 4. Spatial Normalization Interpolation
- 5. Spatial Smoothing Interpolation-like
- End with a 4D data set
- Can be done in other orders
- Not all are done

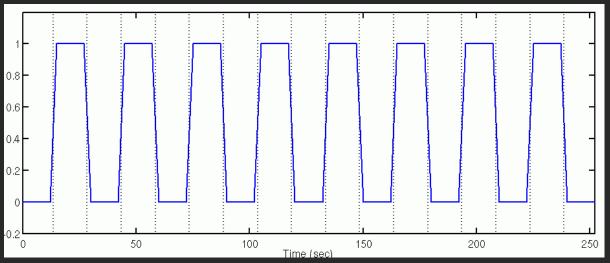
fMRI Time-Series Analysis

fMRI Analysis Overview

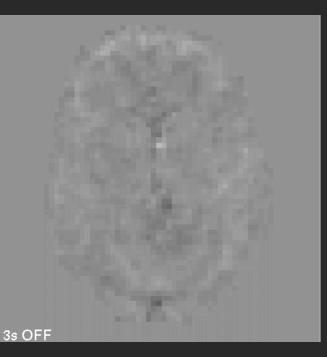


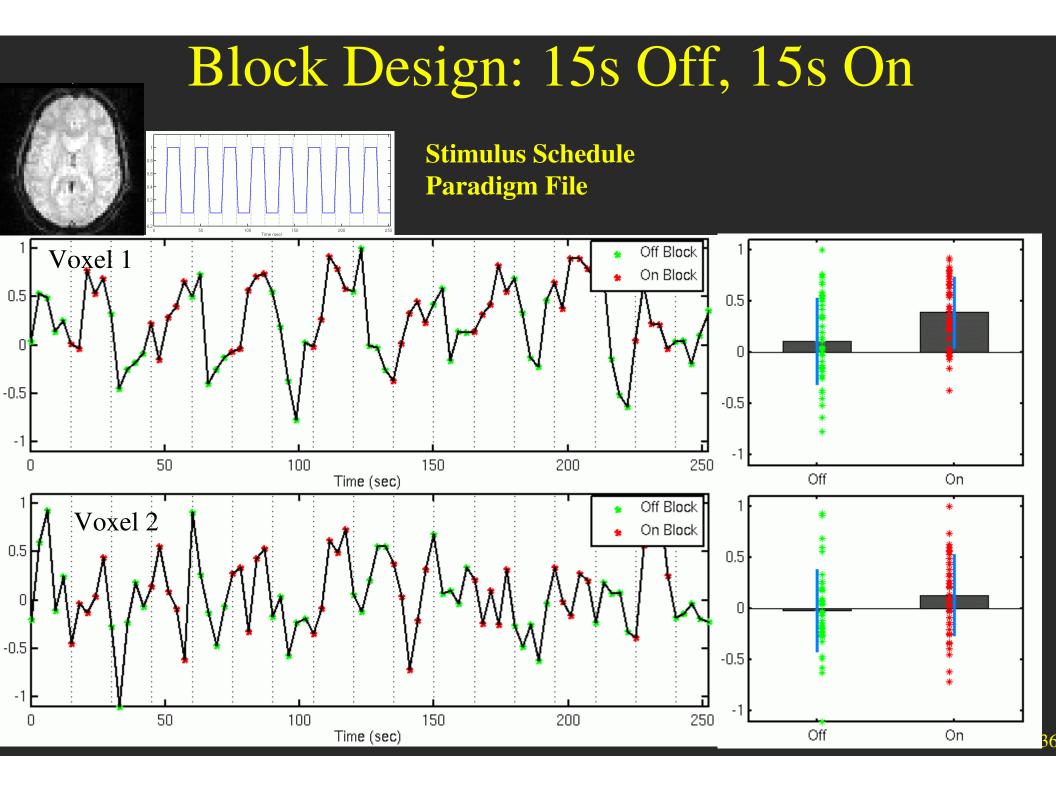
Visual/Auditory/Motor Activation Paradigm



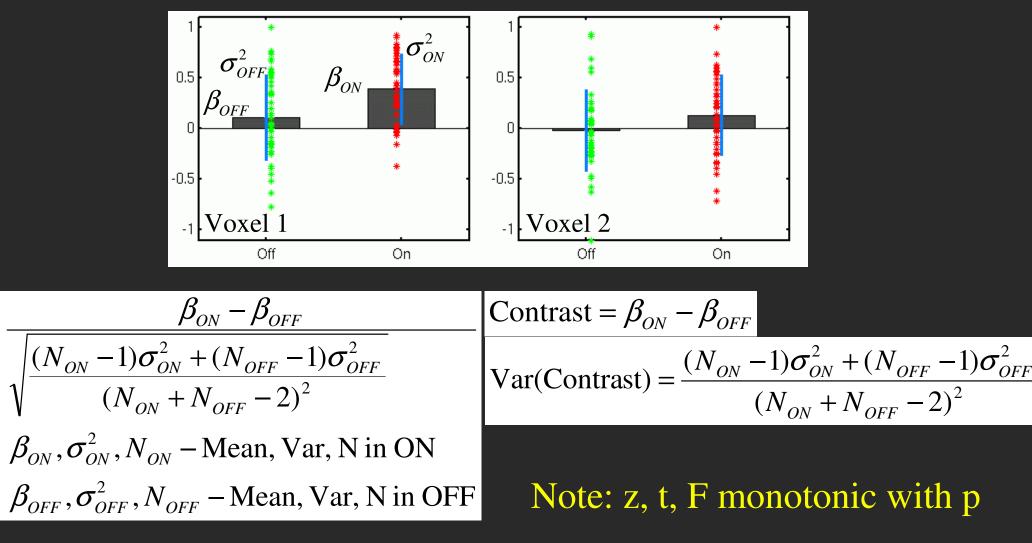


- 15 sec 'ON', 15 sec 'OFF'
- Flickering Checkerboard
- Auditory Tone
- Finger Tapping





