Neuroimaging data analysis

2nd-level analysis (or group-level inference) in SPM12

Sunghyon Kyeong, PhD

Severance Biomedical Science Institute,
Yonsei University College of Medicine
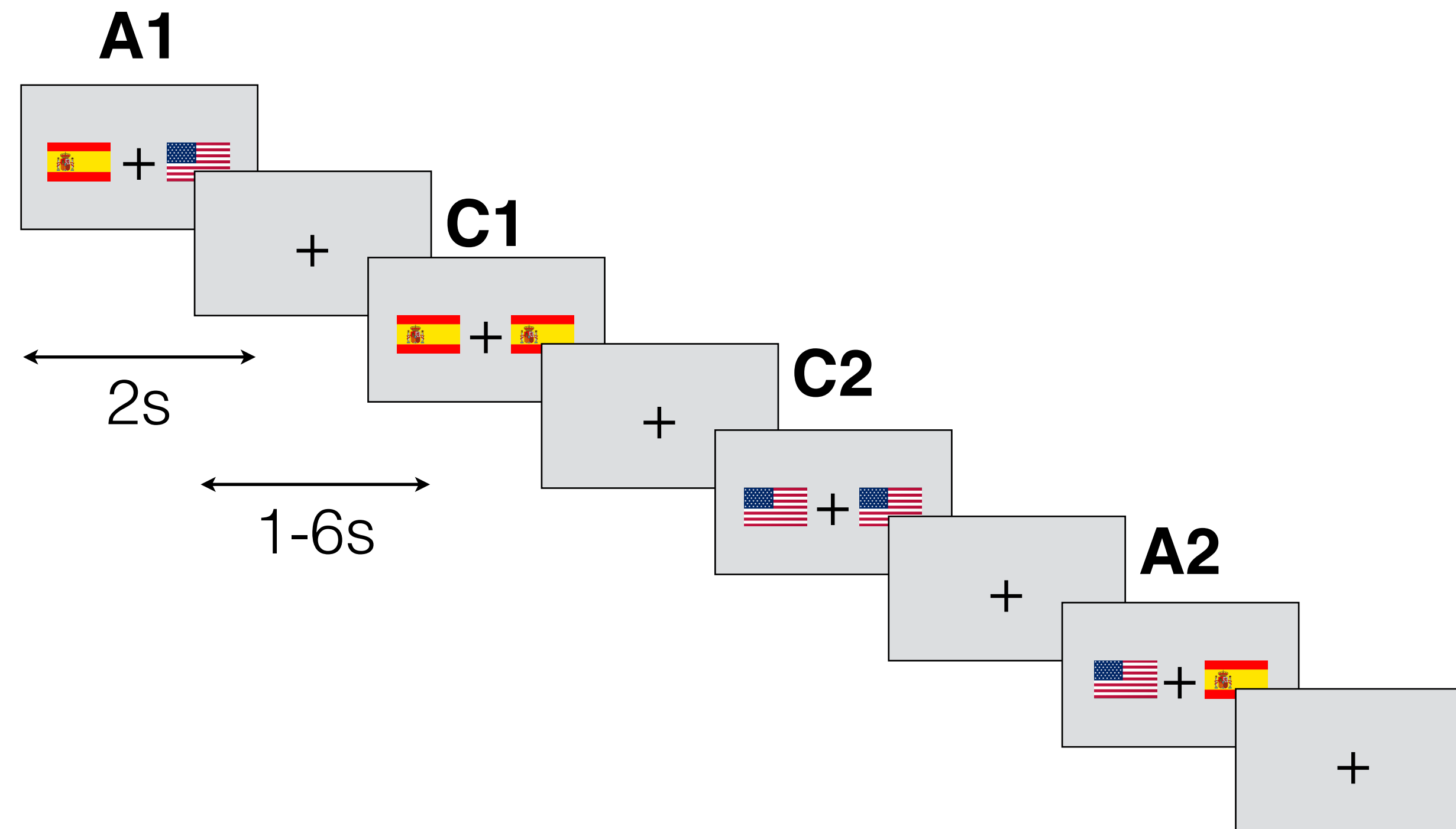
실습 데이터 다운로드

Raw data:
https://openfmri.org/dataset/ds000051/

First-level 분석이 완료된 data:

https://drive.google.com/drive/folders/0B6863JbB_YV-bWFoUE5sbmRvOXc

어떤 데이터 일까?

Cross-language repetition priming

Experiment Information

- (4 x) 2 x 2 factorial event-related fMRI design

- 8 runs (13 subjects)

- (SE, SS, ES, EE) x (abstract vs. concrete) x (1st vs 2nd presentation) of words

- MRI data were acquired using 3T Siemens Allegra system

- 200 Continuous EPI (TE=30ms,TR=2s) per run

- 21 axial slices, 5mm thickness
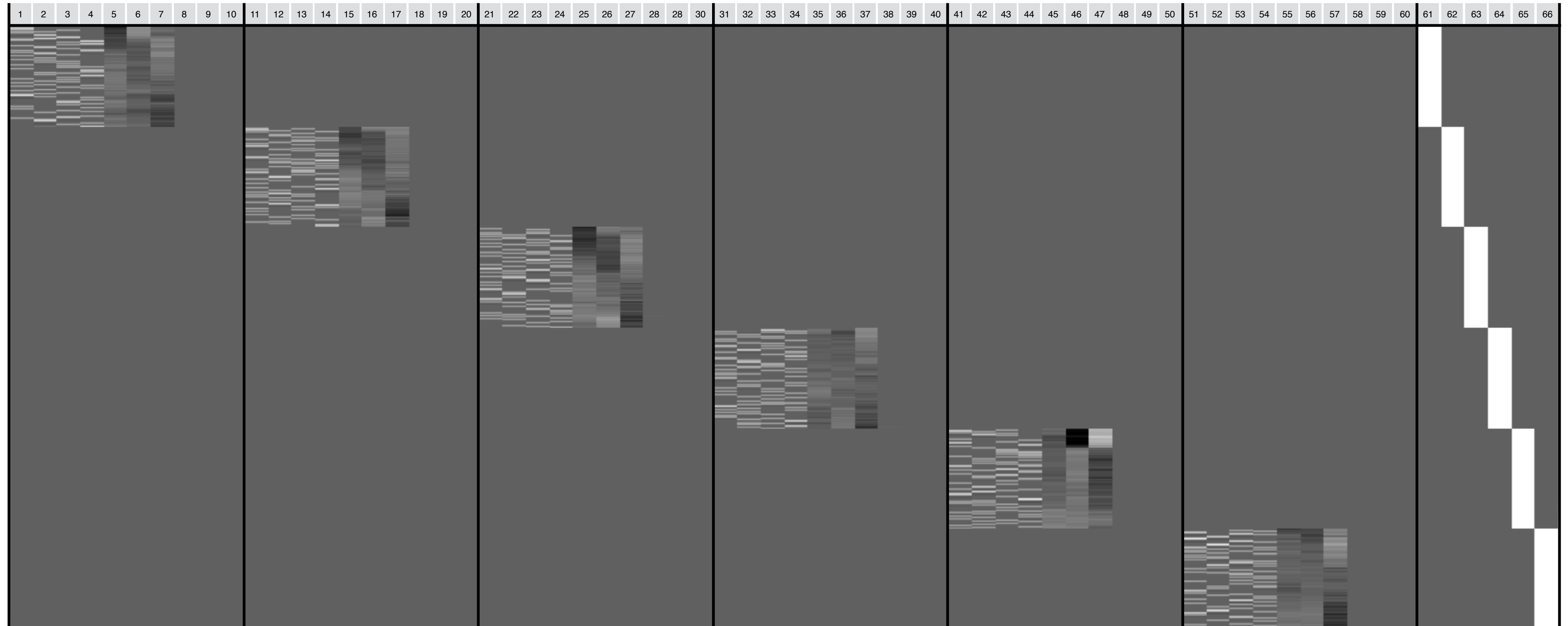
- 200 mm field of view (64x64 3.125x3.125mm^2)

Reference) https://openfmri.org/dataset/ds000051/

GLM for Each fMRI Run
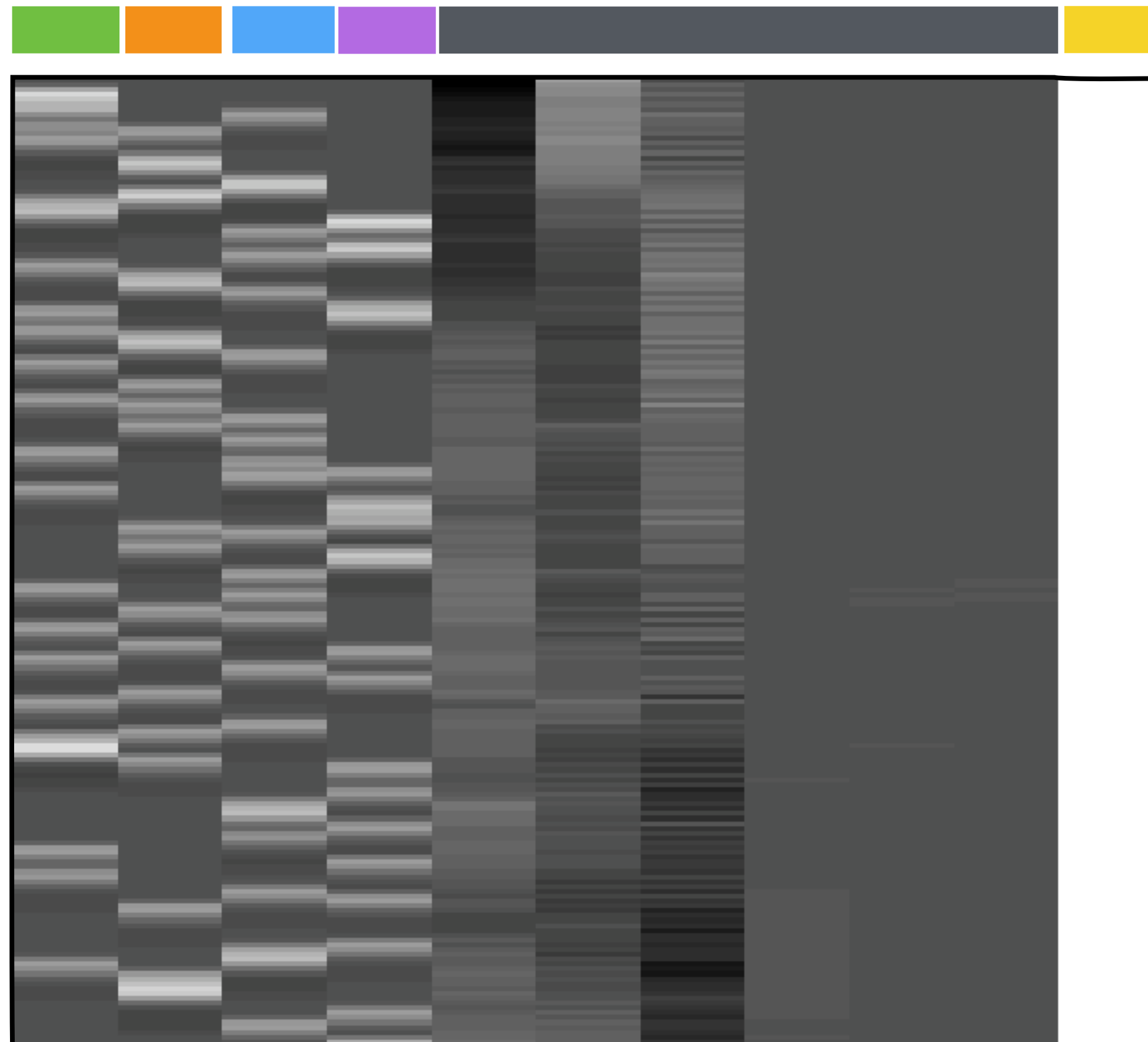
AN: Abstract and novel word

AR: Abstract and repeated word

CN: Concrete and novel word

CR: Concrete and repeated word

Head motion: six rigid head motion parameters

Constant: a constant term in general linear model

1st-level Linear Modeling for 6 Runs

A total of 66 parameters (66 beta images) were estimated.
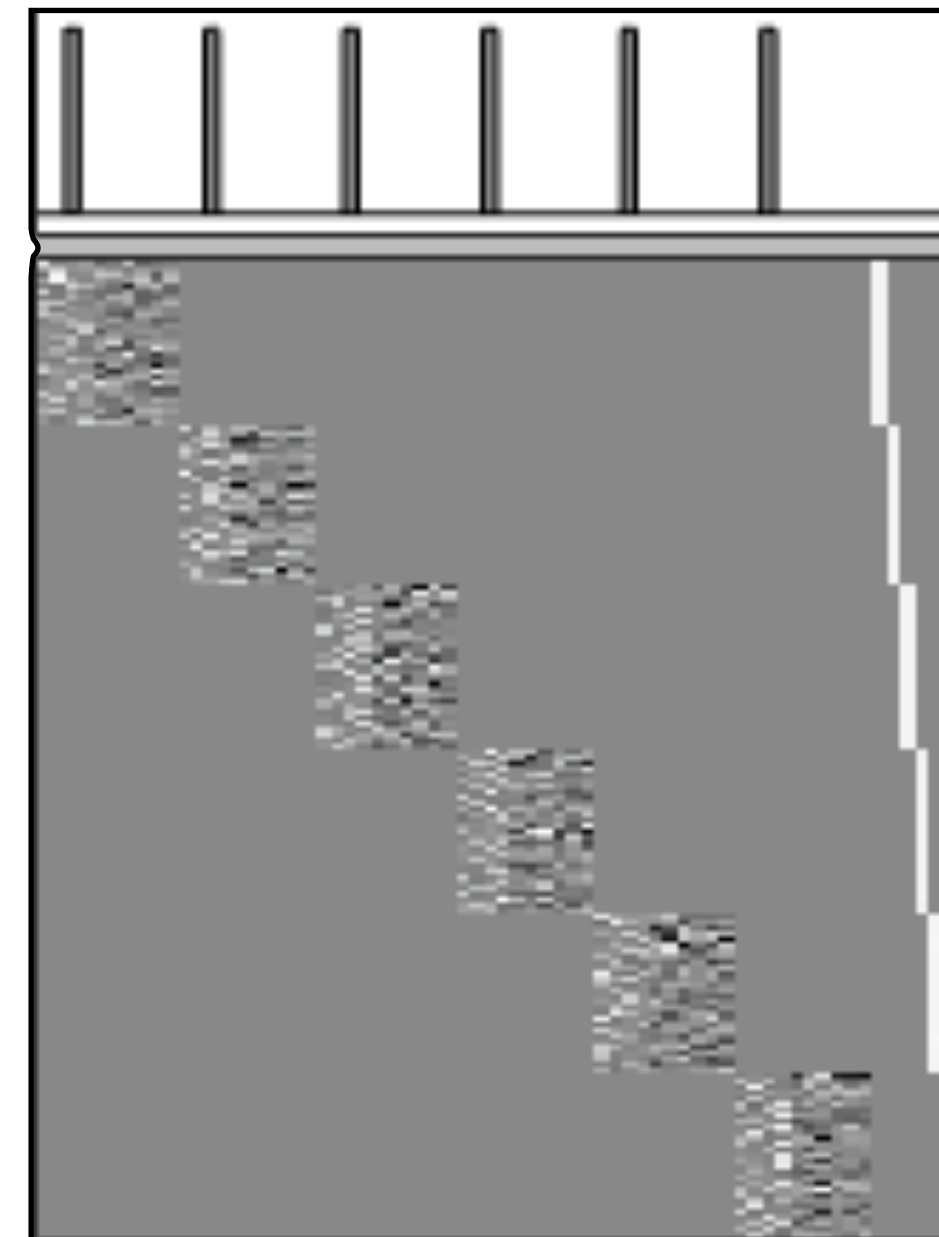
Create Contrast Images

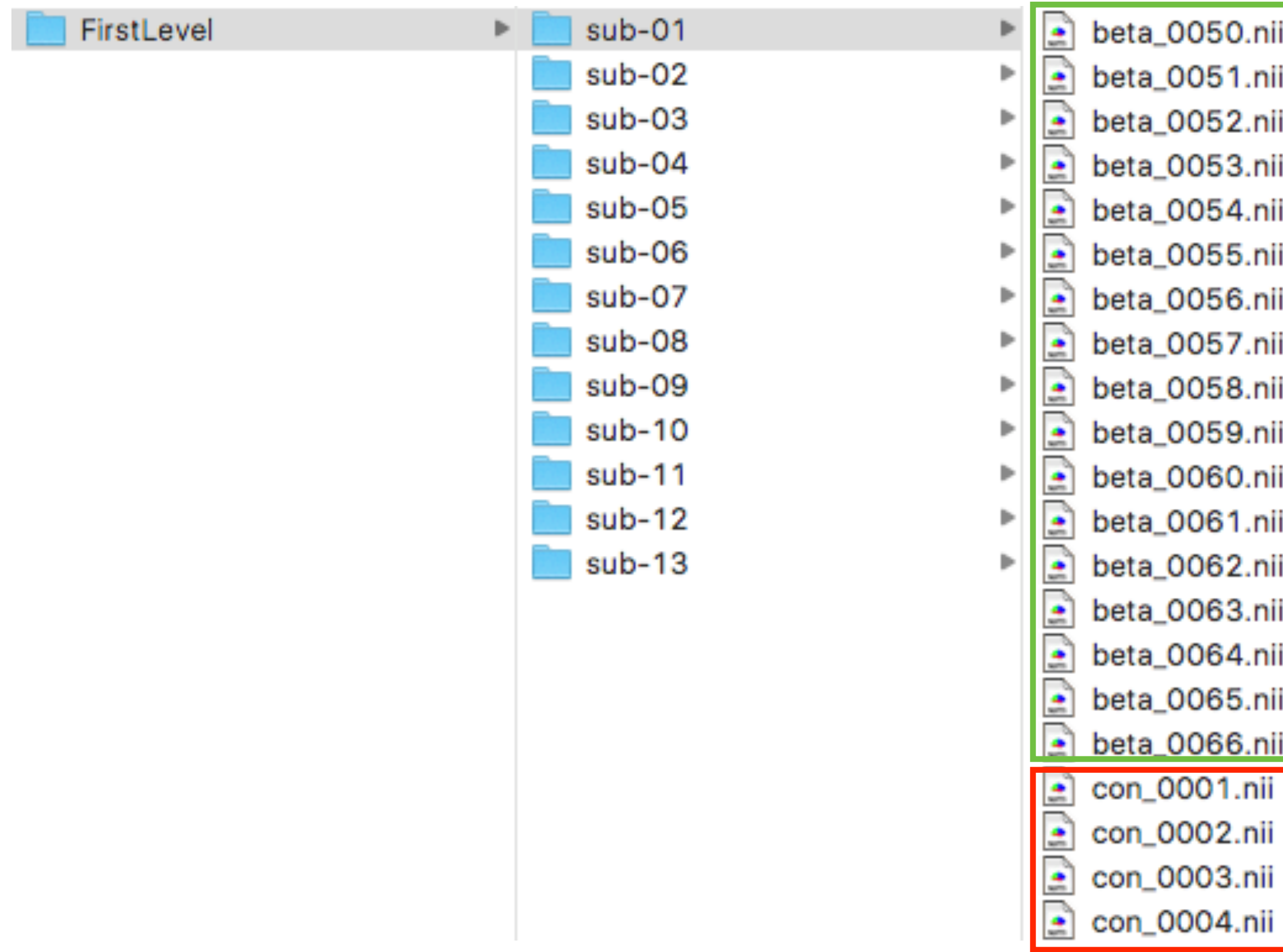| **AN 조건**	**AR 조건**	**CN 조건**	**CR 조건**
con_0001.nii	con_0002.nii	con_0003.nii	con_0004.nii

Contrast Images가 의미하는 바는?

66 beta images

Please note that contrast image is not a average but a summation of interests

```
FirstLevel  ▶   sub-01  ▶   beta_0050.nii
                sub-02  ▶   beta_0051.nii
                sub-03  ▶   beta_0052.nii
                sub-04  ▶   beta_0053.nii
                sub-05  ▶   beta_0054.nii
                sub-06  ▶   beta_0055.nii
                sub-07  ▶   beta_0056.nii
                sub-08  ▶   beta_0057.nii
                sub-09  ▶   beta_0058.nii
                sub-10  ▶   beta_0059.nii
                sub-11  ▶   beta_0060.nii
                sub-12  ▶   beta_0061.nii
                sub-13  ▶   beta_0062.nii
                            beta_0063.nii
                            beta_0064.nii
                            beta_0065.nii
                            beta_0066.nii
                            con_0001.nii
                            con_0002.nii
                            con_0003.nii
                            con_0004.nii
```

con_0001.nii $C_1 = \sum\limits_{i=1,11,21,31,41,51} \beta_i$

(모든 run의 AN조건 합)

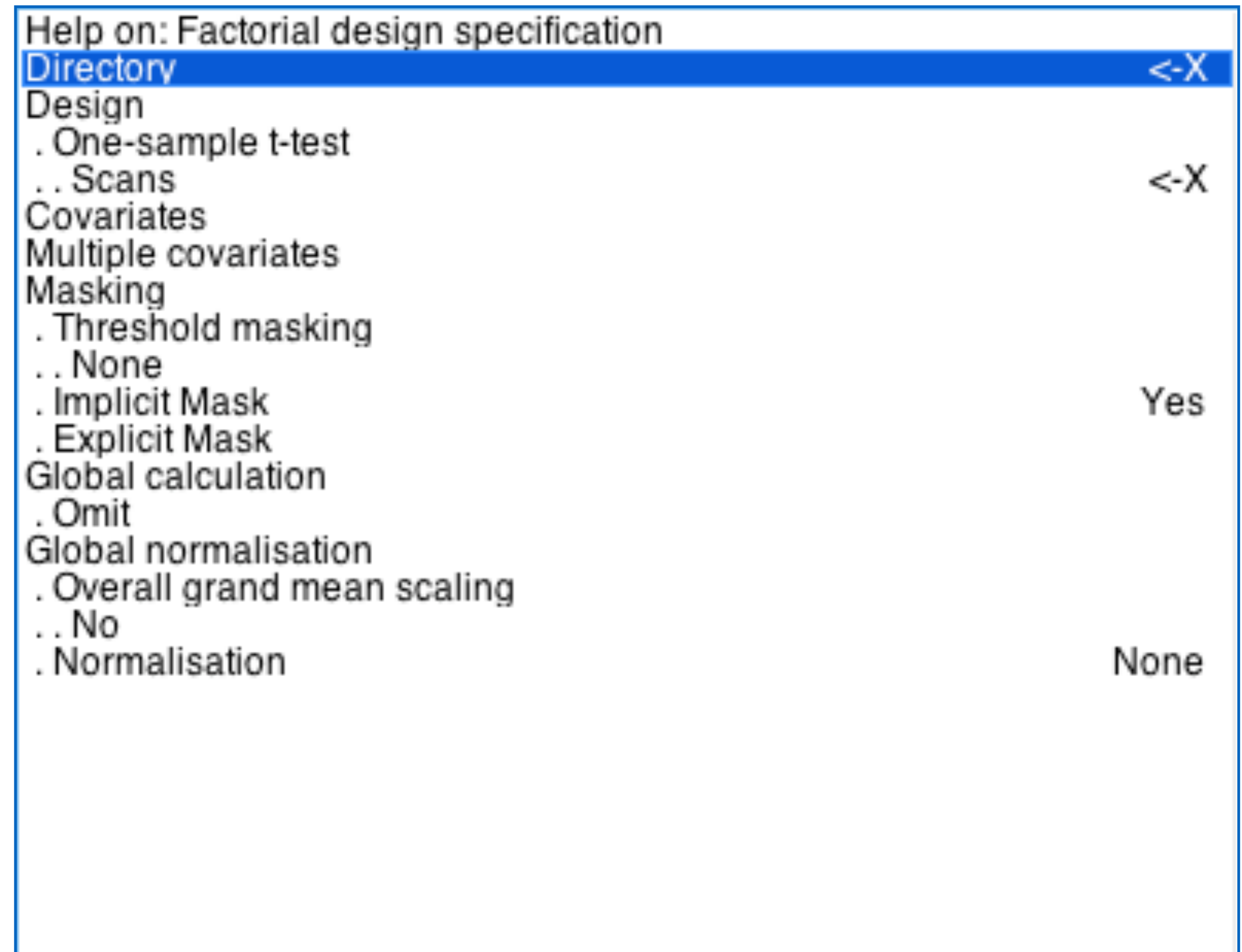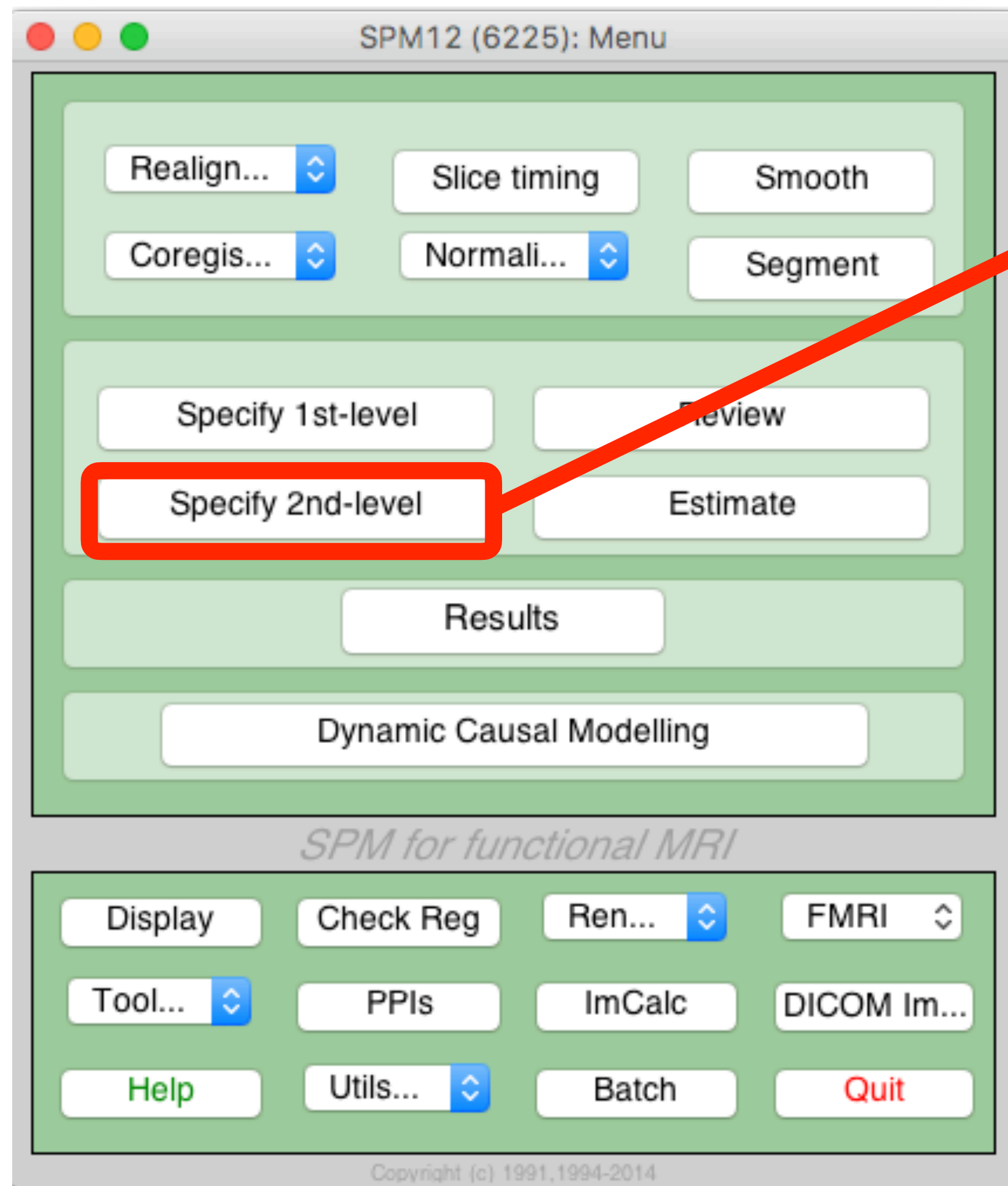**con_0002.nii** $C_2 = \sum\limits_{i=2,12,22,32,42,52} \beta_i$

