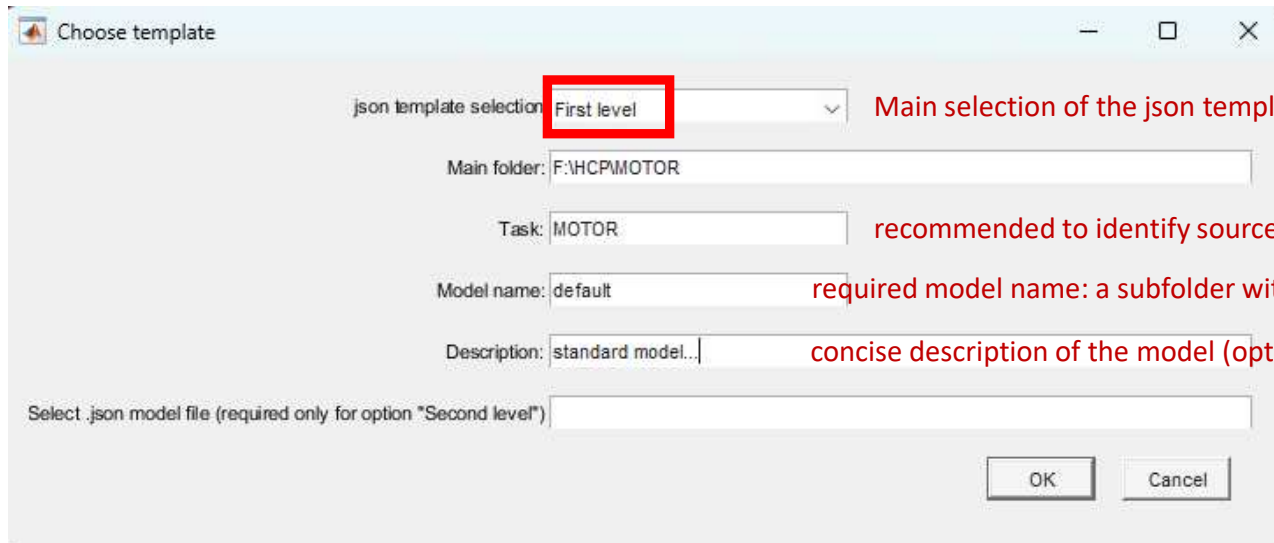


Sequence of user interface dialog boxes in the MATLAB script `ui_spm_batch_creator.m`

Daniel Huber, University of Innsbruck, November 2024

This document intends to show all possible model options for first and second level analysis, which are available in SPM12. On the following pages, these options and the needed inputs are demonstrated on a dataset of the Human Connectome Project (motor task). However, some of the models make no sense for the exemplary dataset shown within the interface. The main purpose is to show the principles of data selection for model definition (not to present valid models).

Main selection window



The 'Choose template' dialog box is shown with the following fields and values:

- json template selection: **First level** (highlighted with a red box)
- Main folder: F:\HCP\MOTOR
- Task: MOTOR
- Model name: default
- Description: standard model...
- Select .json model file (required only for option "Second level"): (empty)

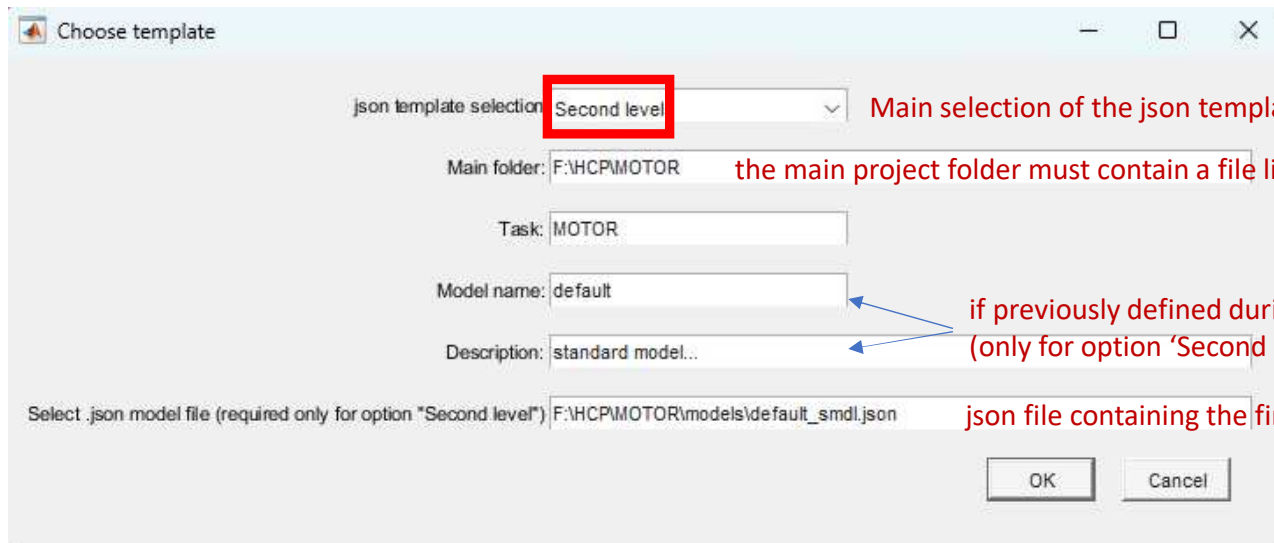
Buttons: OK, Cancel

Main selection of the json template ('First level' and 'First + Second Level' start with the same sequence)

recommended to identify source files; a subfolder 'Task' will be created in the output directory

required model name: a subfolder with the model name will be created in the second level output directory

concise description of the model (optional)



The 'Choose template' dialog box is shown with the following fields and values:

- json template selection: **Second level** (highlighted with a red box)
- Main folder: F:\HCP\MOTOR
- Task: MOTOR
- Model name: default
- Description: standard model...
- Select .json model file (required only for option "Second level"): F:\HCP\MOTOR\models\default_smdl.json

Buttons: OK, Cancel

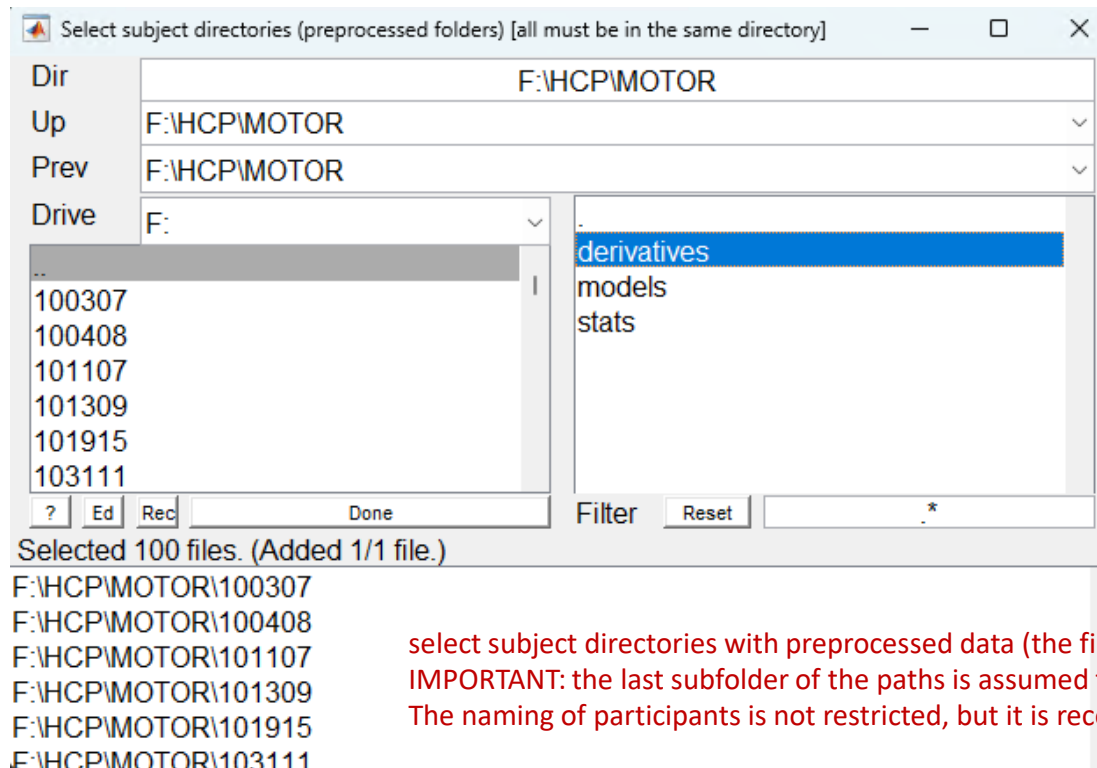
Main selection of the json template -> **'Second level' sequence continues on page 18**

the main project folder must contain a file like 'participants.tsv' in case that covariates shall be included in the model

if previously defined during creation of first level json, these fields may be left empty
(only for option 'Second level')

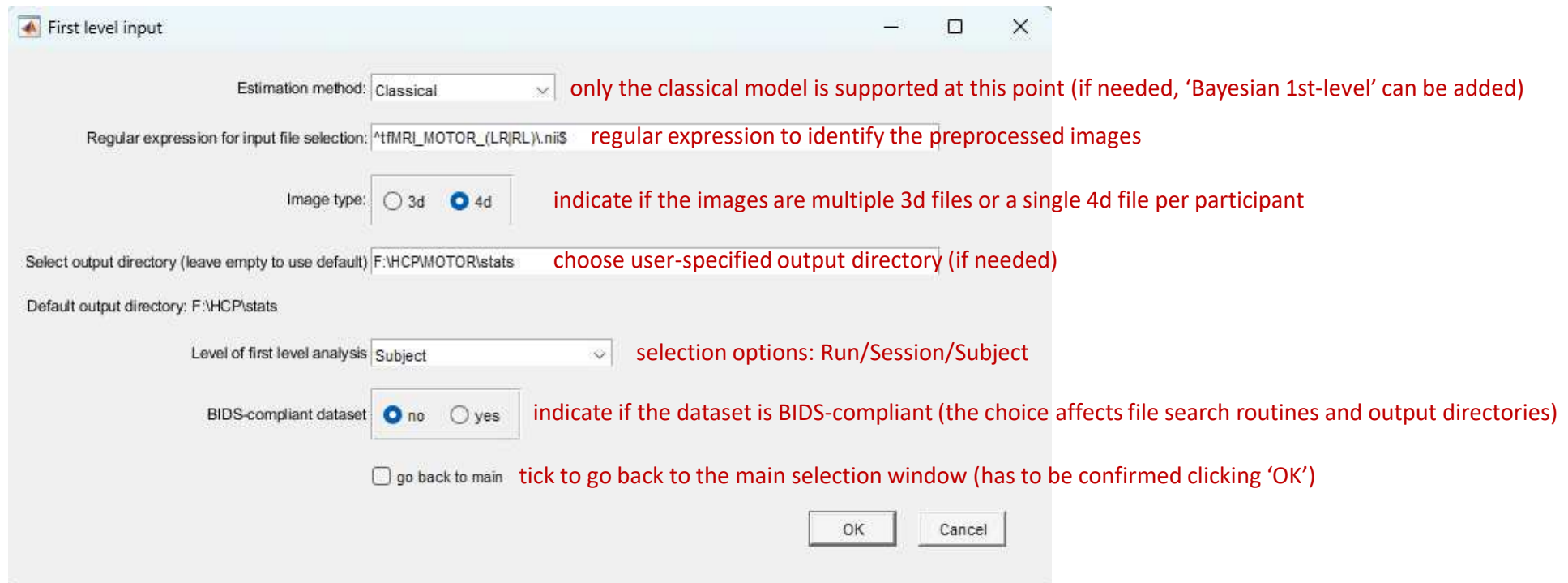
json file containing the first level node -> the second level node will be appended to this file

Options “First level” and “First + Second level”: Selection of subject folders



select subject directories with preprocessed data (the files may be located in subfolders within the chosen ones);
IMPORTANT: the last subfolder of the paths is assumed to be the 'Participant_ID' (in this example '100307', '100408', etc.);
The naming of participants is not restricted, but it is recommended to use sub-01, sub-02, etc.