Contrasts and Inference

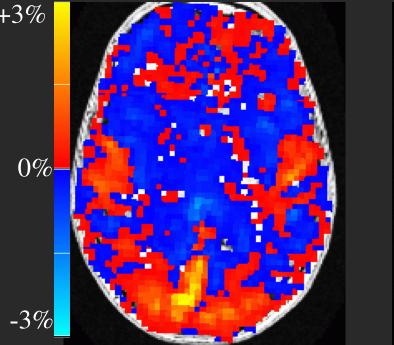


$$p = 10^{-11}$$
, sig=-log10(p) =11

p = .10, sig=-log10(p) =1

37

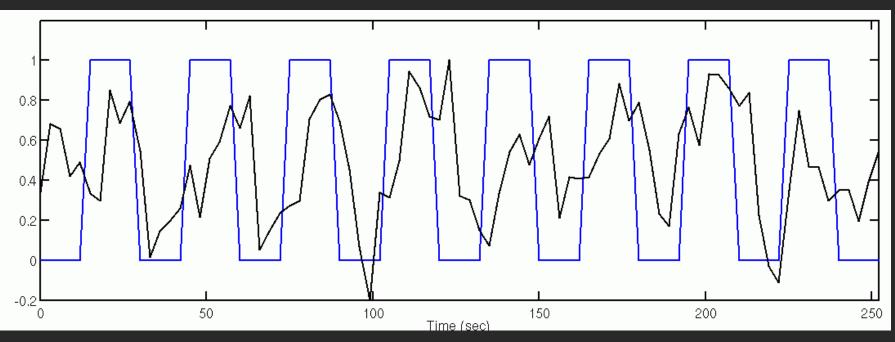
Statistical Parametric Map (SPM)



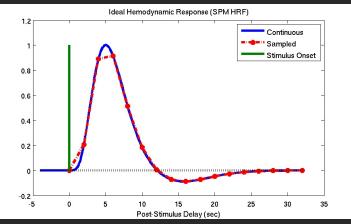
Contrast Amplitude CON, COPE, CES

"Massive Univariate Analysis" -- Analyze each voxel separately Contrast Amplitude Variance (Error Bars) VARCOPE, CESVAR Significance t-Map (p,z,F) (Thresholded p<.01) sig=-log10(p)

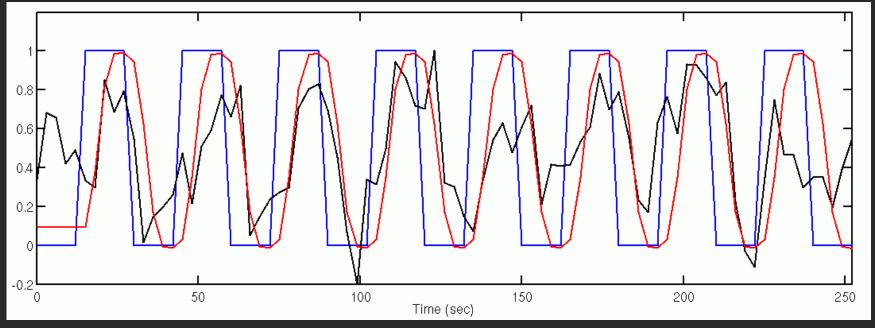
Hemodynamics



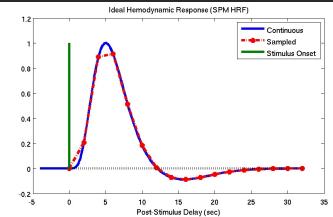
- Delay
- Dispersion
- Grouping by simple time point inaccurate



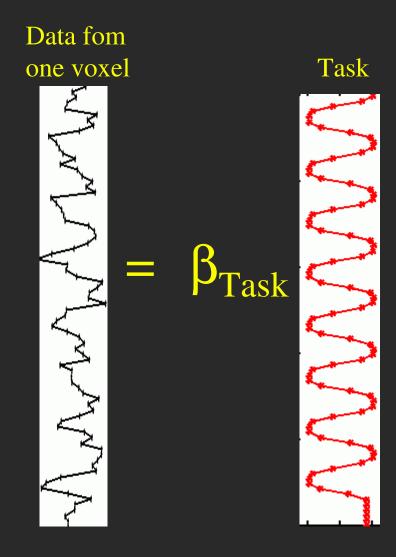
Convolution with HRF



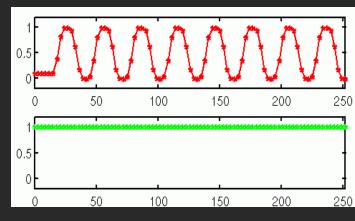
- Shifts, rolls off; more accurate
- Loose ability to simply group time points
- More complicated analysis
- General Linear Model (GLM)



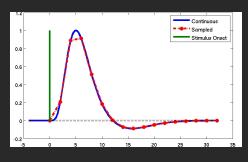
GLM



Baseline Offset (Nuisance) base



 $\beta_{\text{base}} = \beta_{\text{off}}$ $\beta_{\text{Task}} = \beta_{\text{on}} - \beta_{\text{off}}$ •Implicit Contrast •HRF Amplitude