(모든 run의 AR조건 합)

con_0003.nii $C_3 = \sum\limits_{i=3,13,23,33,43,53} \beta_i$

(모든 run의 CN조건 합)

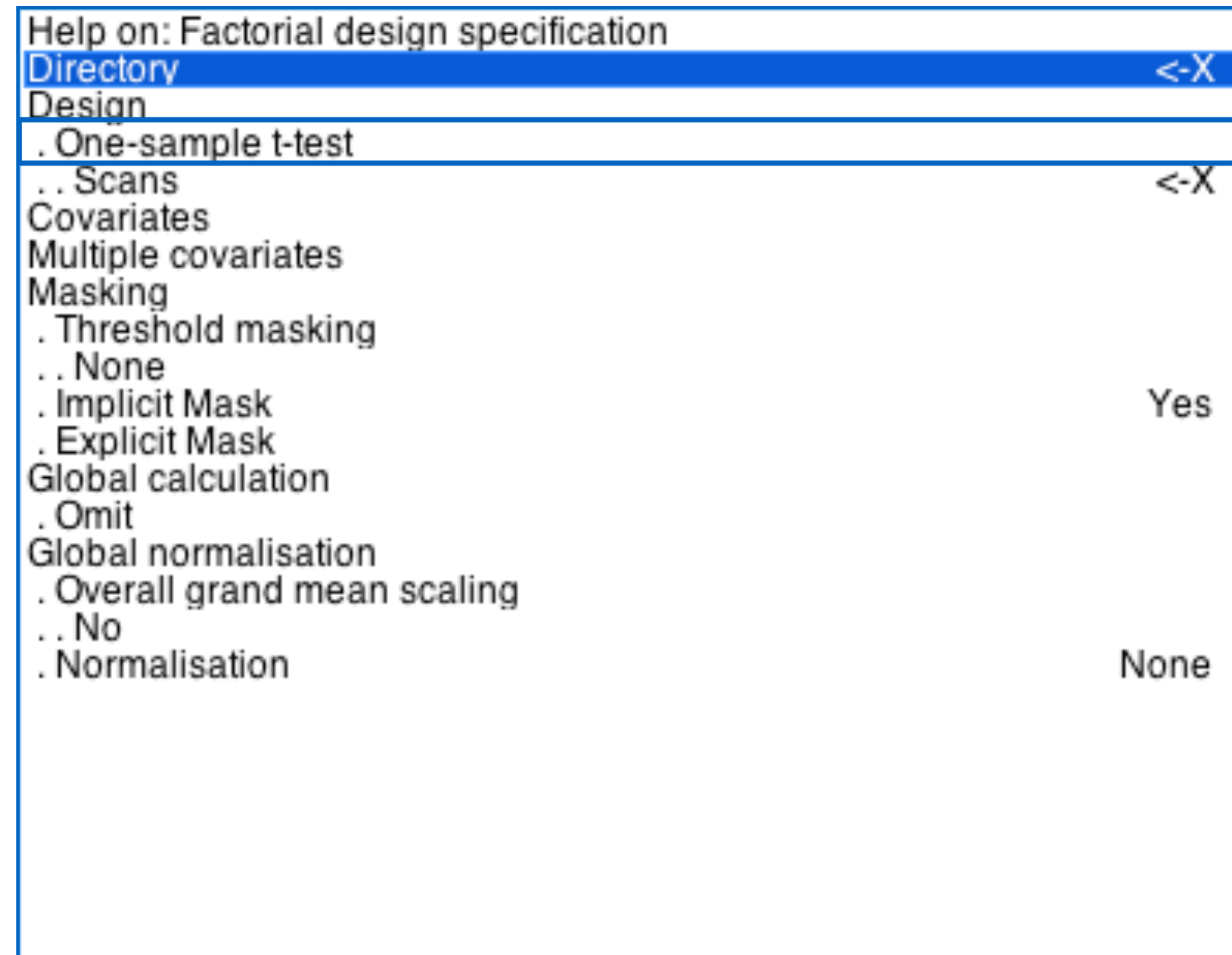**con_0004.nii** $C_4 = \sum\limits_{i=4,14,24,34,44,54} \beta_i$

(모든 run의 CR조건 합)

그룹 통계 분석 (2nd-level analysis)

a. one sample t-test
b. paired sample t-test
c. full factorial
d. flexible factorial

One-sample t-test: Specify model (1/2)
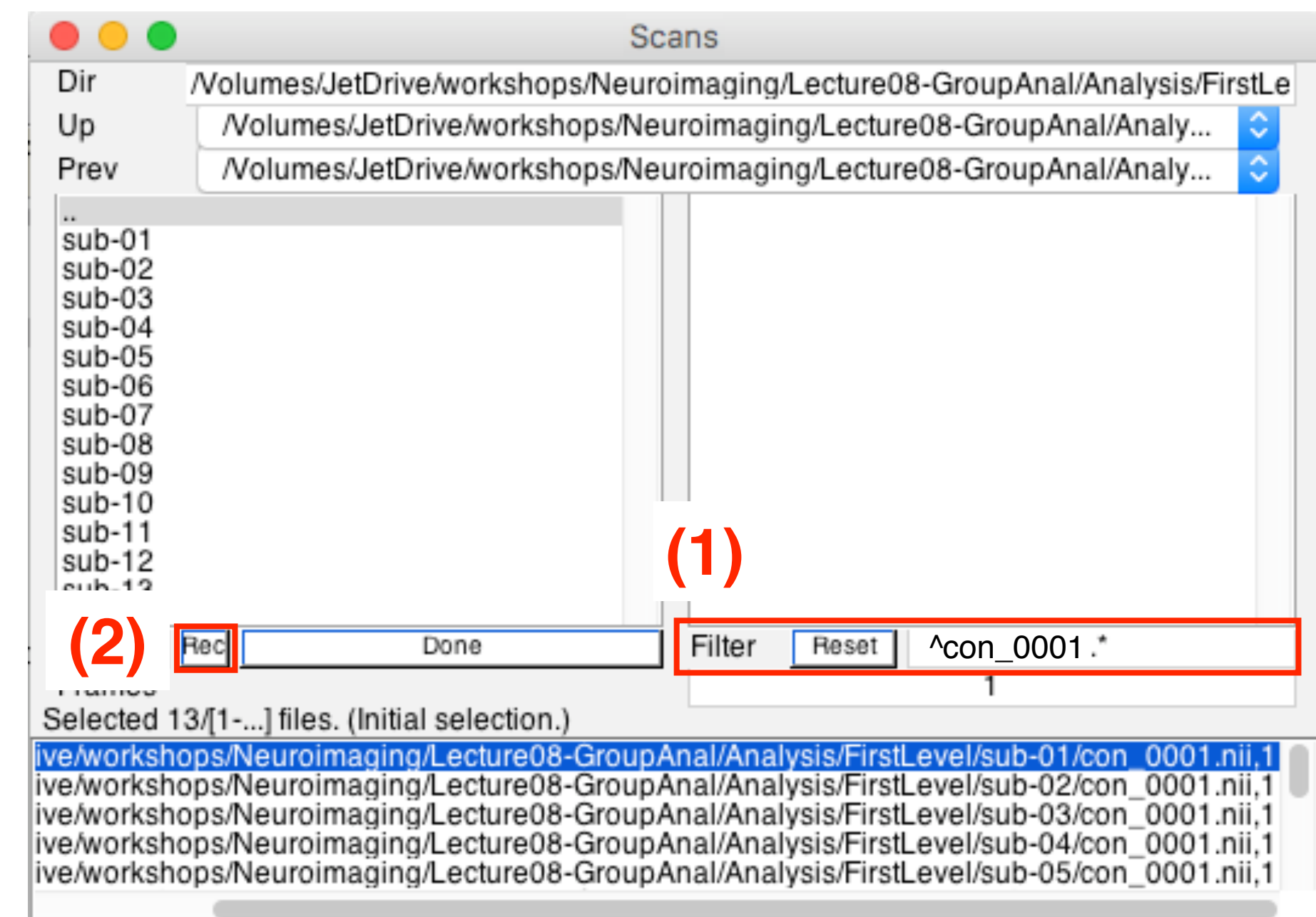
One-sample t-test: Specify model (2/2)

Directory
ex) c:\fMRI\SecondLevel\One sample\Abstract-Novel
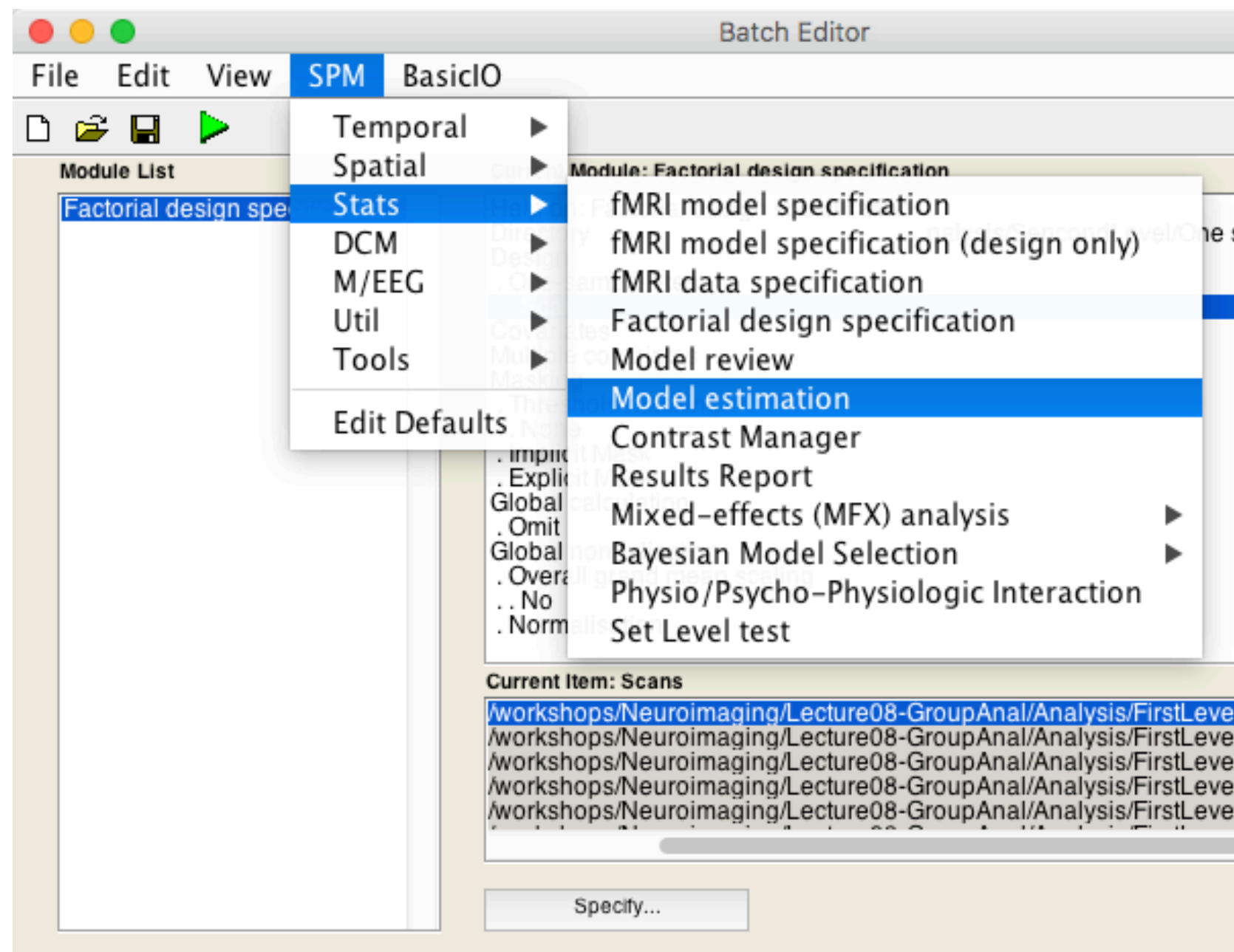
Design
Choose 'One-sample t-test'

Scans
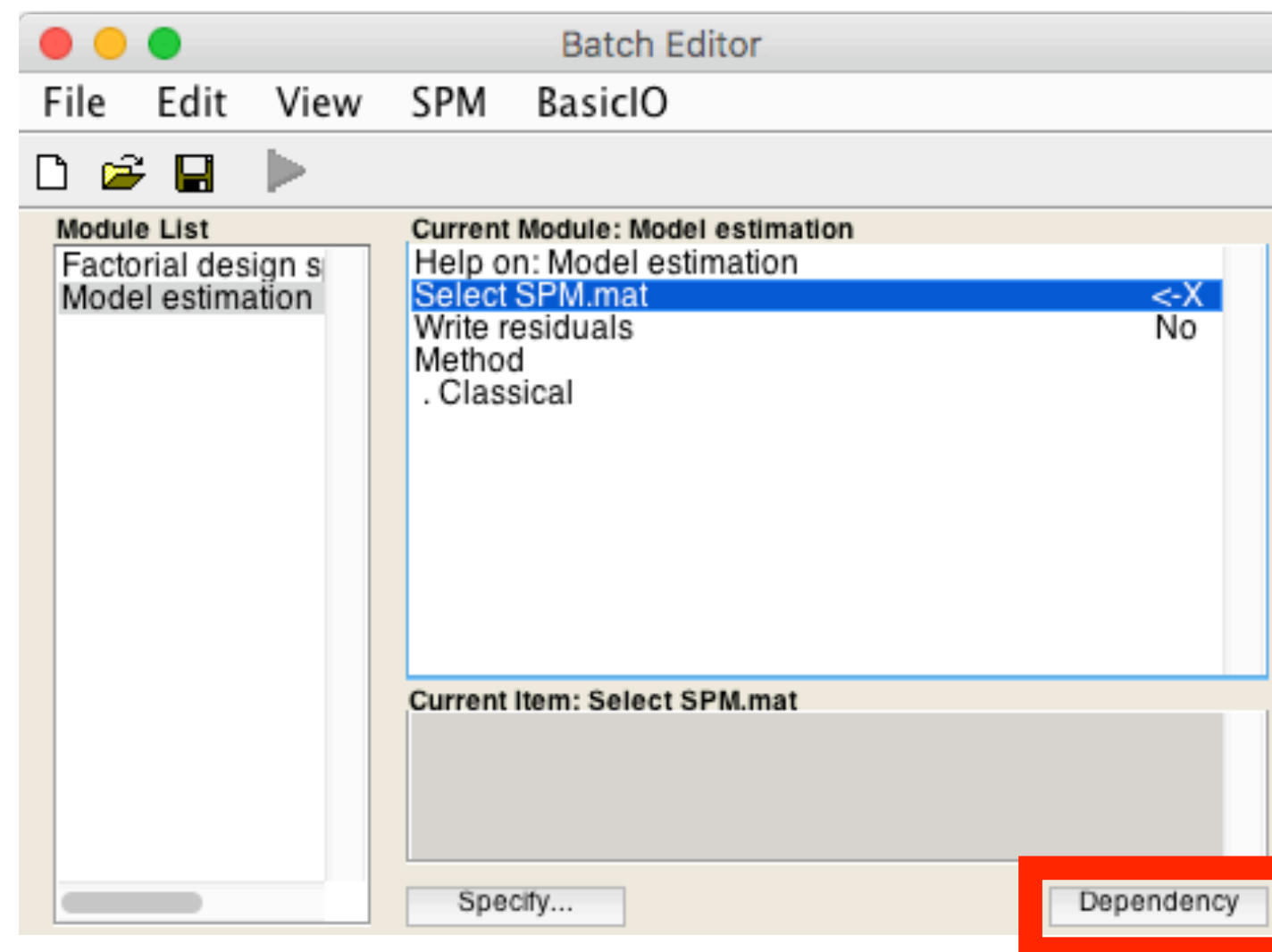Select con_0001.nii files from all subjects
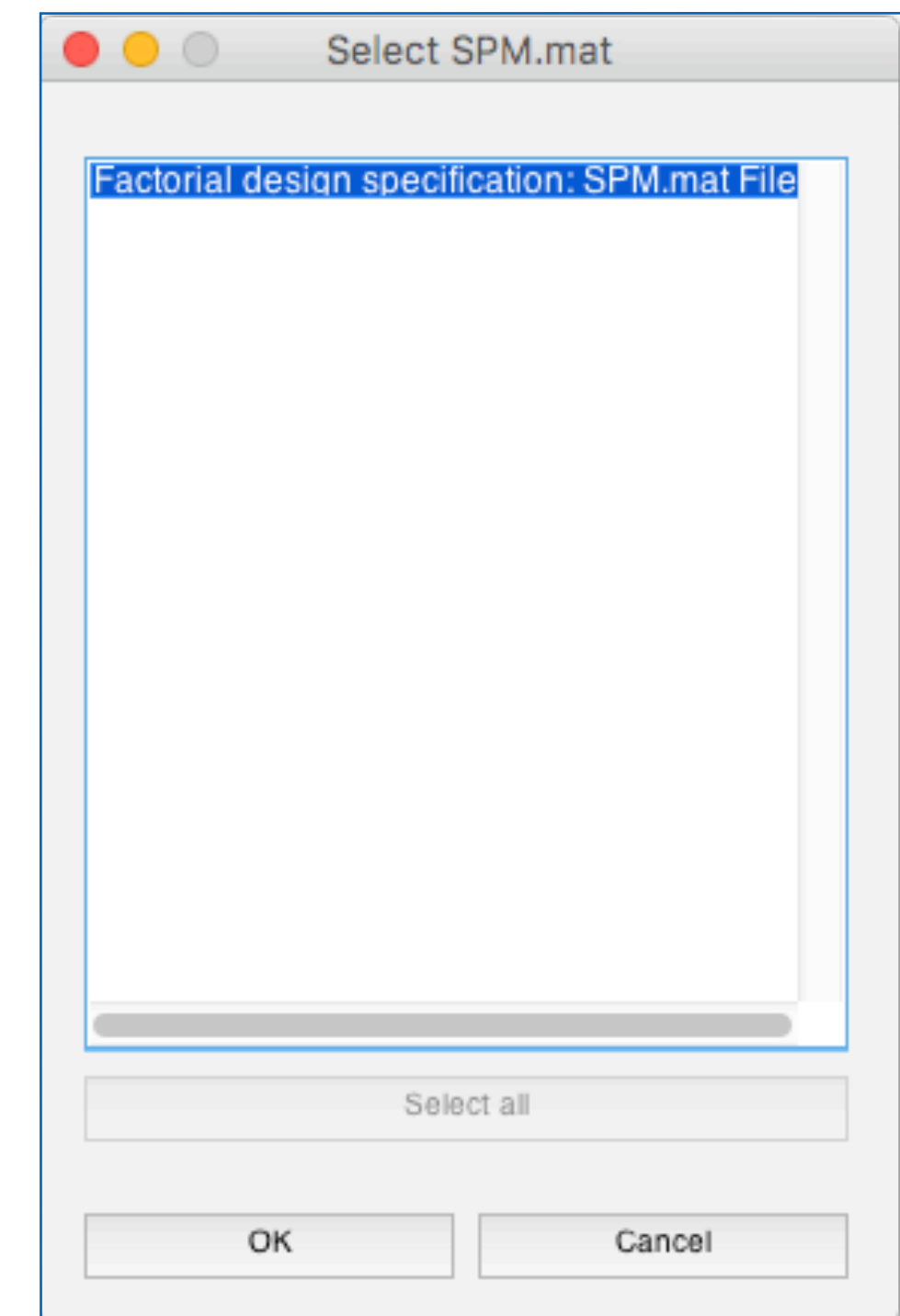
One-sample t-test: Estimation

1. Add 'model estimation' in the module list
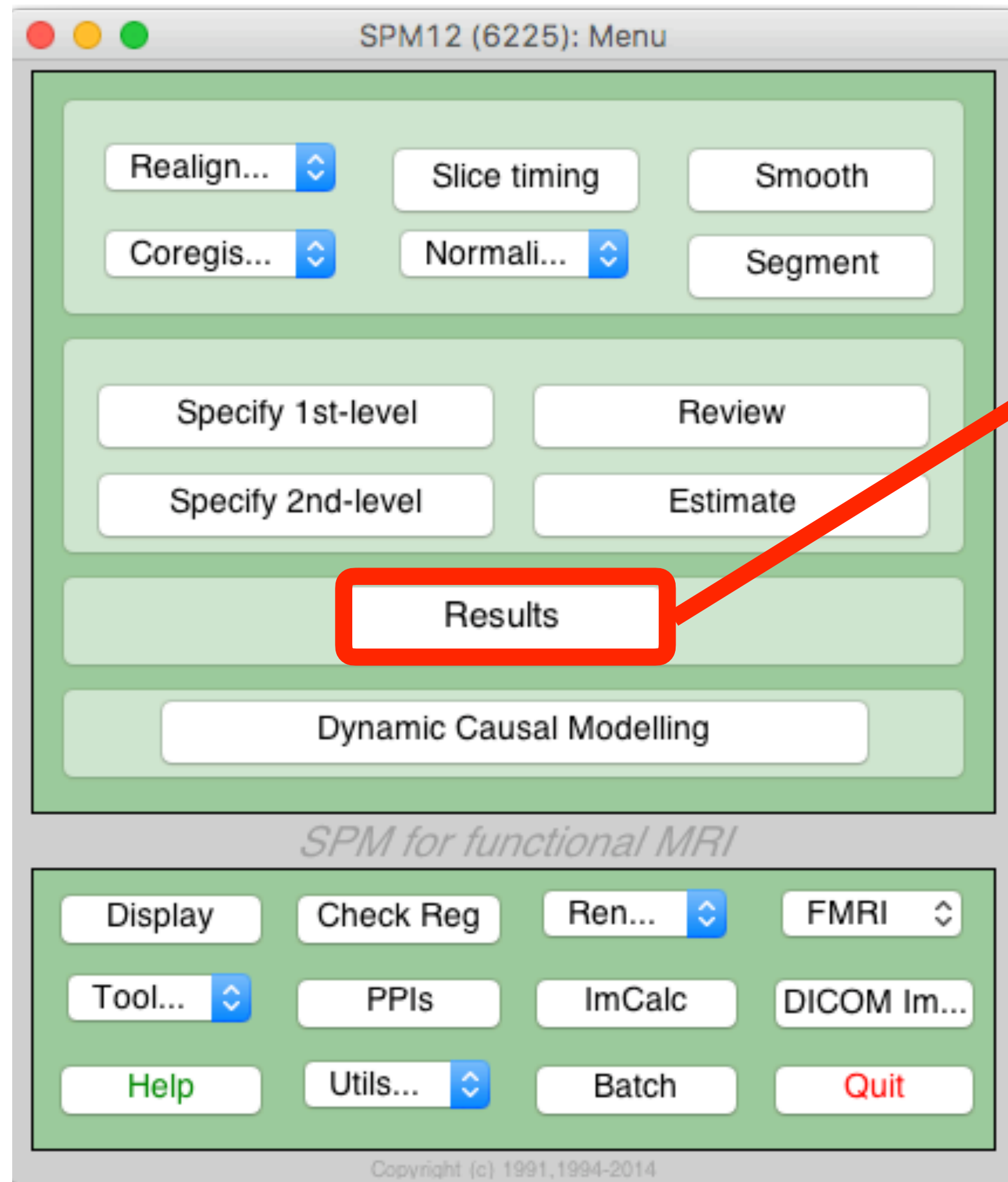(SPM menu → Stats → Model estimation)

