

# Neuroimaging data analysis

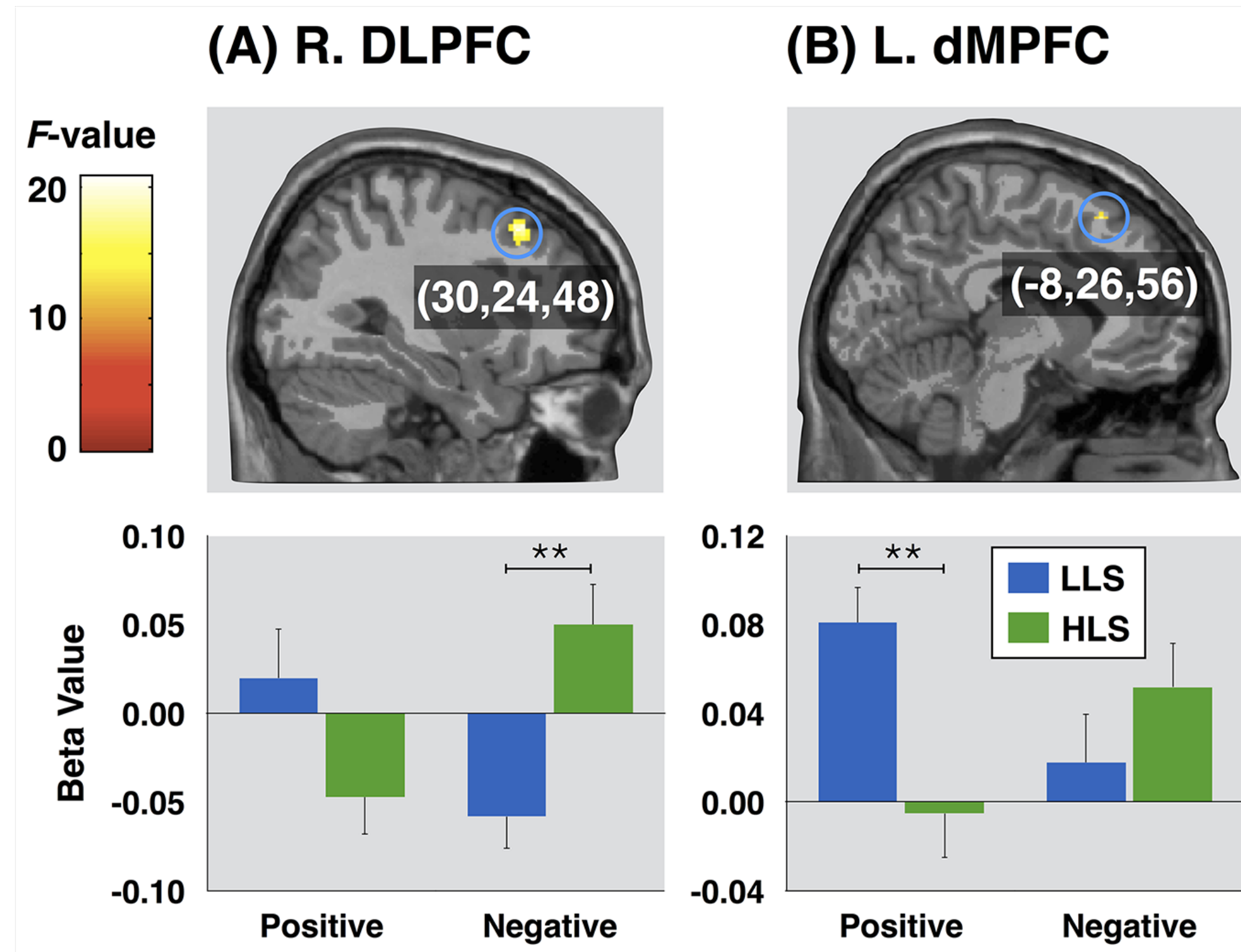
post-hoc analysis using MarsBar (SPM) plug-in toolbox

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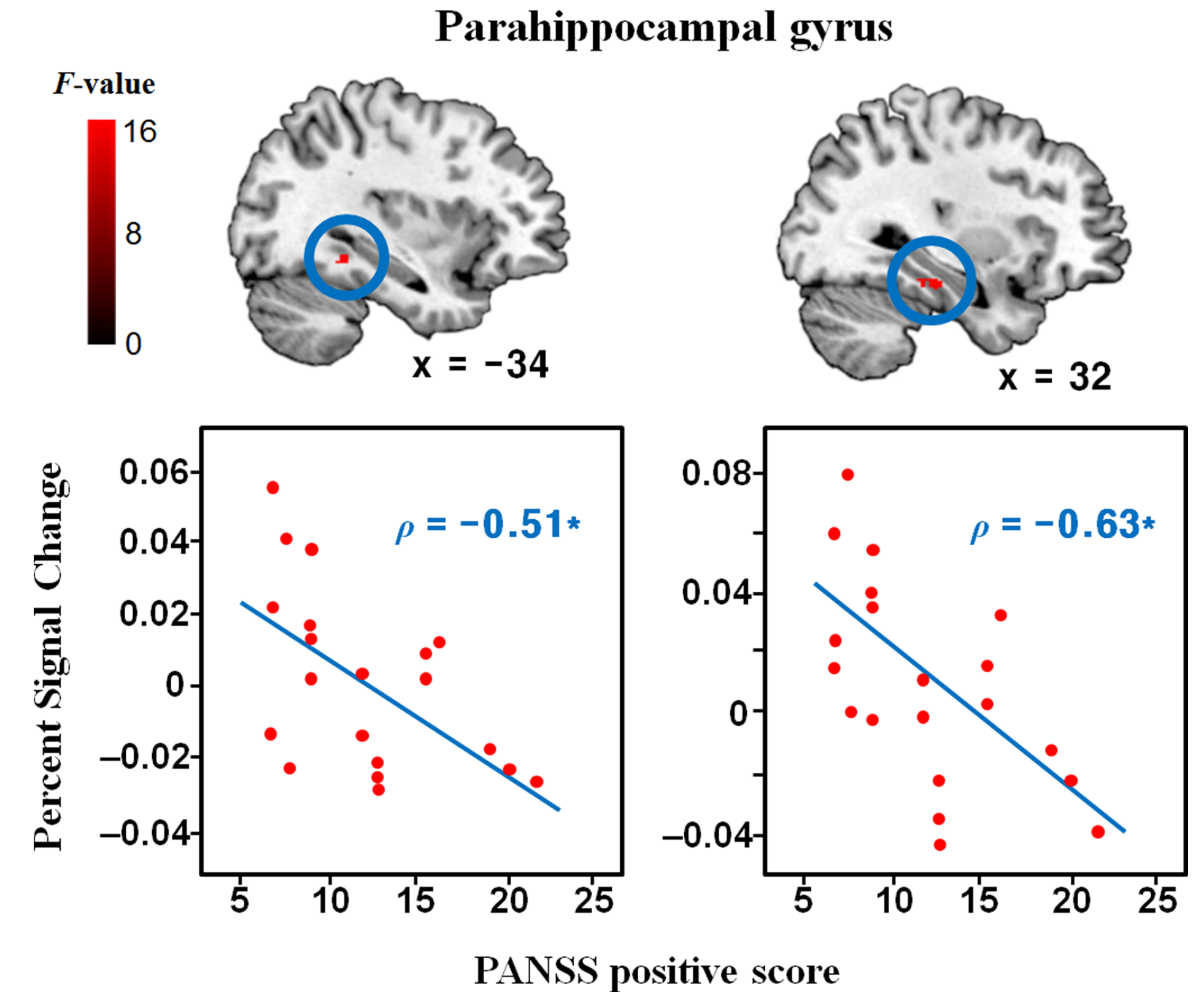
# What are post-hoc analyses?