Matrix Model

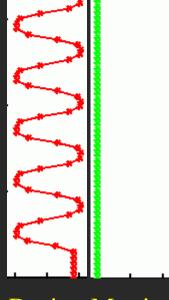
*

Observations

Data from

one voxel

De Re



Χ

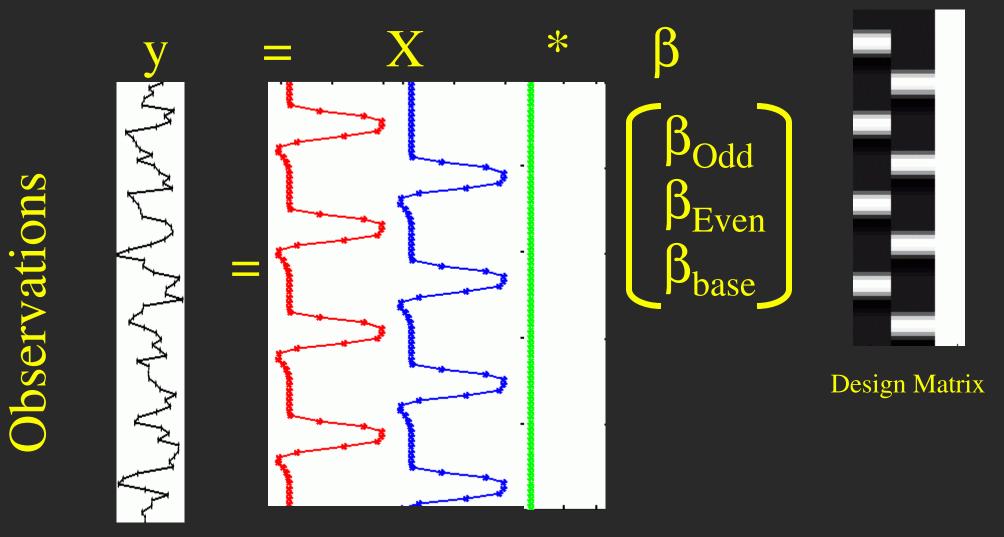
Design Matrix Regressors

ß β_{Task} base

Vector of Regression Coefficients ("Betas")

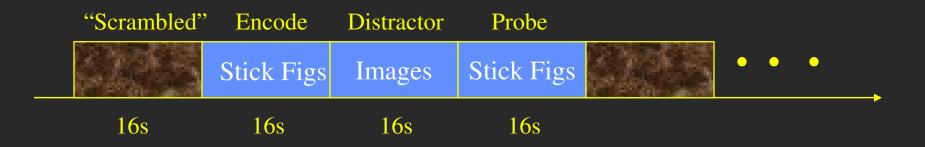
Design Matrix

Two Task Conditions



Data from one voxel Design Matrix Regressors

Working Memory Task (fBIRN)



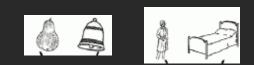
0. "Scrambled" – low-level baseline, no response
1. Encode – series of passively viewed stick figures
Distractor – respond if there is a face

- 2. Emotional
- 3. Neutral

Probe – series of two stick figures (forced choice)

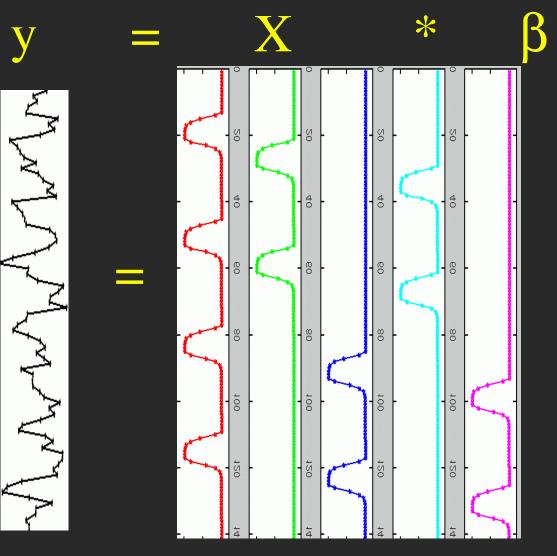
- 4. Following Emotional Distractor
- 5. Following Neutral Distractor

fBIRN: Functional Biomedical Research Network (www.nbirn.net)

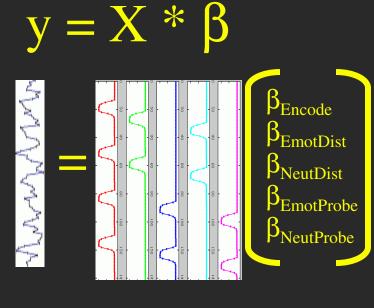




Five Task Conditions



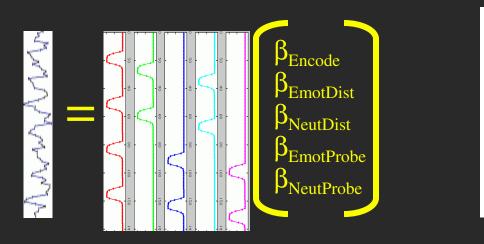
GLM Solution

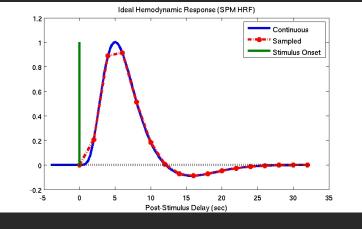


- Set of simultaneous equations
- Each row of X is an equation
- Each column of X is an unknown
- βs are unknown
- 142 Time Points (Equations)
- 5 unknowns

$$\hat{\boldsymbol{\beta}} = (X^T X)^{-1} X^T y$$

Estimates of the HRF Amplitude



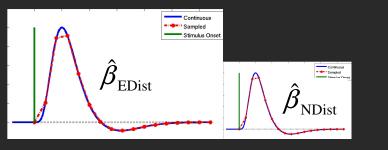


$y = X\beta + n, \quad \hat{\beta} = (X^T X)^{-1} X^T y$

 $\hat{\beta}_{\text{Encode}} = \text{Hemodynami} \text{ c amplitude in response to Encode}$ $\hat{\beta}_{\text{EmotDist}} = \text{Hemodynami} \text{ c amplitude in response to Emotional Distractor}$ $\hat{\beta}_{\text{NeutDist}} = \text{Hemodynami} \text{ c amplitude in response to Neutral Distractor}$ $\hat{\beta}_{\text{EmotProbe}} = \text{Hemodynami} \text{ c amplitude in response to Probe following Emotional Distractor}$ $\hat{\beta}_{\text{NeutProbe}} = \text{Hemodynami} \text{ c amplitude in response to Probe following Neutral Distractor}$