2. Select SPM.mat file
(Click 'Dependency' button)

3. Select SPM.mat file
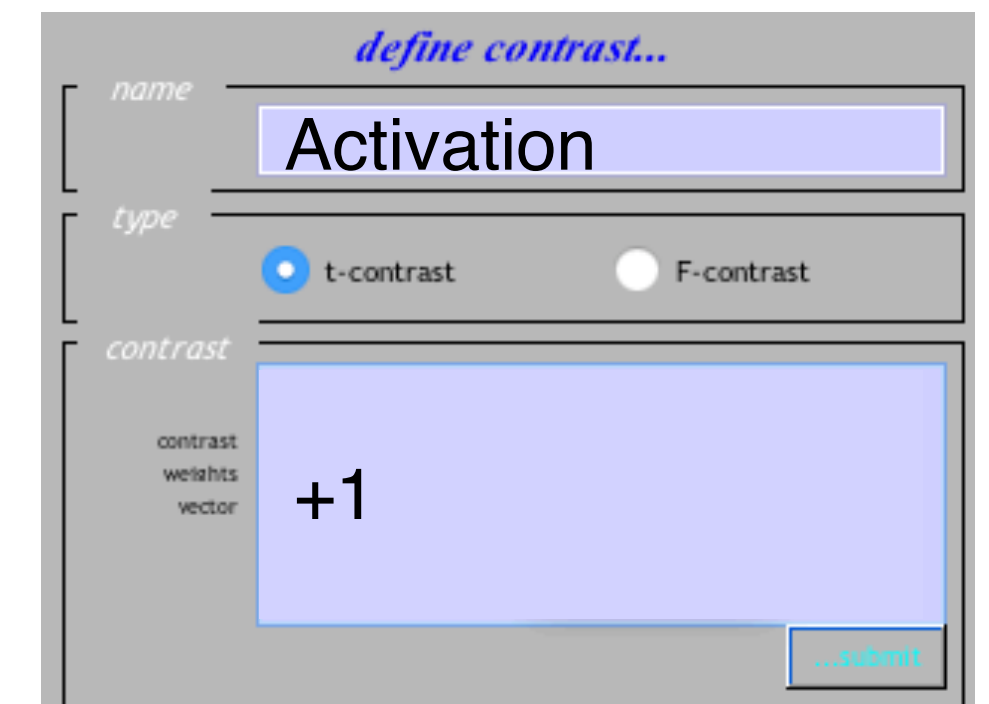(click ▶Run after selection)
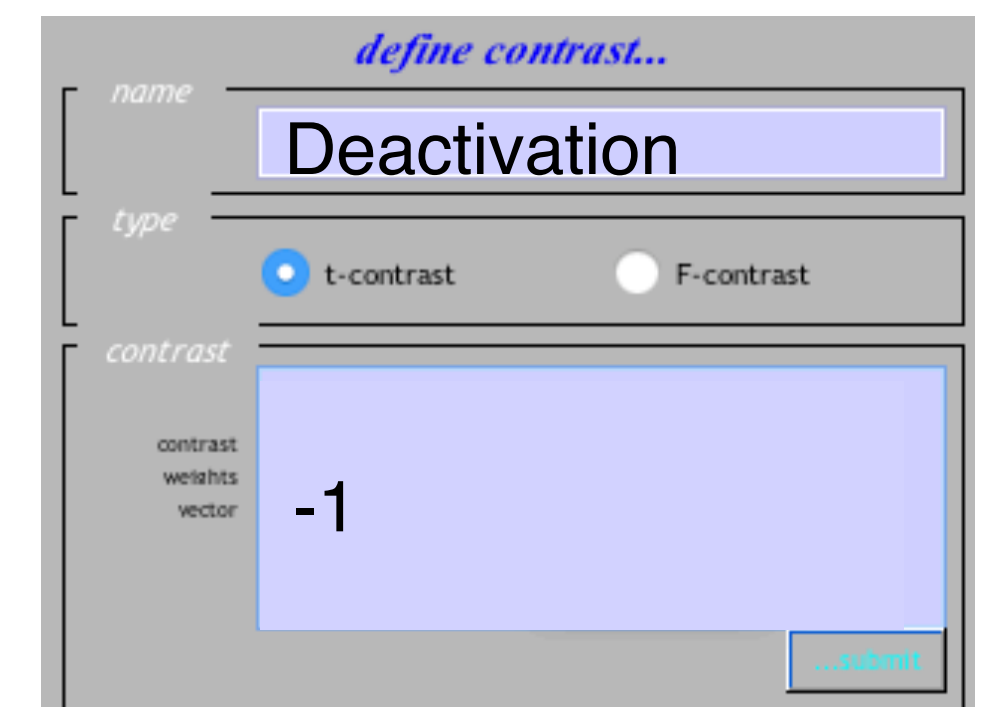
One-sample t-test: Contrast

Select one of existing contrasts or Define net contrast

Activation-contrast

Deactivation-contrast

같은 방법으로 AN, AR, CN, CR 조건에 대해서
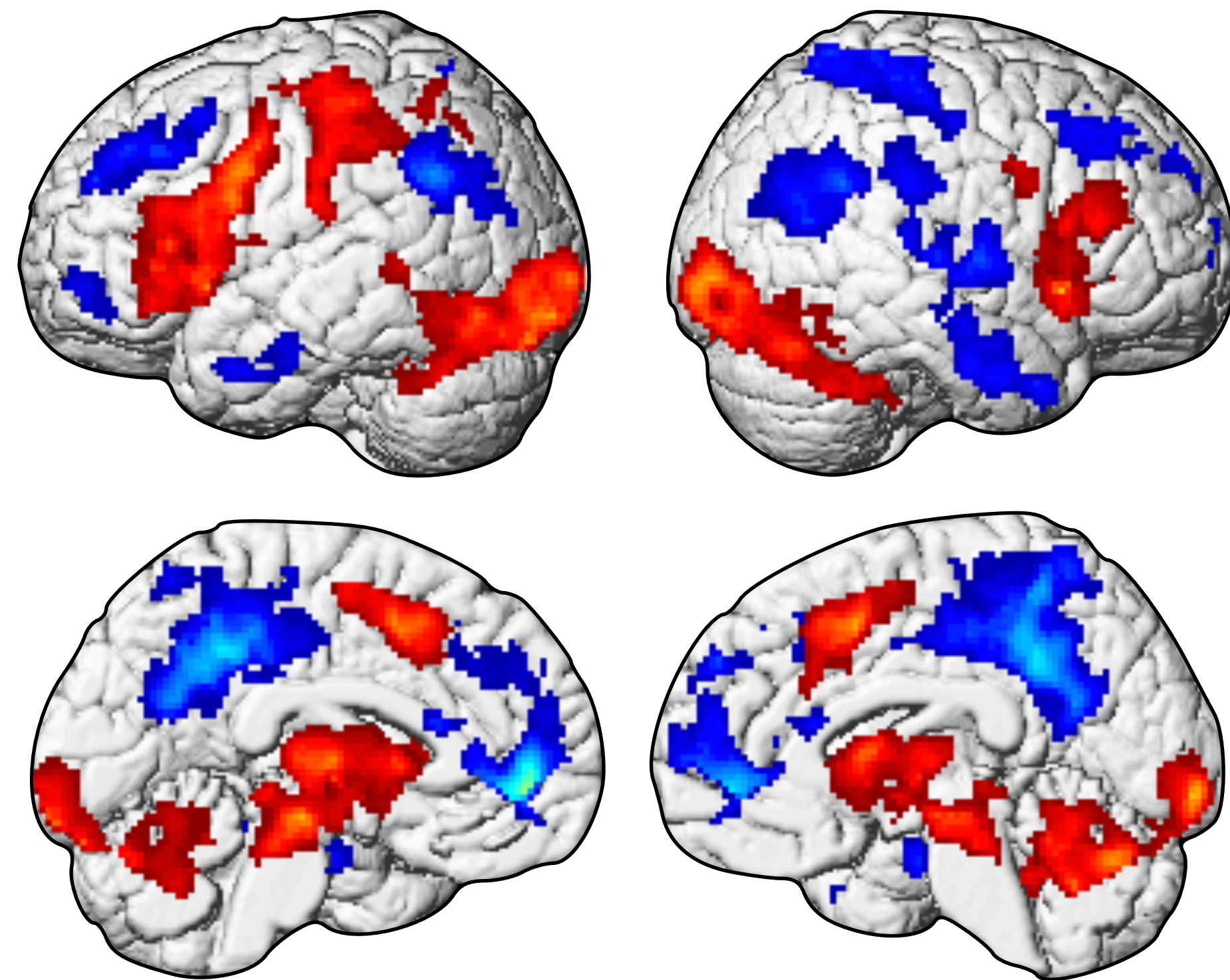One-sample t-test 분석을 진행하고
그 결과를 확인해 본다.

Matlab script for one-sample t-test

```matlab
>> % Directory containing Cross-language data
>> %----------------------------------------------------------------
>> 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);
>>
>> dir_name = 'Abstract-Novel';
>> con_name = 'con_0001.nii';
>>
>>
>> % Specify Model
>> %----------------------------------------------------------------
>> clear matlabbatch;
>> out_dir = fullfile(proj_path,'Analysis','SecondLevel','One sample',dir_name); mkdir(out_dir);
>> confiles = cell(0);
>> for c=1:nsubj,
>>     confiles{c} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},con_name);
>> end
>> matlabbatch{1}.spm.stats.factorial_design.dir = {out_dir};
>> matlabbatch{1}.spm.stats.factorial_design.des.t1.scans = [confiles'];
>> matlabbatch{1}.spm.stats.factorial_design.masking.im = 1;
```
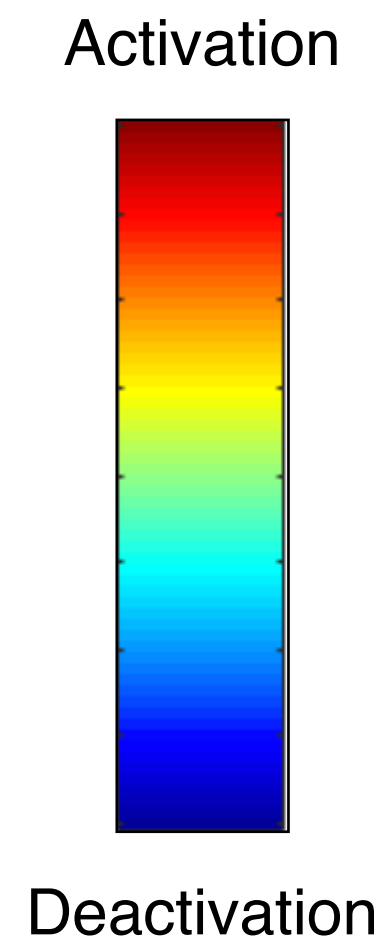
```matlab
>> % Parameter Estimation
>> %----------------------------------------------------------------
>> SPM_mat = fullfile(out_dir,'SPM.mat');
>> matlabbatch{2}.spm.stats.fmri_est.spmmat = {SPM_mat};
>> matlabbatch{2}.spm.stats.fmri_est.write_residuals = 0;
>> matlabbatch{2}.spm.stats.fmri_est.method.Classical = 1;
>>
>>
>> % Create Contrasts
>> %----------------------------------------------------------------
>> matlabbatch{3}.spm.stats.con.spmmat = {SPM_mat};
>> matlabbatch{3}.spm.stats.con.consess{1}.tcon.name = 'Activation';
>> matlabbatch{3}.spm.stats.con.consess{1}.tcon.weights = 1;
>> matlabbatch{3}.spm.stats.con.consess{1}.tcon.sessrep = 'none';
>> matlabbatch{3}.spm.stats.con.consess{2}.tcon.name = 'Deactivation';
>> matlabbatch{3}.spm.stats.con.consess{2}.tcon.weights = -1;
>> matlabbatch{3}.spm.stats.con.consess{2}.tcon.sessrep = 'none';
>> matlabbatch{3}.spm.stats.con.delete = 1;
>> % spm_jobman('interactive',matlabbatch);
>> spm_jobman('run',matlabbatch);
```

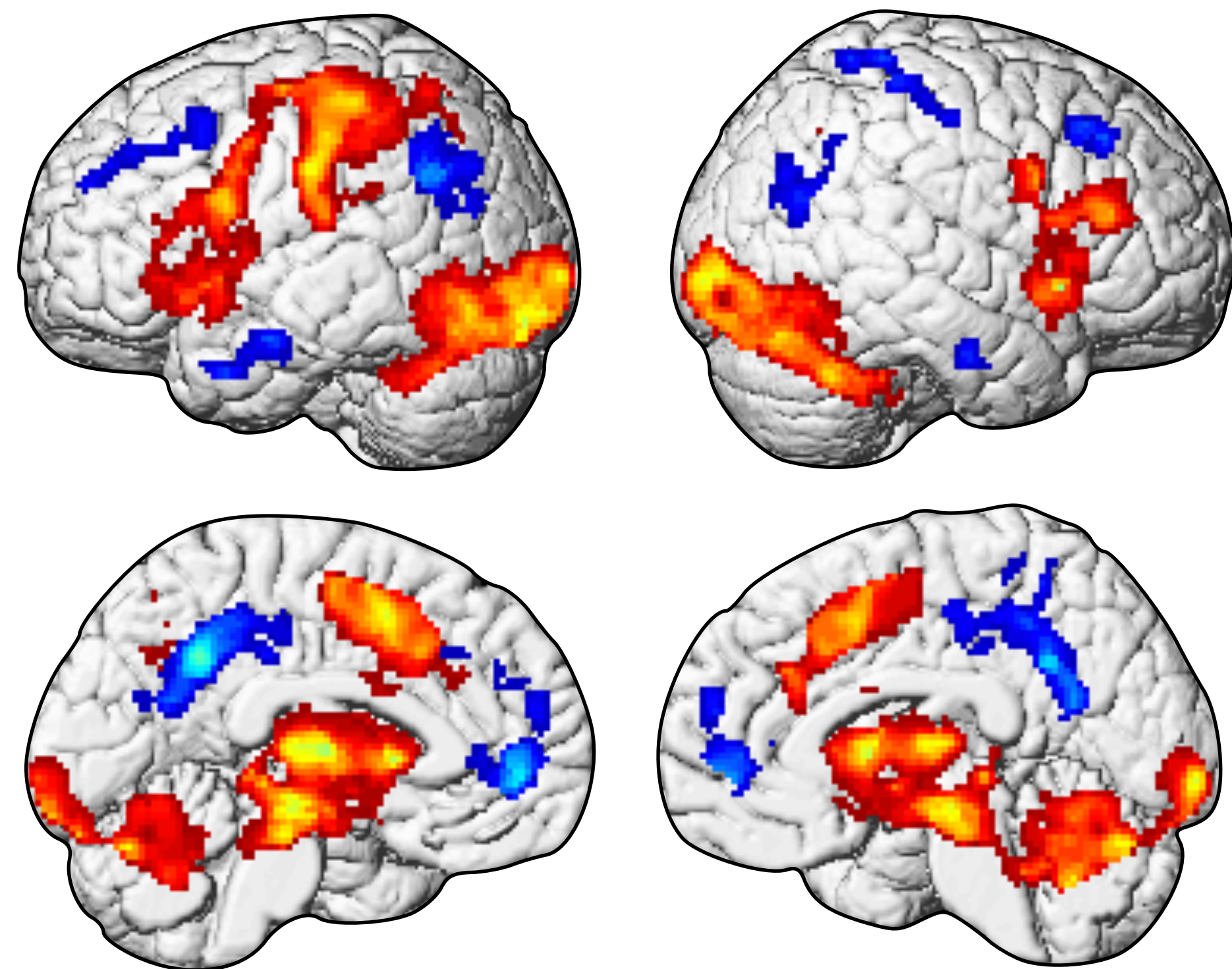# Abstract word condition

Novel-condition

Repeat-condition

Activation

Deactivation
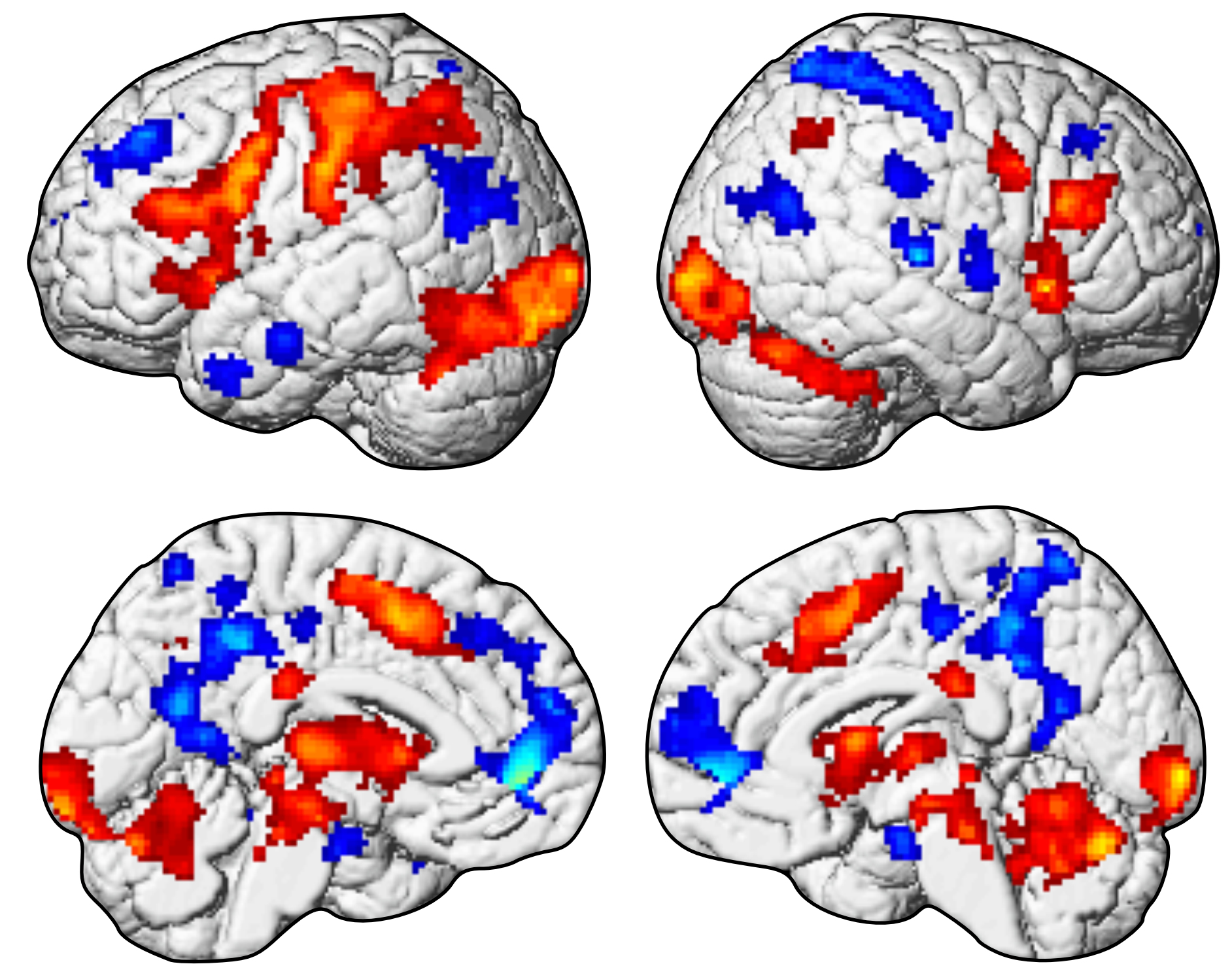
CDT *p*<0.005 & *k*=50

Concrete word condition

Novel-condition

Activation

Deactivation

Repeat-condition
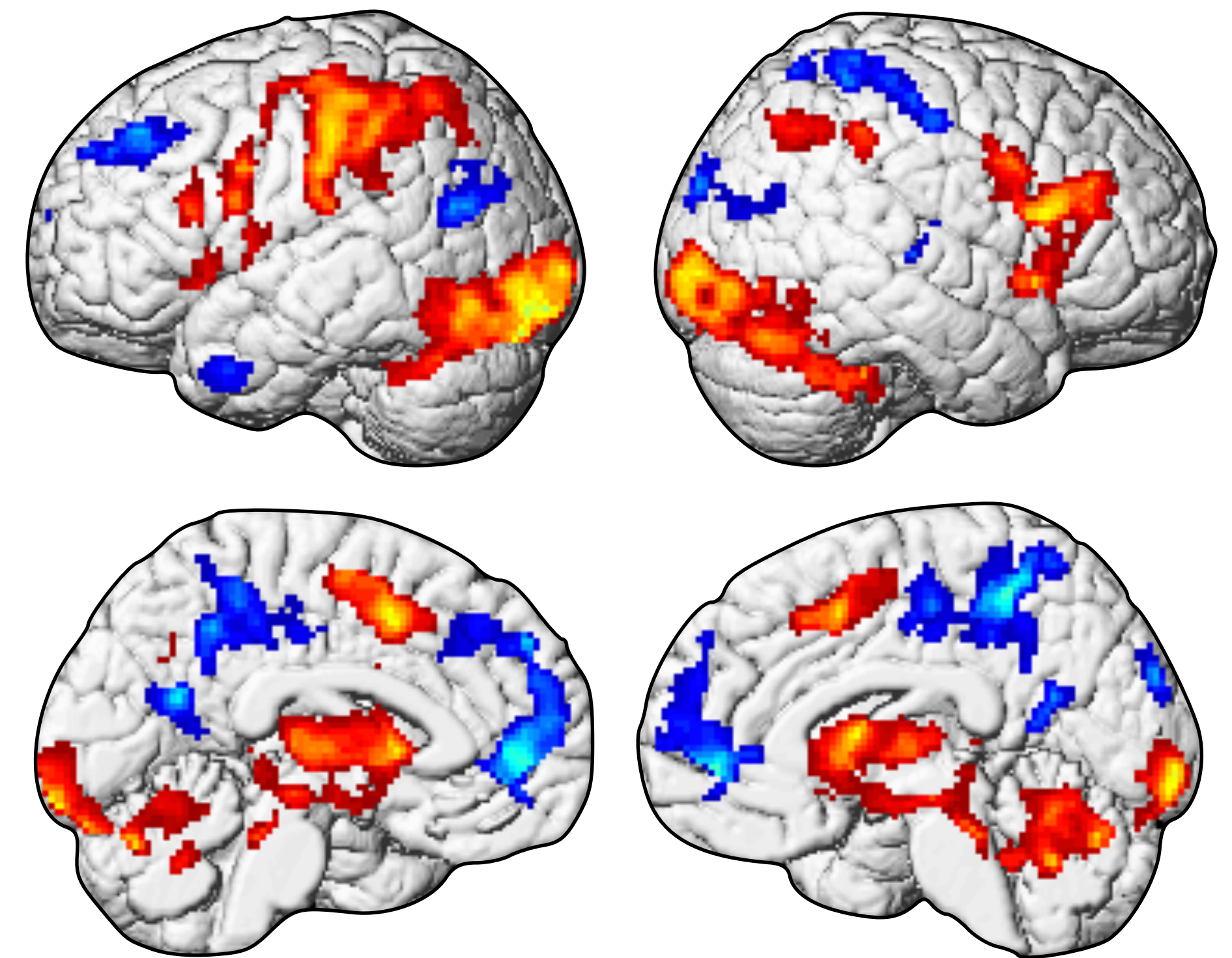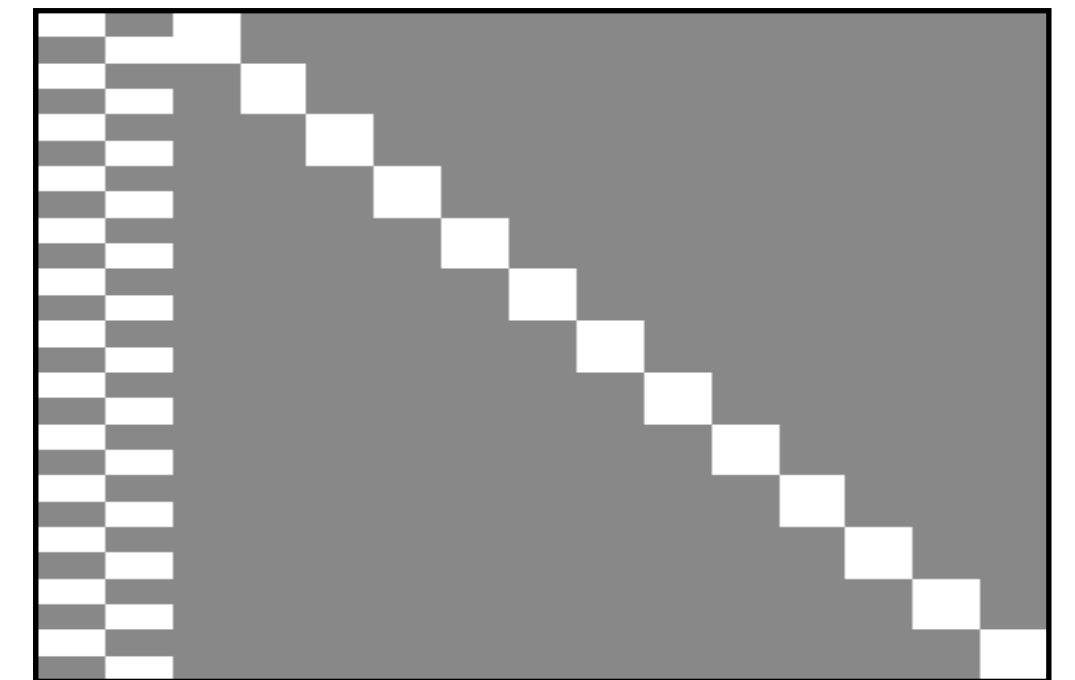
CDT *p*<0.005 & *k*=50

무엇을 알 수 있을까?

