

Functional Image Analysis with a General Linear Model (GLM).

a.k.a "spm" for fun and profit

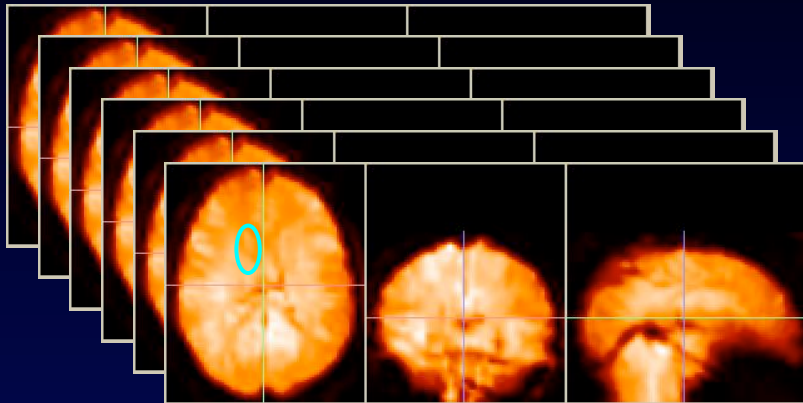
Terry Oakes
troakes@wisc.edu

Image Analysis Goals

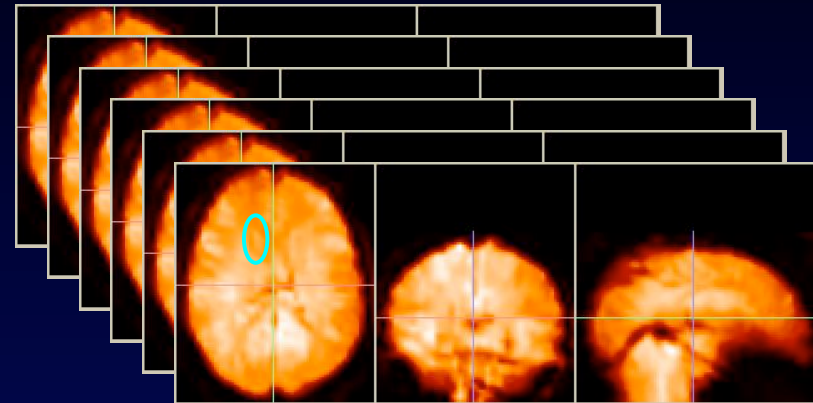
- 1) Does condition X yield a change in function?
- 2) Where do activations occur?
- 3) Where do interesting activations occur?
- 4) Are these activations significant?
- 5) How does an activation compare to others for the same condition? Other conditions? Within and across subjects?

Region of Interest (ROI) Analysis

Depressed

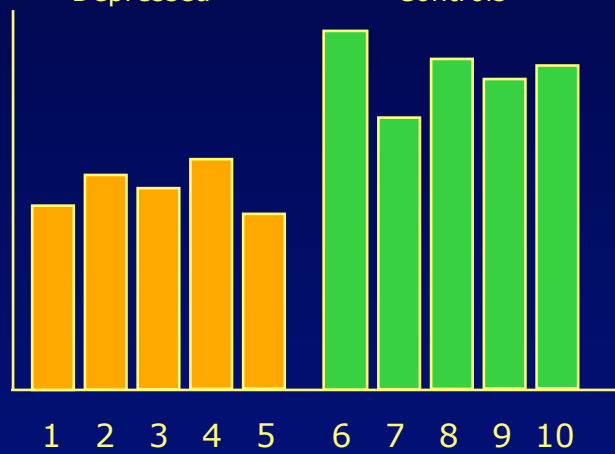


Controls



Depressed

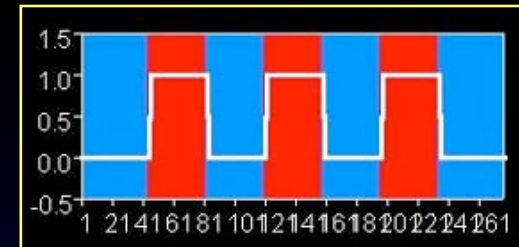
Controls



Where to draw ROIs?

How to assign variance?

Subtraction Image: finding differences



14158.0 #1
64, 64, 36 (X,Y,Z dimensions)
3.12500, 3.12500, 4.50000 (mm voxel dims)
X:\fMRI_data\fMRI_sum_stimulus.img

13964.0 #2
64, 64, 36 (X,Y,Z dimensions)
3.12500, 3.12500, 4.50000 (mm voxel dims)
X:\fMRI_data\fMRI_sum_baseline.img

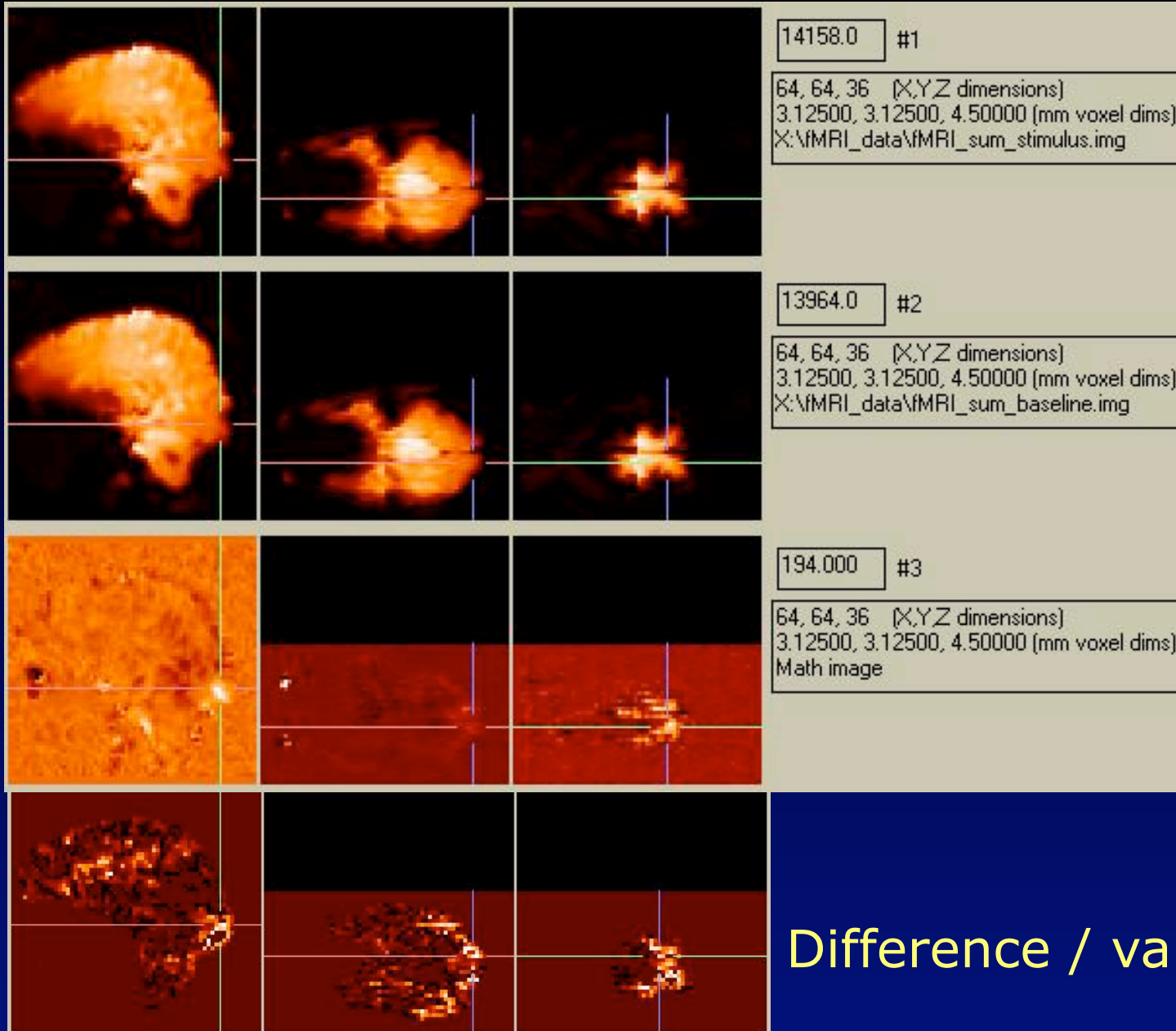
Is the difference in the brain?