Hypotheses and Contrasts

Which voxels respond more/less/differently to the Emotional Distractor than to the Neutral Distractor?



$$\hat{\beta}_{\text{EDist}} > \hat{\beta}_{\text{NDist}}$$
$$\hat{\beta}_{\text{EDist}} < \beta_{\text{NDist}}$$
$$\hat{\beta}_{\text{EDist}} \neq \hat{\beta}_{\text{NDist}}$$

 $\gamma = \hat{\beta}_{\text{EDist}} - \hat{\beta}_{\text{NDist}} > 0, < 0, \neq 0$

Contrast: Assign Weights to each Beta

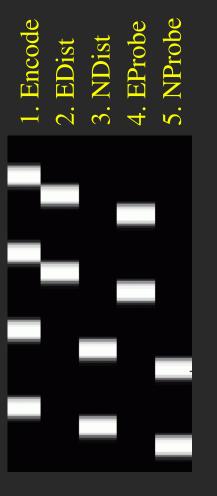
$$\begin{aligned} \gamma &= c_{\text{Encode}} \ \hat{\beta}_{\text{Encode}} + c_{\text{EDist}} \ \hat{\beta}_{\text{EDist}} + c_{\text{NDist}} \ \hat{\beta}_{\text{NDist}} + c_{\text{EProbe}} \ \hat{\beta}_{\text{EProbe}} + c_{\text{NProbe}} \ \hat{\beta}_{\text{NProbe}} \\ c_{\text{Encode}} &= 0 \\ c_{\text{EDist}} &= +1 \\ c_{\text{NDist}} &= -1 \\ c_{\text{EProbe}} &= 0 \\ c_{\text{NProbe}} &= 0 \\ C &= \begin{bmatrix} 0 \\ +1 \\ -1 \\ 0 \end{bmatrix} Contrast Matirx \end{aligned}$$

Hypotheses

• Which voxels respond more to the Emotional Distractor than to the Neutral Distractor?

- Which voxels respond to Encode (relative to baseline)?
- Which voxels respond to the Emotional Distractor?
- Which voxels respond to either Distractor?
- Which voxels respond more to the Probe following the Emotional Distractor than to the Probe following the Neutral Distractor?

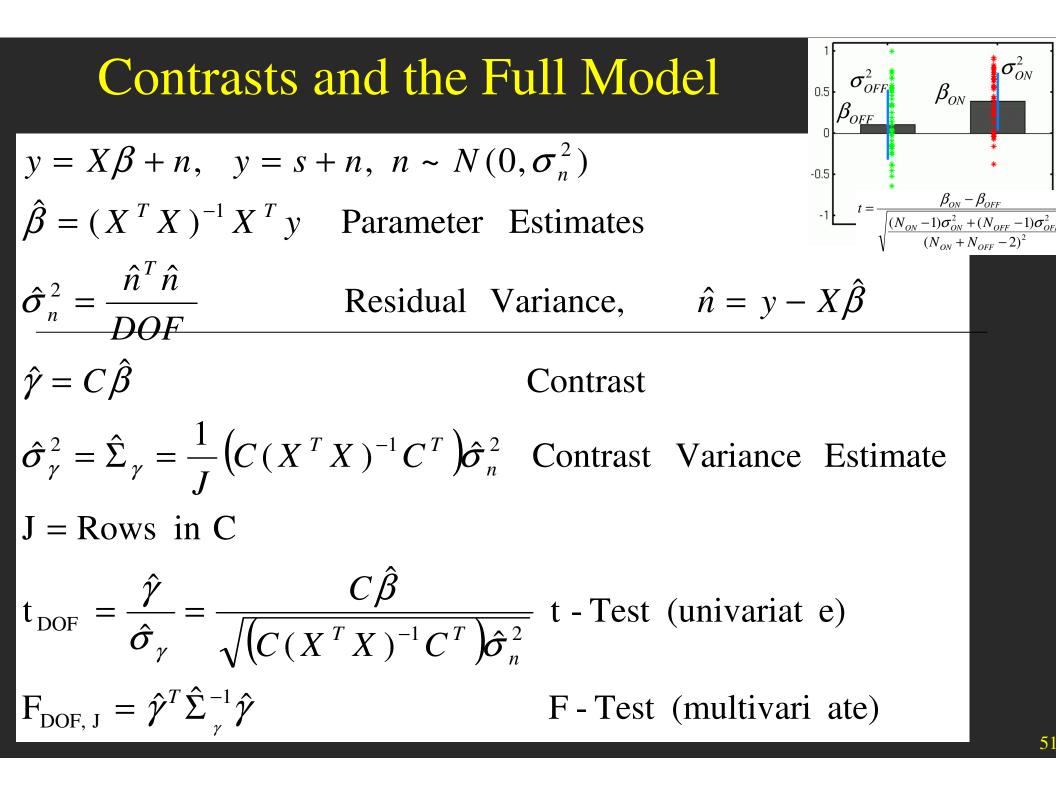
Which voxels respond more to the Emotional Distractor than to the Neutral Distractor?