- One-sample t-test의 결과로 각각의 실험 조건에서 뇌가 활성화 되거나 비활성화 되는 영역을 알 수 있다.

- 하지만, 실험 조건간에 어느 영역이 더욱 활성화 되고, 어느 영역이 덜 활성화 되는지 여부는 알 수 없다. 하지만, 각각의 실험 조건에 관여하는 뇌의 영역을 발견하는 데에는 효과적인 통계분석 방법이다.

그룹 통계 분석 (2nd-level analysis)
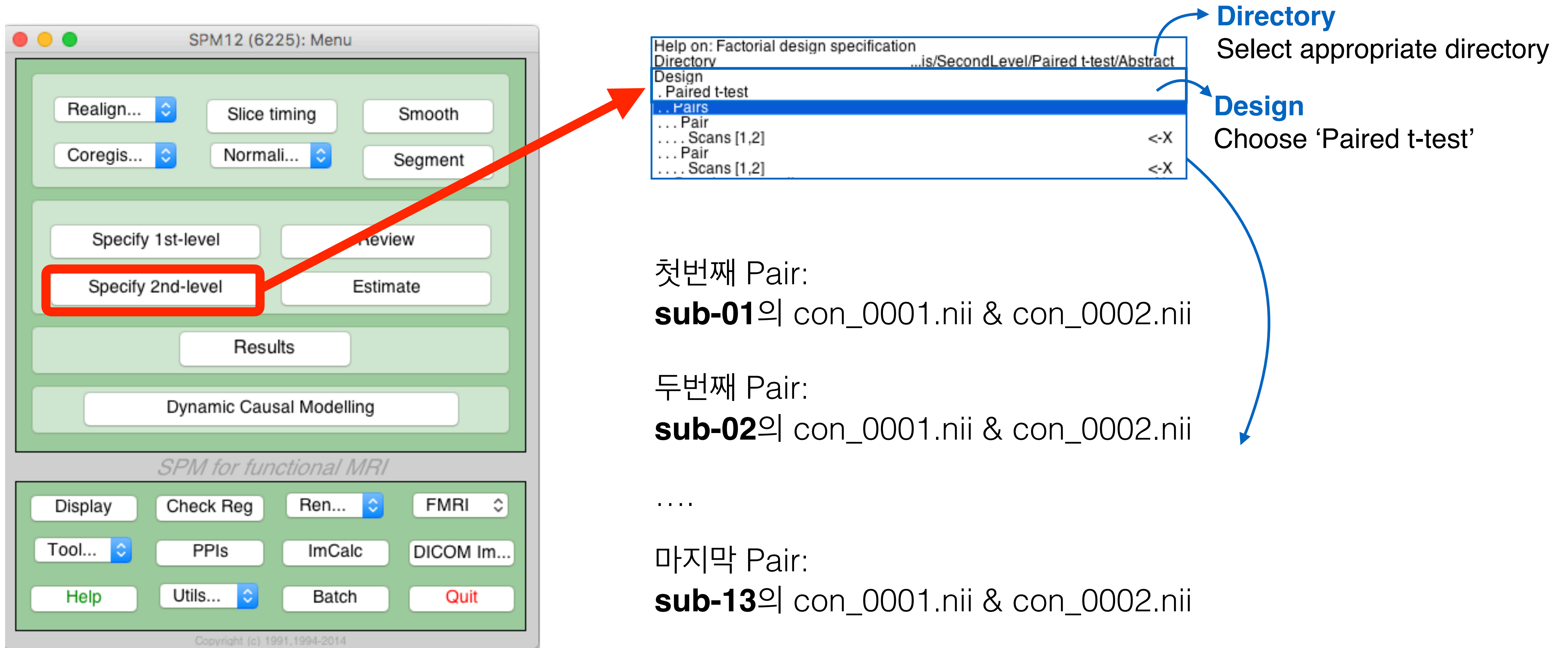
a. one sample t-test

b. paired sample t-test

c. full factorial

d. flexible factorial

Design matrix of
paired sample model

Paired sample t-test: Specify model

Abstract word 단어가 처음 제시되었을 때와 반복되어 제시되었을 때의 뇌반응 차이

Directory
Select appropriate directory

Design
Choose 'Paired t-test'

첫번째 Pair:
sub-01의 con_0001.nii & con_0002.nii

두번째 Pair:
sub-02의 con_0001.nii & con_0002.nii

….

마지막 Pair:
sub-13의 con_0001.nii & con_0002.nii

Paired sample t-test: Estimation

1. Add 'model estimation' in the module list
(SPM menu → Stats → Model estimation)
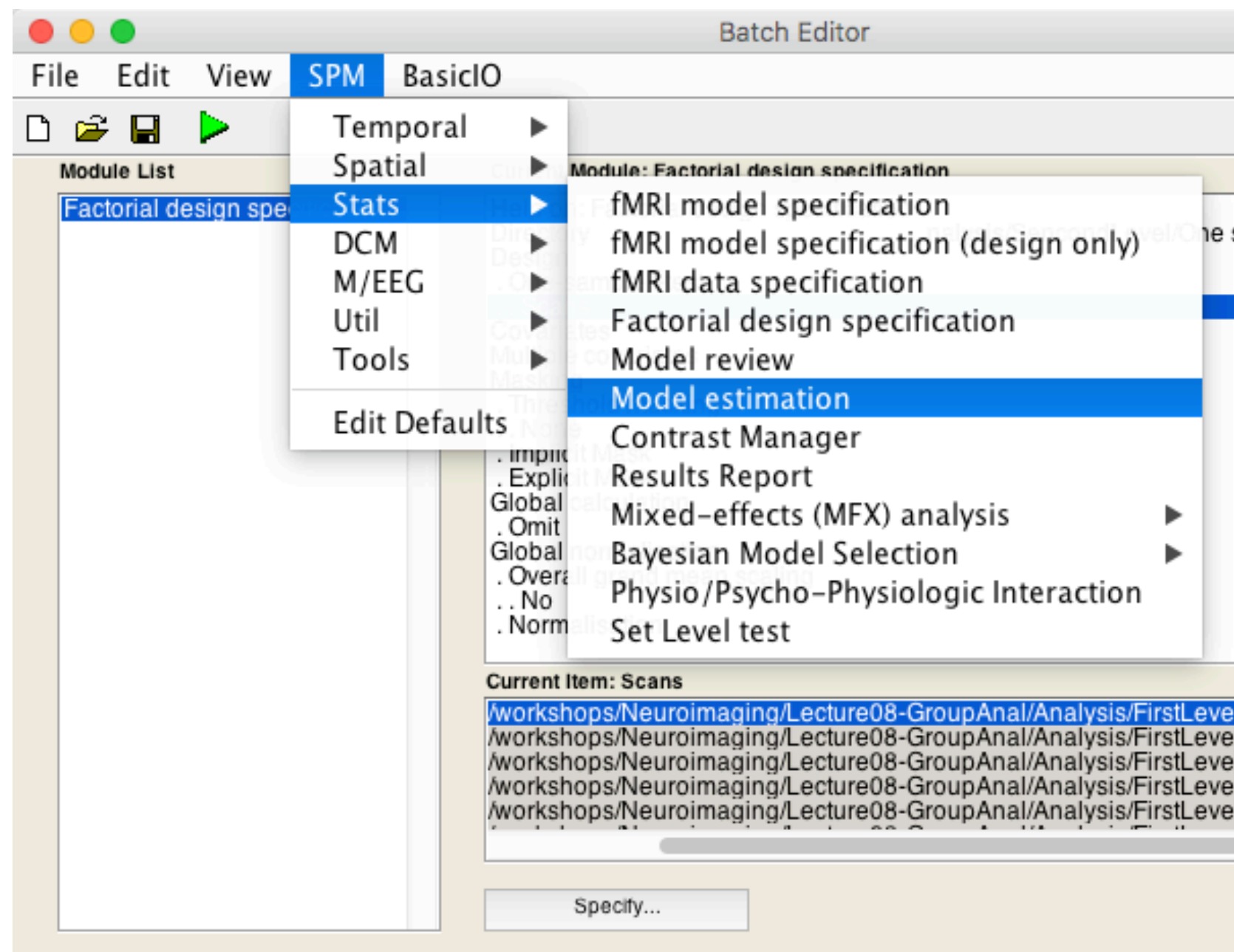
2. Select SPM.mat file
(Click 'Dependency' button)

3. Select SPM.mat file
(click ▶Run after selection)

Paired sample t-test: Contrast

Select one of existing contrasts
or Define net contrast

Contrast of Novel-Repeat

Contrast of Repeat-Novel

Matlab script for paired sample t-test

```matlab
>> % Directory containing Cross-language data
>> %-------------------------------------------------------------
>> 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);
>>
>> dir_name = 'Concrete';
>> con_novel = 'con_0003.nii';
>> con_repeat = 'con_0004.nii';
>>
>>
>> % Specify Model
>> %-------------------------------------------------------------
>> clear matlabbatch;
>> out_dir = fullfile(proj_path,'Analysis','SecondLevel','Paired t-test',dir_name);
   mkdir(out_dir);
>> matlabbatch{1}.spm.stats.factorial_design.dir = {out_dir};
>> for c=1:nsubj,
>>     paired_confiles = cell(0);
>>     paired_confiles{1} =
   fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},con_novel);
>>     paired_confiles{2} =
   fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},con_repeat);
>>     matlabbatch{1}.spm.stats.factorial_design.des.pt.pair(c).scans =
   [paired_confiles'];
>> end
```
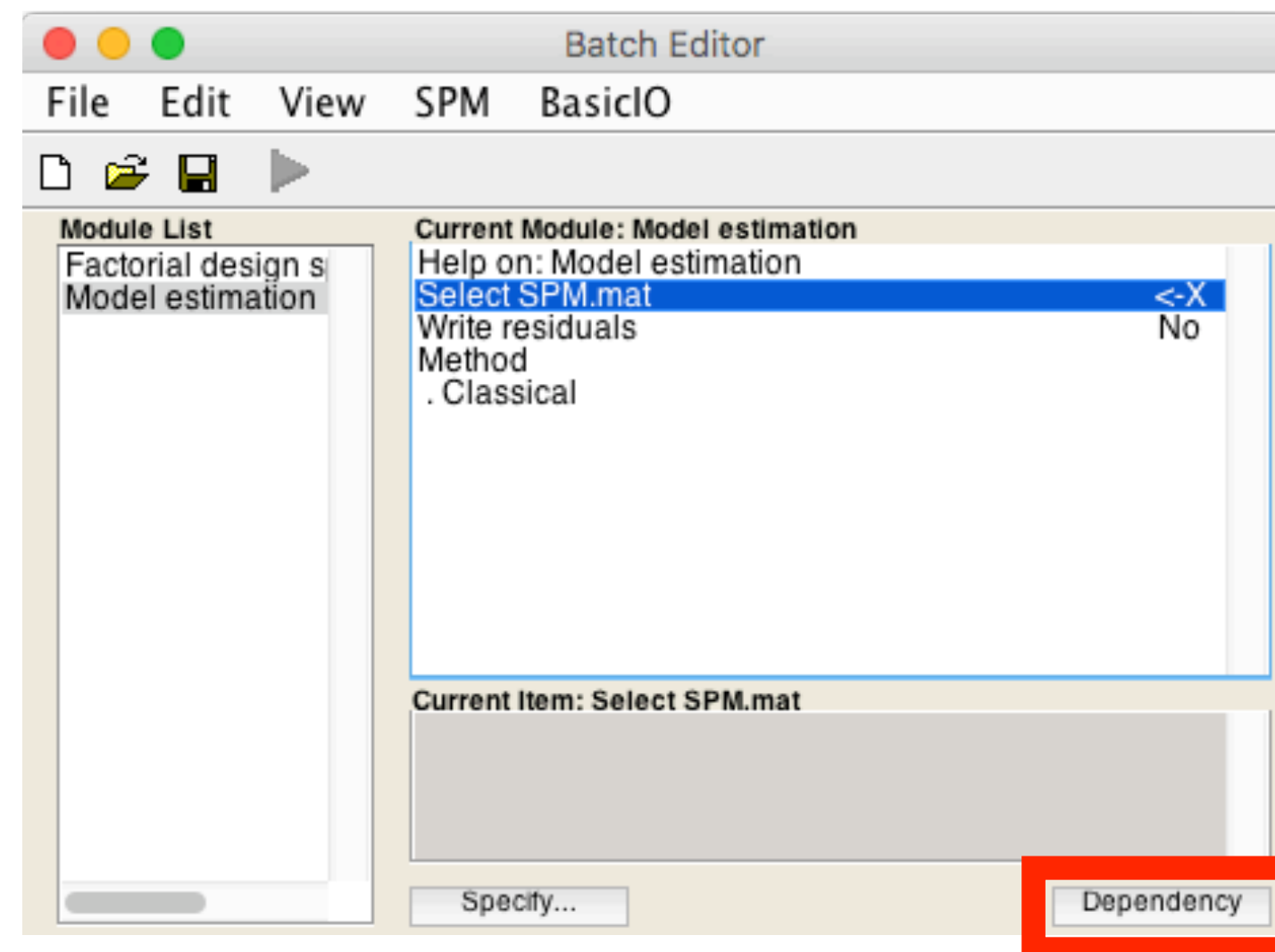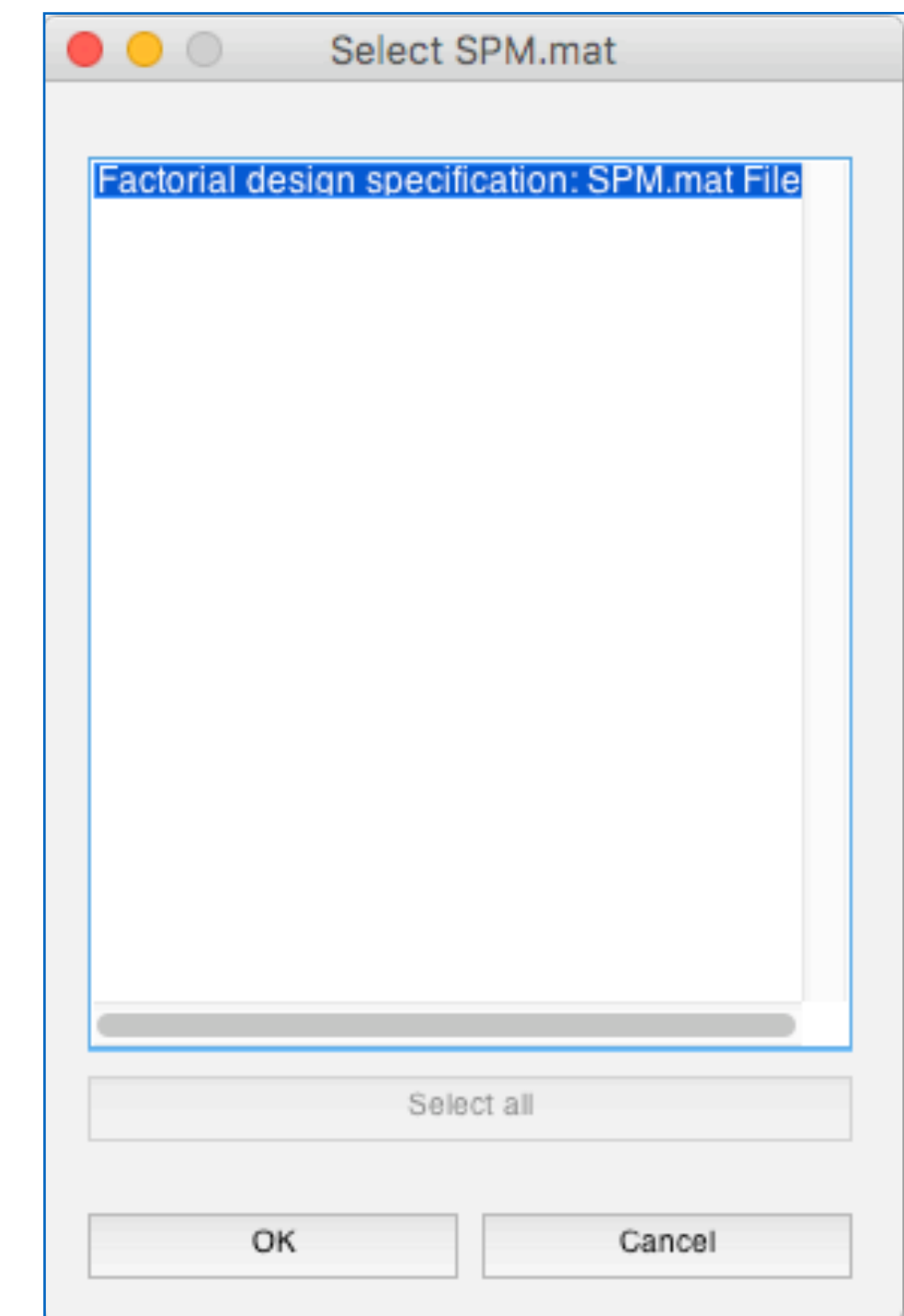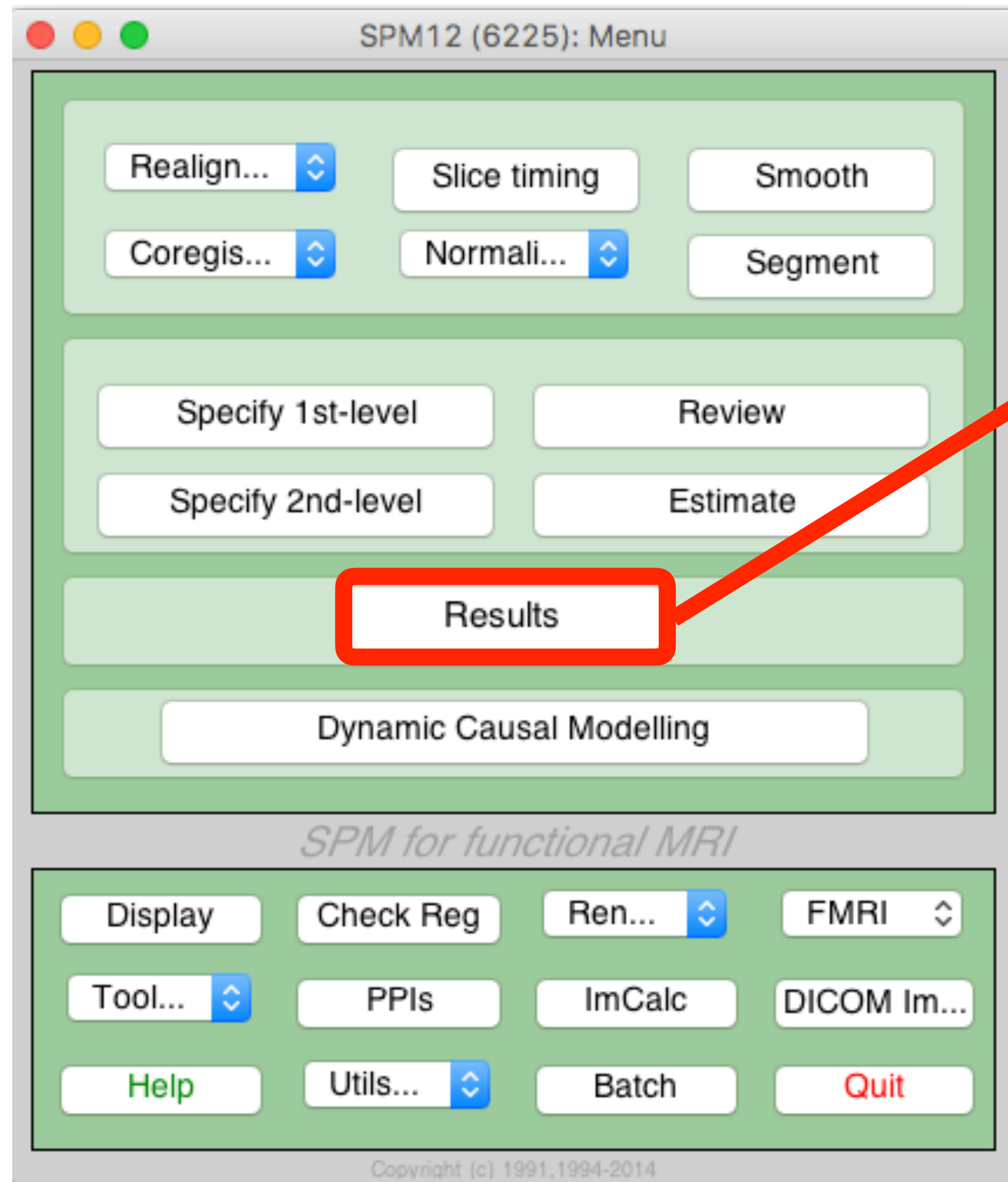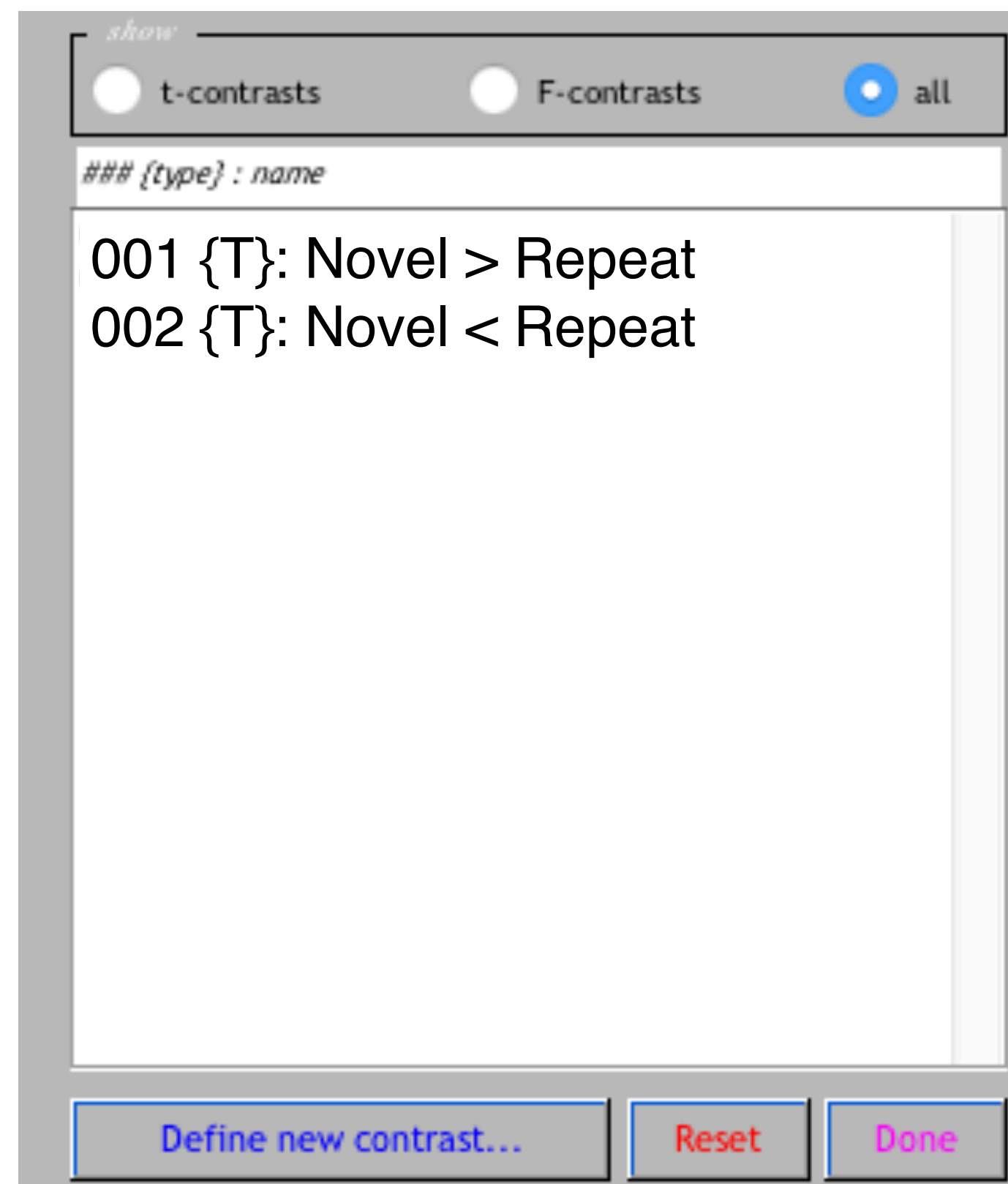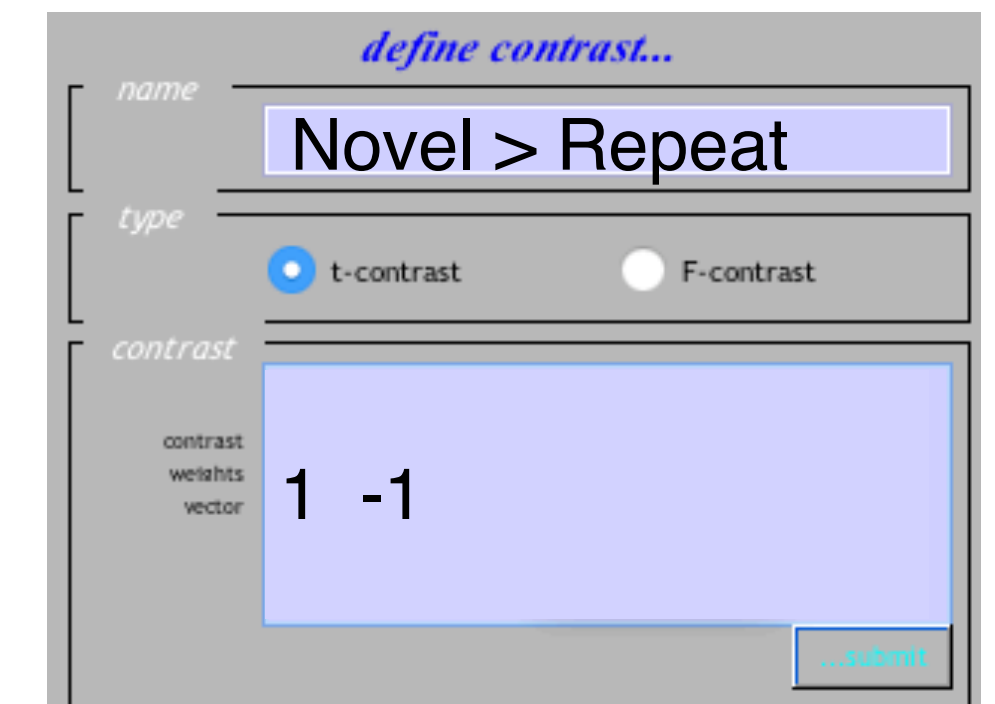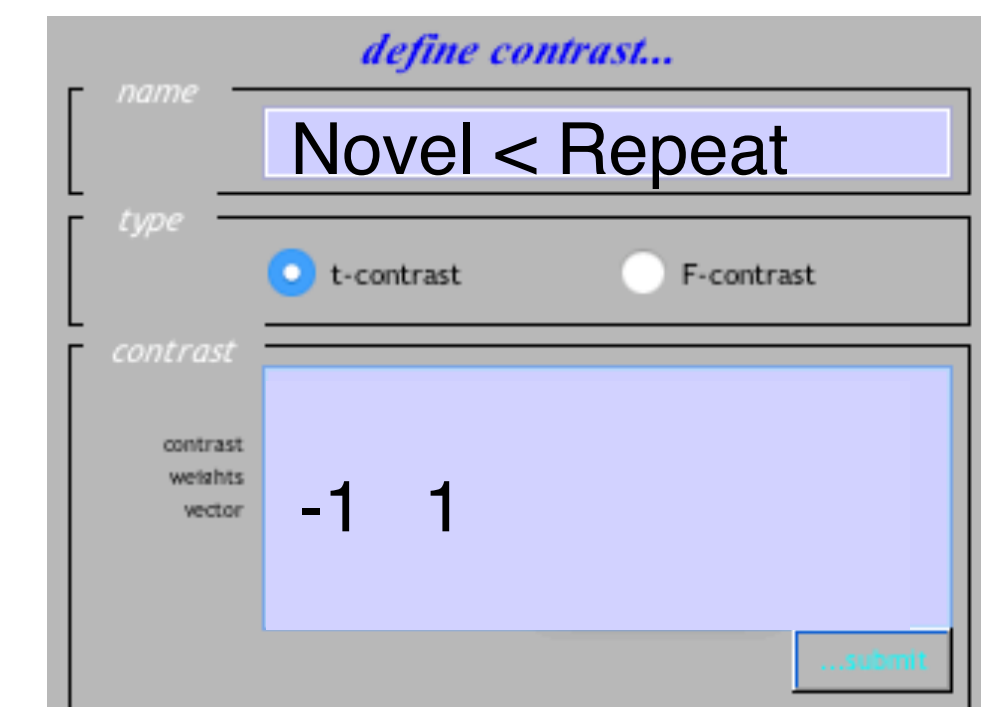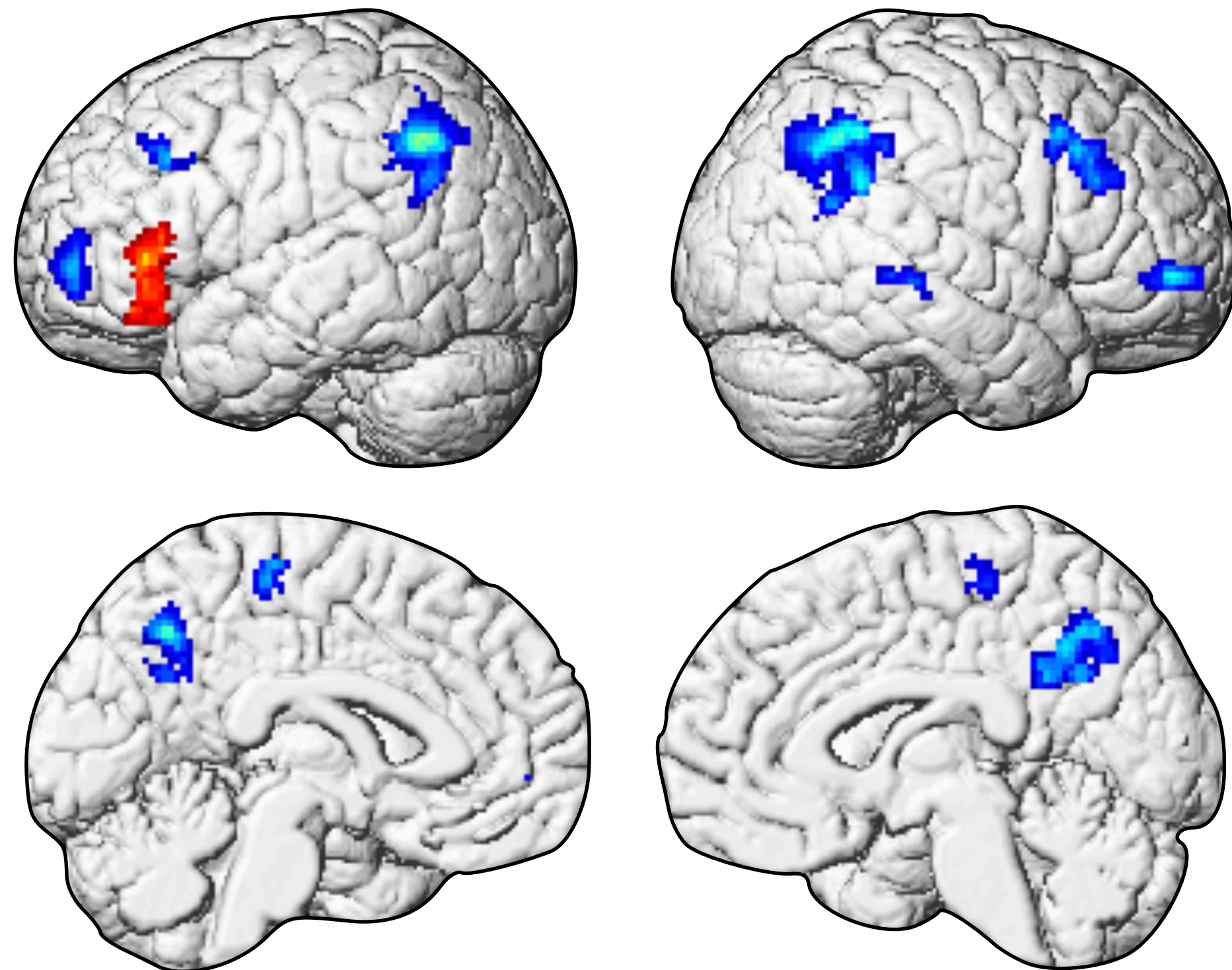
```matlab
>> % Parameter Estimation
>> %-------------------------------------------------------------
>> SPM_mat = fullfile(out_dir,'SPM.mat');
>> matlabbatch{2}.spm.stats.fmri_est.spmmat = {SPM_mat};
>> matlabbatch{2}.spm.stats.fmri_est.write_residuals = 0;
>> matlabbatch{2}.spm.stats.fmri_est.method.Classical = 1;
>>
>>
>> % Create Contrasts
>> %-------------------------------------------------------------
>> matlabbatch{3}.spm.stats.con.spmmat = {SPM_mat};
>> matlabbatch{3}.spm.stats.con.consess{1}.tcon.name = 'Novel > Repeat';
>> matlabbatch{3}.spm.stats.con.consess{1}.tcon.weights = [1 -1];
>> matlabbatch{3}.spm.stats.con.consess{1}.tcon.sessrep = 'none';
>> matlabbatch{3}.spm.stats.con.consess{2}.tcon.name = 'Novel < Repeat';
>> matlabbatch{3}.spm.stats.con.consess{2}.tcon.weights = [-1 1];
>> matlabbatch{3}.spm.stats.con.consess{2}.tcon.sessrep = 'none';
>> matlabbatch{3}.spm.stats.con.delete = 1;
>> % spm_jobman('interactive',matlabbatch);
>> spm_jobman('run',matlabbatch);
```