Flexible analysis → post-hoc t-test



PLoS ONE 11(2): e0149554

Flexible analysis → correlation

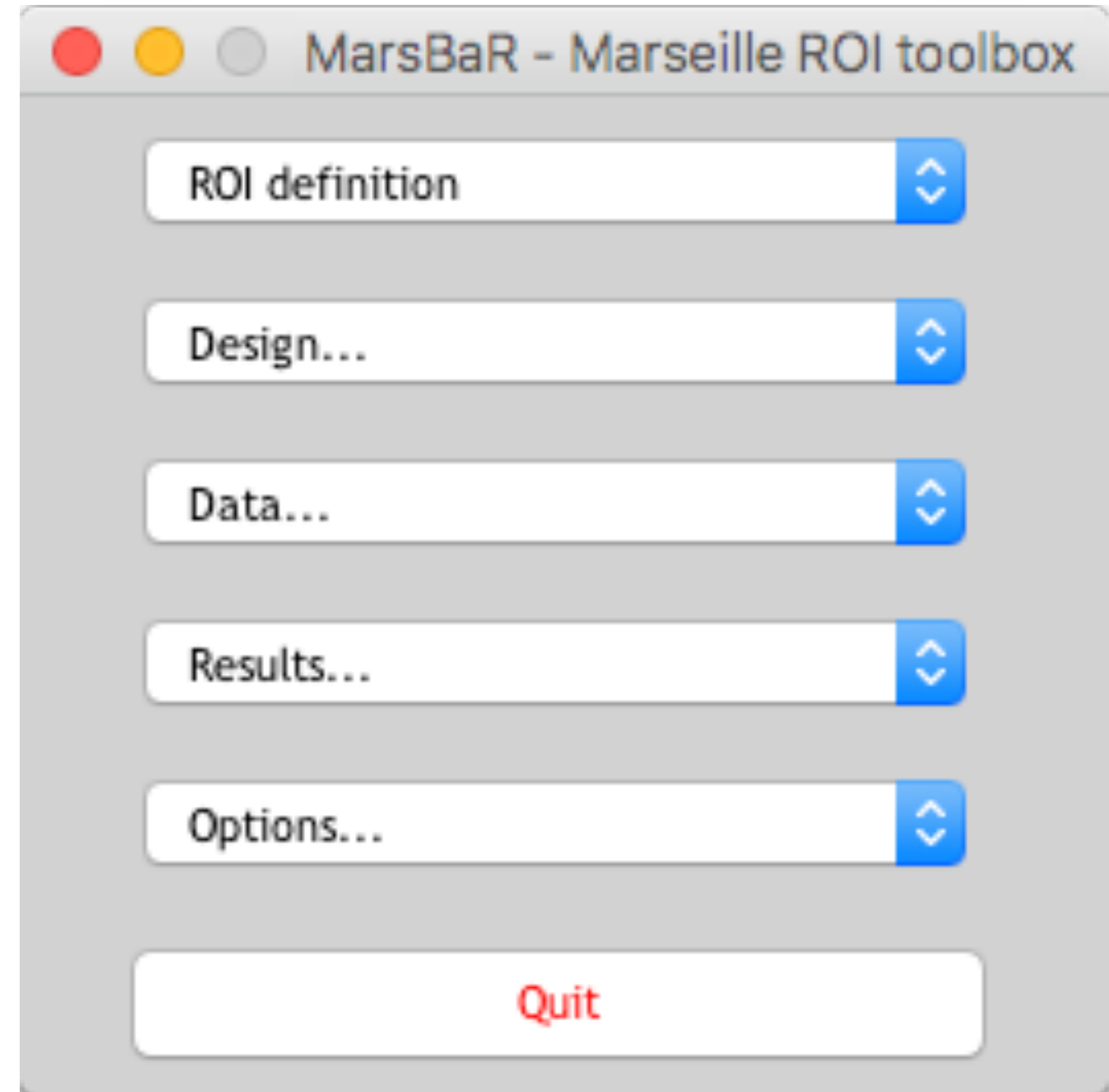


PLoS ONE 10(3): e0120478

# MarsBaR: SPM plug-in toolbox

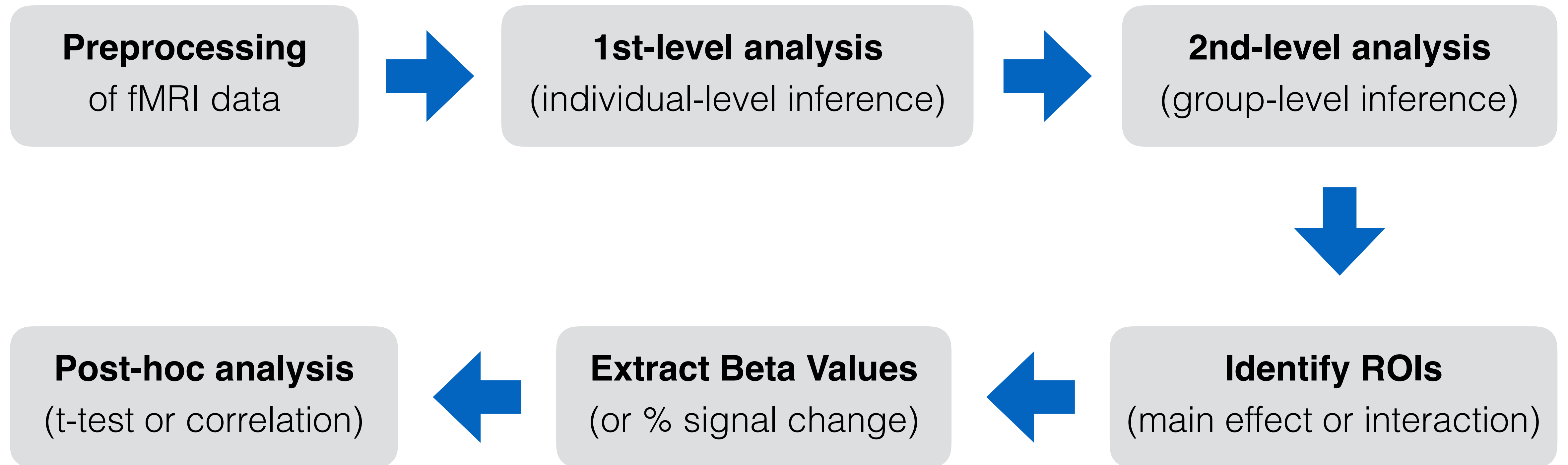
- MarsBaR (MARSeille Boîte À Région d'Intérêt) is a toolbox for SPM which provides routines for region of interest analysis.
- Download toolbox:  
<https://sourceforge.net/projects/marsbar/files/marsbar>
- Online tutorial:  
<http://marsbar.sourceforge.net/tutorial/>
- Manual in PDF:  
<http://marsbar.sourceforge.net/marsbar.pdf>