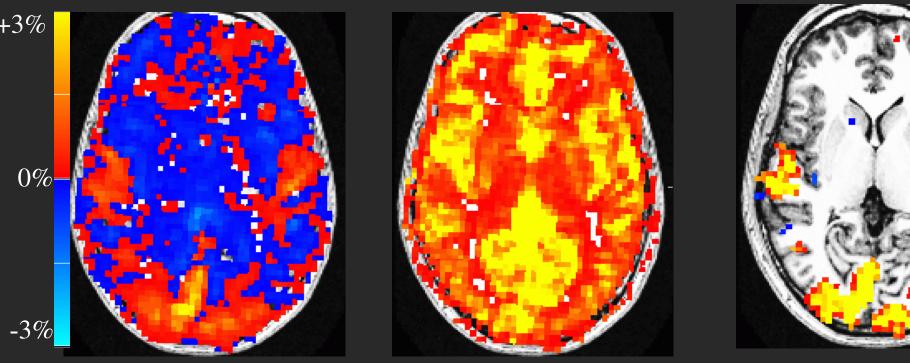
- Only interested in Emotional and Neutral Distractors
- No statement about other conditions

Condition:12345Weight0+1-100

Contrast Matrix C = [0 + 1 - 1 0 0]



First Level GLM Outputs



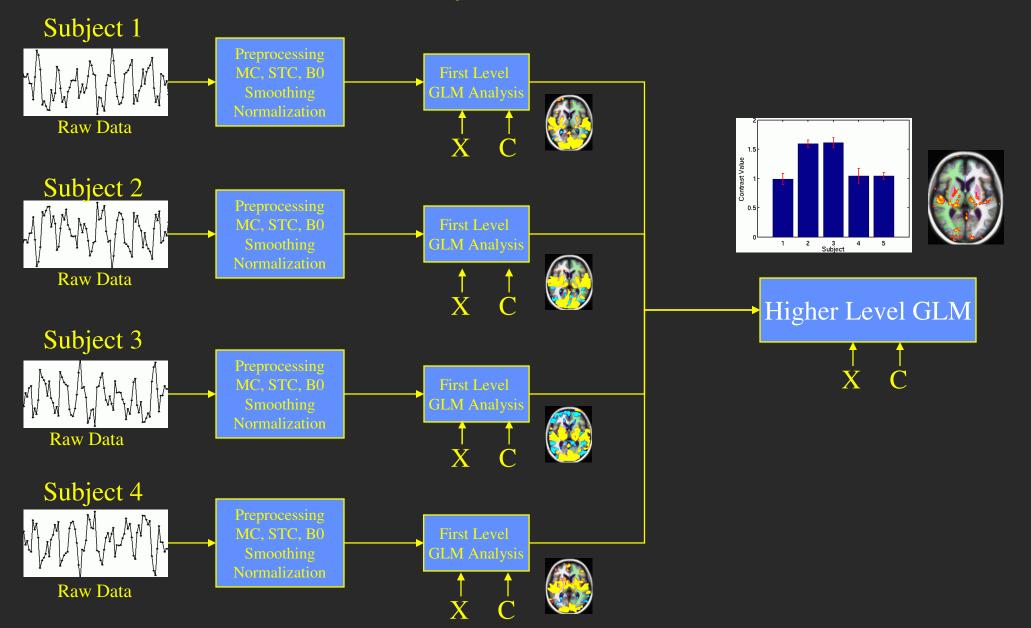
Contrast Amplitude CON, COPE, CES Contrast Amplitude Variance (Error Bars) VARCOPE, CESVAR Significance t-Map (p,z,F) (Thresholded p<.01) sig=-log10(p)

Time Series Analysis Summary

- Correlational
- Design Matrix (HRF shape)
- Estimate HRF amplitude (Parameters)
- Contrasts to test hypotheses
- Results at each voxel:
 - Contrast Value
 - Contrast Value Variance
 - p-value (Volume of Activation)
- Pass Contrast Value and Variance up to higher level analyses

fMRI Group Analysis

fMRI Analysis Overview



Overview

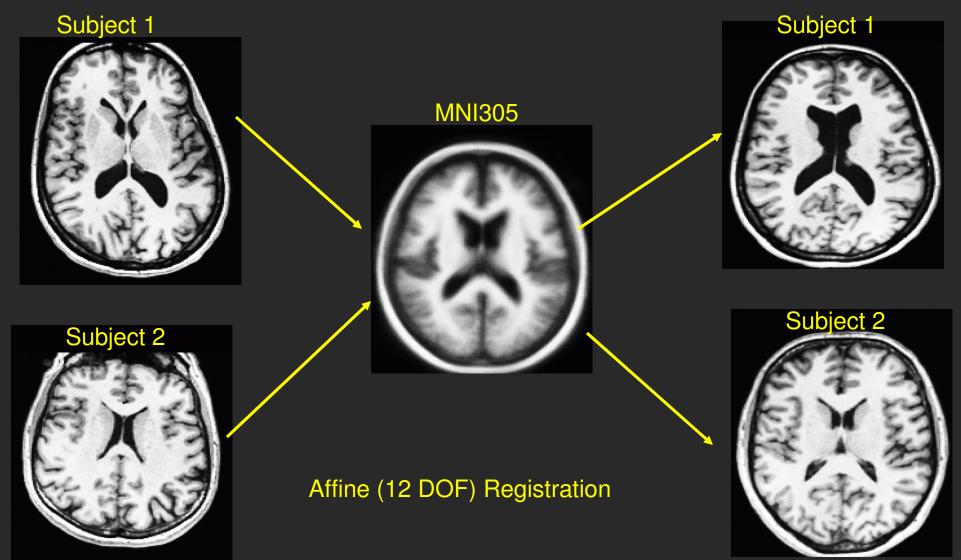
- Goal of Group Analysis
- Types of Group Analysis