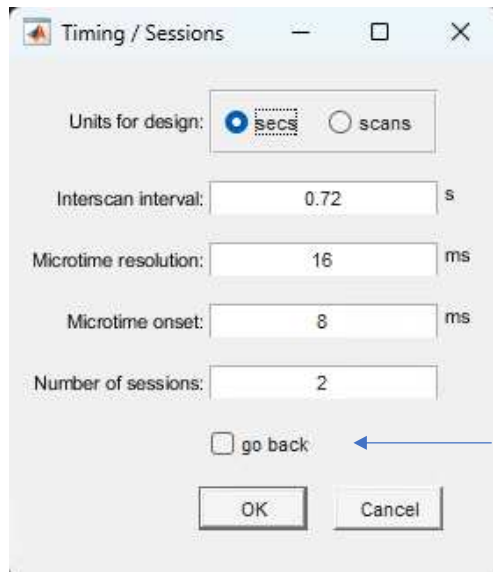
Options “First level” and “First + Second level”: First level input



The screenshot shows the 'First level input' dialog box with the following fields and annotations:

- Estimation method:** Classical (dropdown menu). *only the classical model is supported at this point (if needed, 'Bayesian 1st-level' can be added)*
- Regular expression for input file selection:** ^tfMRI_MOTOR_(LR|RL)\.nii\$ (text field). *regular expression to identify the preprocessed images*
- Image type:** 3d (radio button), 4d (radio button, selected). *indicate if the images are multiple 3d files or a single 4d file per participant*
- Select output directory (leave empty to use default):** F:\HCP\MOTOR\stats (text field). *choose user-specified output directory (if needed)*
- Default output directory:** F:\HCP\stats (text field)
- Level of first level analysis:** Subject (dropdown menu). *selection options: Run/Session/Subject*
- BIDS-compliant dataset:** no (radio button, selected), yes (radio button). *indicate if the dataset is BIDS-compliant (the choice affects file search routines and output directories)*
- go back to main:** (checkbox). *tick to go back to the main selection window (has to be confirmed clicking 'OK')*
- Buttons:** OK, Cancel

Options “First level” and “First + Second level”: Timing parameters & number of sessions

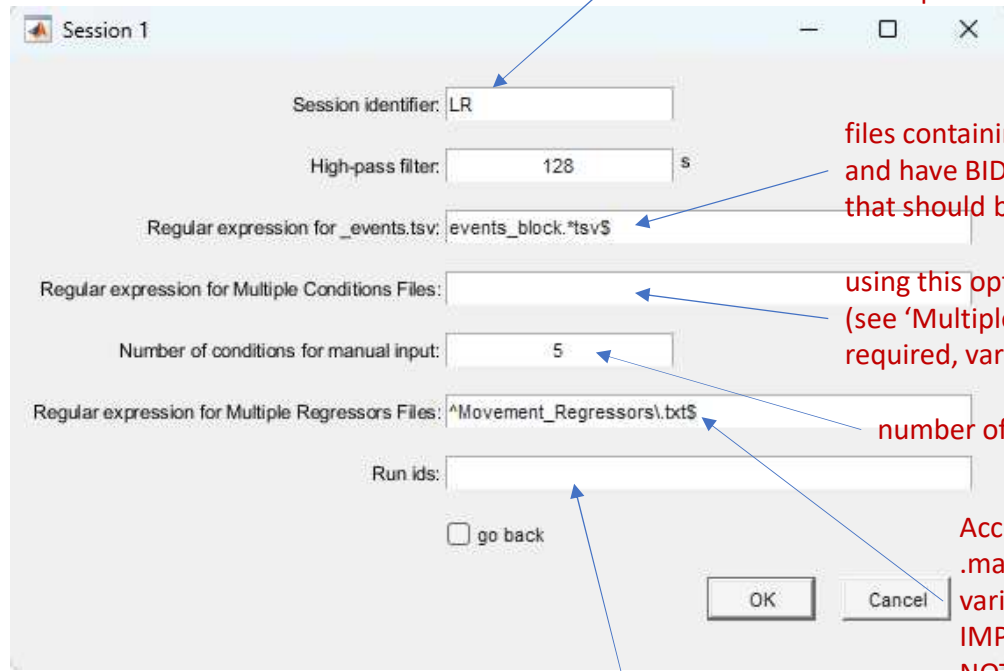


The required fields in this and the upcoming windows are mostly very similar to the ones in SPM's batch editor. Detailed information about the fields can be found there and in the user manual of SPM12.

tick to go back to the previous window (confirm by clicking 'OK'); this option is available in most of the input windows (except for windows which are executed repeatedly); previously entered input is usually saved temporarily;

Options “First level” and “First + Second level”: Session definition

Session identifiers may only consist of either all numbers or all letters (e.g., 01, A, post); This restriction is necessary to identify sessions subfolders in non-BIDS datasets: Session identifiers are expected to be found at the very end of subfolders (e.g., .../.../someFolderName_A)
Note: for BIDS-compliant datasets also mixed entries (e.g., FUNC01) are accepted



files containing event data do not need to be named 'events.tsv', but they must be in format .tsv and have BIDS structure (column names 'trial_type', 'onset', 'duration'); any parametric modulator that should be included in the model must also have its own column in this file;

using this option requires to have a .mat file containing all variables needed to define conditions (see 'Multiple Conditions' in SPM's batch editor): variables 'names', 'onsets', 'durations' are required, variables 'tmod', 'pmod' optional; if this option is used, 'events.tsv' is not needed;

number of conditions, which shall be extracted from 'events.tsv' (details on the next page)

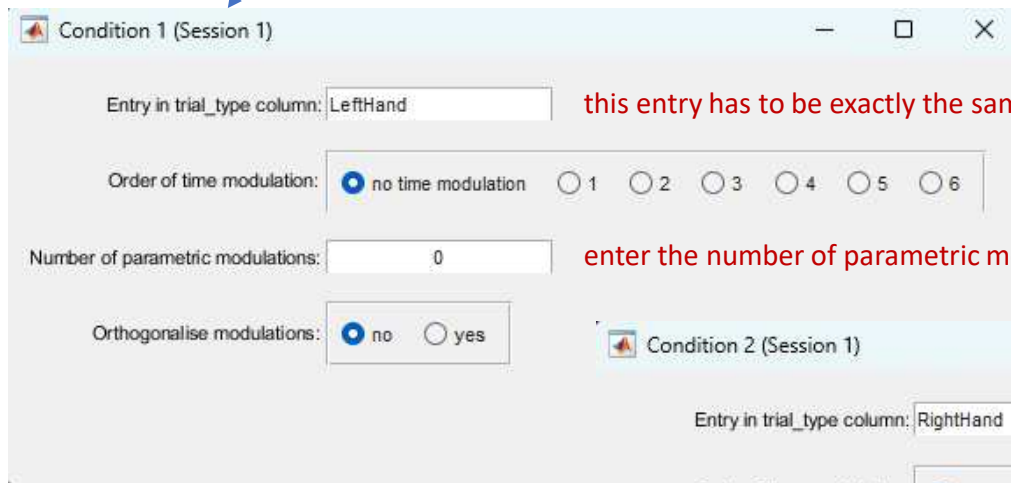
Accepted formats for multiple regressors (e.g., movement parameters) are .txt, .tsv, .mat. If a .mat file is provided, it must contain the variable 'R' (according to SPM12) and the optional variable 'names'. The other formats are converted to .mat.
IMPORTANT: The number of rows in 'R' must be the same as the number of participants!
NOTE: Any missing numbers (NaN) will be replaced by zeros.

Run ids are expected to be numbers (e.g., 01, 02, 03, etc) and have to be entered as a comma-separated list. IMPORTANT: Dedicated files can only be identified by the BIDS-entity 'run-01' or 'run_01' or 'run01'; (this practice is necessary to discriminate run ids from session ids)

Options “First level” and “First + Second level”: Conditions

This window will only appear if a number was entered in ‘Number of conditions for manual input’ in the session window

To keep track of the actual session/condition, the indices are included in the title



Condition 1 (Session 1)

Entry in trial_type column: LeftHand

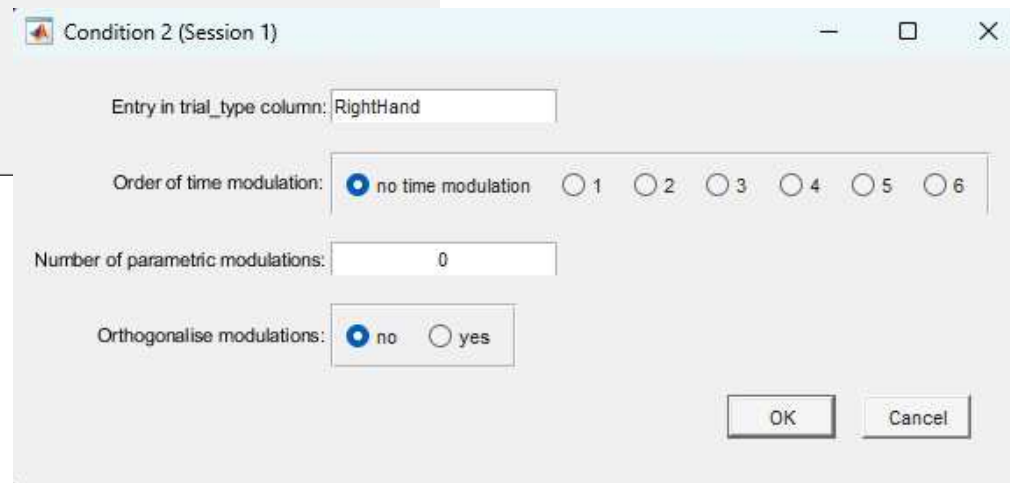
Order of time modulation: ☒ no time modulation ☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6

Number of parametric modulations: 0

Orthogonalise modulations: ☒ no ☐ yes

this entry has to be exactly the same as in the column ‘trial_type’ in events.tsv

enter the number of parametric modulations for this condition (details will be asked for in the next window)



Condition 2 (Session 1)

Entry in trial_type column: RightHand

Order of time modulation: ☒ no time modulation ☐ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6

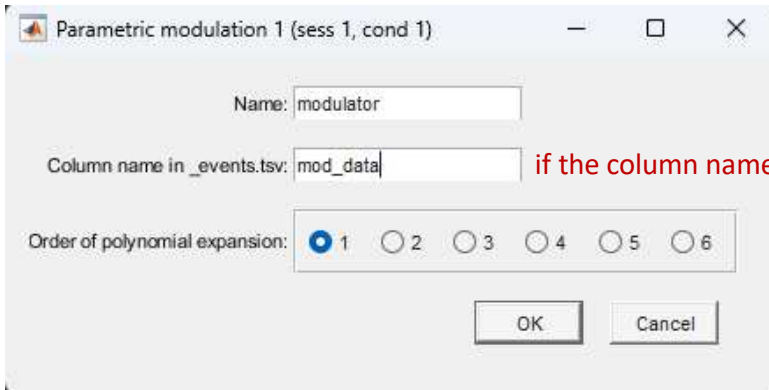
Number of parametric modulations: 0

Orthogonalise modulations: ☒ no ☐ yes

OK Cancel

Options “First level” and “First + Second level”: Parametric modulations

This window will only appear if a number was entered in ‘Number of parametric modulations’ in the condition window



Parametric modulation 1 (sess 1, cond 1)