Paired sample t-test: Mapping
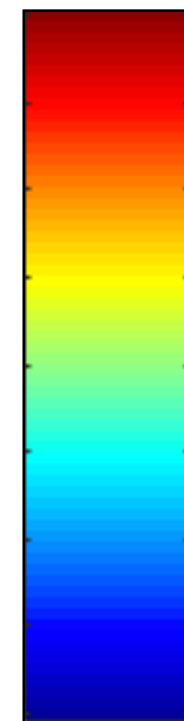
Abstract word condition
(Novel-Repeat)

Concrete word condition
(Novel-Repeat)

Novel > Repeat

Novel < Repeat
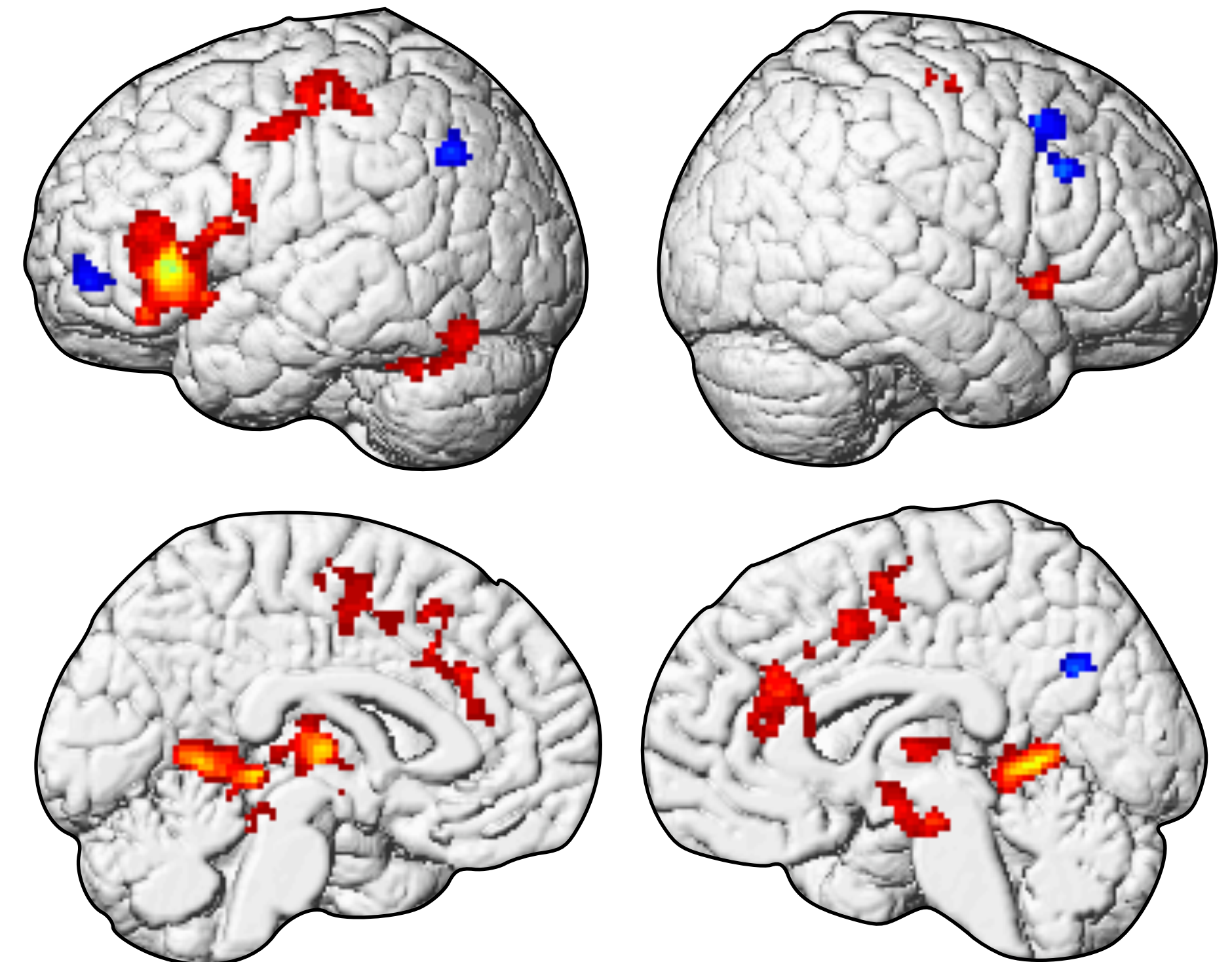
CDT *p*<0.005 & *k*=50

무엇을 알 수 있을까?

- Paired sample t-test의 결과로 Pair로 생각할 수 있는 두개의 조건들 간에 통계적으로 차이가 있는 영역들을 알 수 있다.

- 하지만, 상호작용 효과는 알 수 없다.

상호작용 (Interaction)

Interaction,
Main effect of word condition
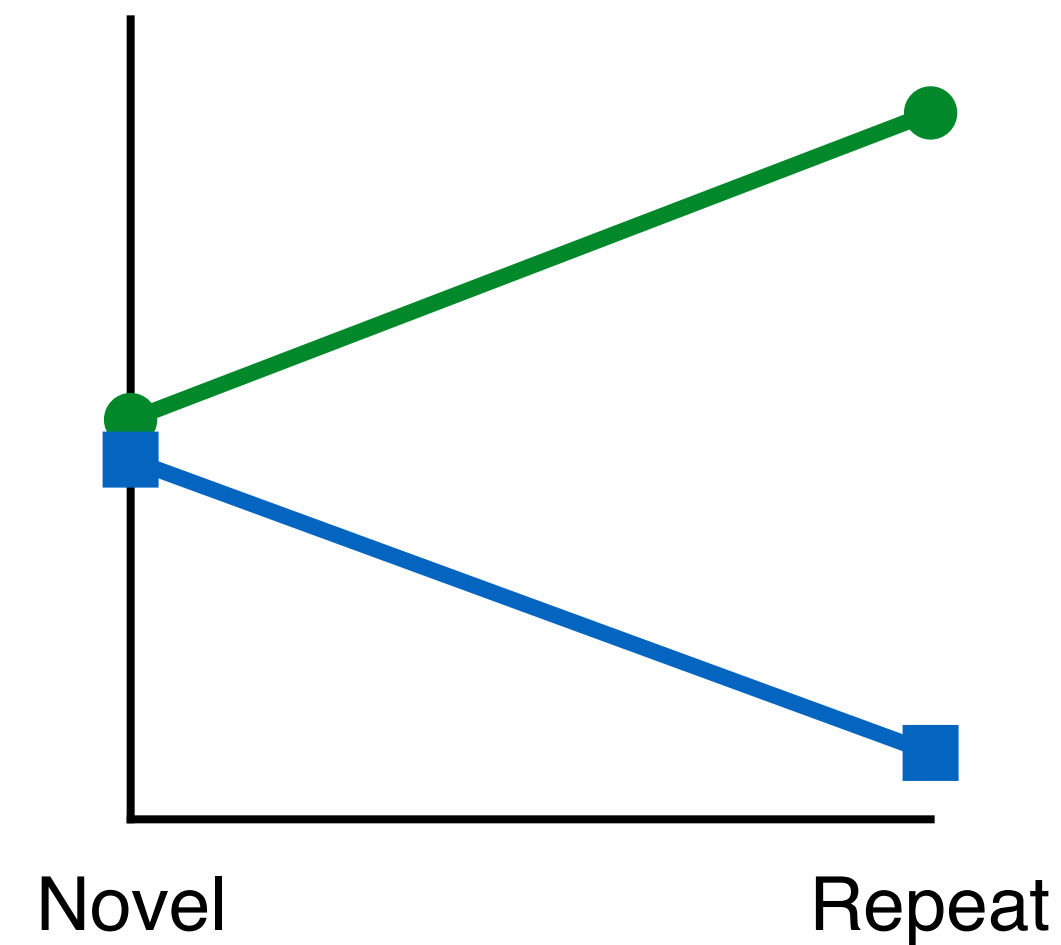
Interaction,
Main effect of repetition
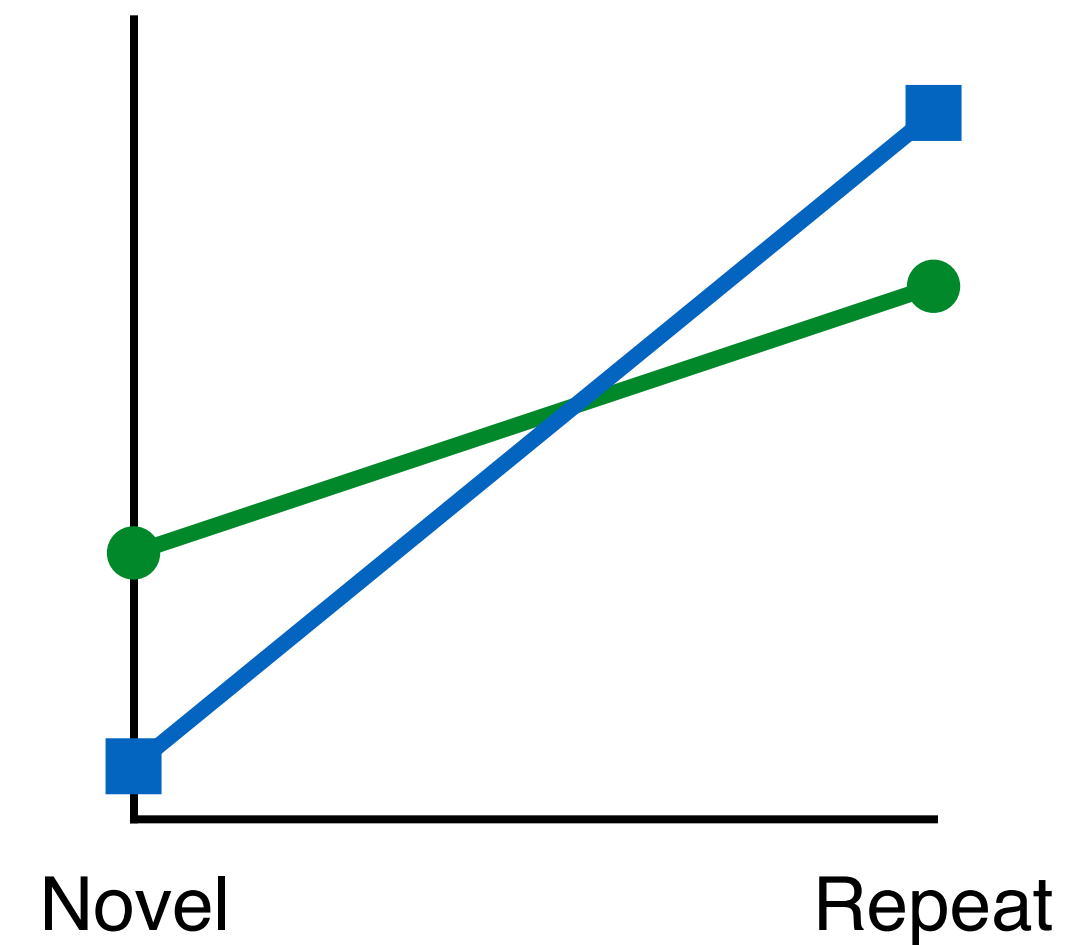
Interaction,
Main effect of word condition
Main effect of repetition
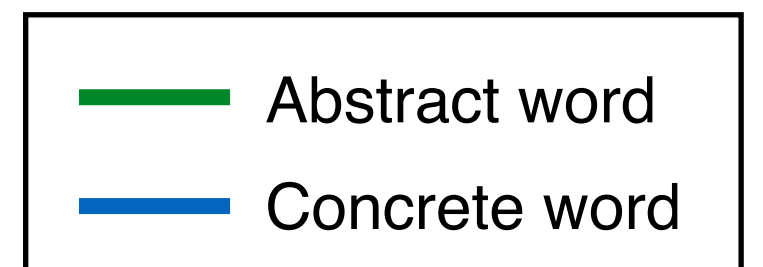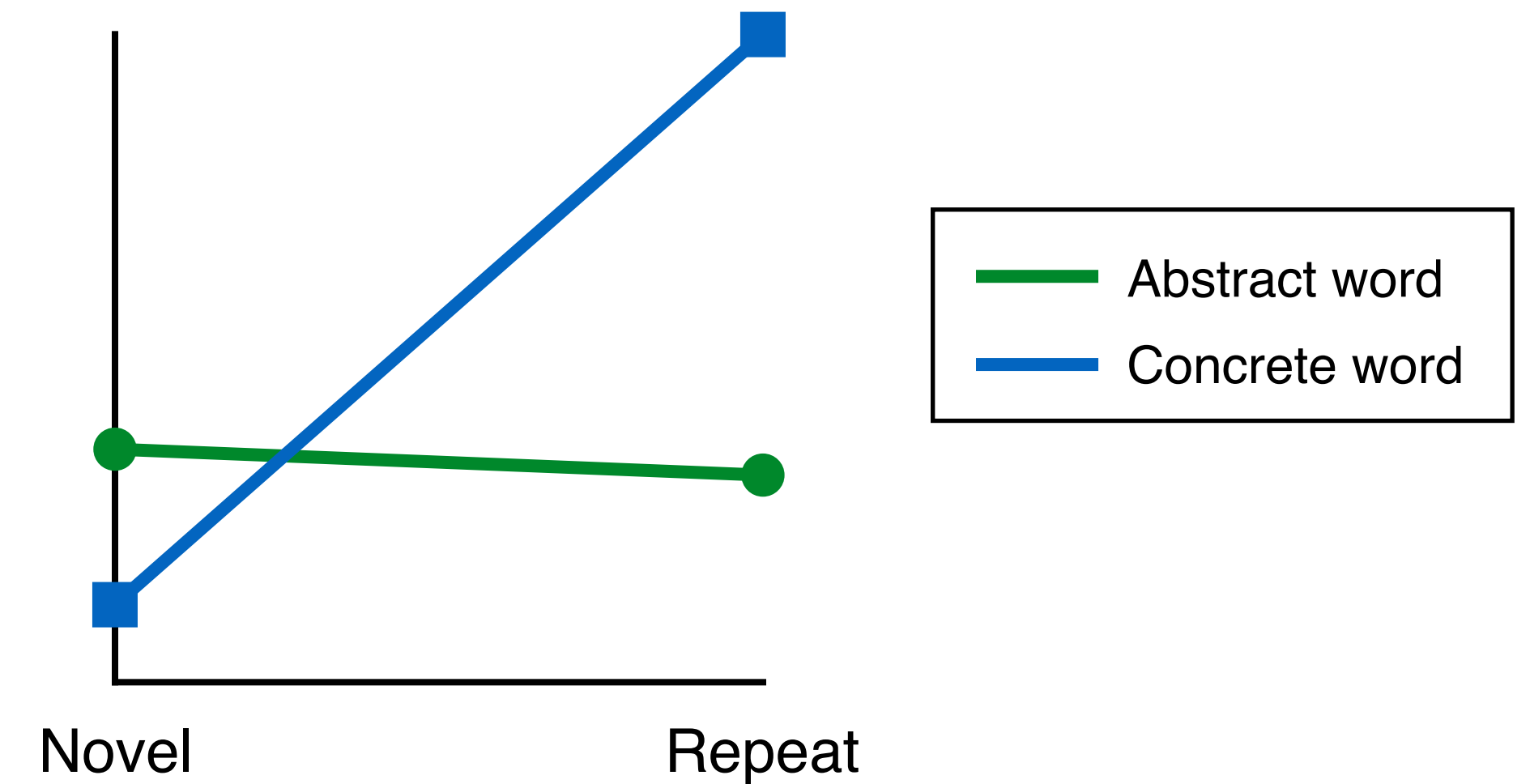
Abstract word
Concrete word

그룹 통계 분석 (2nd-level analysis)

a. one sample t-test
b. paired sample t-test
c. full factorial
d. flexible factorial
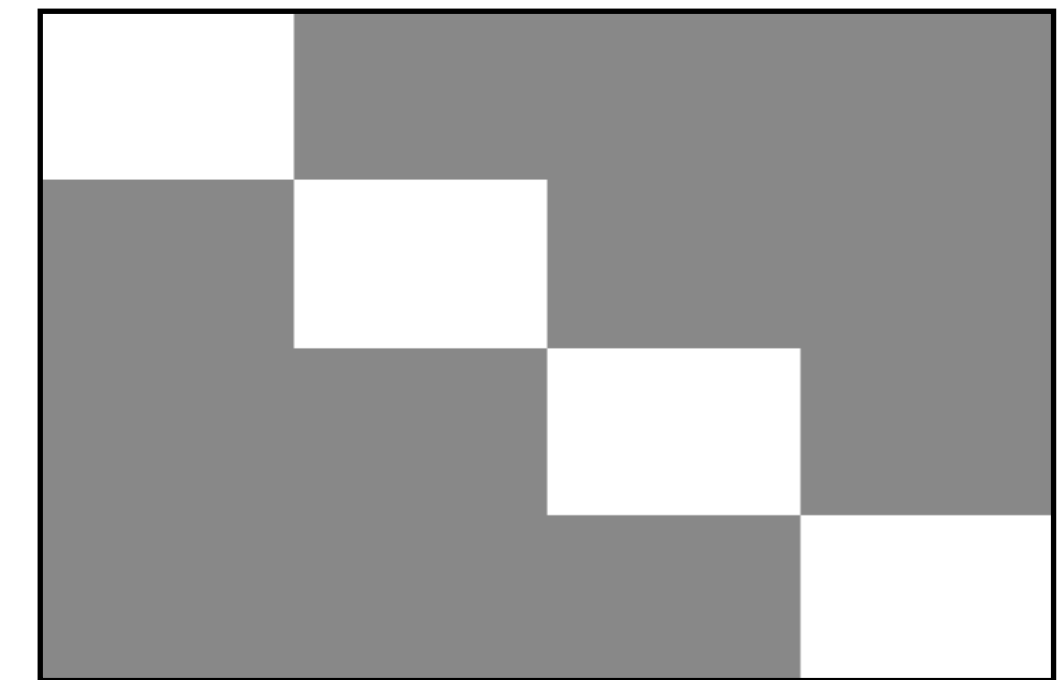
Design matrix of
full factorial model

Factorial design

- If you have a factorial design then SPM can automatically generate the contrasts necessary to test for the main effects and interactions.