Is the difference really due to changes in brain function?

23.0% signal change

1.4% signal change

But is it Reliable?



Difference / variance

Hypothesis Driven Research:

A systematic approach to proving hunches.

Most of the time, we find what we are looking for... even when we shouldn't.*

Science can also involve a discovery.

Preprocessing

Goals:

- 🧠 Focus on structure(s) of interest
- 🧠 Increase sensitivity, specificity

- 🧠 Motion correction
- 🧠 Slice-timing correction
- 🧠 Coregistration to a template
- 🧠 Mask the brain
- 🧠 Spatial, temporal smoothing
- 🧠 Normalize to a global average

Motion correction

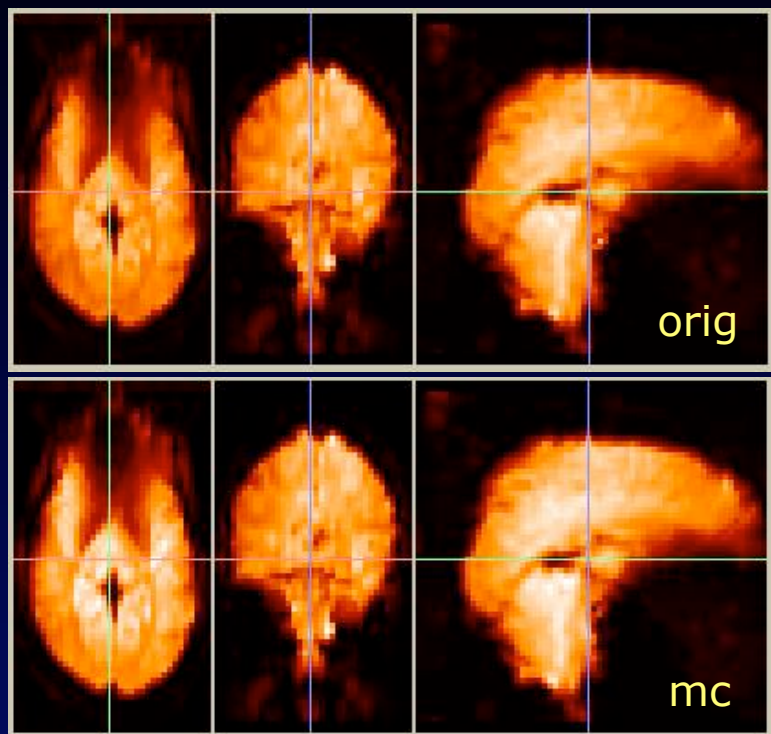
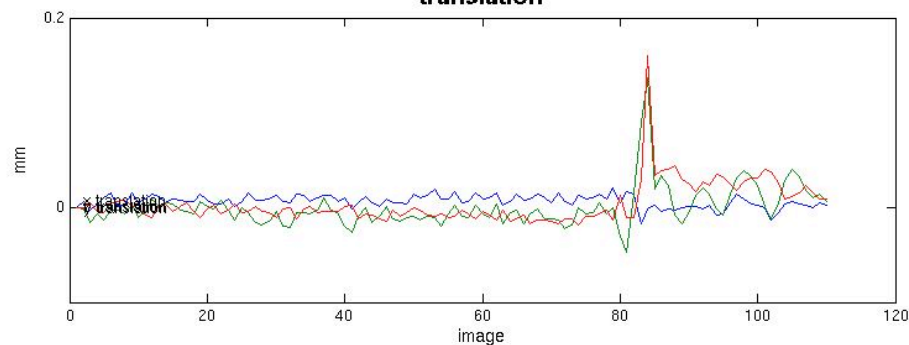


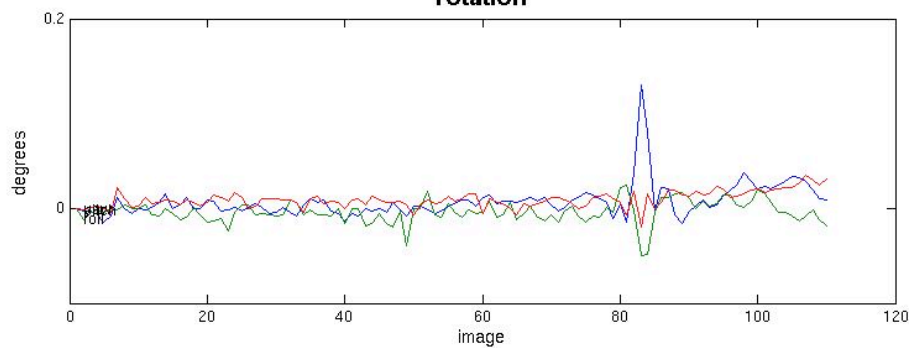
Image realignment

- 1 /scratch/MRI_data/data/fMRI_vis_stim_0000.img
- 2 /scratch/MRI_data/data/fMRI_vis_stim_0001.img
- 3 /scratch/MRI_data/data/fMRI_vis_stim_0002.img
- 4 /scratch/MRI_data/data/fMRI_vis_stim_0003.img
- 5 /scratch/MRI_data/data/fMRI_vis_stim_0004.img
- 6 /scratch/MRI_data/data/fMRI_vis_stim_0005.img
- 7 /scratch/MRI_data/data/fMRI_vis_stim_0006.img
- 8 /scratch/MRI_data/data/fMRI_vis_stim_0007.img
- 9 /scratch/MRI_data/data/fMRI_vis_stim_0008.img
- 10 /scratch/MRI_data/data/fMRI_vis_stim_0009.img
- 11 /scratch/MRI_data/data/fMRI_vis_stim_0010.img
- 12 /scratch/MRI_data/data/fMRI_vis_stim_0011.img
- etc