Name: modulator

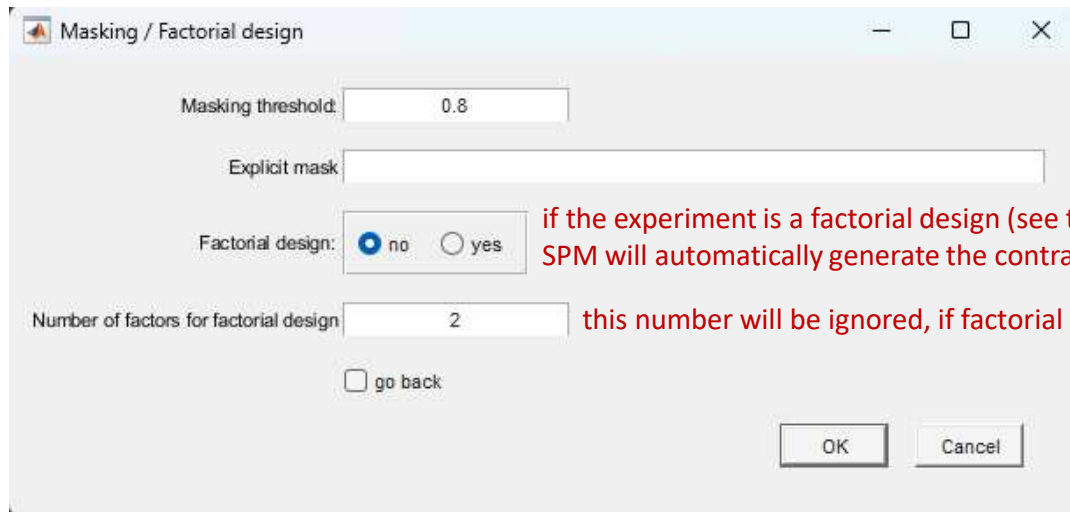
Column name in _events.tsv: mod_data

Order of polynomial expansion: ☒ 1 ☐ 2 ☐ 3 ☐ 4 ☐ 5 ☐ 6

OK Cancel

if the column name is the same as 'Name', this field can be left empty

Options “First level” and “First + Second level”: Masking & Factorial design



The image shows a screenshot of the 'Masking / Factorial design' dialog box in SPM. The dialog box has a title bar with a small icon and the text 'Masking / Factorial design'. It contains several input fields and buttons. The 'Masking threshold' field is set to 0.8. The 'Explicit mask' field is empty. The 'Factorial design' section has two radio buttons: 'no' (selected) and 'yes'. The 'Number of factors for factorial design' field is set to 2. There is a 'go back' checkbox and 'OK' and 'Cancel' buttons at the bottom.

Masking threshold: 0.8

Explicit mask

Factorial design: ☒ no ☐ yes

Number of factors for factorial design: 2

☐ go back

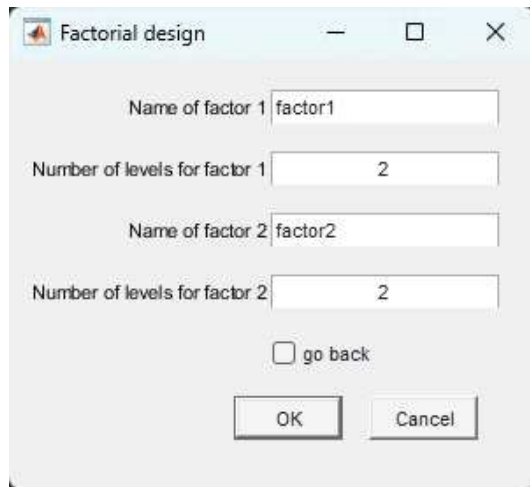
OK Cancel

if the experiment is a factorial design (see the information in SPM's batch editor or the manual of SPM12 for details), SPM will automatically generate the contrasts to test for the main effects and interactions;

this number will be ignored, if factorial design is set to 'no'

Options “First level” and “First + Second level”: Factor definition

This window will only appear if ‘Factorial design’ was set to ‘yes’ in the previous window



Factorial design

Name of factor 1: factor1

Number of levels for factor 1: 2

Name of factor 2: factor2

Number of levels for factor 2: 2

☐ go back

OK Cancel

the first factor is assumed to change slowest

Options “First level” and “First + Second level”: Additional options & basis functions

Additional options / Basis functions

Model interactions Volterra: ☒ no ☐ yes

Global normalisation: ☒ none ☐ scaling

Serial correlations: AR(1) ▼

Basis function type: Canonical HRF ▼

☐ go back

OK Cancel

depending on the chosen option in 'Basis function type', different inputs are required

Options Canonical HRF

Model derivatives: ☒ no ☐ time derivative ☐ time & dispersion derivative

☐ go back

OK Cancel

Additional options / Basis functions

Model interactions Volterra: ☒ no ☐ yes

Global normalisation: ☒ none ☐ scaling

Serial correlations: AR(1) ▼

Basis function type: Fourier set ▼

☐ go back

OK Cancel

Options basis function

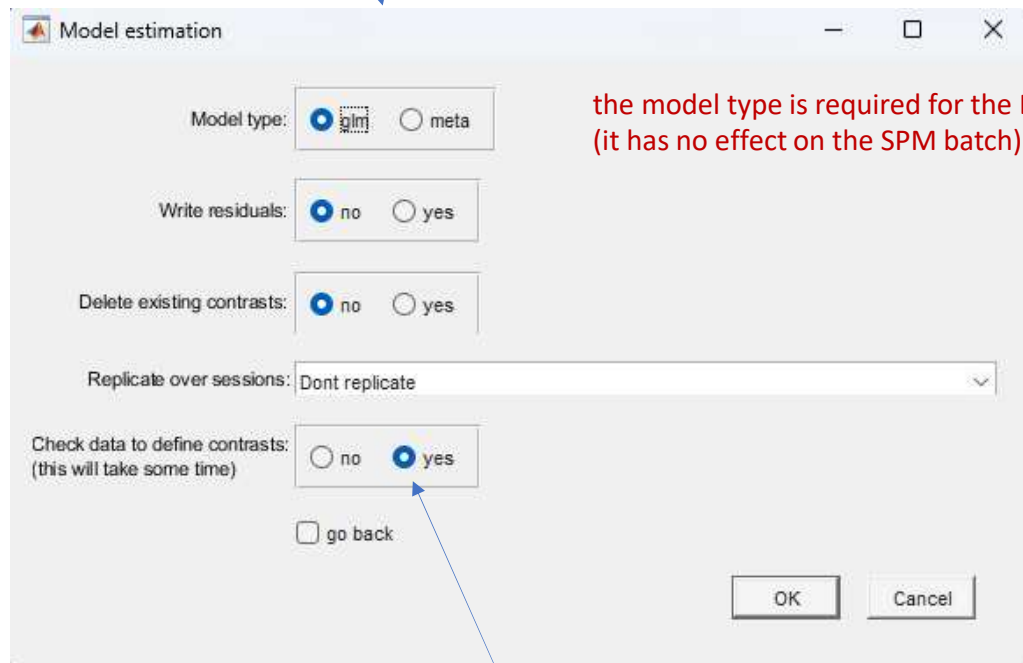
Window length: s

Number of basis functions

☐ go back

OK Cancel

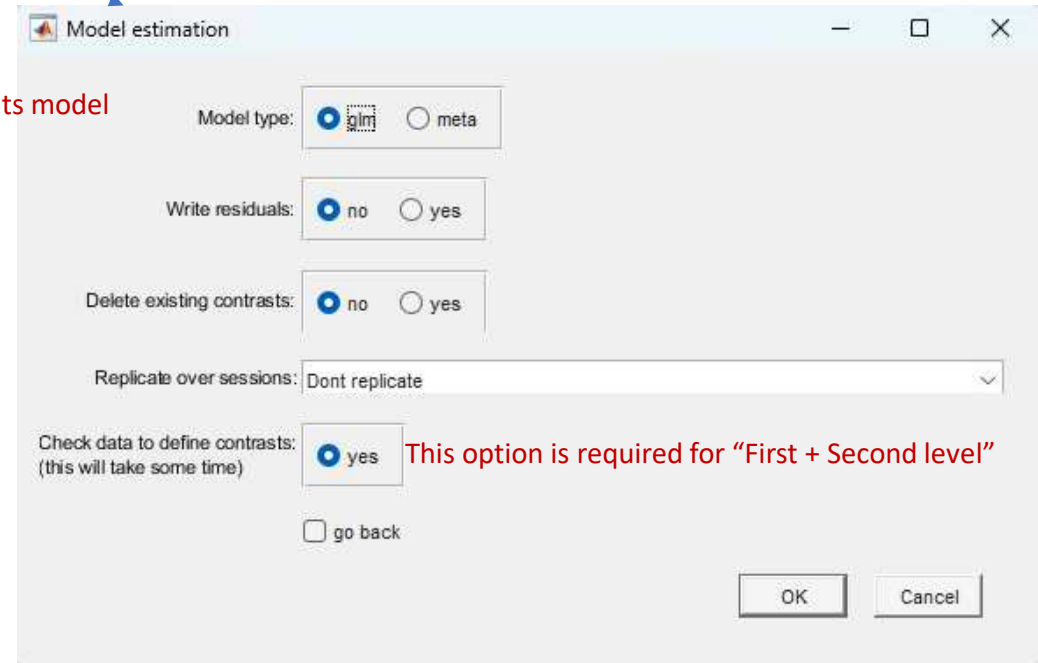
Options “First level” and “First + Second level”: Model estimation



Model estimation dialog box for the first level. The dialog has a title bar with a red triangle icon and the text "Model estimation". It contains the following options:

- Model type: ☒ glm ☐ meta
- Write residuals: ☒ no ☐ yes
- Delete existing contrasts: ☒ no ☐ yes
- Replicate over sessions: Dont replicate (dropdown menu)
- Check data to define contrasts: (this will take some time) ☐ no ☒ yes
- ☐ go back
- OK and Cancel buttons

the model type is required for the BIDS stats model
(it has no effect on the SPM batch)



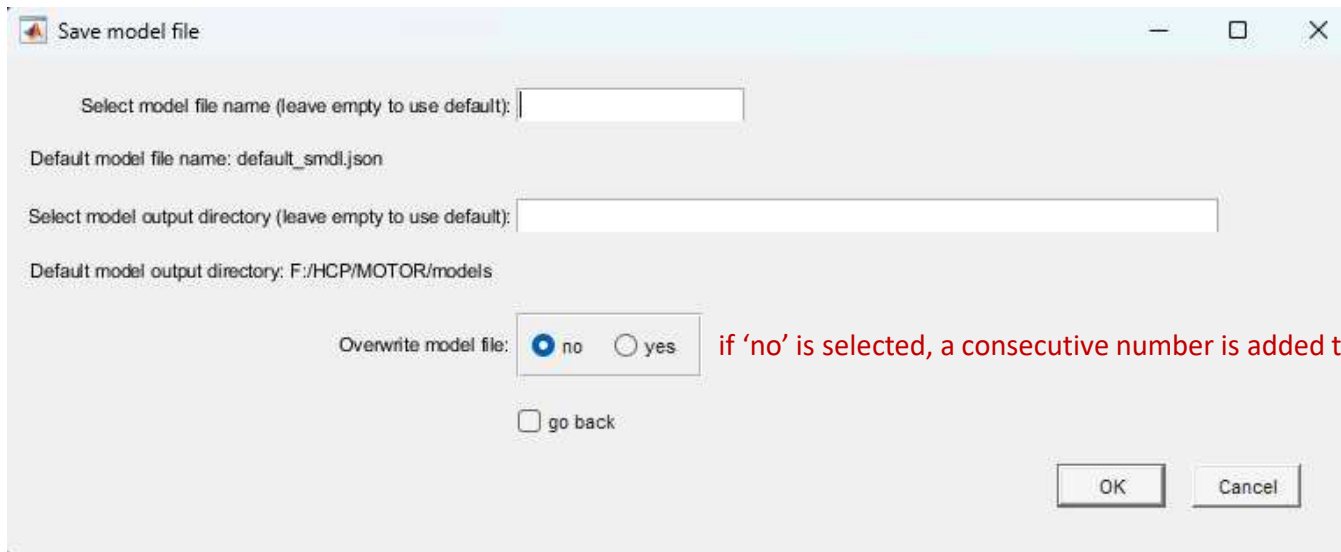
Model estimation dialog box for the first + second level. The dialog has a title bar with a red triangle icon and the text "Model estimation". It contains the following options:

- Model type: ☒ glm ☐ meta
- Write residuals: ☒ no ☐ yes
- Delete existing contrasts: ☒ no ☐ yes
- Replicate over sessions: Dont replicate (dropdown menu)
- Check data to define contrasts: (this will take some time) ☒ yes ☐ no
- ☐ go back
- OK and Cancel buttons

This option is required for “First + Second level”

Choosing ‘yes’ will validate all given inputs for the first levels to finally create the design matrix (the design matrix columns are needed to define contrasts in the next step); since the data of all subjects have to be checked, this may take quite long!
Choosing ‘no’ will skip contrast definition via the user interface. Instead, the contrasts have to be entered directly in the json model file.