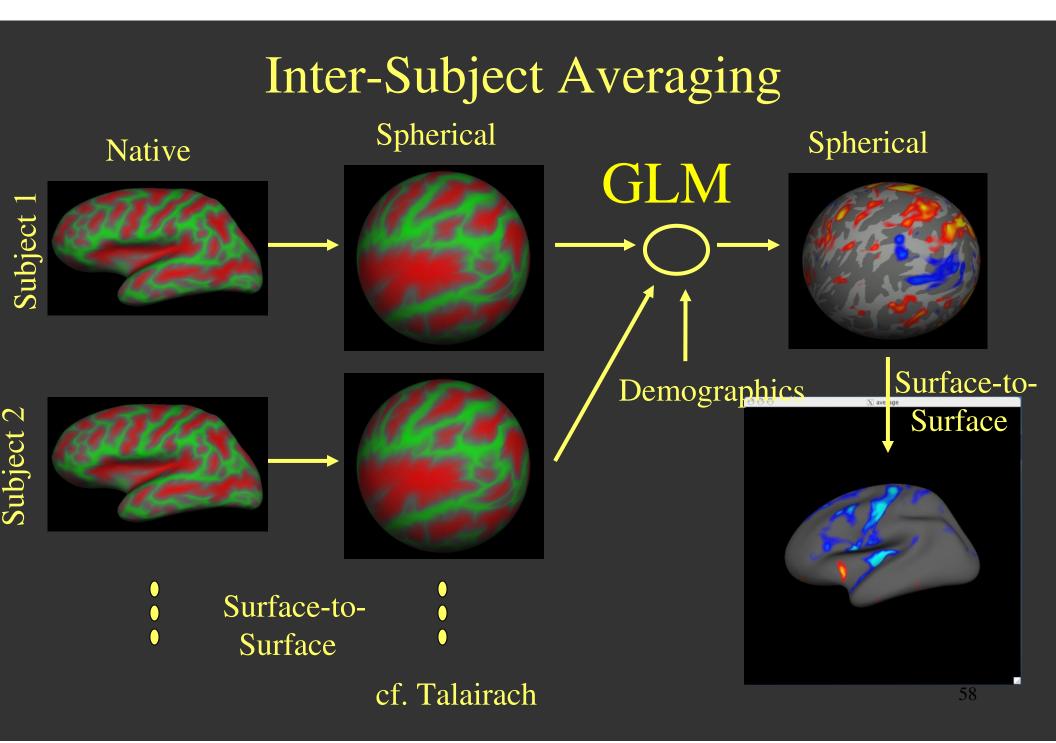
 Random Effects, Mixed Effects, Fixed Effects
- Multi-Level General Linear Model (GLM)