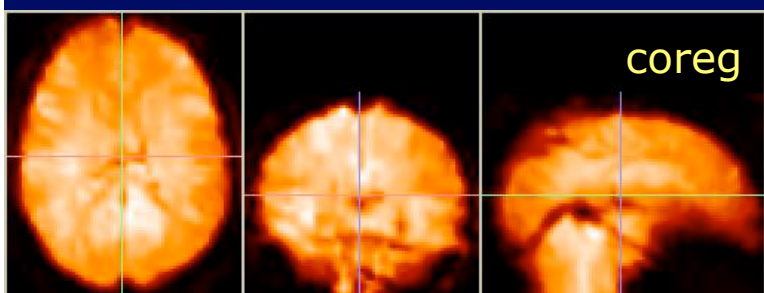
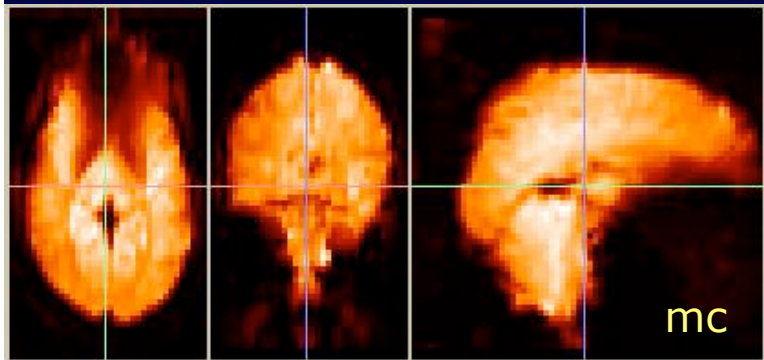
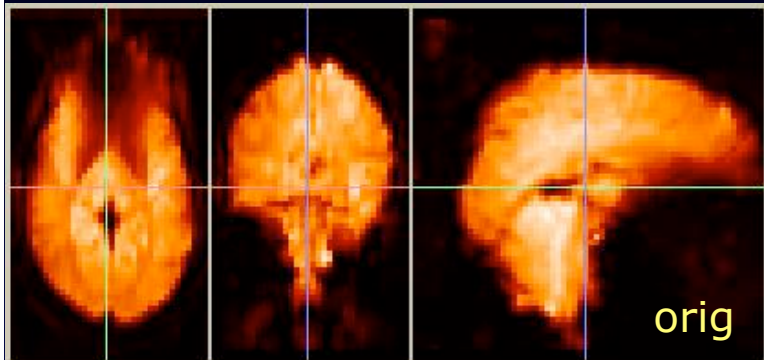
translation



rotation



Coregistration to a template



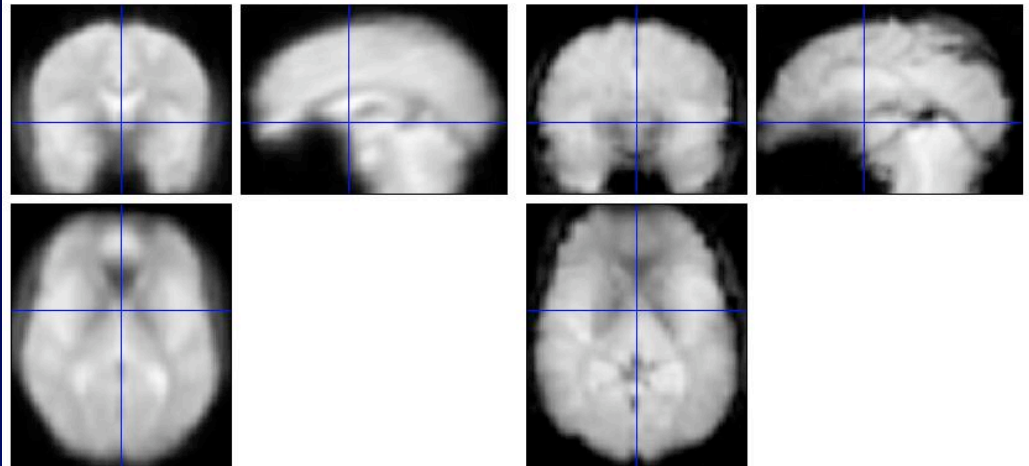
Spatial Normalisation

Image : /scratch/fMRI_data/data/meanfMRI_vis_stim_0000.img
Parameters : /scratch/fMRI_data/data/meanfMRI_vis_stim_0000_sn3d

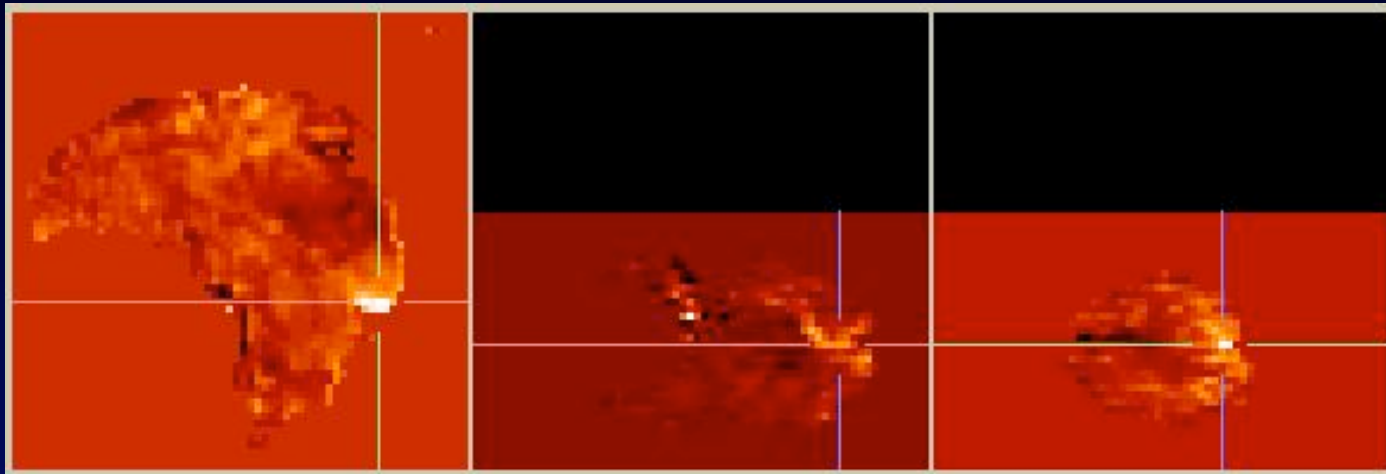
Linear {affine} component - image flipped