Options “First level” and “First + Second level”: Save model (first level node)



The screenshot shows a 'Save model file' dialog box with the following fields and options:

- Select model file name (leave empty to use default):** An empty text input field.
- Default model file name:** default_smdl.json
- Select model output directory (leave empty to use default):** An empty text input field.
- Default model output directory:** F:/HCP/MOTOR/models
- Overwrite model file:** Two radio buttons, 'no' (selected) and 'yes'.
- go back:** A checkbox.
- Buttons:** 'OK' and 'Cancel' buttons at the bottom right.

if 'no' is selected, a consecutive number is added to the file name in case that it already exists

After clicking 'OK', the inputs are saved to the model json file, i.e., the first level node is created. The script ends in case that 'Check data to define contrasts' was not selected in the in the previous window. Otherwise, input data are checked and the design matrix created for all participants. The model json file is then updated with the design matrix columns (Nodes.Model.X and Nodes.Model.HRF.Variables).

Options “First level” and “First + Second level”: Definition of contrasts

This window will only appear if ‘Check data to define contrasts’ was set to ‘yes’ in the ‘Model estimation’ window

separate contrast names by comma and avoid special characters (folders named according to these contrast names will be created during second level analysis)

Definition of Contrasts

Enter contrast names for t-contrasts (separate names by comma): left vs right, hand vs foot, limbs vs tongue, task

Enter contrast names for F-contrasts (separate names by comma): variance

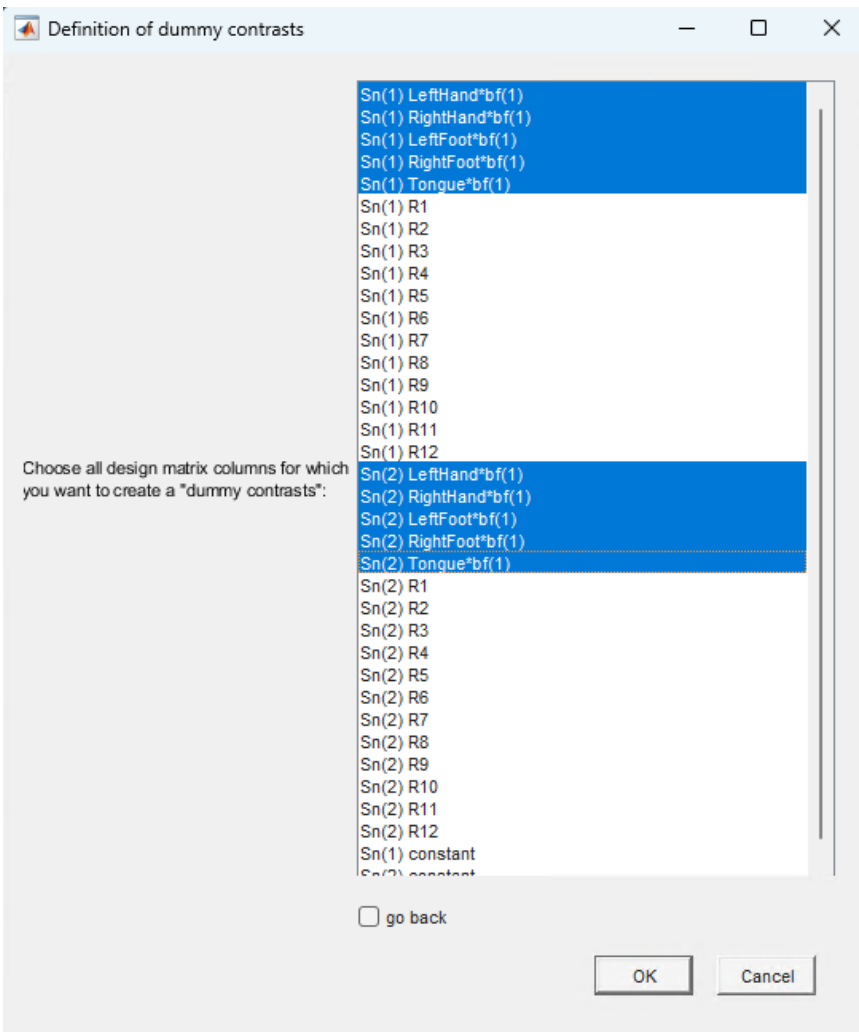
Define *dummy contrasts*: ☐ no ☒ yes

OK Cancel

‘dummy contrasts’ are simple contrasts, which have weight 1 for the chosen variable (i.e., design matrix column) and weight 0 for all others;
In the next window, the desired variables can be selected;

Options “First level” and “First + Second level”: Definition of “dummy contrasts”

This window will only appear if ‘Define “dummy contrasts”’ was selected in the previous window



the list shows all elements of Nodes.Model.X; several entries can be selected pressing Shift or Ctrl

Options “First level” and “First + Second level”: Definition of t-contrasts

This window will only appear if t-contrast names were entered in ‘Definition of Contrasts’

| | Sn(1) LeftHand*bf(1) | Sn(1) RightHand*bf(1) | Sn(1) LeftFoot*bf(1) | Sn(1) RightFoot*bf(1) | Sn(1) Tongue*bf(1) | Sn(1) R1 | Sn(1) R2 | Sn(1) R3 | Sn(1) R4 | Sn(1) R5 | Sn(1) R6 |
|---|----------------------|-----------------------|----------------------|-----------------------|--------------------|----------|----------|----------|----------|----------|----------|
| 1 | -1 | 1 | -1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | -1 | -1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | -0.2500 | -0.2500 | -0.2500 | -0.2500 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |

the weights have to be entered in the table which contains all design matrix columns;
the t-contrast names are listed with consecutive numbers on the left side;
the row indices in the table correspond to the enumeration of the contrasts;

Options “First level” and “First + Second level”: Definition of F-contrasts

This window will only appear if F-contrast names were entered in ‘Definition of Contrasts’

Definition of weights for f-contrast1

Contrast name (f-contrast 1): variance

Weights:

| | g | Sn(1) R10 | Sn(1) R11 | Sn(1) R12 | Sn(2) LeftHand*bf(1) | Sn(2) RightHand*bf(1) | Sn(2) LeftFoot*bf(1) | Sn(2) RightFoot*bf(1) | Sn(2) Tongue*bf(1) | Sn(2) R1 | Sn(2) R2 |
|----|---|-----------|-----------|-----------|----------------------|-----------------------|----------------------|-----------------------|--------------------|----------|----------|
| 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 11 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 14 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 21 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 22 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 23 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

☐ go back

OK Cancel

the weights have to be entered in the table which contains all design matrix columns;
the row indices in the table also correspond to the design matrix columns (-> n x n matrix);
the f-contrast name to which the table is assigned, is indicated above the table

After clicking ‘OK’, the model json file is updated with the defined contrasts. For the option “First level”, the script ends at this point: To create and execute the SPM batches defined in the json, type `SPM_batch_creator(1)`;
For the option “First + Second level”, the user interface continues with the input for the second level analysis.

Options “Second level” and “First + Second level”: Second level input

The screenshot shows the 'Second level input' dialog box. The 'Design type' is set to 'One sample t-test' and the 'Estimation method' is 'Classical'. The 'Check data to define contrasts' section has 'yes' selected. The 'Write second level node' section has 'append to existing file' selected. The 'Enter new file name' field contains 'default_smdl'. The 'go back to main' checkbox is unchecked. Red text annotations explain the 'yes' selection and the file name field.

Design type: One sample t-test

Estimation method: Classical

Select output directory (leave empty to use default):

Default output directory: F:/HCP/MOTOR/group_stats

Check data to define contrasts: (this will take some time) ☐ no ☒ yes

Write second level node: ☒ append to existing file ☐ write new file

Enter new file name: default_smdl

☐ go back to main

OK Cancel

For the option “Second level”, the input data for the second level model can be validated and the design matrix created supposed that the first level analyses have already been done.

ignored if node is appended

use ‘write new file’ if several second level models shall be tested on the same first level analysis

The screenshot shows the 'Second level input' dialog box with a dropdown menu open for 'Design type'. The menu lists several options: 'One sample t-test', 'Two sample t-test', 'Paired t-test', 'Multiple Regression', 'One Way ANOVA', 'One Way ANOVA within subject', 'Full Factorial', and 'Flexible Factorial'. The 'Design type' is currently set to 'One sample t-test' and the 'Estimation method' is 'Classical'. Red text annotations point to the dropdown menu and the 'Contrasts have to be defined directly in the .json model file' text.

Design type: One sample t-test

Estimation method: Classical

Select output directory (leave empty to use default):

Default output directory: F:/HCP/MOTOR/group_stats

Contrasts have to be defined directly in the .json model file

OK Cancel

options for the second level factorial design

For the option “First + Second level”, it is not possible to check the data, since the first level analysis has not been executed yet (i.e., the contrast files do not exist)

Options “Second level” and “First + Second level”: One-sample t-test

Input One-sample t-test

Input file type: ☒ con ☐ beta ☐ other

Select all contrast names for which you want to perform a one-sample t-test: (ignored if "Input file type" is "beta")

- left vs right
- hand vs foot
- limbs vs tongue
- task
- tongue
- variance
- Sn(1) LeftHand*bf(1)
- Sn(1) RightHand*bf(1)
- Sn(1) LeftFoot*bf(1)
- Sn(1) RightFoot*bf(1)
- Sn(1) Tongue*bf(1)
- Sn(2) LeftHand*bf(1)
- Sn(2) RightHand*bf(1)
- Sn(2) LeftFoot*bf(1)

Select all beta names for which you want to perform a one-sample t-test: (only needed if "Input file type" is "beta", otherwise ignored)

- Sn(1) LeftHand*bf(1)
- Sn(1) RightHand*bf(1)
- Sn(1) LeftFoot*bf(1)
- Sn(1) RightFoot*bf(1)
- Sn(1) Tongue*bf(1)
- Sn(1) R1
- Sn(1) R2
- Sn(1) R3
- Sn(1) R4
- Sn(1) R5
- Sn(1) R6
- Sn(1) R7
- Sn(1) R8
- Sn(1) R9

Regular expression for input file selection: (only needed if "Input file type" is "other")

☐ go back

OK Cancel

The option 'con' uses the con_####.nii files created in the first level analysis as the input files. This option is the default and requires only the input of the list directly below; Alternatively, the 'beta' files of the first levels can be used for the second level analysis. This option requires the input from the second list below (which contains Nodes.Model.X of the first level node). This option allows to test simple contrasts on the second level, which were not originally created during first level analysis. The option 'other' allows to assign user-specified files to the contrasts chosen in the upper list. The user-specified files are identified using the regular expression(s) in the field at the bottom.

the list shows all contrast names (including “dummy contrasts”) that are defined in the first level node

the list shows all entries from the first level Nodes.Model.X. As these are the names of the design matrix columns, for each of them a beta_####.nii file exists, which can be used as an input for the second level analysis. NOTE: It is not possible to use both 'con' and 'beta' files in the same model.