# MarsBaR GUI tool

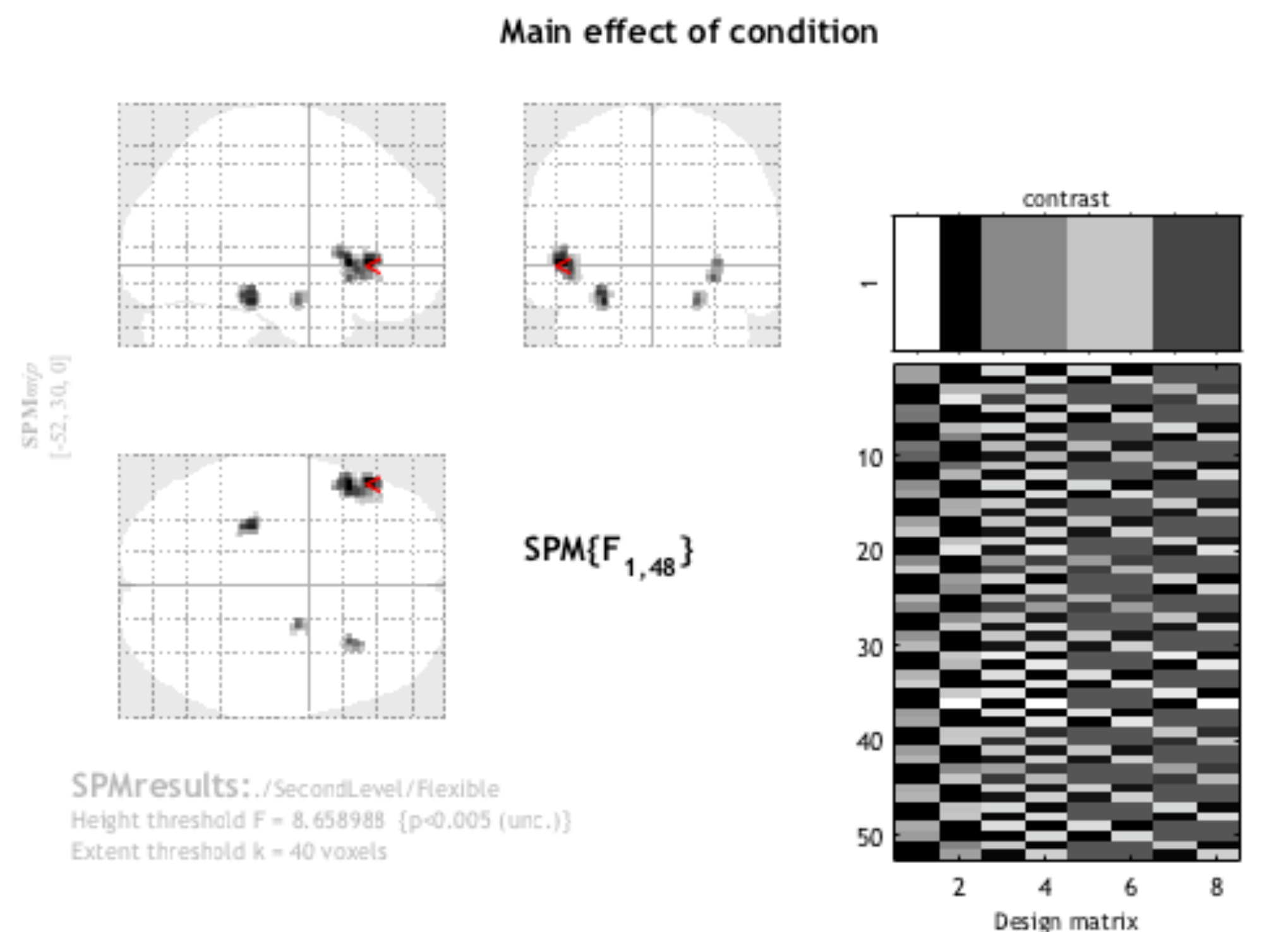




# Flowchart for fMRI Data Analysis



# Check Results



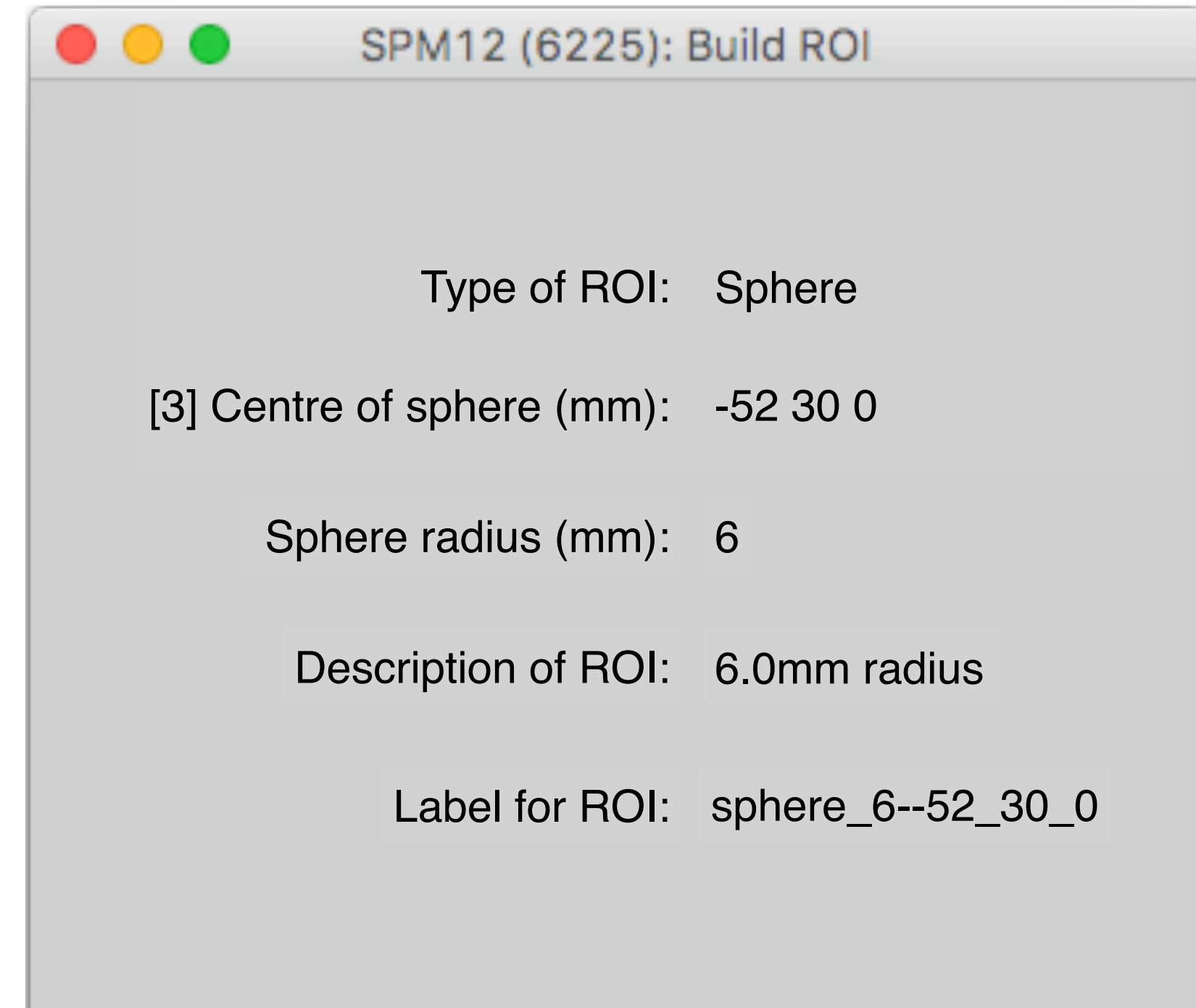