$$\begin{aligned} X1 &= -0.953*X - 0.007*Y + 0.039*Z + 1.241 \\ Y1 &= 0.059*X + 0.914*Y + 0.035*Z - 19.540 \\ Z1 &= 0.035*X - 0.172*Y + 0.941*Z - 0.722 \end{aligned}$$

12 nonlinear iterations
7 x 8 x 7 basis functions



Masking









Threshold = 7000 (range = 0-25000)

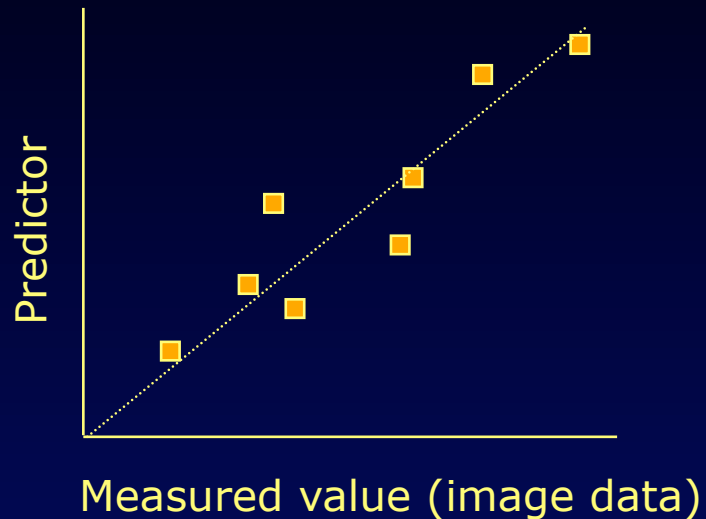
SPM: statistical parametric map

A map showing the location, spatial extent, and relative magnitude of statistically significant activations to an experiment.

Software:

 AFNI	(fMRI)
 BrainVoyager	(fMRI)
 fmristat	(fMRI, PET)
 FSL	(fMRI)
 SPM2	(fMRI, PET)
 VoxBo	(fMRI)

General Linear Model (GLM)



$$Y_i = (\beta * X_i) + c + E_i$$

Effect
magnitude

Uncertainty
(error)

Student's t-statistic:
 $t = \beta / E$

All statistics are calculated voxelwise.