regular expression(s) assigned to the contrasts chosen in the upper list; regular expressions must be separated by commas; the number of regular expressions must match the number of chosen contrasts (upper list)

Options “Second level” and “First + Second level”: Two-sample t-test

Input Two-sample t-test

Input file type: ☒ con ☐ beta ☐ other

Select all contrast names for which you want to perform a two-sample t-test: (ignored if "Input file type" is "beta")

- left vs right
- hand vs foot
- limbs vs tongue
- task
- tongue
- variance
- Sn(1) LeftHand*bf(1)
- Sn(1) RightHand*bf(1)
- Sn(1) LeftFoot*bf(1)
- Sn(1) RightFoot*bf(1)
- Sn(1) Tongue*bf(1)
- Sn(2) LeftHand*bf(1)
- Sn(2) RightHand*bf(1)
- Sn(2) LeftFoot*bf(1)

Select all beta names for which you want to perform a two-sample t-test: (only needed if "Input file type" is "beta", otherwise ignored)

- Sn(1) LeftHand*bf(1)
- Sn(1) RightHand*bf(1)
- Sn(1) LeftFoot*bf(1)
- Sn(1) RightFoot*bf(1)
- Sn(1) Tongue*bf(1)
- Sn(1) R1
- Sn(1) R2
- Sn(1) R3
- Sn(1) R4
- Sn(1) R5
- Sn(1) R6
- Sn(1) R7
- Sn(1) R8
- Sn(1) R9

Regular expression for input file selection (Group 1): (only needed if "Input file type" is "other")

Regular expression for input file selection (Group 2): (only needed if "Input file type" is "other")

☐ go back

OK Cancel

The meaning of these options is described in detail on page 19

select subjects by Participant_ID for both groups

it is possible to define different regular expressions for the two groups of subjects

Options Two-sample t-test

Subjects Group 1:

- 118528
- 118730
- 118932
- 120111
- 122317
- 122620
- 123117
- 123925
- 124422
- 125525
- 126325
- 127630
- 127933
- 128127

Subjects Group 2:

- 118932
- 120111
- 122317
- 122620
- 123117
- 123925
- 124422
- 125525
- 126325
- 127630
- 127933
- 128127
- 128632
- 129028

Independence: ☐ no ☒ yes

Variance: ☒ equal ☐ unequal

Grand mean scaling: ☒ no ☐ yes

ANCOVA: ☒ no ☐ yes

☐ go back

OK Cancel

Options “Second level” and “First + Second level”: Paired t-test

Input paired t-test

Input file type for first image of a pair: ☒ con ☐ beta ☐ other

Select all contrast names for the first image of a pair, for which you want to perform a paired t-test: (ignored if "Input file type" is "beta")

task
tongue
variance
Sn(1) LeftHand*bf(1)
Sn(1) RightHand*bf(1)
Sn(1) LeftFoot*bf(1)
Sn(1) RightFoot*bf(1)

Select all beta names for the first image of a pair, for which you want to perform a paired t-test: (only needed if "Input file type" is "beta", otherwise ignored)

Sn(1) LeftHand*bf(1)
Sn(1) RightHand*bf(1)
Sn(1) LeftFoot*bf(1)
Sn(1) RightFoot*bf(1)
Sn(1) Tongue*bf(1)
Sn(1) R1
Sn(1) R2

Regular expression for input file selection (first image of pair): (only needed if "Input file type" is "other")

Input file type for second image of a pair: ☒ con ☐ beta ☐ other

Select all contrast names for the second image of a pair, for which you want to perform a paired t-test: (ignored if "Input file type" is "beta")

Sn(1) LeftHand*bf(1)
Sn(1) RightHand*bf(1)
Sn(1) LeftFoot*bf(1)
Sn(1) RightFoot*bf(1)
Sn(1) Tongue*bf(1)
Sn(2) LeftHand*bf(1)
Sn(2) RightHand*bf(1)

Select all beta names for the first image of a pair, for which you want to perform a paired t-test: (only needed if "Input file type" is "beta", otherwise ignored)

Sn(1) LeftHand*bf(1)
Sn(1) RightHand*bf(1)
Sn(1) LeftFoot*bf(1)
Sn(1) RightFoot*bf(1)
Sn(1) Tongue*bf(1)
Sn(1) R1
Sn(1) R2

Regular expression for input file selection (second image of pair): (only needed if "Input file type" is "other")

☐ go back

OK Cancel

The meaning of these options is described in detail on page 19

the chosen contrasts are combined with the chosen subjects for the first image of a pair

the chosen contrasts are combined with the chosen subjects for the second image of a pair

the example shown here results in the following pairs:

Pair1:

- LeftHand-100307
- RightHand-100307

Pair2:

- LeftFoot-100307
- RightFoot-100307

IMPORTANT: since the order of the lists cannot be changed here, it might have to be adjusted directly in the json file (after finishing the user interface dialog) to obtain the desired pairs

Options Paired t-test

Select subjects for first image of a pair: 100307
100408
101107
101309
101915
103111
103414
103818
105014
105115
106016
108828
110411
111312

Select subjects for second image of a pair: 100307
100408
101107
101309
101915
103111
103414
103818
105014
105115
106016
108828
110411
111312

Grand mean scaling: ☒ no ☐ yes

ANCOVA: ☒ no ☐ yes

☐ go back

OK Cancel

Options “Second level” and “First + Second level”: Paired t-test (example)

Input paired t-test

Input file type for first image of a pair: ☒ con ☐ beta ☐ other

Select all contrast names for the first image of a pair, for which you want to perform a paired t-test: (ignored if "Input file type" is "beta")

| |
|-----------------------|
| task |
| tongue |
| variance |
| Sn(1) LeftHand*bf(1) |
| Sn(1) RightHand*bf(1) |
| Sn(1) LeftFoot*bf(1) |
| Sn(1) RightFoot*bf(1) |

Select all beta names for the first image of a pair, for which you want to perform a paired t-test: (only needed if "Input file type" is "beta", otherwise ignored)

| |
|-----------------------|
| Sn(1) LeftHand*bf(1) |
| Sn(1) RightHand*bf(1) |
| Sn(1) LeftFoot*bf(1) |
| Sn(1) RightFoot*bf(1) |
| Sn(1) Tongue*bf(1) |
| Sn(1) R1 |
| Sn(1) R2 |

Regular expression for input file selection (first image of pair): (only needed if "Input file type" is "other")

Input file type for second image of a pair: ☒ con ☐ beta ☐ other

Select all contrast names for the second image of a pair, for which you want to perform a paired t-test: (ignored if "Input file type" is "beta")

| |
|-----------------------|
| Sn(1) LeftHand*bf(1) |
| Sn(1) RightHand*bf(1) |
| Sn(1) LeftFoot*bf(1) |
| Sn(1) RightFoot*bf(1) |
| Sn(1) Tongue*bf(1) |
| Sn(2) LeftHand*bf(1) |
| Sn(2) RightHand*bf(1) |

Select all beta names for the first image of a pair, for which you want to perform a paired t-test: (only needed if "Input file type" is "beta", otherwise ignored)

| |
|-----------------------|
| Sn(1) LeftHand*bf(1) |
| Sn(1) RightHand*bf(1) |
| Sn(1) LeftFoot*bf(1) |
| Sn(1) RightFoot*bf(1) |
| Sn(1) Tongue*bf(1) |
| Sn(1) R1 |
| Sn(1) R2 |

Regular expression for input file selection (second image of pair): (only needed if "Input file type" is "other")

☐ go back

OK Cancel

NOTE: The intention of this example is to demonstrate the mechanism of creating pairs. It does not have any practical sense.

relevant for the first image of a pair

relevant for the second image of a pair

the example shown here results in the following pairs:

Pair1:

- LeftHand-100307
- RightHand-101309

Pair2:

- LeftHand-100408
- RightHand-101915

Pair3:

- LeftHand-101107
- RightHand-103111

Pair4:

- LeftFoot-100307
- RightFoot-101309

Pair5:

- LeftFoot-100408
- RightFoot-101915

Pair6:

- LeftFoot-101107
- RightFoot-103111

Options Paired t-test

Select subjects for first image of a pair:

| |
|--------|
| 100307 |
| 100408 |
| 101107 |
| 101309 |
| 101915 |
| 103111 |
| 103414 |
| 103818 |
| 105014 |
| 105115 |
| 106016 |
| 108828 |
| 110411 |
| 111312 |

Select subjects for second image of a pair:

| |
|--------|
| 100307 |
| 100408 |
| 101107 |
| 101309 |
| 101915 |
| 103111 |
| 103414 |
| 103818 |
| 105014 |
| 105115 |
| 106016 |
| 108828 |
| 110411 |
| 111312 |

Grand mean scaling: ☒ no ☐ yes

ANCOVA: ☒ no ☐ yes

☐ go back

OK Cancel

Options “Second level” and “First + Second level”: Multiple regression

Input file type: ☒ con ☐ beta ☐ other

Select all contrast names, which you want to include for the chosen subjects: (ignored if "Input file type" is "beta")

- left vs right
- hand vs foot
- limbs vs tongue
- task
- tongue
- variance
- Sn(1) LeftHand*bf(1)
- Sn(1) RightHand*bf(1)
- Sn(1) LeftFoot*bf(1)
- Sn(1) RightFoot*bf(1)
- Sn(1) Tongue*bf(1)
- Sn(2) LeftHand*bf(1)
- Sn(2) RightHand*bf(1)
- Sn(2) LeftFoot*bf(1)

Select all beta names, which you want to include for the chosen subjects: (only needed if "Input file type" is "beta", otherwise ignored)

- Sn(1) LeftHand*bf(1)
- Sn(1) RightHand*bf(1)
- Sn(1) LeftFoot*bf(1)
- Sn(1) RightFoot*bf(1)
- Sn(1) Tongue*bf(1)
- Sn(1) R1
- Sn(1) R2
- Sn(1) R3
- Sn(1) R4
- Sn(1) R5
- Sn(1) R6
- Sn(1) R7
- Sn(1) R8
- Sn(1) R9

Regular expression for input file selection: (only needed if "Input file type" is "other")

Number of covariates: 2

Intercept: ☒ no ☐ yes

☐ go back

OK Cancel

The meaning of these options is described in detail on page 19

Covariate name: age

Regular expression to find file containing covariate: ^participants\.tsv\$

Corresponding column in file: age_yrs

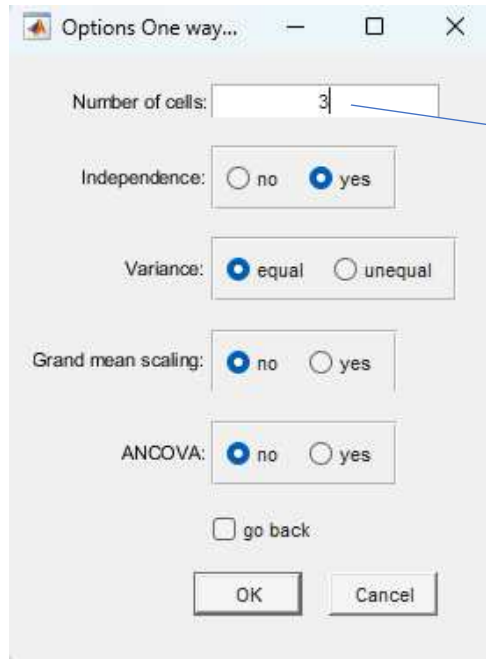
Centering: Overall mean

☐ go back

OK Cancel

if the column name is the same as 'Covariate name', this field can be left empty

Options “Second level” and “First + Second level”: One-way ANOVA (between subjects)



Options One way...