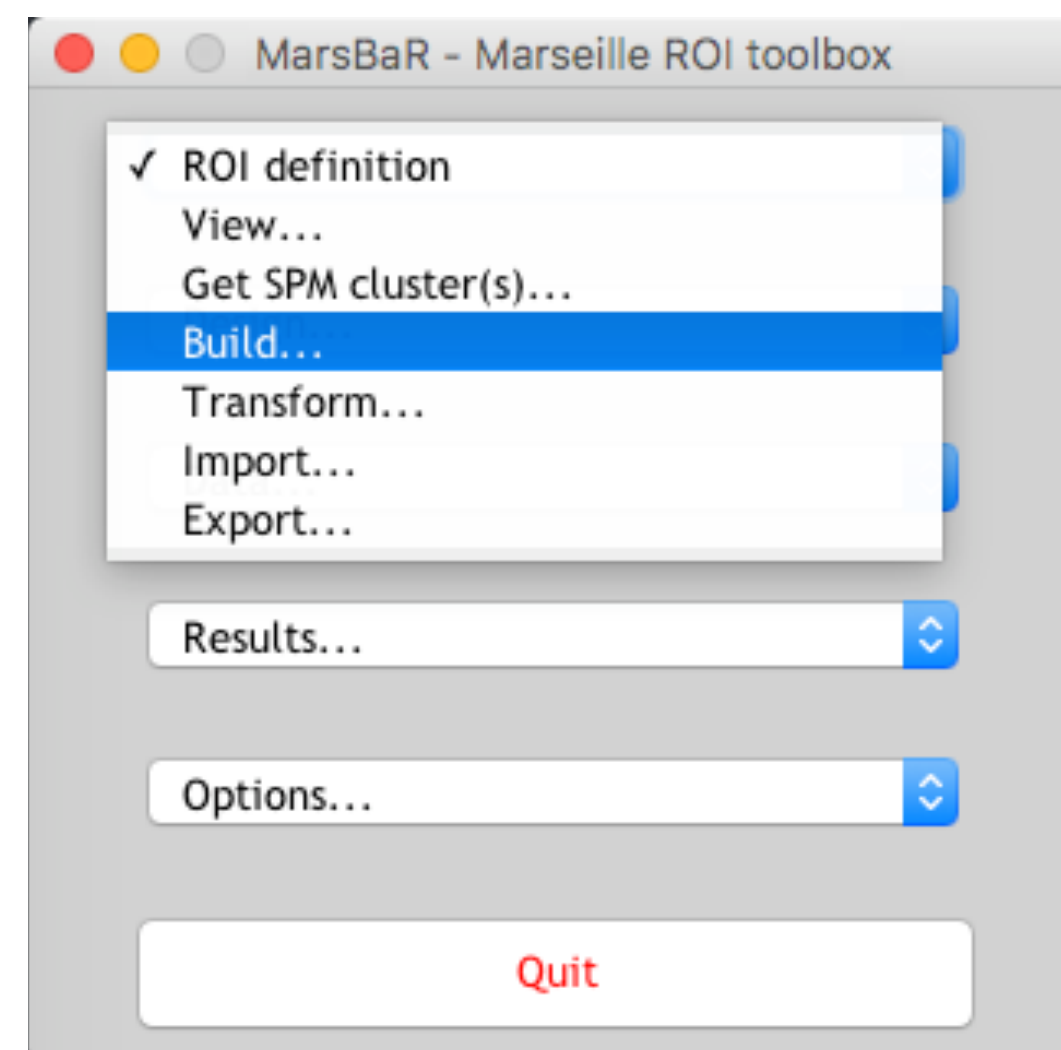
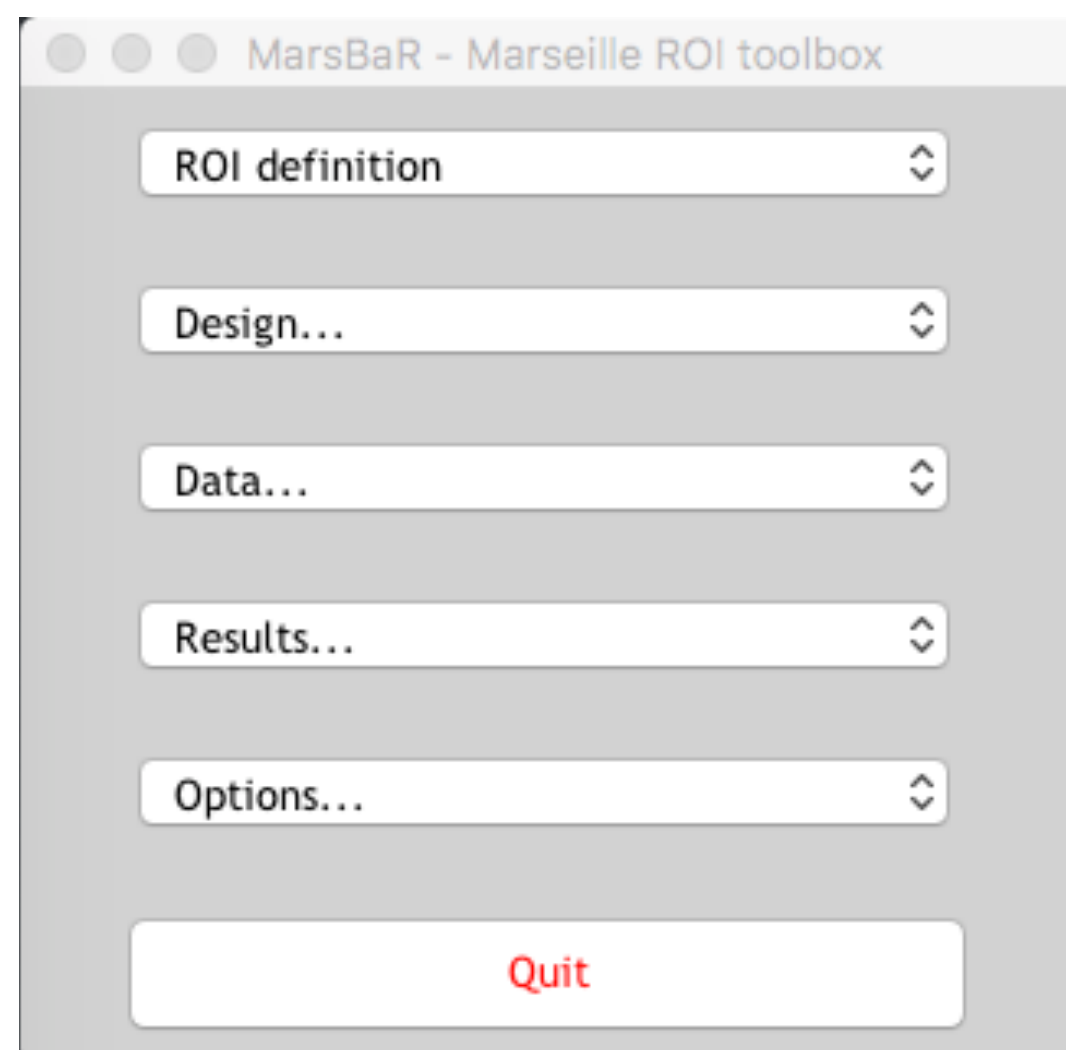
Peak coordinate of Broca's area is  
MNI = [-52 30 0];