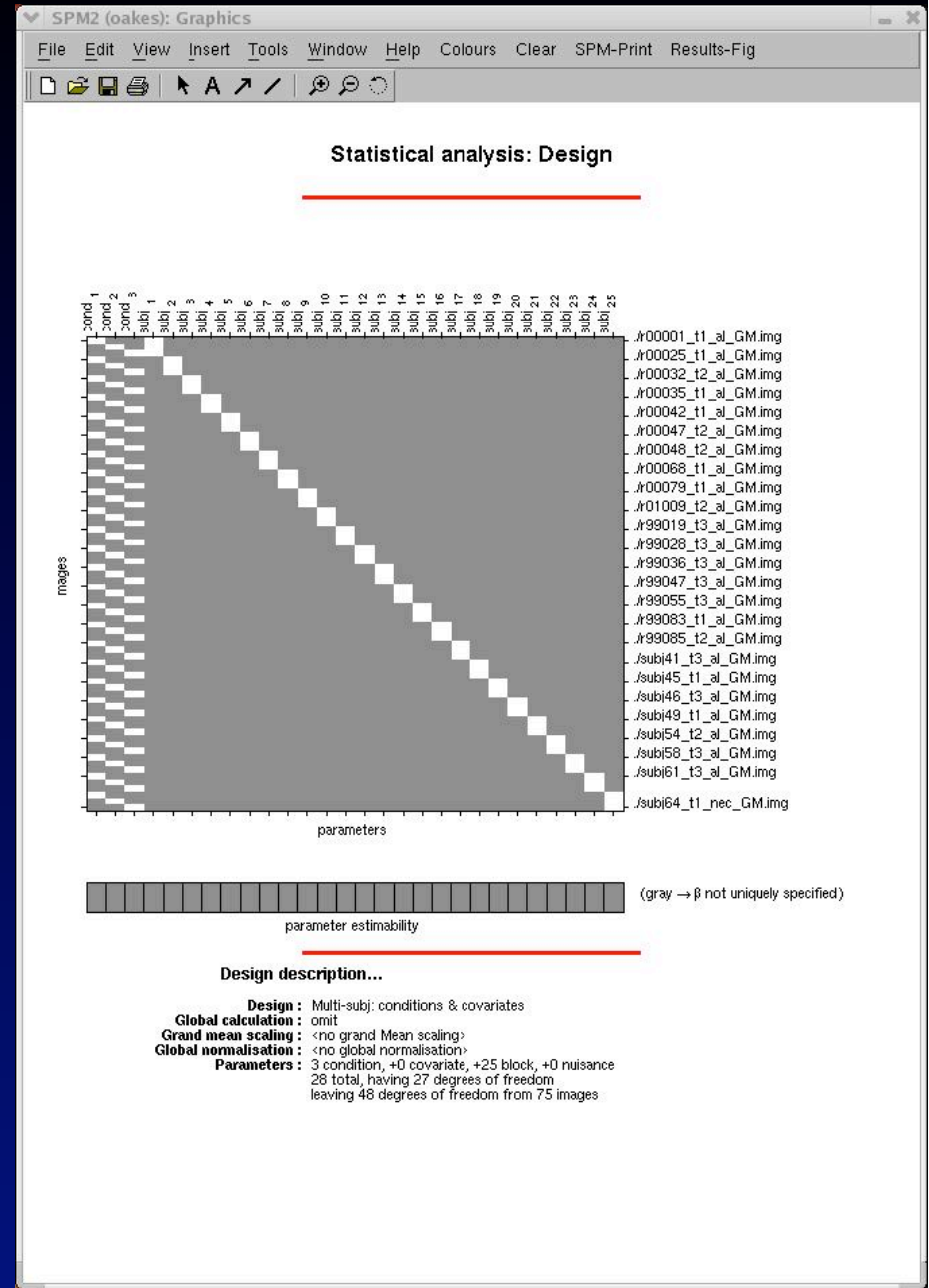
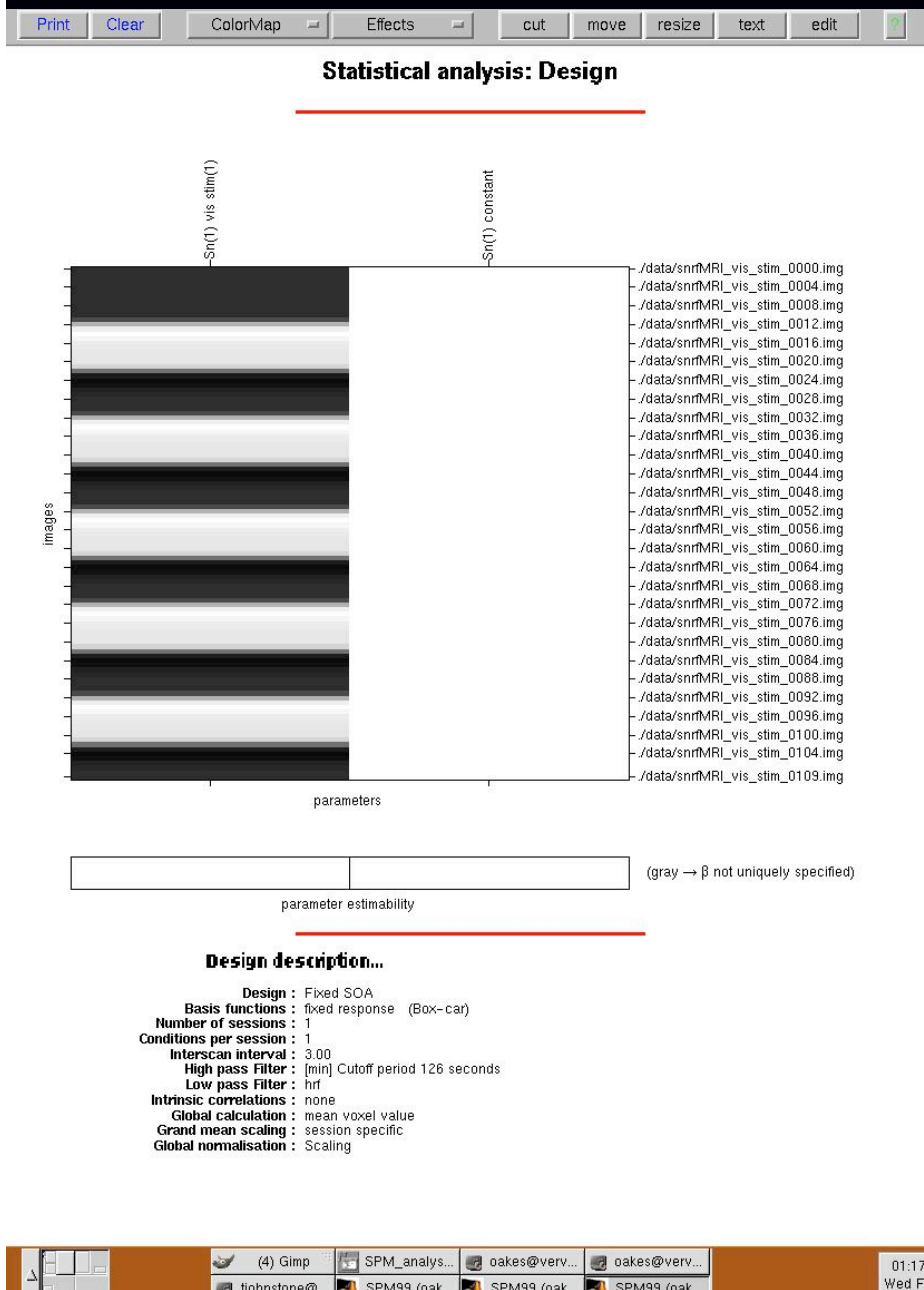
Best GLM explanation: <http://www.mrc-cbu.cam.ac.uk/Imaging/Common/spmstats.shtml>

GLM parts

- β -estimates (effect magnitude)
- contrast indicators
- con*** (t-stat) or ess*** (F-stat)
- ResMS (residual error)
- spmT*** or spmF***

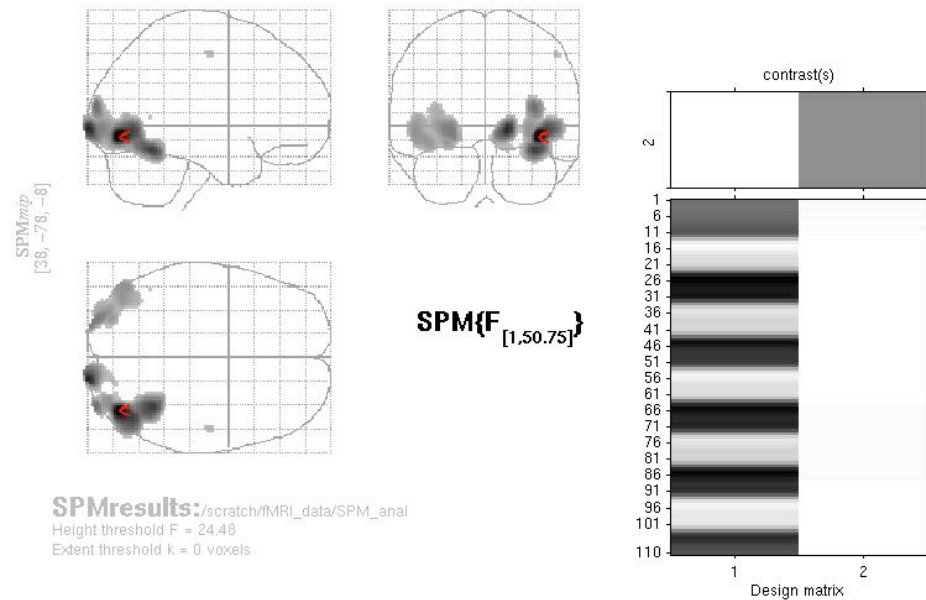
$$Y_i = (\beta * X_i) + c + E_i$$

SPM2 design matrix



Results example

Session 1: vis stim



Statistics: volume summary (p-values corrected for entire volume)