- This includes the F-contrasts necessary to test for these effects at the within-subject level (first level) and the simple contrasts necessary to generate the contrast images for a between-subject (second-level) analysis.

- What is a factor? For example, if you have 2-by-3 design in your contingency table, you have two factors. One has 2-levels and another has 3-levels.

Concreteness (C/A)

Repetition (1/2/3)

A1	C1
A2	C2
A3	C3

Full factorial: Specify model (1/2)

Directory
Select appropriate directory

Design
Choose 'Full factorial'

Factor 1
Name: Condition
Levels: 2
Independence: Yes

Factor 2
Name: Repetition
Levels: 2
Independence: No

Full factorial: Specify model (2/2)

```
. . Cells
. . . Cell
. . . . Levels                                    [1 1]
. . . . Scans                                  13 files
. . . Cell
. . . . Levels                                    [1 2]
. . . . Scans                                  13 files
. . . Cell
. . . . Levels                                    [2 1]
. . . . Scans                                  13 files
. . . Cell
. . . . Levels                                    [2 2]
. . . . Scans                                  13 files
```

Cell 1 (Abstract & Novel)
Levels: [1 1]
Scans: select con_0001.nii files from all participants

Cell 2 (Abstract & Repeat)
Levels: [1 2]
Scans: select con_0002.nii files from all participants

Cell 3 (Concrete & Novel)
Levels: [2 1]
Scans: select con_0003.nii files from all participants

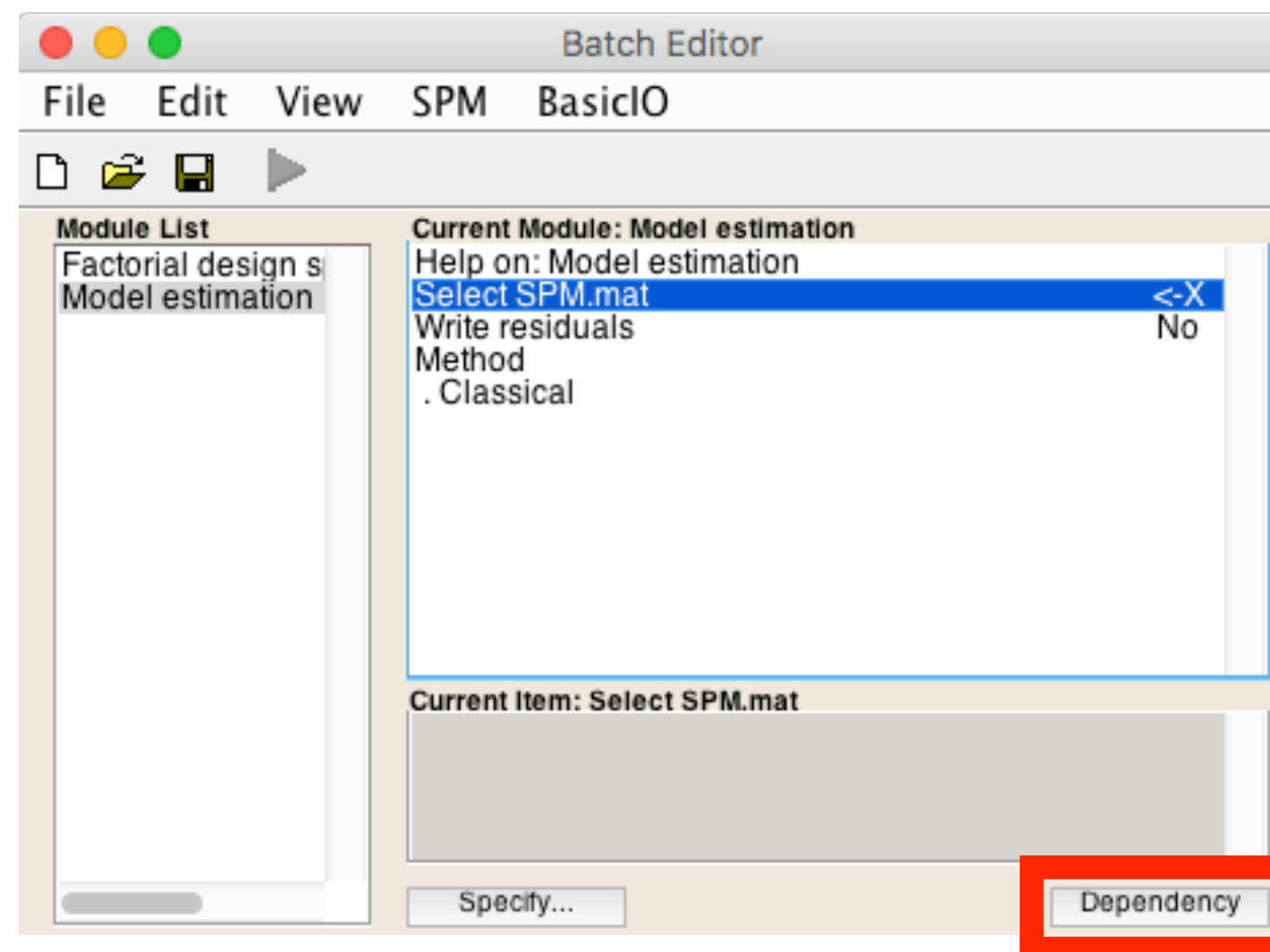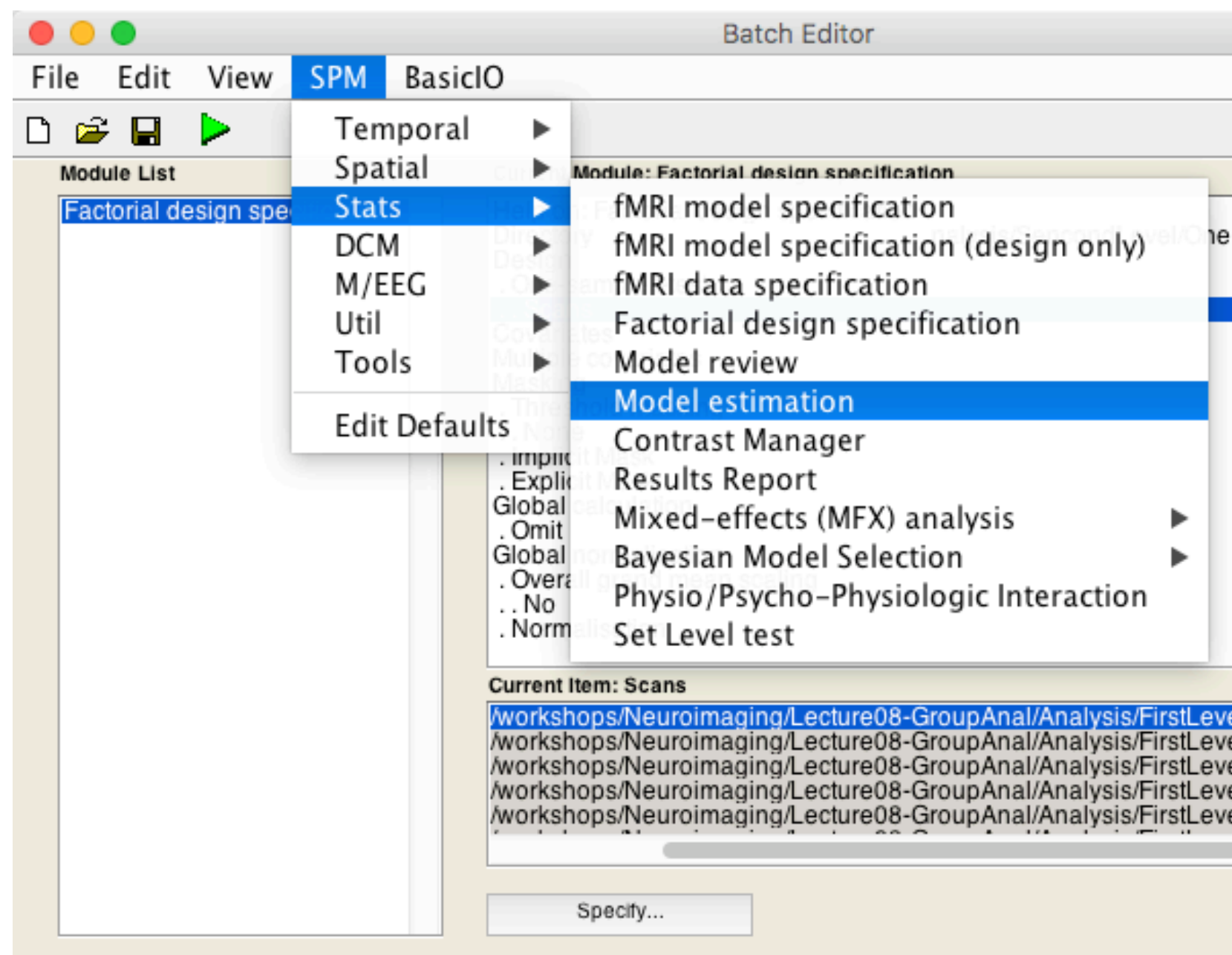**Cell 3 (Concrete & Repeat)**
Levels: [2 2]
Scans: select con_0004.nii files from all participants

Full factorial: Estimation

1. Add 'model estimation' in the module list
(SPM menu → Stats → Model estimation)

2. Select SPM.mat file
(Click 'Dependency' button)
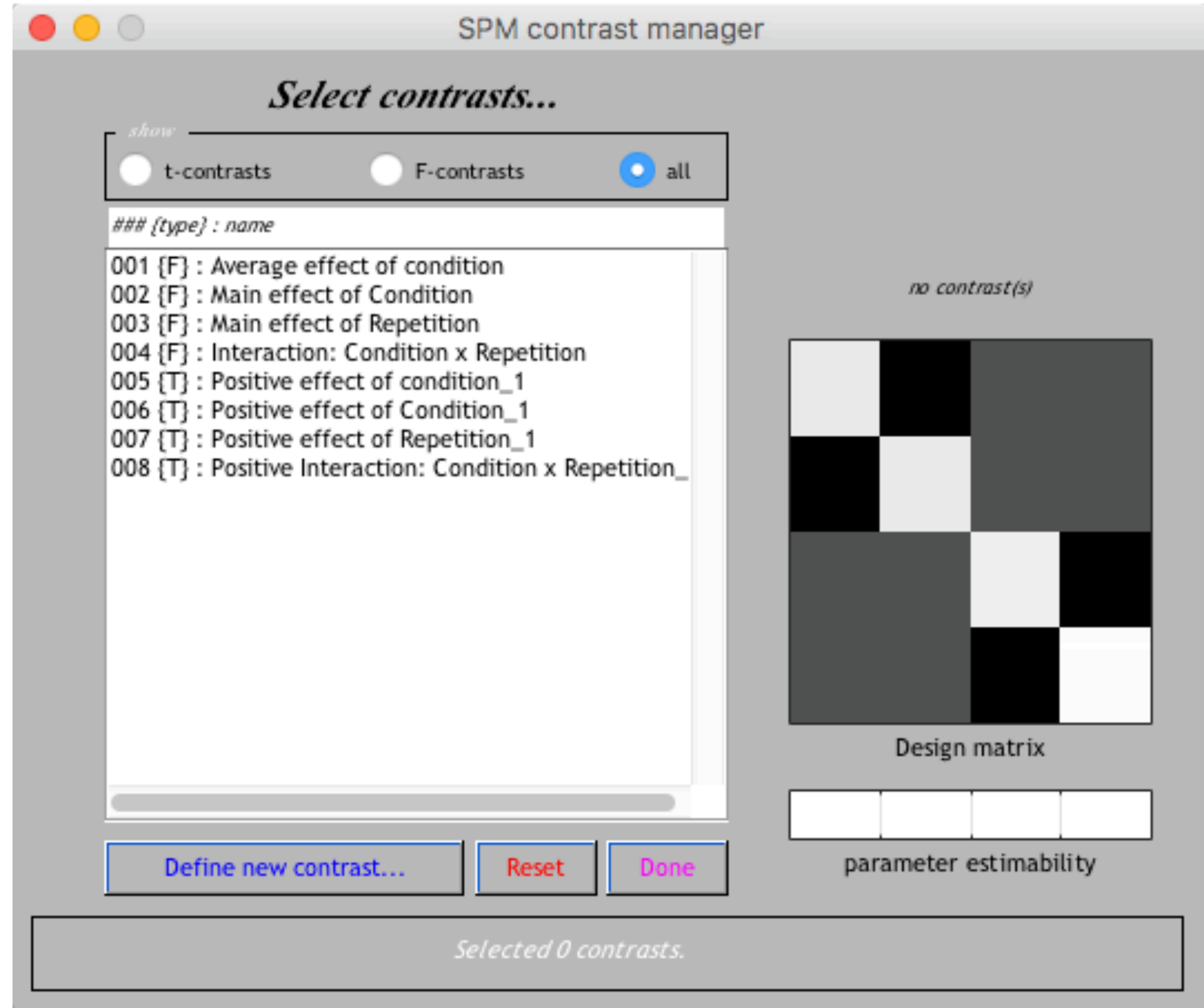
3. Select SPM.mat file
(click ▶Run after selection)

Full factorial design에서는 Estimation을 수행하고 나면, 자동으로 contrasts가 생성됨

Matlab script for full factorial analysis

```matlab
>> % Directory containing Cross-language data
>> %----------------------------------------------------------------
>> 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);
>>
>>
>> % Specify Model
>> %----------------------------------------------------------------
>> clear matlabbatch;
>> out_dir = fullfile(proj_path,'Analysis','SecondLevel','Factorial'); mkdir(out_dir);
>> con1files = cell(0);
>> con2files = cell(0);
>> con3files = cell(0);
>> con4files = cell(0);
>>
>> for c=1:nsubj,
>>     con1files{c} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0001.nii');
>>     con2files{c} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0002.nii');
>>     con3files{c} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0003.nii');
>>     con4files{c} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0004.nii');
>> end
>>
```

```matlab
>> matlabbatch{1}.spm.stats.factorial_design.dir = {out_dir};
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(1).name = 'Condition';
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(1).levels = 2;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(1).dept = 0;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(1).variance = 1;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(1).gmsca = 0;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(1).ancova = 0;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(2).name = 'Repetition';
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(2).levels = 2;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(2).dept = 1;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(2).variance = 1;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(2).gmsca = 0;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.fact(2).ancova = 0;
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(1).levels = [1 1];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(1).scans = [con1files'];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(2).levels = [1 2];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(2).scans = [con2files'];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(3).levels = [2 1];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(3).scans = [con3files'];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(4).levels = [2 2];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.icell(4).scans = [con4files'];
>> matlabbatch{1}.spm.stats.factorial_design.des.fd.contrasts = 1;
>>
>>
>> % Parameter Estimation
>> %----------------------------------------------------------------
>> SPM_mat = fullfile(out_dir,'SPM.mat');
>> matlabbatch{2}.spm.stats.fmri_est.spmmat = {SPM_mat};
>> matlabbatch{2}.spm.stats.fmri_est.write_residuals = 0;
>> matlabbatch{2}.spm.stats.fmri_est.method.Classical = 1;
>>
>> % spm_jobman('interactive',matlabbatch);
>> spm_jobman('run',matlabbatch);
```

Full factorial: Results

SPM contrast manager

Select contrasts...

show
○ t-contrasts   ○ F-contrasts   ● all

{type} : name
001 {F} : Average effect of condition
002 {F} : Main effect of Condition
003 {F} : Main effect of Repetition
004 {F} : Interaction: Condition x Repetition
005 {T} : Positive effect of condition_1
006 {T} : Positive effect of Condition_1
007 {T} : Positive effect of Repetition_1
008 {T} : Positive Interaction: Condition x Repetition_

Define new contrast...   Reset   Done

no contrast(s)

Design matrix

parameter estimability

Selected 0 contrasts.

Full factorial model에서는 연구자가 F- or T- contrasts 를 정의하지 않아도, 자동으로 가능한 모든 contrasts가 생성해 준다.

Full factorial: Mapping

Main effect of condition
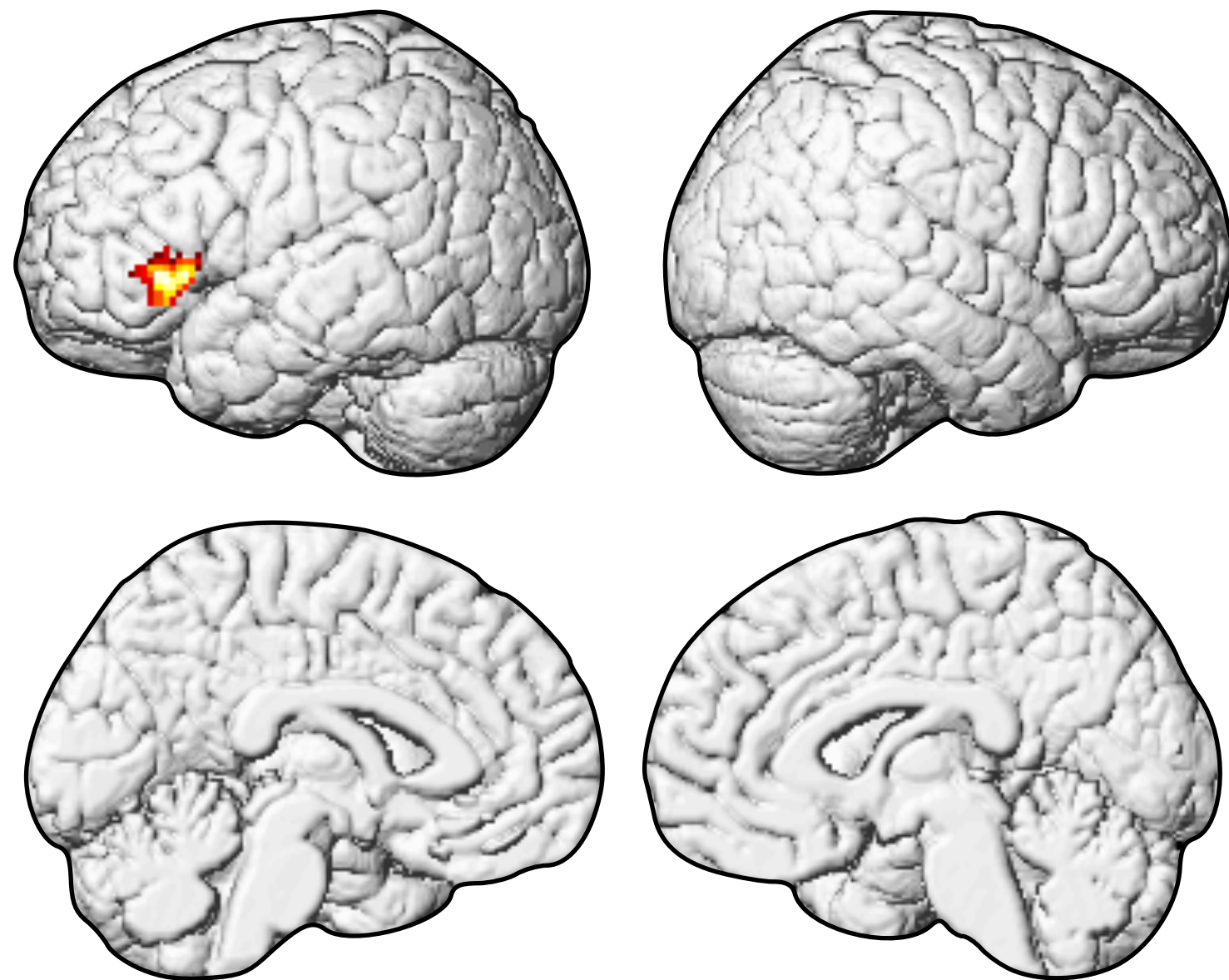
Main effect of repetition
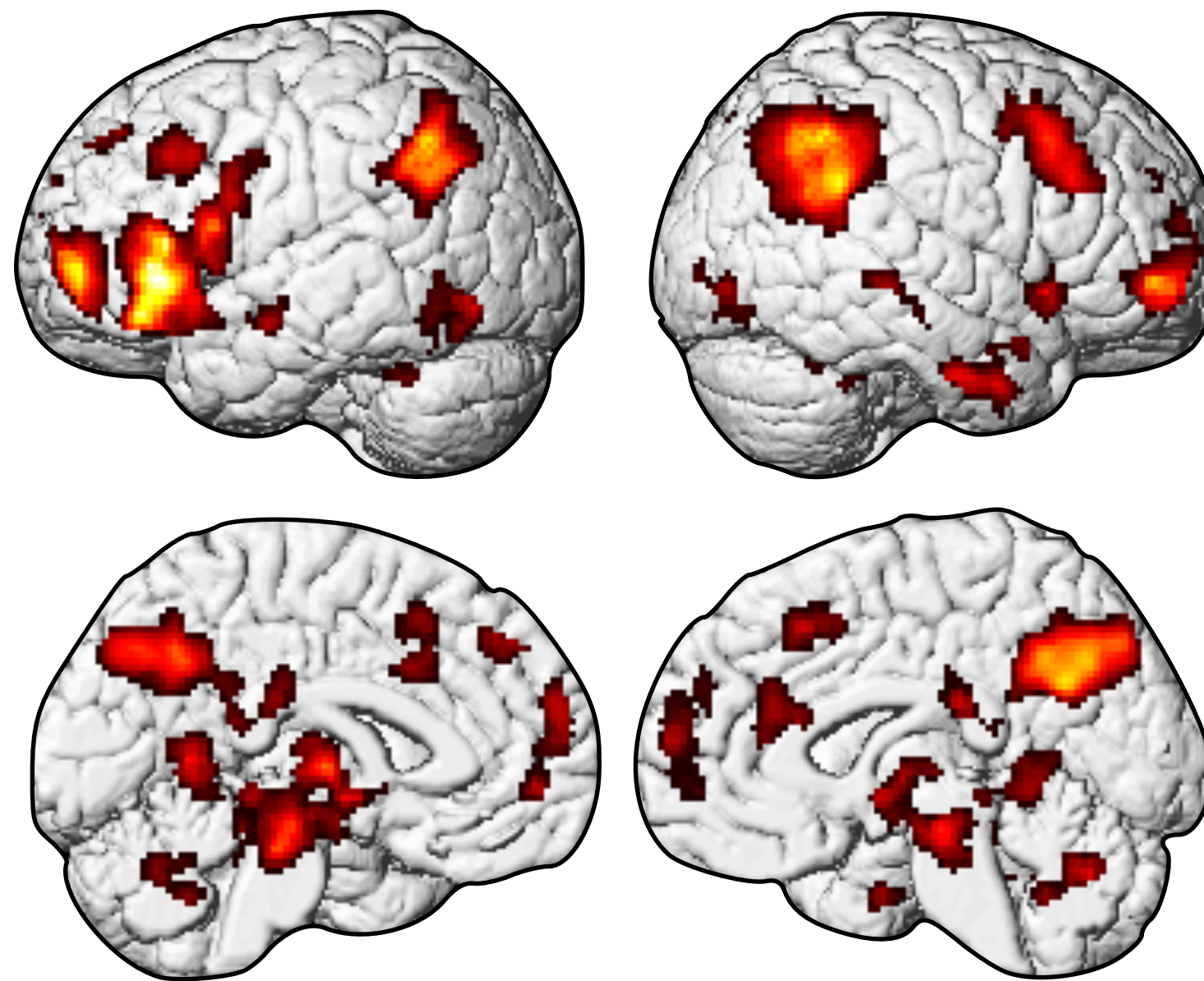
Interaction effect
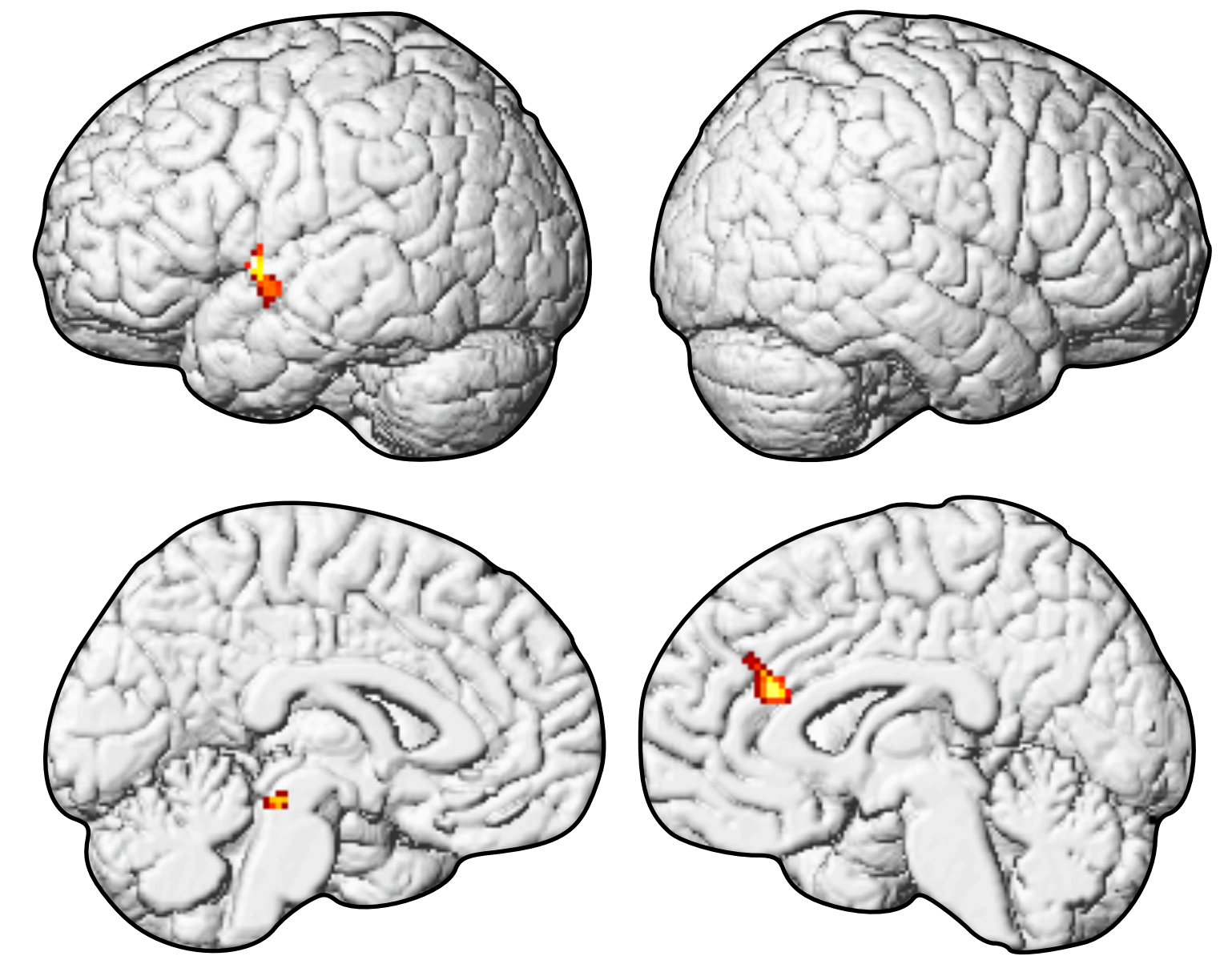
CDT *p*<0.005 & *k*=50