Spatial Normalization, Atlas Space

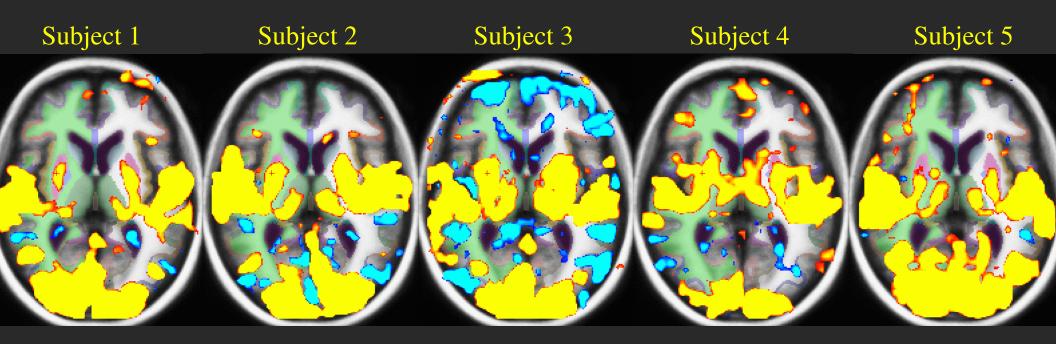
Native Space

MNI305 Space

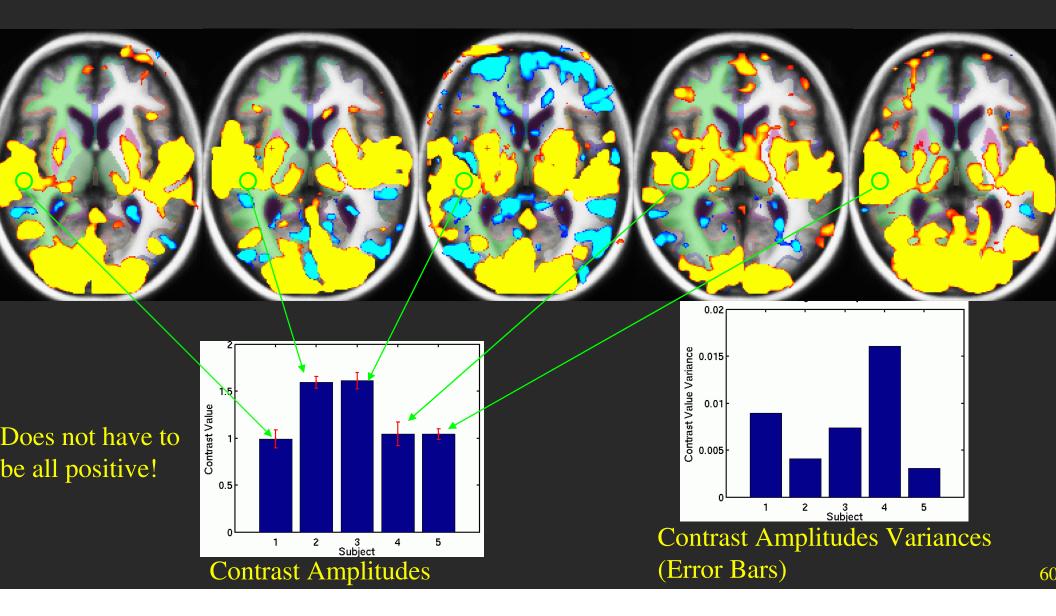




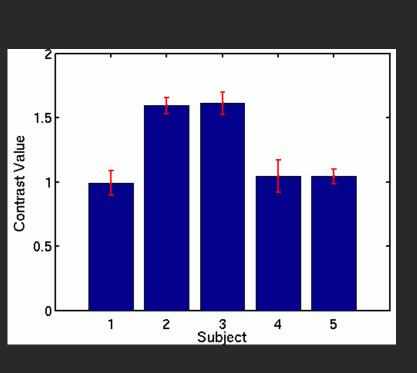
Is Pattern Repeatable Across Subject?

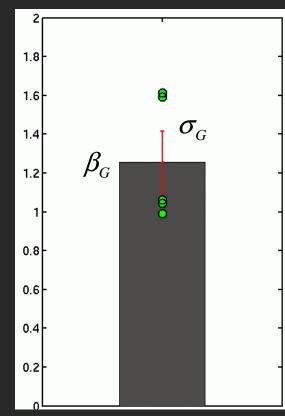


Group Analysis

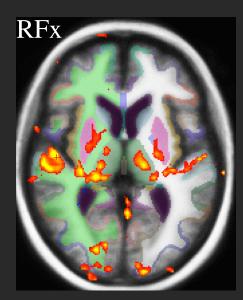


"Random Effects (RFx)" Analysis



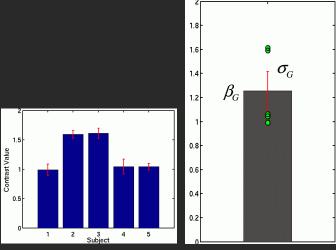


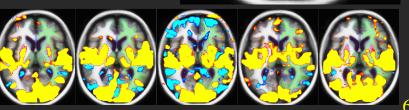
$$t = \frac{\beta_G}{\sigma_{\beta_G}}, \sigma_{\beta_G}^2 = \frac{\sigma_G^2}{N_G}$$
$$\sigma_G^2 = \frac{\sum (\beta_G - \beta_i)^2}{(N_G - 1)}$$
$$DOF = N_G - 1$$



"Random Effects (RFx)" Analysis

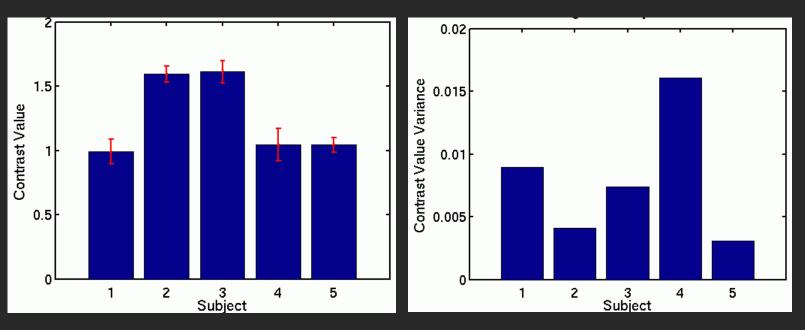
- Model Subjects as a Random Effect
- Variance comes from a single source: variance across subjects
 - Mean at the population mean
 - Variance of the population variance
- Does not take first-level noise into account (assumes 0)
- "Ordinary" Least Squares (OLS)
- Usually less activation than individuals

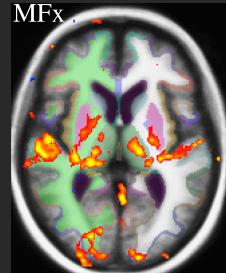




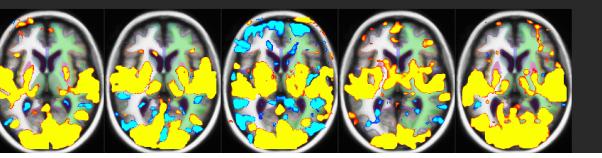
RFx

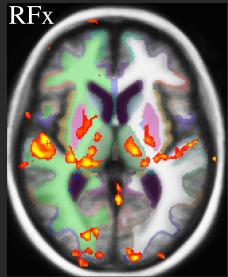
"Mixed Effects (MFx)" Analysis





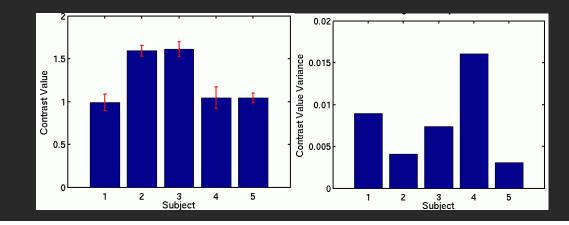
- Down-weight each subject based on variance.
- Weighted Least Squares vs ("Ordinary" LS)





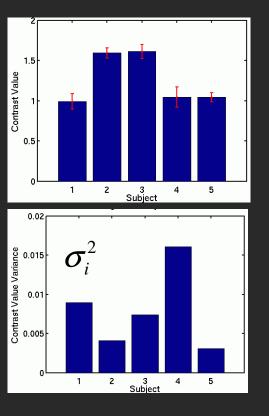
"Mixed Effects (MFx)" Analysis

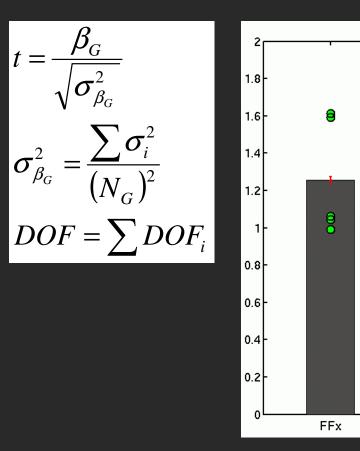
- Down-weight each subject based on variance.
- Weighted Least Squares vs ("Ordinary" LS)
- Protects against unequal variances across group or groups ("heteroskedasticity")
- May increase or decrease significance with respect to simple Random Effects
- More complicated to compute
- "Pseudo-MFx" simply weight by first-level variance (easier to compute)