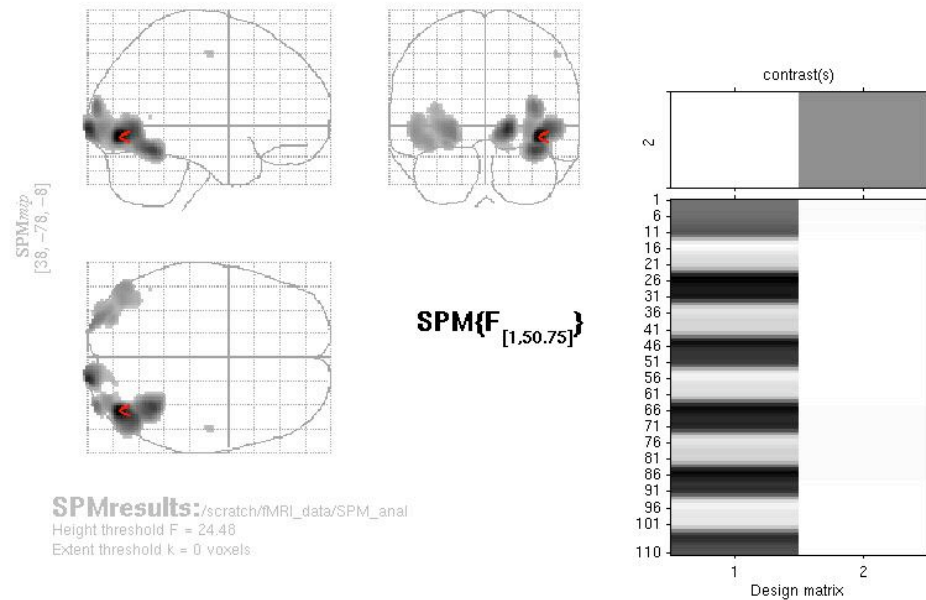
set-level		cluster-level			voxel-level			x,y,z (mm)
p	c	p corrected	k _E	p uncorrected	p corrected	F (Z _≡)	p uncorrected	
0.000	4		2085		0.000	65.06 (6.34)	0.000	38 -78 -8
					0.000	57.02 (6.04)	0.000	16 -100 -2
					0.000	52.88 (5.88)	0.000	36 -54 -18
			1009		0.001	40.93 (5.33)	0.000	-24 -96 -4
					0.002	36.46 (5.03)	0.000	-50 -74 -4
					0.002	35.62 (5.04)	0.000	-42 -76 -10
			7		0.016	28.56 (4.59)	0.000	50 -14 52
			1		0.049	24.54 (4.30)	0.000	-48 -56 6

table shows at most local maxima > 8.0mm apart per cluster

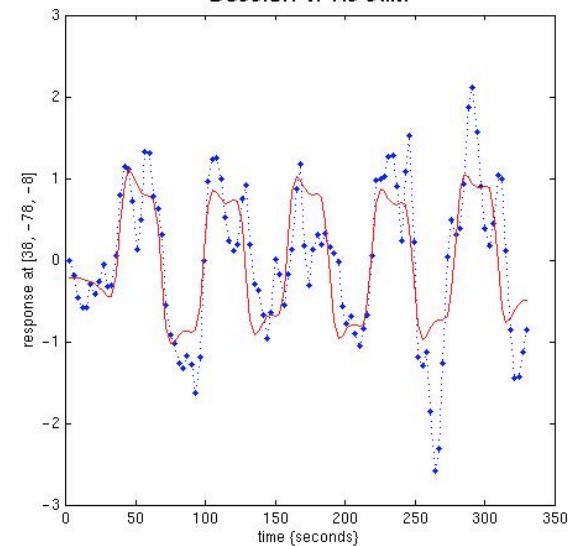
Height threshold: F = 24.48, p = 0.000 (0.050 corrected) Degrees of freedom = [1.0, 50.8]
 Extent threshold: k = 0 voxels, p = 1.000 (0.050 corrected) Smoothness FWHM = 18.6 21.4 25.1 (mm) = 9.3 10.7 12.5 (voxels)
 Expected voxels per cluster, <k> = 27.750 Search volume: S = 1423664 mm³ = 177958 voxels = 131.9 resels
 Expected number of clusters, <c> = 0.05 Voxel size: [2.0, 2.0, 2.0] mm (1 resel = 1248.03 voxels)