무엇을 알 수 있을까?

- Full factorial model로 데이터를 분석하게 되면, 각각의 요인에 대한 주요 효과(Main effect)와 요인과 요인 간에 상호작용 효과가 나타나는 뇌 영역을 알 수 있다.

- 하지만, subject에 대한 random effects가 모델에 포함되지 않는다.

그룹 통계 분석 (2nd-level analysis)

a. one sample t-test
b. paired sample t-test
c. full factorial
d. flexible factorial

Flexible factorial

- This option is best used for one-way, two-way, or three-way ANOVAs but where you do not wish to test for all possible main effects and interactions.

- A typical example here would be a group-by-drug-by-task analysis where, perhaps, only (i) group-by-drug or (ii) group-by-task interactions are of interest. In this case it is only necessary to have two-blocks in the design matrix - one for each interaction. The three-way interaction can then be tested for using a contrast that computes the difference between (i) and (ii).

- There are two reserved words for the names of factors. There are 'subject' and 'repl' (standing for replication). If you use these factor names then SPM will automatically create replication and/or subject factors without you having to type in an extra entry in the condition vector.

Flexible factorial: Specify model (1/2)
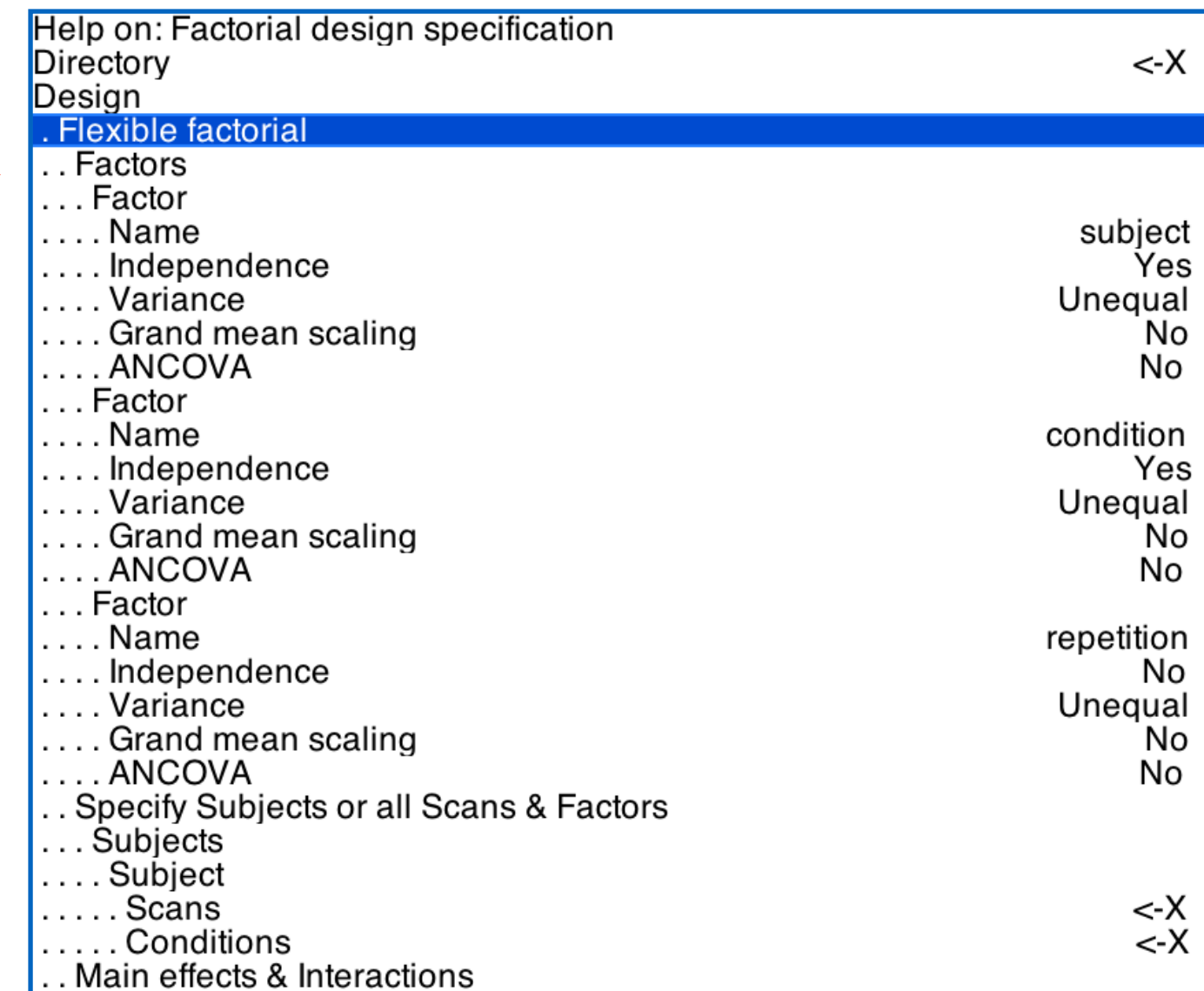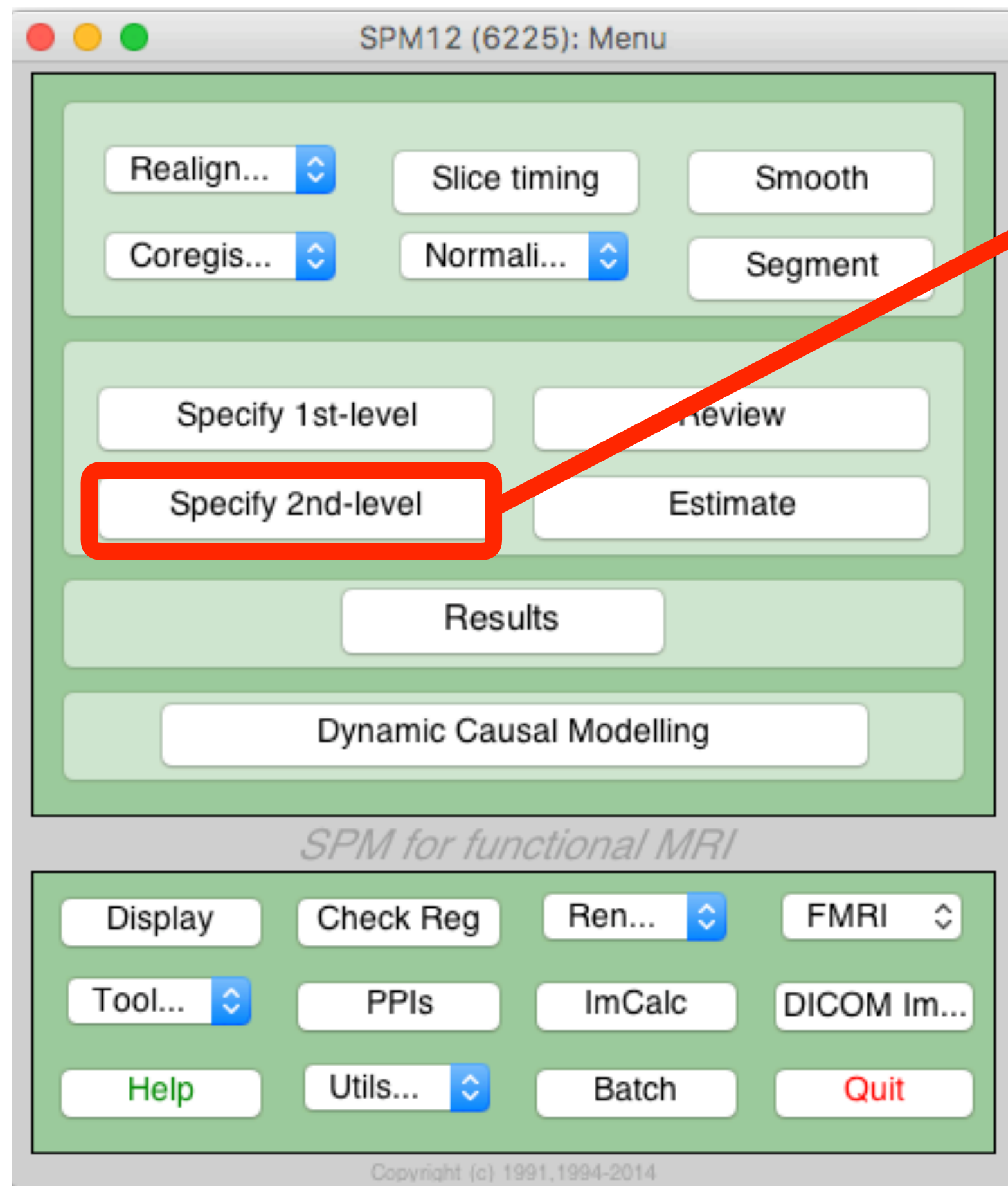
Directory
Select appropriate directory

Design
Choose 'Flexible factorial'

Factor 1
Name: subject
Independence: Yes

Factor 2
Name: condition
Independence: Yes

Factor 3
Name: repetition
Independence: No

Flexible factorial: Specify model (2/2)

```
. . . . ANCOVA                                          No
. . Specify Subjects or all Scans & Factors
. . . Subjects
. . . . Subject
. . . . . Scans                                      4 files
. . . . . Conditions                              4x2 double
. . . . Subject
. . . . . Scans                                      4 files
. . . . . Conditions                              4x2 double
. . . . Subject
. . . . . Scans                                         <-X
. . . . . Conditions                                    <-X
. . . . Subject
. . . . . Scans                                         <-X
. . . . . Conditions                                    <-X
. . . . Subject
. . . . . Scans                                         <-X
. . . . . Conditions                                    <-X
```

Subject 1
Scans: con_0001, con_0002, con_0003, con_0004 of sub-001
Conditions: [1 1; 1 2; 2 1; 2 2];

Subject 2
Scans: con_0001, con_0002, con_0003, con_0004 of sub-0012
Conditions: [1 1; 1 2; 2 1; 2 2];

Subject 3
Scans: con_0001, con_0002, con_0003, con_0004 of sub-0012
Conditions: [1 1; 1 2; 2 1; 2 2];

```
. . Main effects & Interactions
. . . Main effect
. . . . Factor number                                    2
. . . Main effect
. . . . Factor number                                    3
. . . Interaction
. . . . Factor numbers                                [2 3]
```

Main effect of condition
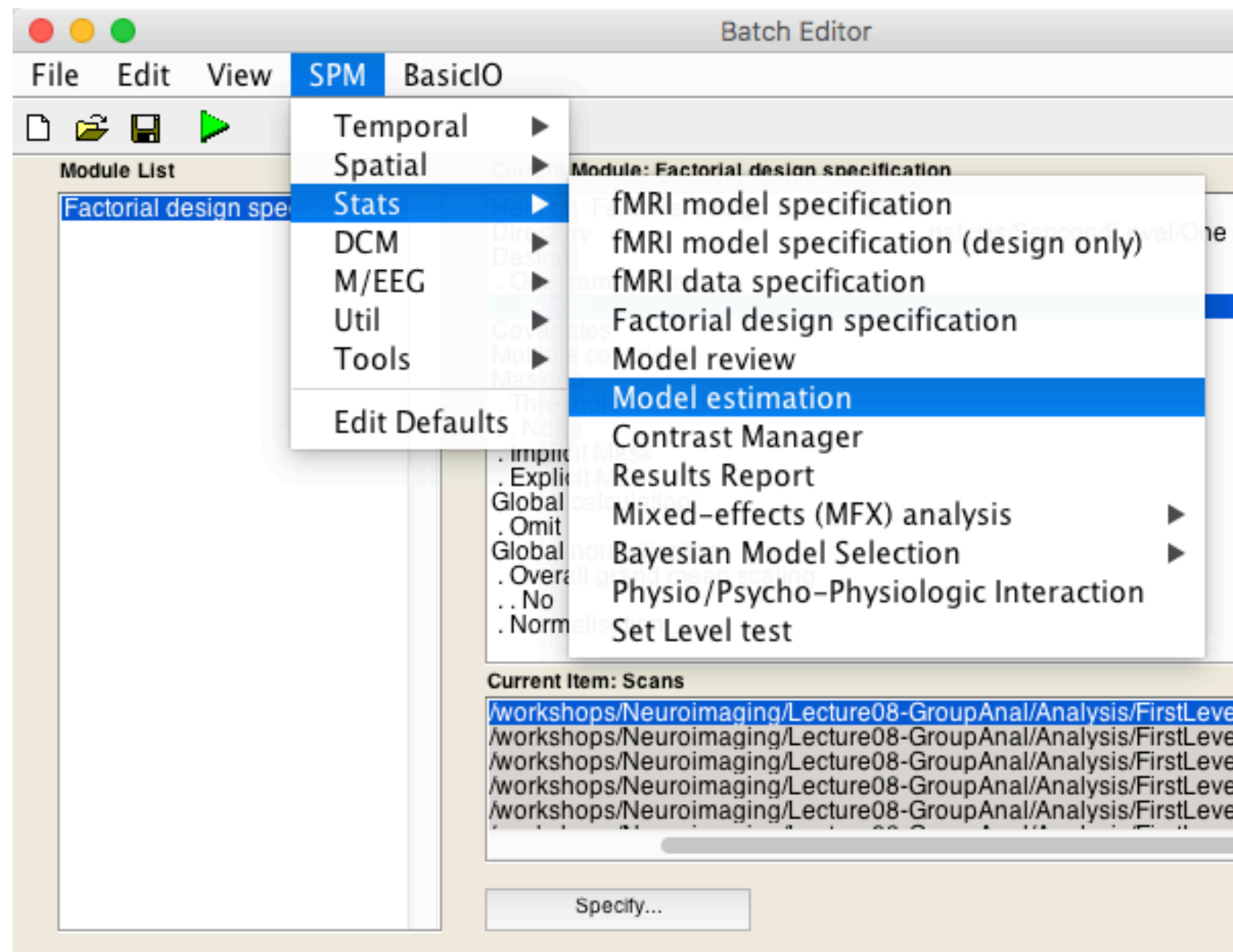Factor number: 2

Main effect of repetition
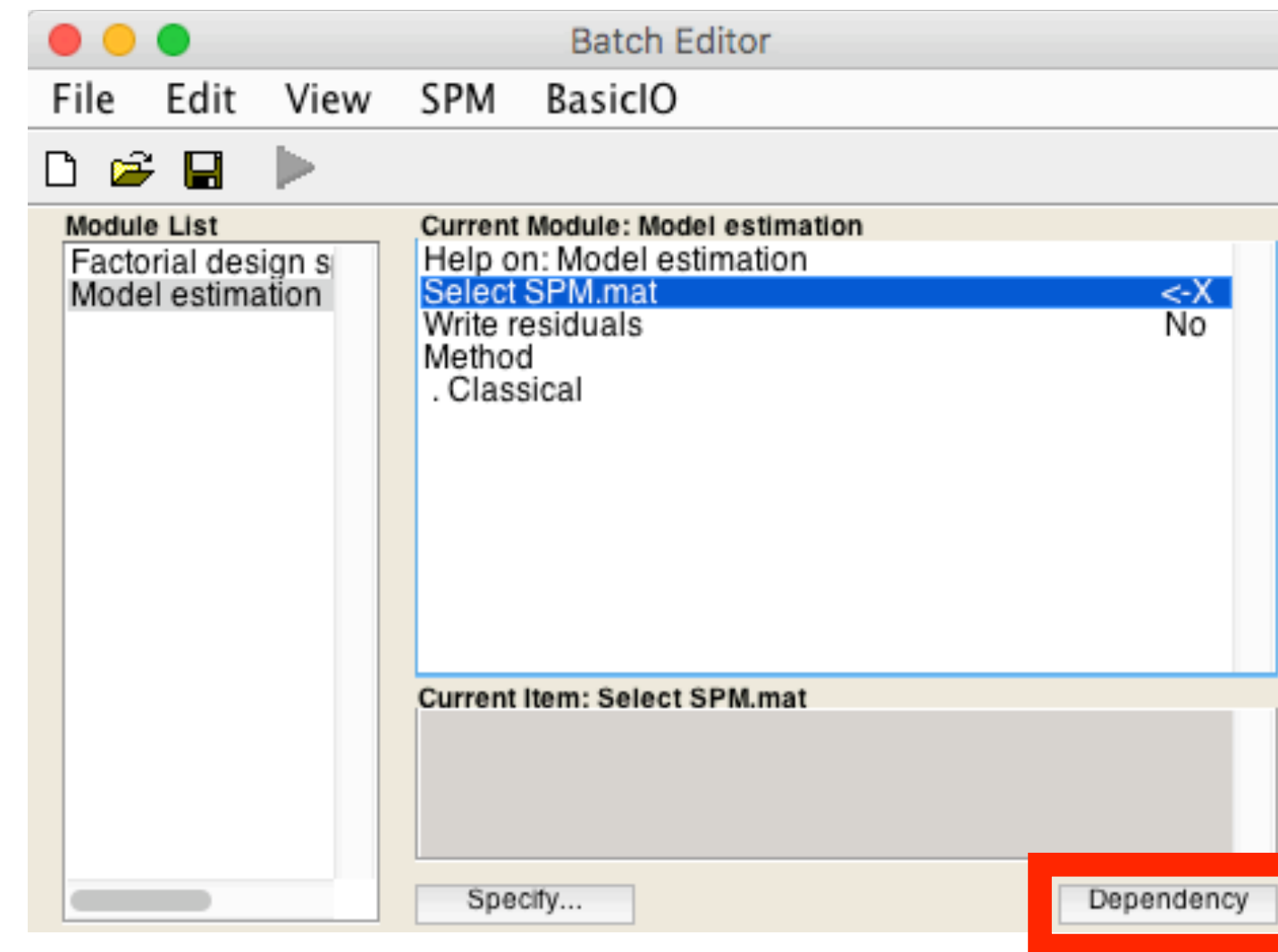Factor number: 3

Interaction
Factor numbers: [2 3]