Statistics: *p-values adjusted for search volume*

set-level		cluster-level				peak-level					mm mm mm		
<i>p</i>	<i>c</i>	<i>p</i> <sub>FWE-corr</sub>	<i>q</i> <sub>FDR-corr</sub>	<i>k</i> <sub>E</sub>	<i>p</i> <sub>uncorr</sub>	<i>p</i> <sub>FWE-corr</sub>	<i>q</i> <sub>FDR-corr</sub>	<i>F</i>	( <i>Z</i> <sub>max</sub> )	<i>p</i> <sub>uncorr</sub>			
0.838	4	0.014		274	0.000	0.996	1.000	16.45	3.56	0.000	-52	30	0
						0.996	1.000	16.39	3.56	0.000	-48	20	0
						1.000	1.000	10.00	2.78	0.003	-44	36	-10
		0.767		81	0.024	1.000	1.000	15.16	3.43	0.000	-28	-32	-20
		0.943				1.000	1.000	13.48	3.24	0.001	30	20	-8
						1.000	1.000	12.74	3.15	0.001	32	24	0
		0.992		45	0.081	1.000	1.000	13.11	3.19	0.001	22	-8	-20

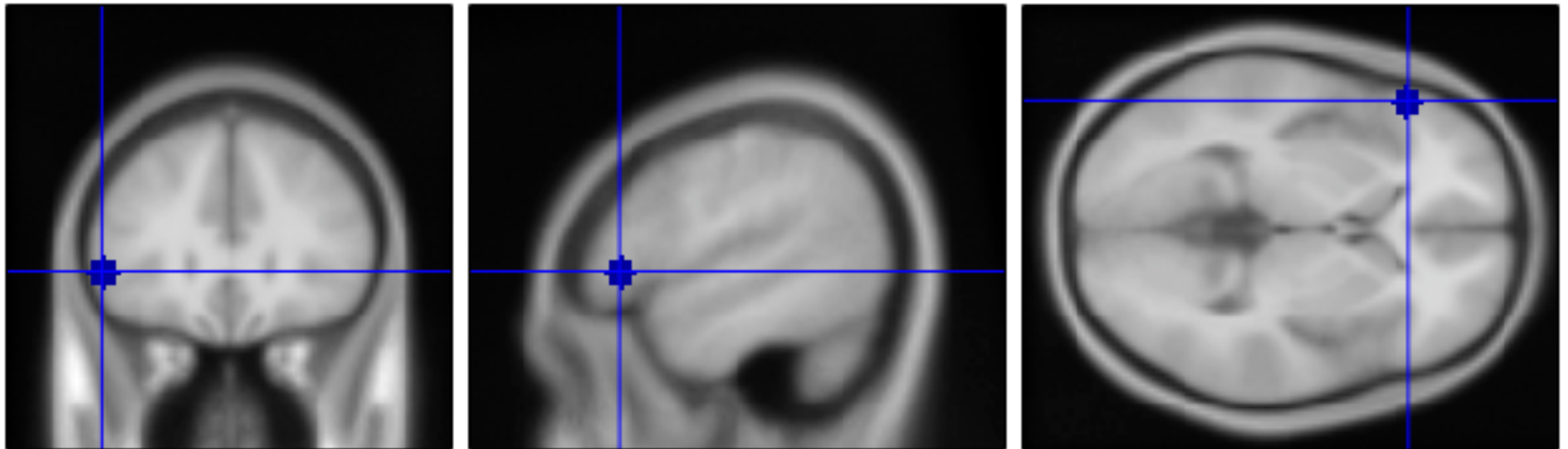
# Create ROIs in MarsBaR

Creating a sphere ROI with 6mm radius from MarsBaR  
(MarsBaR → ROI definition → Build → Sphere)