Number of cells:

Independence: ☐ no ☒ yes

Variance: ☒ equal ☐ unequal

Grand mean scaling: ☒ no ☐ yes

ANCOVA: ☒ no ☐ yes

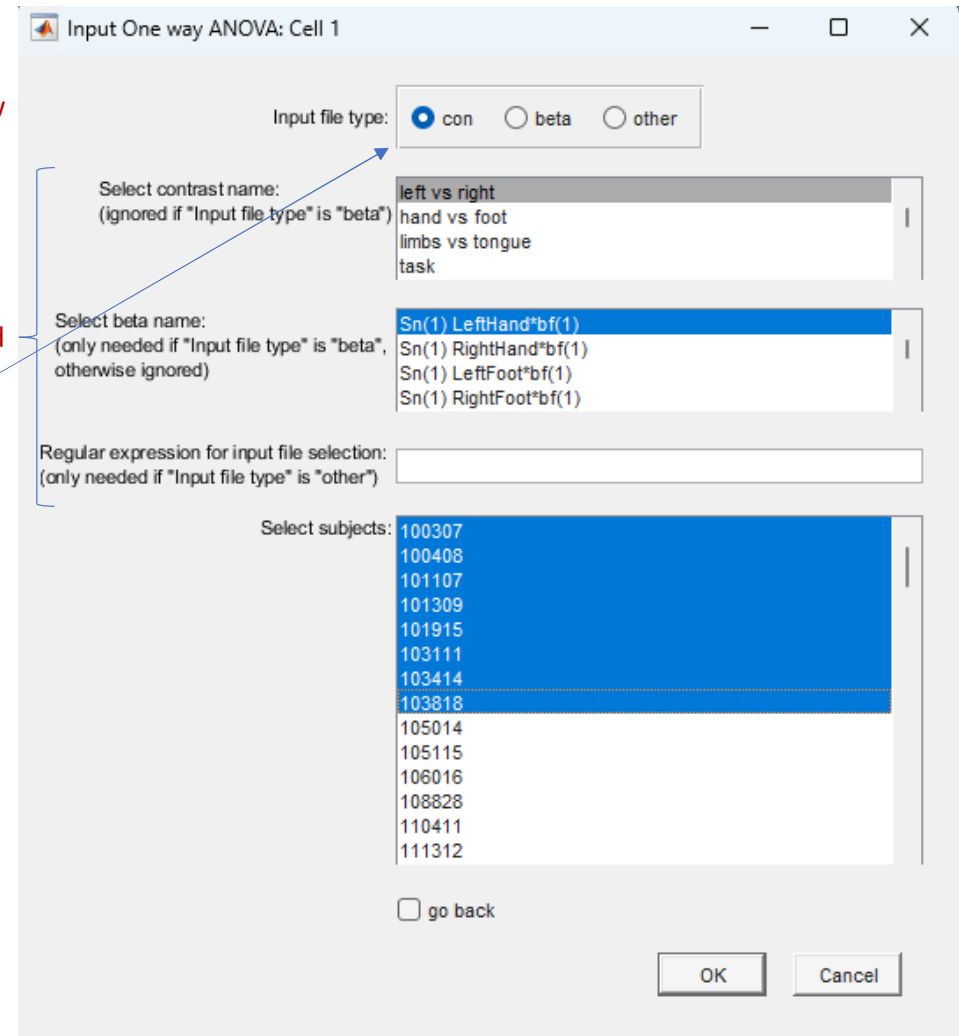
☐ go back

OK Cancel

scans for each cell are defined in a separate window

only a single contrast can be chosen for this method

The meaning of these options is described in detail on page 19



Input One way ANOVA: Cell 1

Input file type: ☒ con ☐ beta ☐ other

Select contrast name:
(ignored if "Input file type" is "beta")

- left vs right
- hand vs foot
- limbs vs tongue
- task

Select beta name:
(only needed if "Input file type" is "beta", otherwise ignored)

- Sn(1) LeftHand*bf(1)
- Sn(1) RightHand*bf(1)
- Sn(1) LeftFoot*bf(1)
- Sn(1) RightFoot*bf(1)

Regular expression for input file selection:
(only needed if "Input file type" is "other")

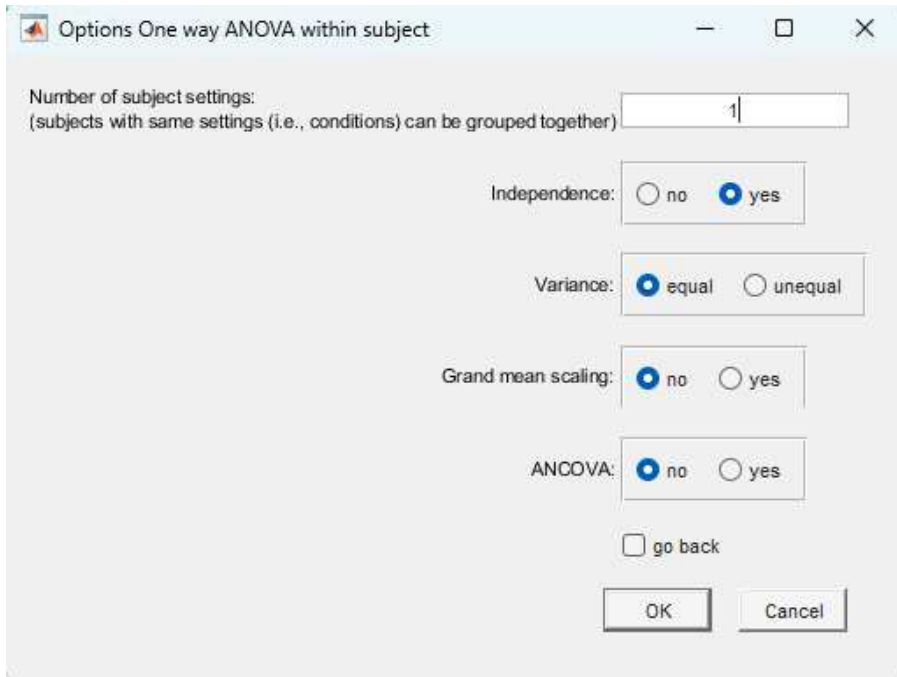
Select subjects:

- 100307
- 100408
- 101107
- 101309
- 101915
- 103111
- 103414
- 103818
- 105014
- 105115
- 106016
- 108828
- 110411
- 111312

☐ go back

OK Cancel

Options “Second level” and “First + Second level”: One-way ANOVA – within subject



Options One way ANOVA within subject

Number of subject settings:
(subjects with same settings (i.e., conditions) can be grouped together)

Independence: ☐ no ☒ yes

Variance: ☒ equal ☐ unequal

Grand mean scaling: ☒ no ☐ yes

ANCOVA: ☒ no ☐ yes

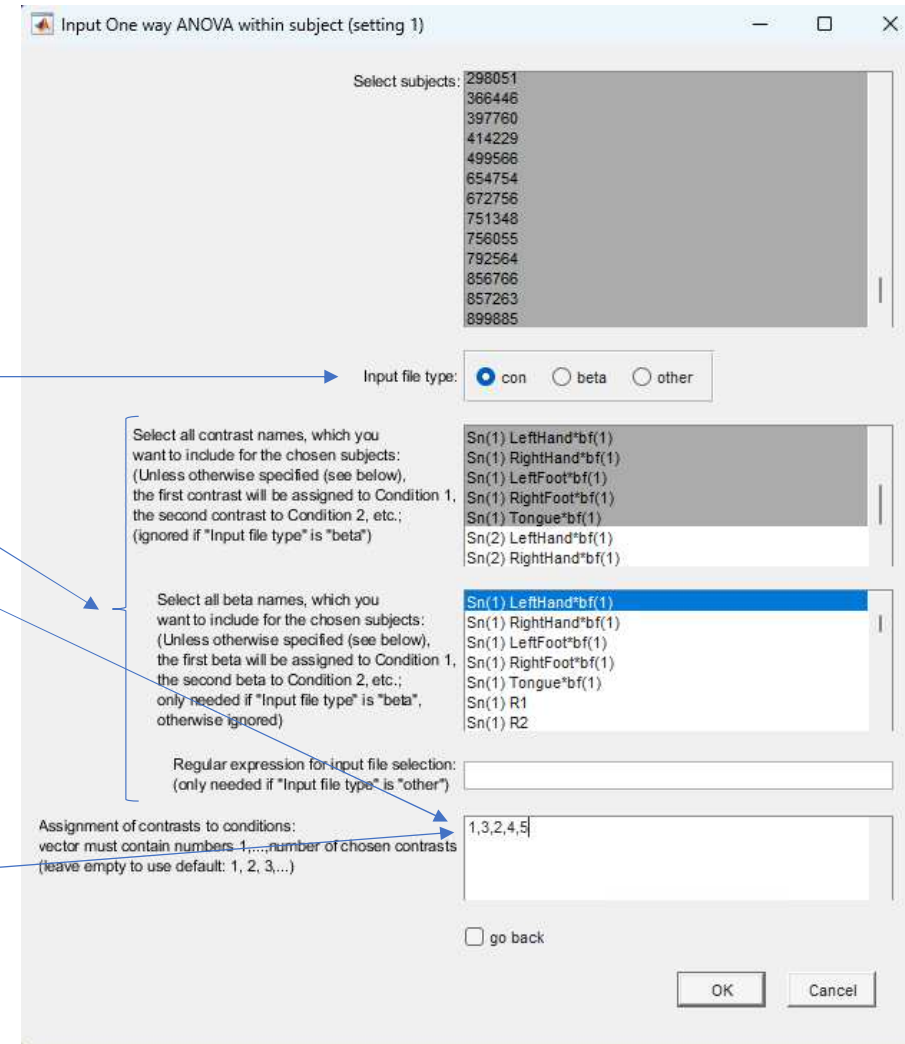
☐ go back

OK Cancel

The meaning of these options is described in detail on page 19

if the chosen contrasts and their assignment to conditions is the same for several subjects, they can be grouped within the same setting

in this example, 5 contrasts are selected -> they have to be assigned to conditions 1 to 5



Input One way ANOVA within subject (setting 1)

Select subjects:

Input file type: ☒ con ☐ beta ☐ other

Select all contrast names, which you want to include for the chosen subjects:
(Unless otherwise specified (see below), the first contrast will be assigned to Condition 1, the second contrast to Condition 2, etc.; (ignored if "Input file type" is "beta")

Select all beta names, which you want to include for the chosen subjects:
(Unless otherwise specified (see below), the first beta will be assigned to Condition 1, the second beta to Condition 2, etc.; only needed if "Input file type" is "beta", otherwise ignored)

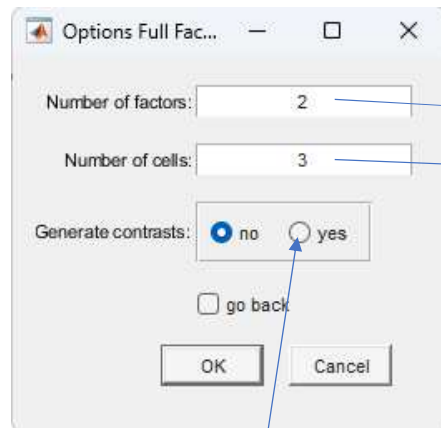
Regular expression for input file selection:
(only needed if "Input file type" is "other")

Assignment of contrasts to conditions:
vector must contain numbers 1,..., number of chosen contrasts
(leave empty to use default: 1, 2, 3,...)