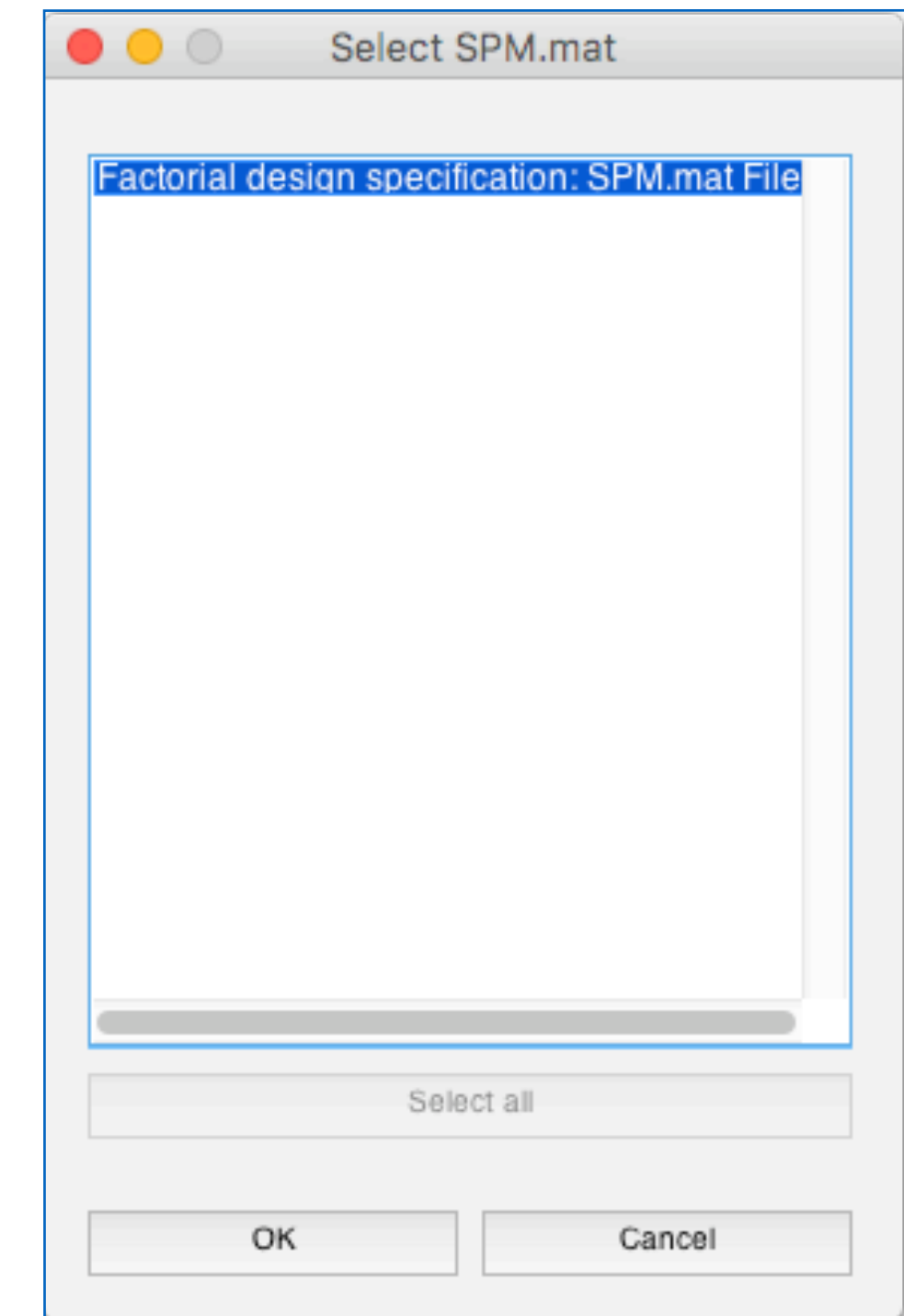# Flexible factorial: Estimation

1. Add 'model estimation' in the module list
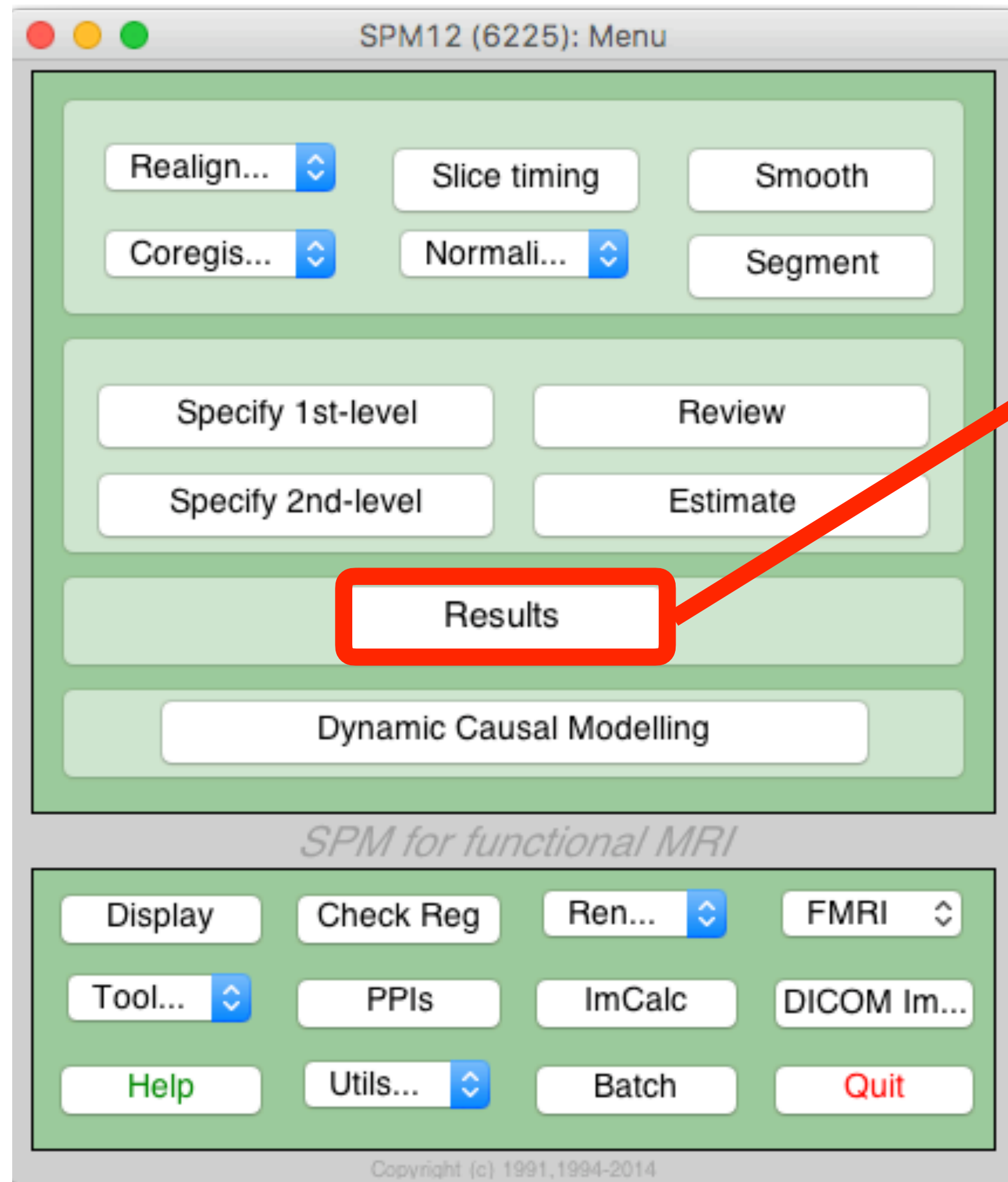   (SPM menu → Stats → Model estimation)

2. Select SPM.mat file
   (Click 'Dependency' button)

3. Select SPM.mat file
   (click ▶Run after selection)

Flexible factorial: Contrast

Select one of existing contrasts
or Define net contrast
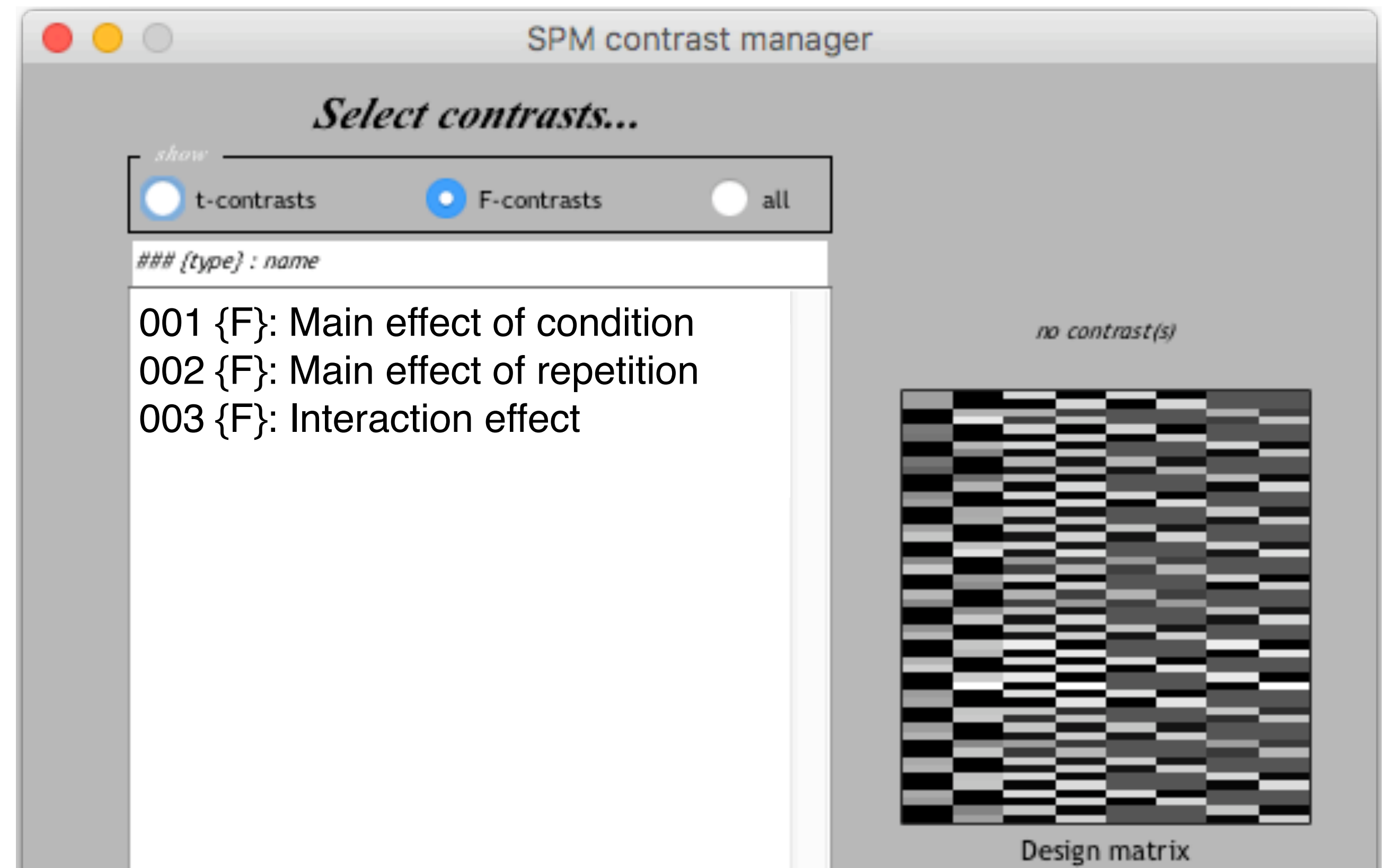
More on F-contrasts

Contrast name	Abstract	Concrete	Novel	Repeat	Abstract & Novel	Abstract & Repeat	Concrete & Novel	Concrete & Repeat
001 {F}: Main effect of condition	1	-1	0	0	0.5	0.5	-0.5	-0.5
002 {F}: Main effect of repetition	0	0	1	-1	0.5	-0.5	0.5	-0.5
003 {F}: Interaction effect	0	0	0	0	1	-1	-1	1

다양한 F-contrast에 대한 예시

Contrast weights in flexible factorial design with multiple groups of subjects

Jan Gläscher[1] and Darren Gitelman[2]

[1] Div. of Humanities and Social Science, Caltech
[2] Dept. of Neurology and Radiology, Northwestern
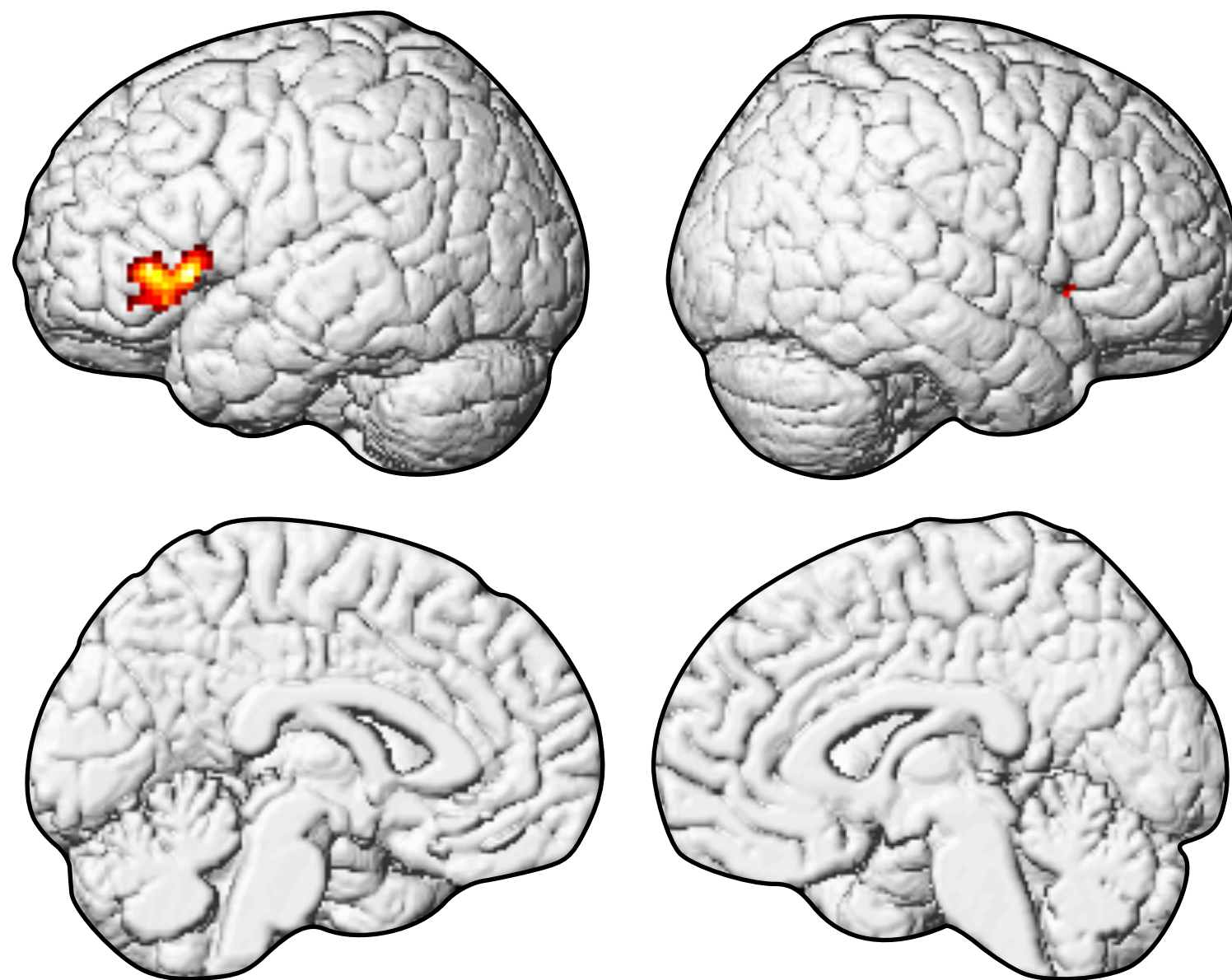
March 18, 2008

contact: glascher@hss.caltech.edu

Matlab script for flexible factorial analysis

```matlab
>> % Directory containing Cross-language data
>> %----------------------------------------------------------------
>> 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);
>>
>>
>> % Specify Model
>> %----------------------------------------------------------------
>> clear matlabbatch;
>> out_dir = fullfile(proj_path,'Analysis','SecondLevel','Flexible'); mkdir(out_dir);
>>
>> matlabbatch{1}.spm.stats.factorial_design.dir = {out_dir};
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(1).name = 'subject';
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(1).dept = 0;
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(1).variance = 1;
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(2).name = 'condition';
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(2).dept = 0;
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(2).variance = 1;
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(3).name = 'repetition';
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(3).dept = 1;
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.fac(3).variance = 1;
>>
>>
>> for c=1:nsubj,
>>     confiles = cell(0);
>>     confiles{1} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0001.nii');
>>     confiles{2} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0002.nii');
>>     confiles{3} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0003.nii');
>>     confiles{4} = fullfile( proj_path,'Analysis','FirstLevel',subjlist{c},'con_0004.nii');
>>
>>     matlabbatch{1}.spm.stats.factorial_design.des.fblock.fsuball.fsubject(c).scans = [confiles'];
>>     matlabbatch{1}.spm.stats.factorial_design.des.fblock.fsuball.fsubject(c).conds = [1 1; 1 2; 2 1; 2 2];
>>
>> end
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.maininters{1}.fmain.fnum = 2;
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.maininters{2}.fmain.fnum = 3;
>> matlabbatch{1}.spm.stats.factorial_design.des.fblock.maininters{3}.inter.fnums = [2 3];
```
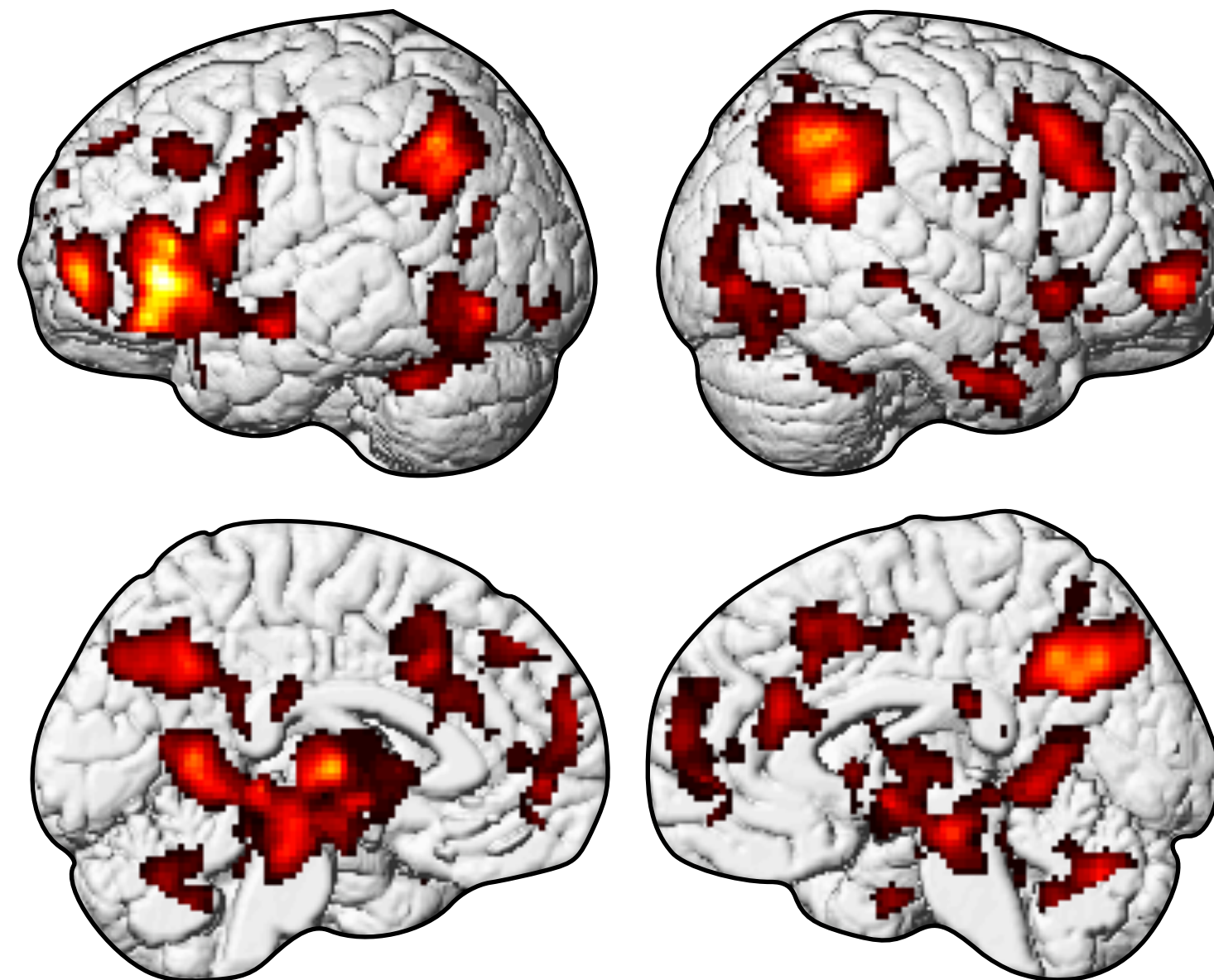
```matlab
>> % Parameter Estimation
>> %----------------------------------------------------------------
>> SPM_mat = fullfile(out_dir,'SPM.mat');
>> matlabbatch{2}.spm.stats.fmri_est.spmmat = {SPM_mat};
>> matlabbatch{2}.spm.stats.fmri_est.write_residuals = 0;
>> matlabbatch{2}.spm.stats.fmri_est.method.Classical = 1;
>>
>>
>> % Create Contrasts
>> %----------------------------------------------------------------
>> matlabbatch{3}.spm.stats.con.spmmat = {SPM_mat};
>> matlabbatch{3}.spm.stats.con.consess{1}.fcon.name = 'Main effect of condition';
>> matlabbatch{3}.spm.stats.con.consess{1}.fcon.weights = [1 -1 0 0 0.5 0.5 -0.5 -0.5];
>> matlabbatch{3}.spm.stats.con.consess{1}.fcon.sessrep = 'none';
>> matlabbatch{3}.spm.stats.con.consess{2}.fcon.name = 'Main effect of repetition';
>> matlabbatch{3}.spm.stats.con.consess{2}.fcon.weights = [0 0 1 -1 0.5 -0.5 0.5 -0.5];
>> matlabbatch{3}.spm.stats.con.consess{2}.fcon.sessrep = 'none';
>> matlabbatch{3}.spm.stats.con.consess{3}.fcon.name = 'Interaction';
>> matlabbatch{3}.spm.stats.con.consess{3}.fcon.weights = [0 0 0 0 1 -1 -1 1];
>> matlabbatch{3}.spm.stats.con.consess{3}.fcon.sessrep = 'none';
>> matlabbatch{3}.spm.stats.con.delete = 1;
>>
>>
>> % spm_jobman('interactive',matlabbatch);
>> spm_jobman('run',matlabbatch);
```
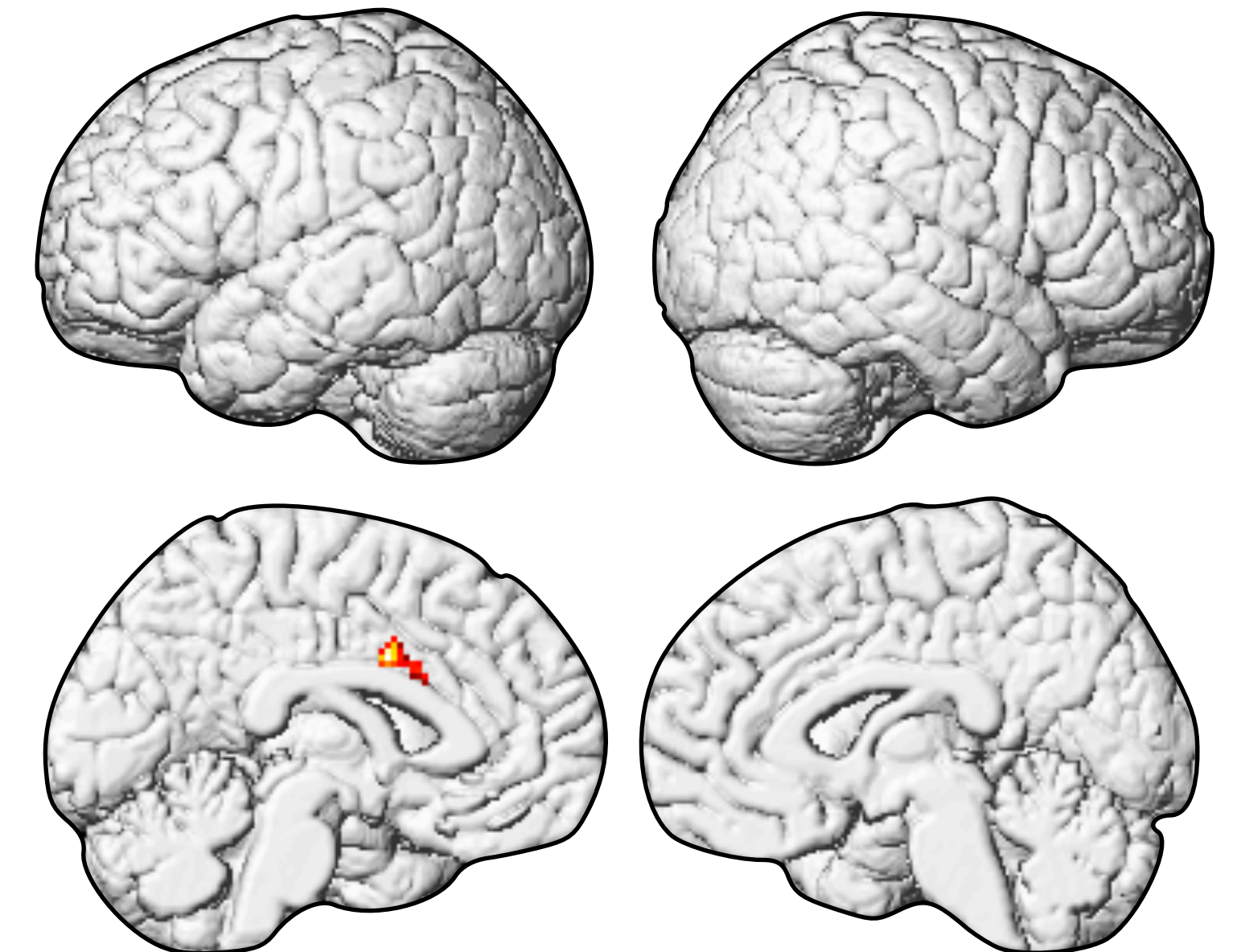
Flexible factorial: Mapping

Main effect of condition

Main effect of repetition

Interaction effect

CDT *p*<0.005 & *k*=50