# Check ROI data

This is Broca's area - core region in the language processing





# Extract Beta Values

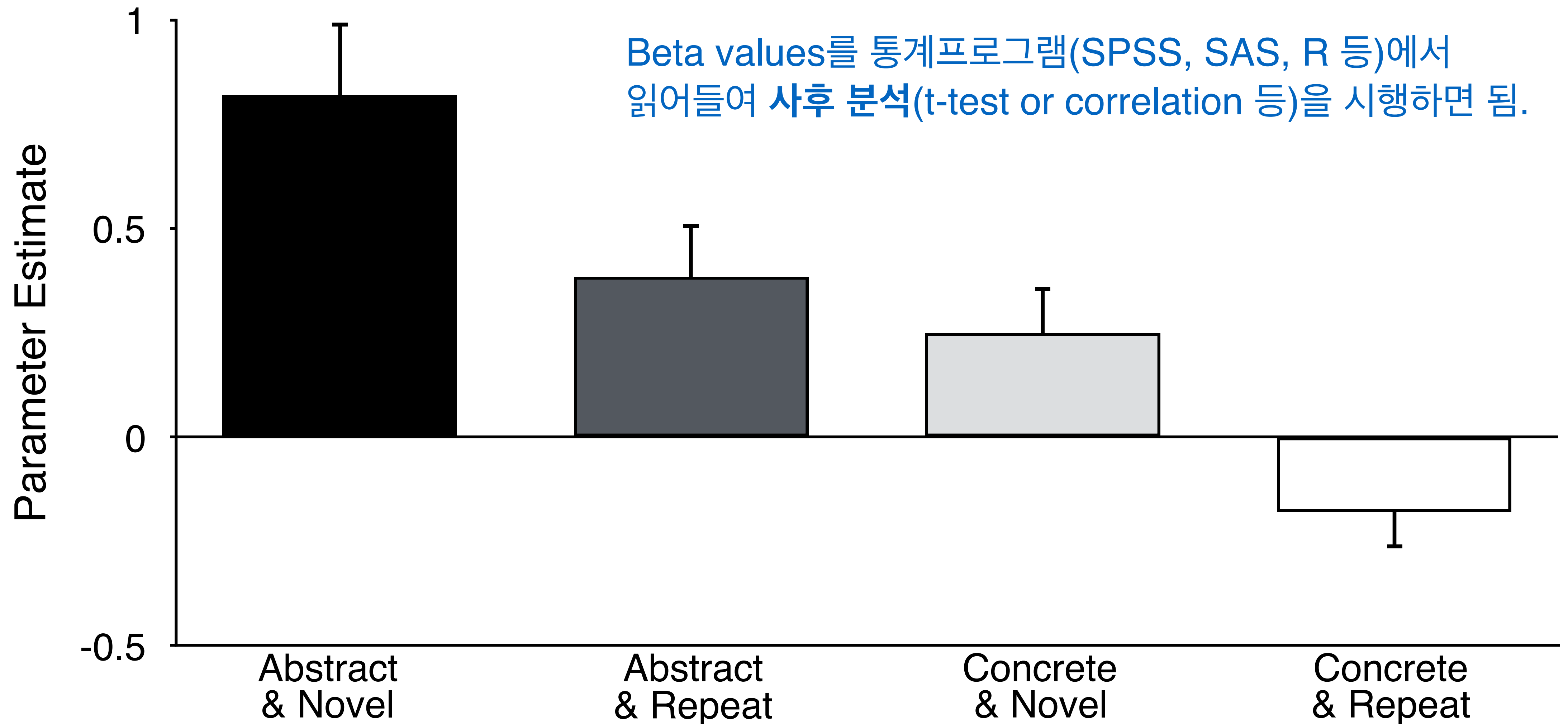
```
>> % Start marsbar to make sure spm_get works
>> marsbar('on')
>>
>>
>> % You might want to define the path for your project
>> %-----
>> proj_path = '/Volumes/JetDrive/workshops/Neuroimaging/Lecture08-GroupAnal';
>> fn_xls     = fullfile(proj_path,'subjlist.xlsx');
>>
>> T = readtable(fn_xls);
>> subjlist = T.subjname;
>> nsubj = length(subjlist);
>>
>> %-----
>> % Create ROI using marsbar script
>> %-----
>> % MNIcenters: center coordinates of ROI
>> % RADIUS: radius of ROI
>> % roi_dir: output directory to save ROI image
>> % fn_mask(optional): file path of mask image (to define image space)
>>
>> RADIUS = 6;
>> clear MNIcenters;
>> MNIcenters{1} = [-52 30 0];
>> MNIcenters{2} = [52 30 0];
>>
>> fn_mask = fullfile(proj_path,'Analysis','SecondLevel','Flexible','mask.nii');
>> roi_dir = fullfile(proj_path,'Analysis','rois'); mkdir(roi_dir);
>> roi_files = create_ROI(MNIcenters,RADIUS,roi_dir,fn_mask);
```

```
>> %-----
>> % MarsBaR estimation to extract beta values in each ROI
>> %-----
>> nroi = length(roi_files);
>> ncond = 4;
>> event_duration = 0; % default SPM event duration
>>
>> BetaValues = zeros(nsubj,ncond,nroi);
>> for c = 1:nsubj
>>     subjname = subjlist{c};
>>     spm_name = fullfile(proj_path,'Analysis','FirstLevel',subjname,'SPM.mat');
>>
>>     % Make marsbar design object
>>     D = mardo(spm_name);
>>
>>     for r=1:length(roi_files),
>>         % Make marsbar ROI object
>>         R = maroi(roi_files{r});
>>         % Fetch data into marsbar data object
>>         Y = get_marsy(R,D,'mean');
>>         % Get contrasts from original design
>>         xCon = get_contrasts(D);
>>         % Estimate design on ROI data
>>         E = estimate(D,Y);
>>         % Get design betas
>>         b = betas(E);
>>         for cond_i=1:length(xCon),
>>             con_vec = xCon(cond_i).c;
>>             BetaValues(c,cond_i,r) = mean(b(con_vec==1)); % average across sessions
>>         end
>>     end
>> end
>>
>> dlmwrite('~\Desktop/BetaValues.csv',BetaValues(:,:,:),1); % Save for ROI1
```

# Beta values for each condition

Subject	Abstract-Novel	Abstract-Repeat	Concrete-Novel	Concrete-Repeat
sub-01	1.3395	0.80875	-0.019458	-0.10004
sub-02	-0.37783	-0.49522	-0.41541	-0.63272
sub-03	2.3721	1.1551	0.72135	-0.00027128
sub-04	0.58861	0.23596	-0.11531	-0.57674
sub-05	0.9733	0.18268	0.3968	-0.16907
sub-06	0.81145	0.90324	0.29943	-0.12184
sub-07	0.36319	0.12021	-0.09805	-0.41842
sub-08	0.78794	0.15813	0.038025	-0.42258
sub-09	0.3722	-0.053752	-0.096797	-0.46269
sub-10	0.60333	0.22182	0.30693	-0.012669
sub-11	0.89011	0.32513	0.65178	-0.053054
sub-12	0.93845	0.87265	0.69751	0.46067
sub-13	0.99807	0.55706	0.85932	0.18776