☐ go back

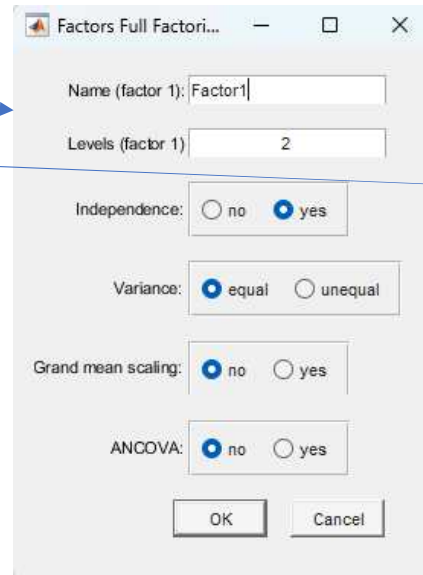
OK Cancel

Options “Second level” and “First + Second level”: Full factorial

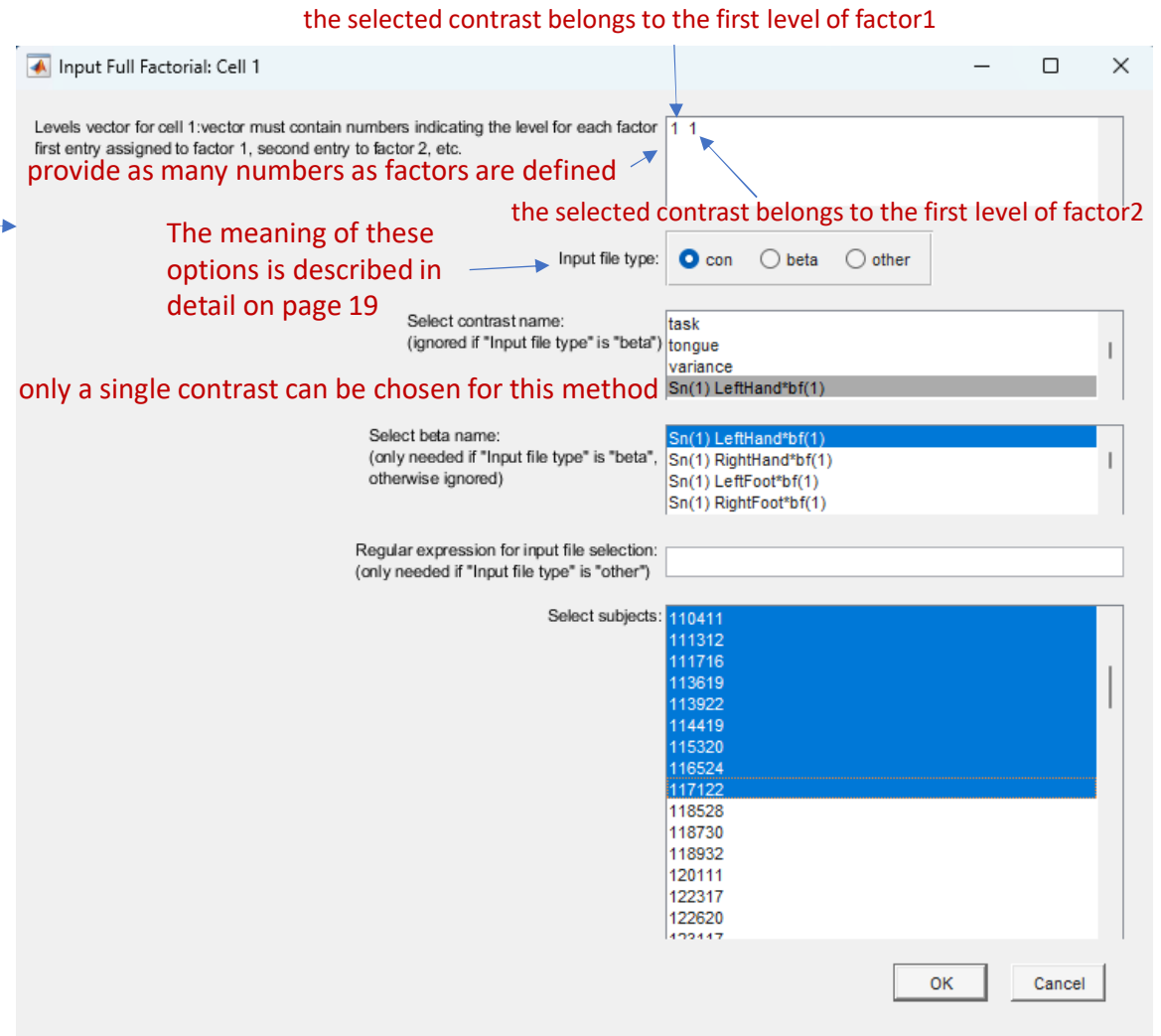


Options Full Fac... dialog box. Number of factors: 2. Number of cells: 3. Generate contrasts: ☒ no ☐ yes. ☐ go back. OK Cancel.

contrasts necessary to test for all main effects and interactions will automatically be generated (without an additional “Contrast Manager”)

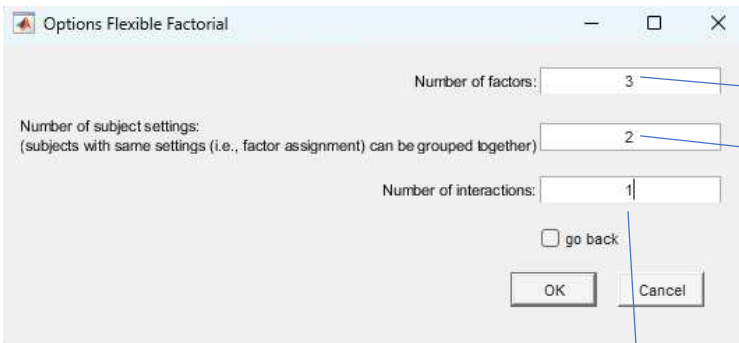


Factors Full Factori... dialog box. Name (factor 1): Factor1. Levels (factor 1): 2. Independence: ☐ no ☒ yes. Variance: ☒ equal ☐ unequal. Grand mean scaling: ☒ no ☐ yes. ANCOVA: ☒ no ☐ yes. OK Cancel.



Input Full Factorial: Cell 1 dialog box. Levels vector for cell 1: vector must contain numbers indicating the level for each factor first entry assigned to factor 1, second entry to factor 2, etc. provide as many numbers as factors are defined. the selected contrast belongs to the first level of factor1. the selected contrast belongs to the first level of factor2. Input file type: ☒ con ☐ beta ☐ other. Select contrast name: (ignored if "Input file type" is "beta") task, tongue, variance, Sn(1) LeftHand*bf(1). Select beta name: (only needed if "Input file type" is "beta", otherwise ignored) Sn(1) LeftHand*bf(1), Sn(1) RightHand*bf(1), Sn(1) LeftFoot*bf(1), Sn(1) RightFoot*bf(1). Regular expression for input file selection: (only needed if "Input file type" is "other"). Select subjects: 110411, 111312, 111716, 113619, 113922, 114419, 115320, 116524, 117122, 118528, 118730, 118932, 120111, 122317, 122620, 122117. OK Cancel.

Options “Second level” and “First + Second level”: Flexible factorial



Options Flexible Factorial

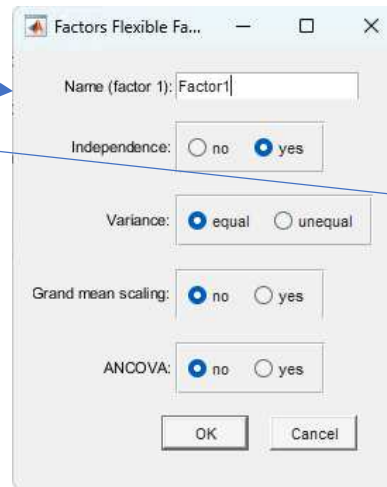
Number of factors: 3

Number of subject settings:
(subjects with same settings (i.e., factor assignment) can be grouped together): 2

Number of interactions: 1

☐ go back

OK Cancel



Factors Flexible Factorial

Name (factor 1): Factor1

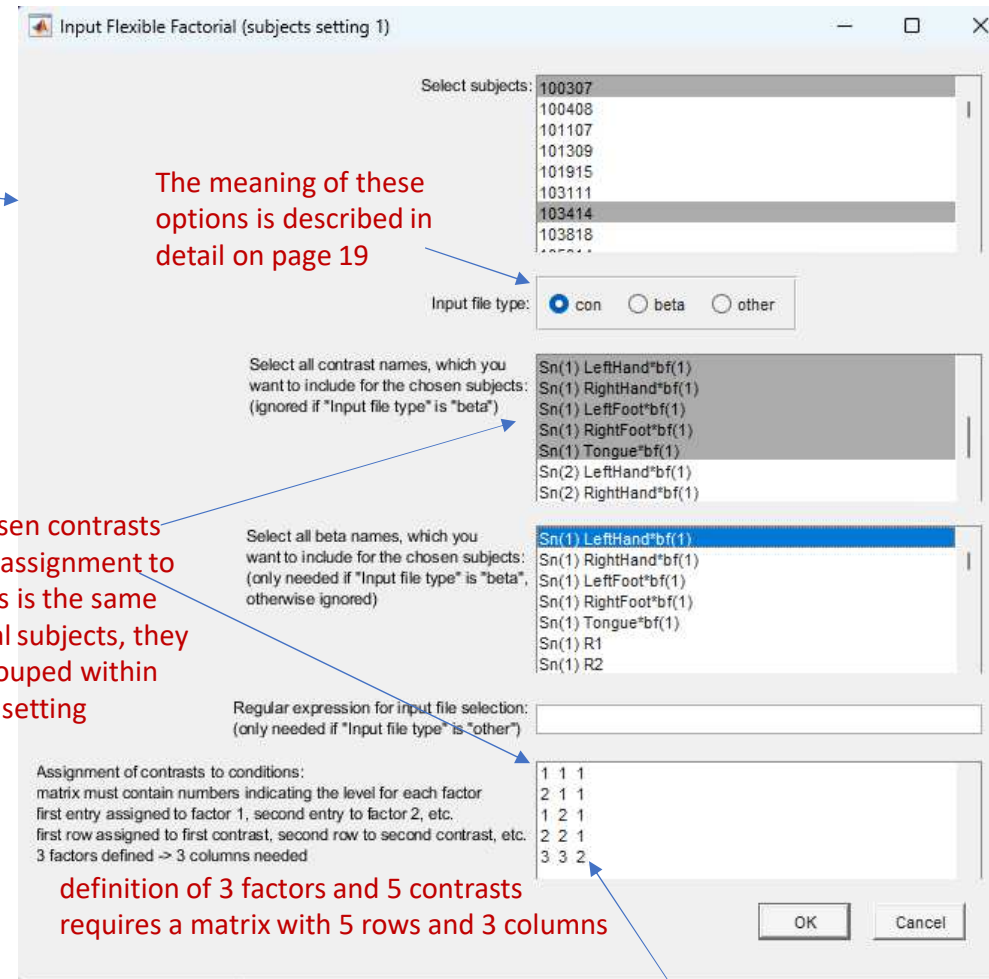
Independence: ☐ no ☒ yes

Variance: ☒ equal ☐ unequal

Grand mean scaling: ☒ no ☐ yes

ANCOVA: ☒ no ☐ yes

OK Cancel



Input Flexible Factorial (subjects setting 1)

Select subjects: 100307, 100408, 101107, 101309, 101915, 103111, 103414, 103818

Input file type: ☒ con ☐ beta ☐ other

Select all contrast names, which you want to include for the chosen subjects:
(ignored if "Input file type" is "beta")

Sn(1) LeftHand*bf(1)
Sn(1) RightHand*bf(1)
Sn(1) LeftFoot*bf(1)
Sn(1) RightFoot*bf(1)
Sn(1) Tongue*bf(1)
Sn(2) LeftHand*bf(1)
Sn(2) RightHand*bf(1)

Select all beta names, which you want to include for the chosen subjects:
(only needed if "Input file type" is "beta", otherwise ignored)

Sn(1) LeftHand*bf(1)
Sn(1) RightHand*bf(1)
Sn(1) LeftFoot*bf(1)
Sn(1) RightFoot*bf(1)
Sn(1) Tongue*bf(1)
Sn(1) R1
Sn(1) R2

Regular expression for input file selection:
(only needed if "Input file type" is "other")

Assignment of contrasts to conditions:
matrix must contain numbers indicating the level for each factor
first entry assigned to factor 1, second entry to factor 2, etc.
first row assigned to first contrast, second row to second contrast, etc.
3 factors defined -> 3 columns needed

| | | |
|---|---|---|
| 1 | 1 | 1 |
| 2 | 1 | 1 |
| 1 | 2 | 1 |
| 2 | 2 | 1 |
| 3 | 3 | 2 |

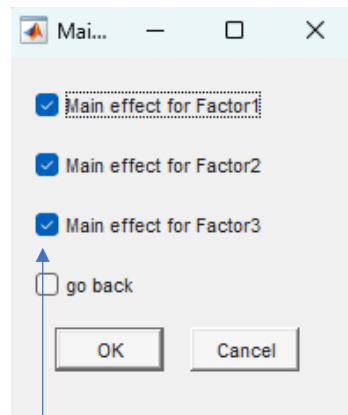
OK Cancel

The meaning of these options is described in detail on page 19

if the chosen contrasts and their assignment to conditions is the same for several subjects, they can be grouped within the same setting

definition of 3 factors and 5 contrasts requires a matrix with 5 rows and 3 columns

ATTENTION: If this window is re-opened after switching between windows ('go back' etc.), the matrix is automatically transformed to a single column. This has to be corrected by the user manually!