Plot of data and fit

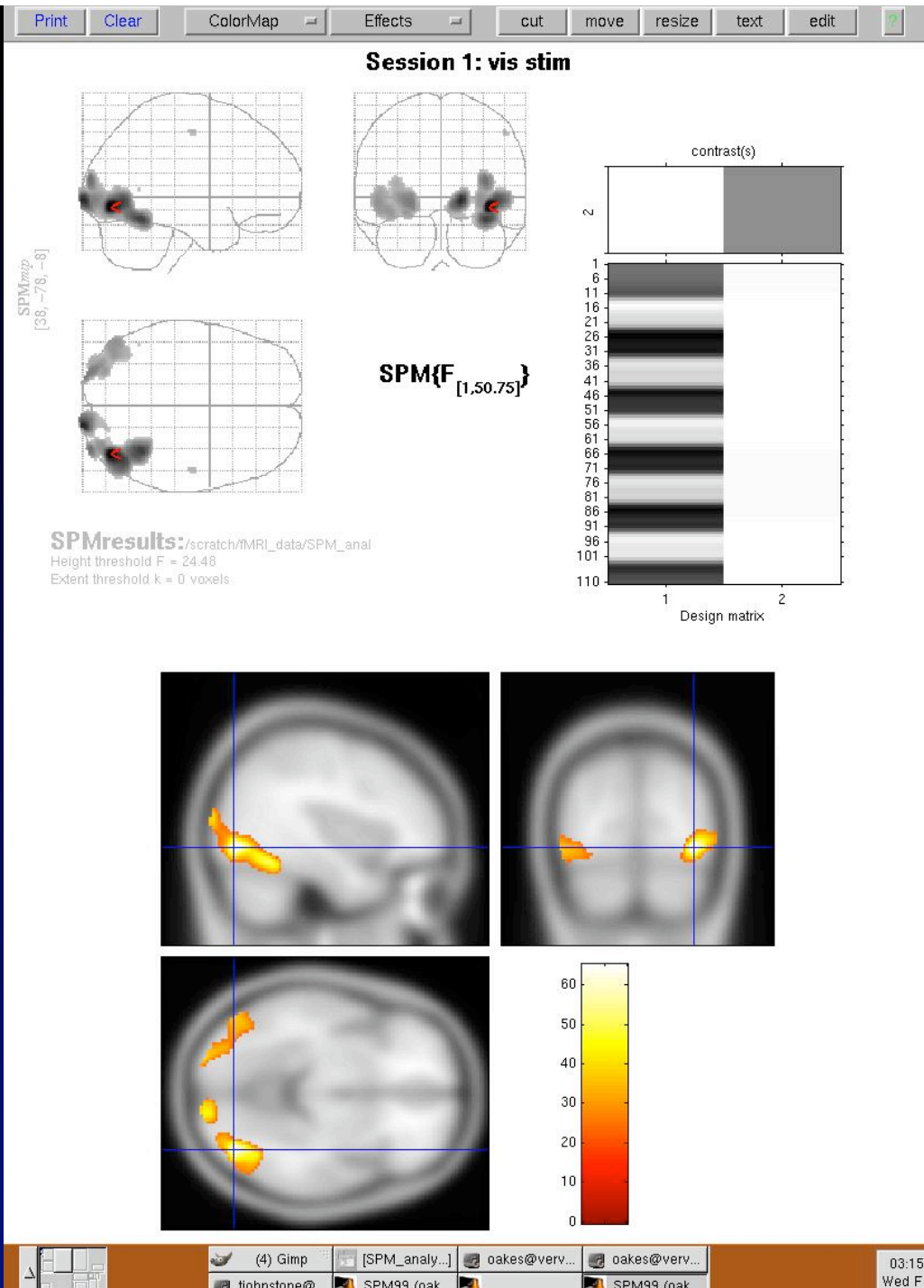
Session 1: vis stim



Fitted and adjusted responses Session 1: vis stim

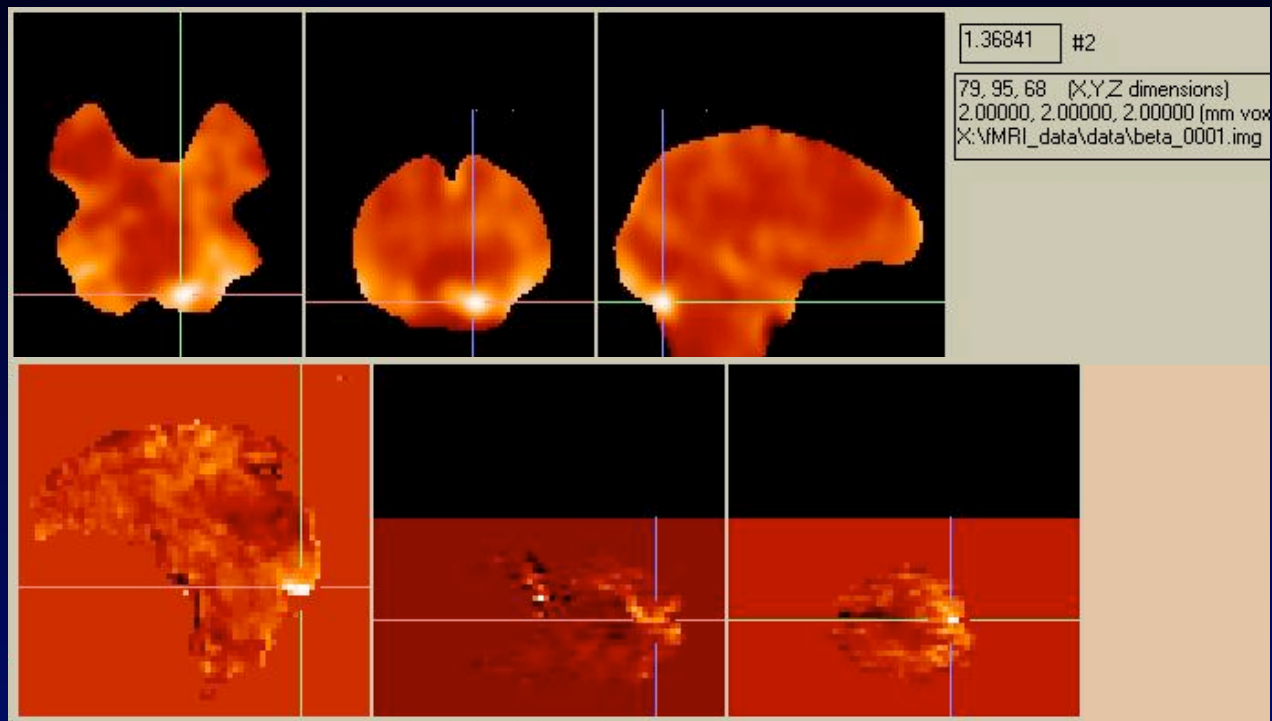


Results: overlay



GLM effect size

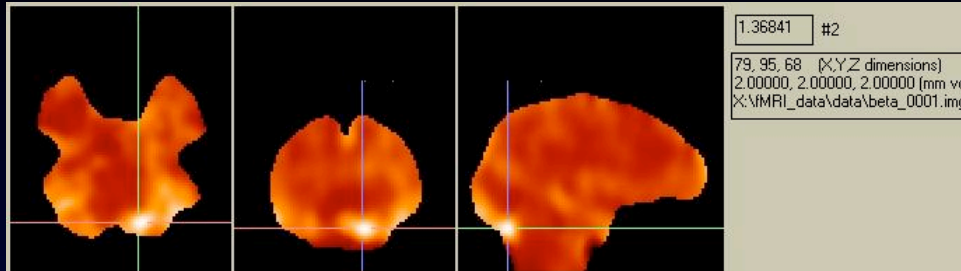
SPM β
image



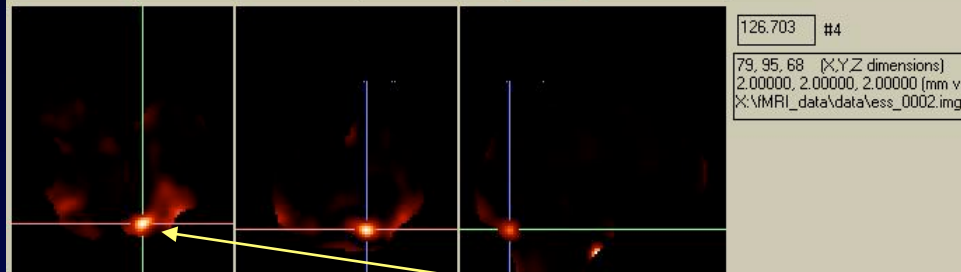
Subtraction
image

GLM components from SPM

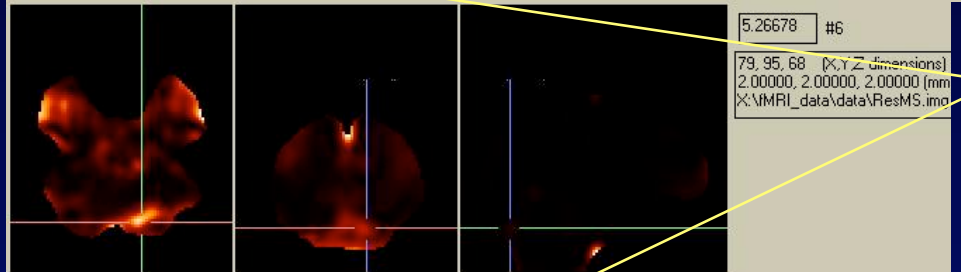
β image



β image
weighted with
contrast

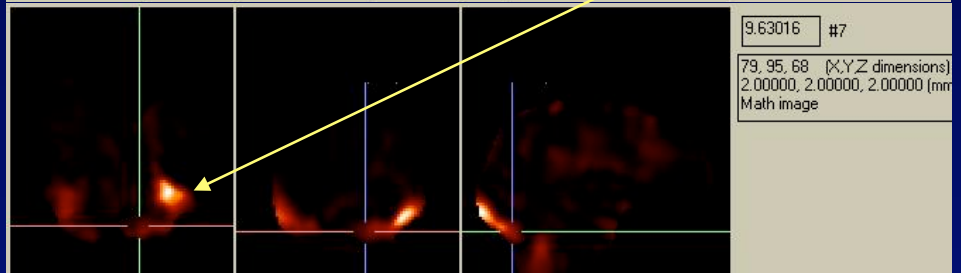


error estimate



t-statistic map:

$\frac{\text{weighted } \beta}{\text{error}}$



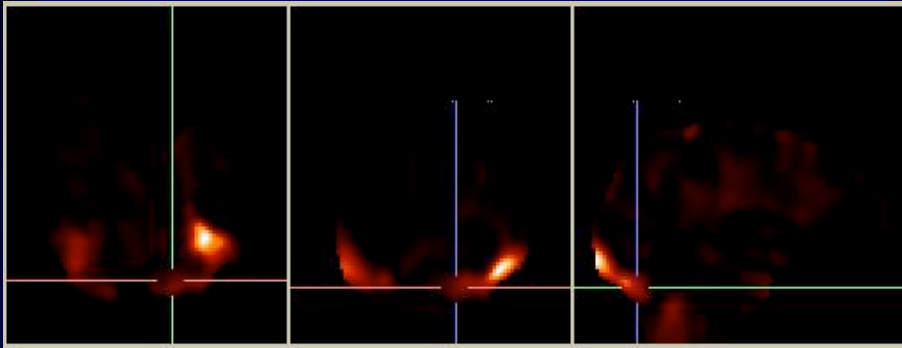
Why the difference?

The spm shows where we are SURE there is a difference.

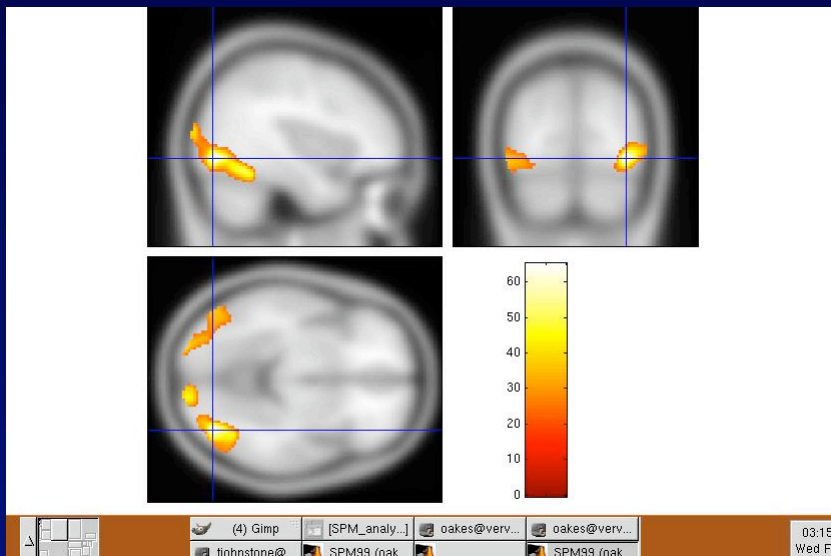
This is different than a subtraction image, which shows areas of large but possibly unreliable differences.

Thresholding

- Localization
- Remove non-significant regions
- Compare cluster sizes



How do we get clusters from a continuous spm?



Statistical threshold:
 $p < 0.05$

Limit results to the most significant pixels (95% confidence level).

Approx. 500,000 pixels in the brain!
=> 25,000 significant pixels.

Multiple Comparisons

Bonferroni correction: $p' = p / N$

$$p' = 0.05 / 500,000 = 1.0e-7$$



Too conservative!

Most image data are not independent.

Challenge: find N which represents the true number of independent data points.

In SPM and fmristat, this is done via Random Field Theory and resolution elements (resels).

Sample GLM script with fmristat

```