# Plot Mean Values for each condition



# Extract % Signal Change

```
>> % Start marsbar to make sure spm_get works
>> marsbar('on')
>>
>> % You might want to define the path for your project
>> %-----
>> proj_path = '/Volumes/JetDrive/workshops/Neuroimaging/Lecture08-GroupAnal';
>> fn_xls    = fullfile(proj_path,'subjlist.xlsx');
>> T         = readtable(fn_xls);
>> subjlist  = T.subjname;
>> nsubj     = length(subjlist);
>>
>>
>> % Create ROI using marsbar script
>> %-----
>> % MNIcenters: center coordinates of ROI
>> % RADIUS: radius of ROI
>> % roi_dir: output directory to save ROI image
>> % fn_mask(optional): file path of mask image (to define image space)
>>
>> RADIUS = 6;
>> clear MNIcenters;
>> MNIcenters{1} = [-52 30 0];
>> MNIcenters{2} = [52 30 0];
>>
>> fn_mask = fullfile(proj_path,'Analysis','SecondLevel','Flexible','mask.nii');
>> roi_dir = fullfile(proj_path,'Analysis','rois'); mkdir(roi_dir);
>> roi_files = create_ROI(MNIcenters,RADIUS,roi_dir,fn_mask);
>>
>> % MarsBaR estimation to extract beta values in each ROI
>> %-----
>> nroi = length(roi_files);
>> ncond = 4;
>> event_duration = 0; % default SPM event duration
```

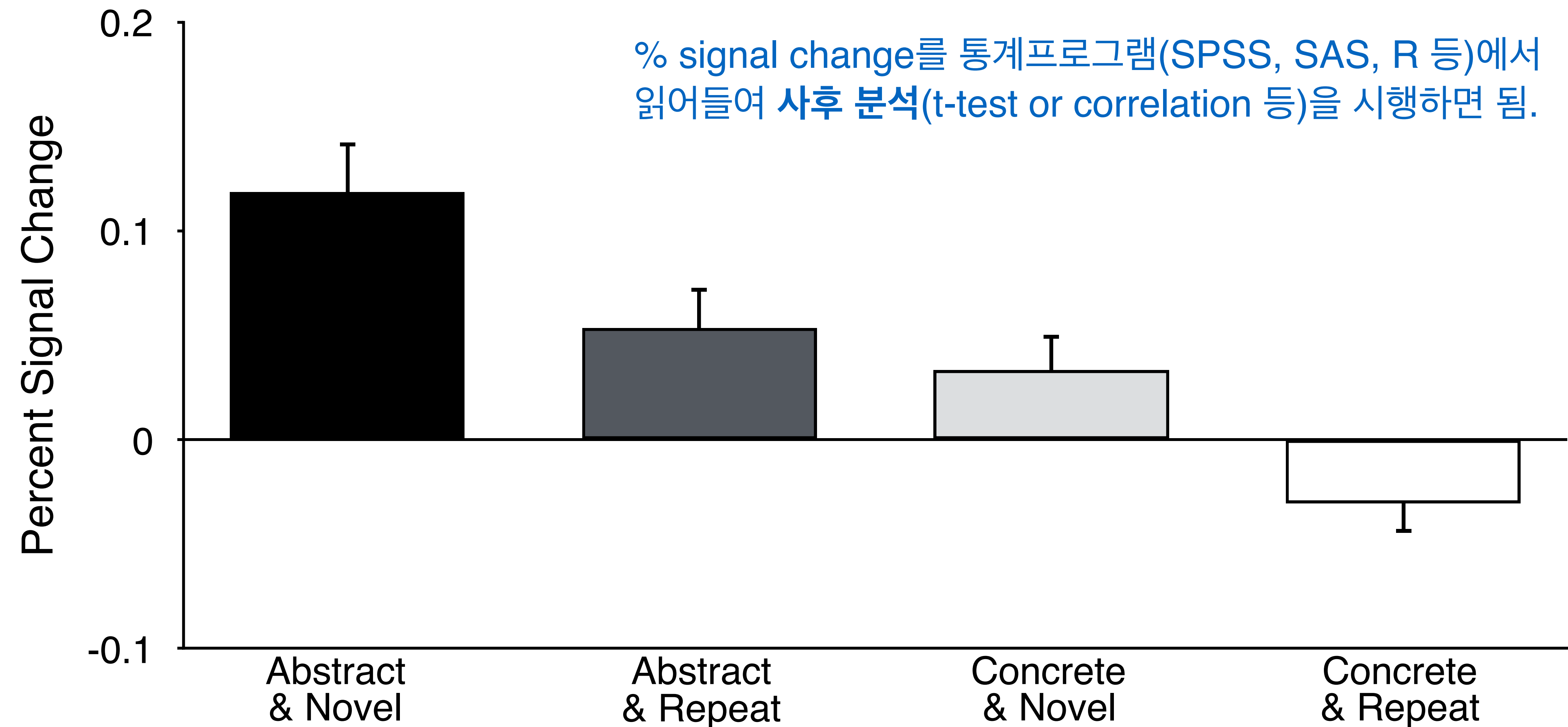
```
>> PCT_EVT = zeros(nsubj,ncond,nroi);
>> for c = 1:nsubj
>>     subjname = subjlist{c};
>>     spm_name = fullfile(proj_path,'Analysis','FirstLevel',subjname,'SPM.mat');
>>
>>     % Make marsbar design object
>>     D = mardo(spm_name);
>>
>>     for r=1:length(roi_files),
>>         % Make marsbar ROI object
>>         R = maroi(roi_files{r});
>>         % Fetch data into marsbar data object
>>         Y = get_marsy(R,D,'mean');
>>         % Get contrasts from original design
>>         xCon = get_contrasts(D);
>>         % Estimate design on ROI data
>>         E = estimate(D,Y);
>>         % Get definition of all events in model
>>         [e_specs, e_names] = event_specs(E);
>>         n_events = size(e_specs,2);
>>         % Return percent signal estimate for all events in design
>>         pct_ev = zeros(n_events,1);
>>         for e_s = 1:n_events,
>>             pct_ev(e_s) = event_signal(E, e_specs(:,e_s),event_duration);
>>         end
>>         % Compute average value over sessions
>>         for cond_i=1:length(xCon),
>>             PCT_EVT(c,cond_i,r) = mean(pct_ev(e_specs(2,:)==cond_i)); % average over sessions
>>         end
>>     end
>> end
>>
>> dlmwrite('~\Desktop\PCT_EVT.csv',PCT_EVT(:,:,:),1); % Save for ROI1
```