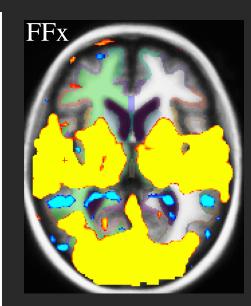




"Fixed Effects (FFx)" Analysis

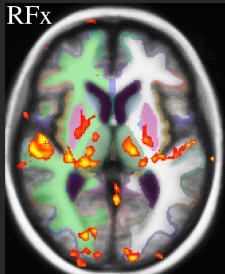


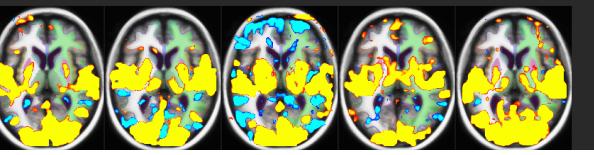




0

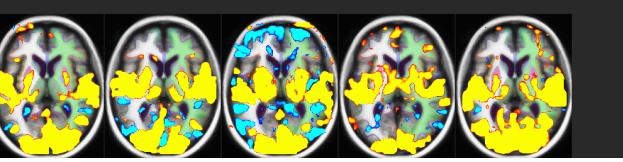
RFx

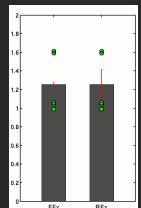


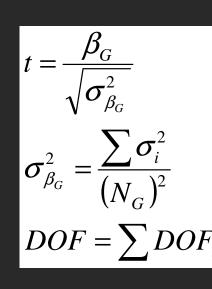


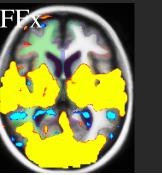
"Fixed Effects (FFx)" Analysis

- As if all subjects treated as a single subject (fixed effect)
- Small error bars (with respect to RFx)
- Large DOF
- Same mean as RFx
- Huge areas of activation
- Not generalizable beyond <u>sample</u>.

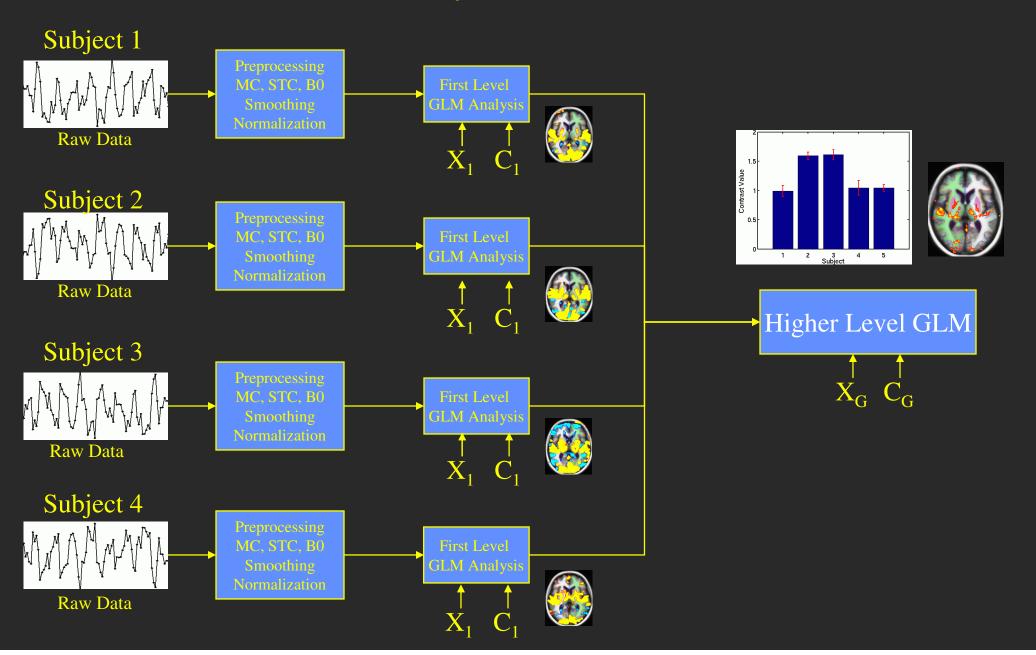








fMRI Analysis Overview



Higher Level GLM Analysis

X

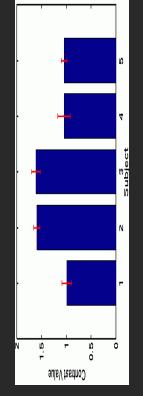
Design Matrix

(Regressors)

*

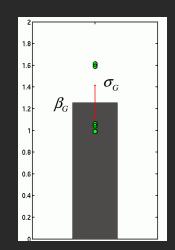
ß





Data from one voxel

Vector of Regression Coefficients ("Betas")



Contrast Matrix: C = [1]Contrast = $C*\beta = \beta_G$

Summary

- Preprocessing MC, STC, B0, Normalize, Smooth
- First Level GLM Analysis Design matrix, HRF, Nuisance
- Contrasts, Hypothesis Testing contrast matrix
- Group Analysis
 - Random, Mixed, Fixed
 - Multi-level GLM (Design and Contrast Matrices)