hrf_parameters = [5.4 5.2 10.8 7.35 0.35];
frametimes = (0:138)*2;
slicetimes = zeros(1, 30);
onsets = [5 22 39 56 73 90 107 124 141 158 175 192 209 212 217 220 224 230 235 241 244 248 253 257];
eventid = [1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2];
duration = zeros(1,24);
height = ones(1,24);
events = [ eventid', onsets', duration', height' ]

X_cache = fmridesign( frametimes, slicetimes, events, [], hrf_parameters )

imagesc( squeeze( X_cache.X( :,1,1,:) ) )           % hrf go
imagesc( squeeze( X_cache.X( :,2,1,:) ) )           % hrf nogo
imagesc( squeeze( X_cache.X( :,1,2,:) ) )           %hfr deriv go

contrast = [1 0; % slow only
            0 1; % fast only
            1 1]; % both

which_stats = [1 1 1 1 1 1 1 1 1];

[mtr_df_016 p] = fmriilm( filename, output_file_base, X_cache, contrast, [], which_stats )

% saves workspace as fmristat.mat to task directory
save /study/fMRI_tools/analysis/fmristat/016/mtr/fmristat.mat

% load workspace & view different stats images
load /study/fMRI_tools/analysis/fmristat/016/mtr/fmristat.mat

t_file = '/study/fMRI_tools/analysis/fmristat/016/mtr/both_Stat_mag_t.img';
view_slices( t_file, maskfile );

blur_file = gauss_blur ( t_file, 8, '/study/fMRI_tools/analysis/fmristat/016/mtr/both_t')

sigT = stat_threshold( 3.75*(64*64)*30*5, 64*64*30, 0, mtr_df_016);
glass_brain( t_file, sigT, maskfile );
```

Web resources

http://brainimaging.waisman.wisc.edu/~oakes/spm/visual_stim_demo/fmri_visual_stim.html

<http://www.mrc-cbu.cam.ac.uk/Imaging/Common/spmstats.shtml>