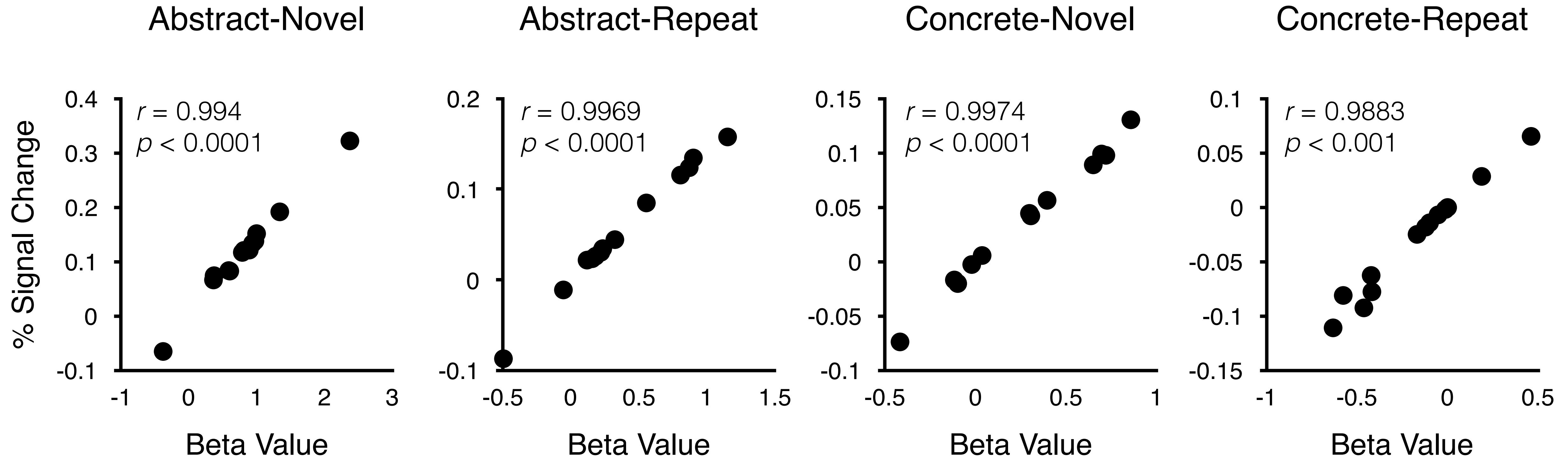
# % Signal Changes for each condition

Subject	Abstract-Novel	Abstract-Repeat	Concrete-Novel	Concrete-Repeat
sub-01	0.19174	0.11564	-0.0025961	-0.0142
sub-02	-0.065152	-0.087084	-0.073777	-0.11084
sub-03	0.32225	0.15774	0.097879	-0.00012068
sub-04	0.083695	0.034442	-0.016796	-0.081029
sub-05	0.13811	0.025992	0.056459	-0.024865
sub-06	0.12077	0.13454	0.044472	-0.01819
sub-07	0.06646	0.021772	-0.019675	-0.077661
sub-08	0.11709	0.023317	0.0057108	-0.062635
sub-09	0.074297	-0.01115	-0.020075	-0.092477
sub-10	0.082783	0.030389	0.042174	-0.0019255
sub-11	0.12138	0.044363	0.089104	-0.0069162
sub-12	0.1336	0.12382	0.099087	0.065301
sub-13	0.15167	0.084881	0.13055	0.02847

# Plot Mean % Signal Change for each condition

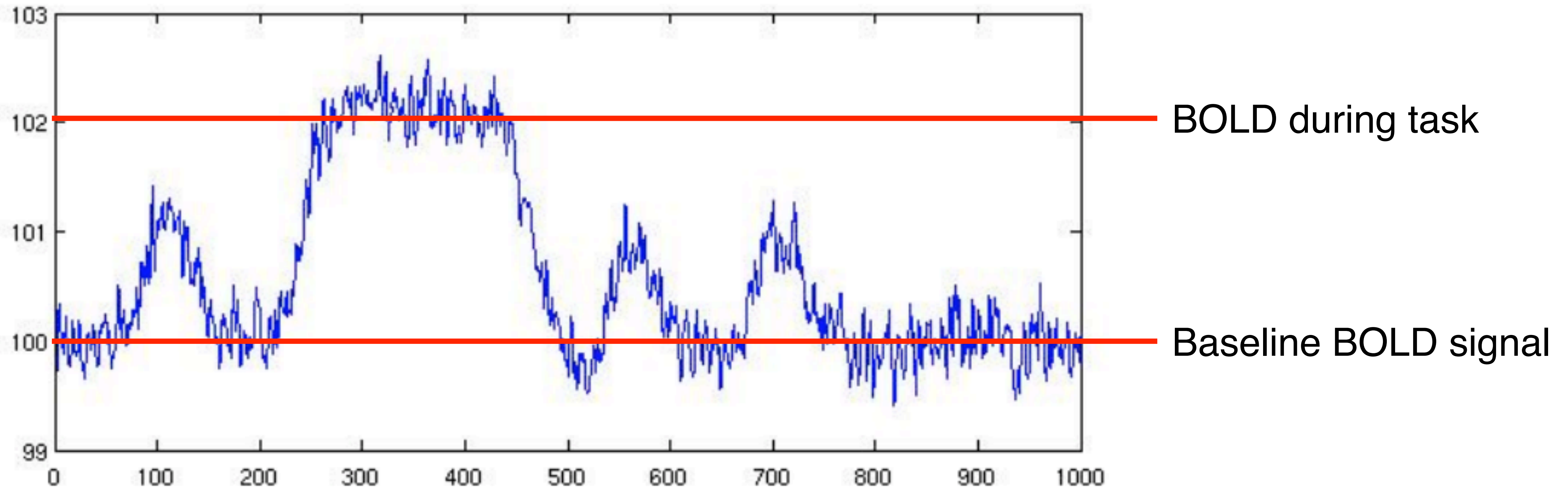


# Beta vs % signal change



Almost similar, but there are some differences!

# What is the % signal change calculated?



Simulated block and event design, where block is a linear superposition of closely spaced events (about 3 secs apart). When the GLM is correctly scaled, the block height is 2% whether the data is modeled as a block or as overlapping events. Mean of the time-series is 100.6.

Reference) Paul Mazaika, Percent Signal Change for fMRI calculation



# Limitations of Percent Signal Change

- **Statistical Maps do not require percent signal change.** All SPM statistics are scale invariant so quantified results are not needed. The maps are used to spatially localize regions of the brain that show a significant effect different from zero (null hypothesis).
- **Quantitative results do not interpret neural excitations.** The scaling does not extend back to neural excitation, because neither the BOLD effect (neural excitation to change in local dHb blood levels), or scanner effects (dHb change to recorded signal change) are well defined. Thus, this analysis of percent signal change is only in the mathematical estimation domain, not the biology or physics domains.
- **The assumption of linear superposition can be violated in real data.** For block experiments, the measured shape of the block response may not be particularly flat on top [Glover, 1999] due to saturation and other effects. These unusual shapes can make it tricky to define the peak or average value of even a simple block effect.