Main effect selection

☒ Main effect for Factor1

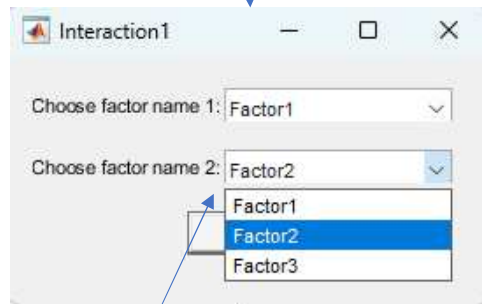
☒ Main effect for Factor2

☒ Main effect for Factor3

☐ go back

OK Cancel

select the factors for which their main effect shall be included in the model



Interaction1

Choose factor name 1: Factor1

Choose factor name 2: Factor2

Factor1
Factor2
Factor3

select the factors for which their interaction shall be included in the model

Options “Second level” and “First + Second level”: Covariates



Covariates

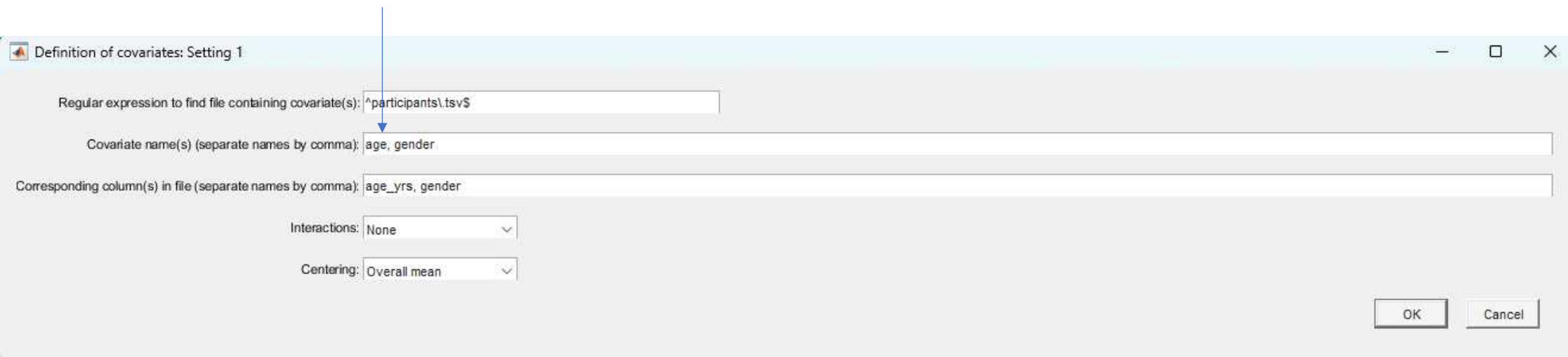
How many different settings for covariates do you want to specify?
Settings include source files (e.g. participants.tsv) and the SPM options "Interactions" and "Centering".
If all covariates are specified in the same file and settings for "Interactions" and "Centering" are the same, you only need to specify one setting.

1

☐ go back to second level main selection

OK Cancel

if several covariates are taken from the same file and the options ('Interactions', 'Centering') are the same, they can be summarized in one covariates setting:
covariate names and their related column names have to be separated by commas;



Definition of covariates: Setting 1

Regular expression to find file containing covariate(s): ^participants\.tsv\$

Covariate name(s) (separate names by comma): age, gender

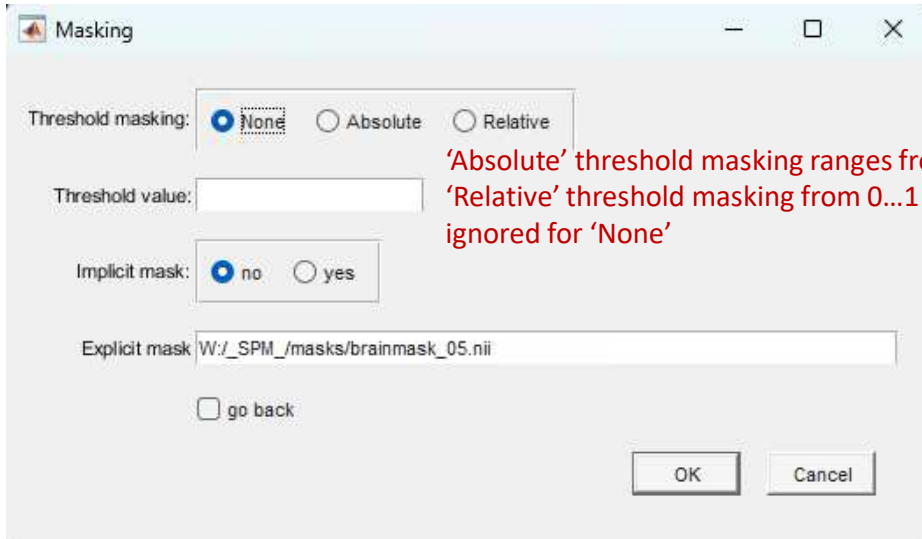
Corresponding column(s) in file (separate names by comma): age_yrs, gender

Interactions: None

Centering: Overall mean

OK Cancel

Options “Second level” and “First + Second level”: Masking

A screenshot of a software dialog box titled "Masking". It contains several controls: a "Threshold masking:" section with three radio buttons labeled "None", "Absolute", and "Relative", where "None" is selected; a "Threshold value:" text input field; an "Implicit mask:" section with two radio buttons labeled "no" and "yes", where "no" is selected; an "Explicit mask:" text input field containing the path "W:/_SPM_/masks/brainmask_05.nii"; a "go back" checkbox; and "OK" and "Cancel" buttons at the bottom right.

Masking

Threshold masking: ☒ None ☐ Absolute ☐ Relative

Threshold value:

Implicit mask: ☒ no ☐ yes

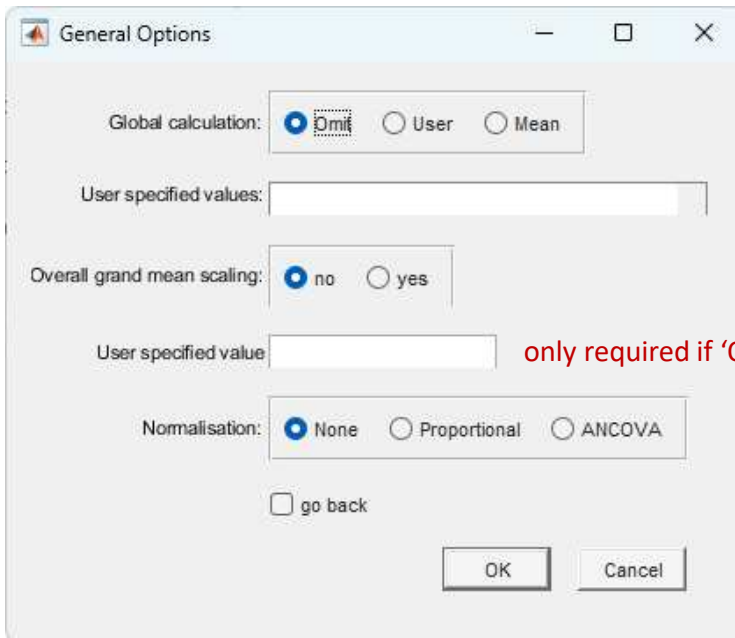
Explicit mask:

☐ go back

OK Cancel

‘Absolute’ threshold masking ranges from 0...x (default value of 100 is used if left empty),
‘Relative’ threshold masking from 0...1 (proportion of global value; if left empty a default value of 0.8 is used);
ignored for ‘None’

Options “Second level” and “First + Second level”: General options



General Options

Global calculation: ☒ Omit ☐ User ☐ Mean

User specified values:

Overall grand mean scaling: ☒ no ☐ yes

User specified value:

Normalisation: ☒ None ☐ Proportional ☐ ANCOVA

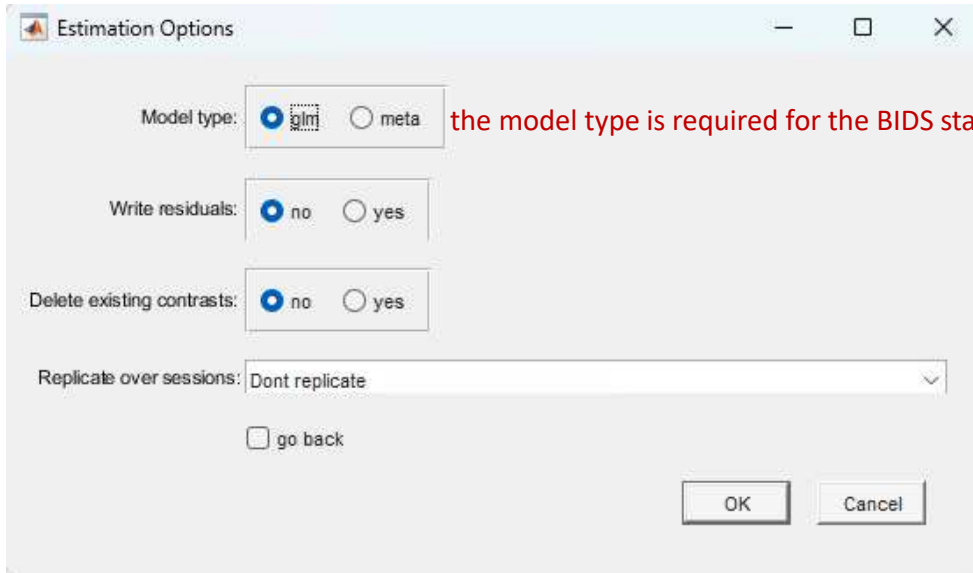
☐ go back

OK Cancel

only required for option 'User': the number of values must match the total number of scans used in the model

only required if 'Overall grand mean scaling' is set to 'yes' (if still left empty a default value of 50 is used)

Options “Second level” and “First + Second level”: Estimation options



Model type: ☒ glm ☐ meta

Write residuals: ☒ no ☐ yes

Delete existing contrasts: ☒ no ☐ yes

Replicate over sessions: Dont replicate

☐ go back

OK Cancel

the model type is required for the BIDS stats model (it has no effect on the SPM batch)

After clicking ‘OK’, the inputs are saved to the model json file, i.e., the second level node is created. The script ends for the option “First + Second level” and in case that ‘Check data to define contrasts’ was not selected in the Second level input window (page 18). Otherwise, input data are checked and the design matrix created. The model json file is then updated with the design matrix columns (Nodes.Model.X). The user interface continues with contrast definition already described on pages 14-17. After contrast definition, to create and execute the SPM batches defined in the json, type `SPM_batch_creator(2);`

For the option “First + Second level”, first execute `SPM_batch_creator(1)` to create and execute the first level batch, then execute `SPM_batch_creator(2)` to get the design matrix columns needed to define the contrasts, which has to be done directly in the json file. Finally, once more execute `SPM_batch_creator(2)` to create and execute the second level batches.