Table of Contents

[Information about Scripts 1](#_Toc30760483)

[Files required 1](#_Toc30760484)

[Information about Scripts 1](#_Toc30760485)

[Template 1](#_Toc30760486)

[~~~ template\_one\_subj2.fsf ~~~ 1](#_Toc30760487)

[~~~ template\_one\_subj\_stats2.fsf ~~~ 2](#_Toc30760488)

[~~~ multi\_subj.sh ~~~ 2](#_Toc30760489)

[~~~ multi\_subj\_stats.sh ~~~ 3](#_Toc30760490)

[~~~ run\_multi\_subj\_stats.sh ~~~ 4](#_Toc30760491)

[~~~ run\_multi\_subj.sh ~~~ 5](#_Toc30760492)

[~~~ run\_all\_multi\_subj.sh ~~~ 6](#_Toc30760493)

[Error codes 7](#_Toc30760494)

[Terminal 8](#_Toc30760495)

[Feat design files: 8](#_Toc30760496)

# Information about Scripts

**Stored:** Users/colette/sourcedata/code/StatsSkip/Scripts/multi\_subj

Note – if you are testing out the scripts, test them in the order that they are here:

# Files required

template\_one\_subj2.fsf

template\_one\_subj\_stats2.fsf

Multi\_subj.sh

Multi\_subj\_stats.sh

Run\_multi\_subj.sh

Run\_multi\_subj\_select.sh

# Information about Scripts

## Template

Script Name:

Usage:

Scripts/ inputs required:

Output:

Other Info:

## ~~~ template\_one\_subj2.fsf ~~~

**Script Name:** template\_one\_subj2.fsf

**Usage:** Feat design file template, FEAT design for running one subject through full analysis

**Scripts/ inputs required:** Data sets in the bids format e.g. sub-01\_task-hyper\_acq-default\_asl.nii.gz

**Output:** none

**Other Info:** can be run using multi\_subj

## ~~~ template\_one\_subj\_stats2.fsf ~~~

**Script Name:** template\_one\_subj\_stats2.fsf

**Usage:** FEAT template, FEAT design for running a subject through the FSL Feat and creating the 'stats' output folder

**Scripts/ inputs required:** full feat analysis with the input file name followed by extension .feat e.g sub-01\_task-hyper\_acq-default\_asl.feat

**Output:** none

**Other Info:** can be run using multi\_subj\_stats.sh

## ~~~ multi\_subj.sh ~~~

**Script Name:** multi\_subj.sh

**Usage:** Takes the template\_one\_subj2.fsf design template and modifies it to run a full feat analysis for the subject number and MRI parameter inputted to output the feat stats for one subject

Usage: $0 <sourcedata folder> <SubjectNumber> <MRIParameter> e.g [default] (default,paramA,paramB) [options] Output: .Feat Full analysis folder. e.g. ./multi\_subj.sh /Users/colette/sourcedata/ sub-01 paramA creates sub-01\_FullparamA.feat

**Scripts/ inputs required:** template\_one\_subj2.fsf, datasets in the bids format e.g. sub-01\_task-hyper\_acq-default\_asl.nii.gz

**Output:** full feat analysis with the input file name followed by extension .feat e.g sub-01\_FullparamA.feat

Output directory: {sourcedata folder} /design{MRI Parameter}.fsf

**Other Info:**

Prints arguments (sourcedata folder, subject number, MRIparameter)

Creates folder ‘/{sourcedata folder}/derivatives/’ for output data

Creates folder ‘/{sourcedata folder}/derivatives/{subject number}’ for output data organised by subject number

Creates a design{MRI parameter}.fsf design file to be run with the specific subject number and MRI parameter - not required once the .feat and stats folder has been created

## ~~~ multi\_subj\_stats.sh ~~~

**Script Name:** multi\_subj\_stats.sh

**Usage:** runs the subject through the template\_one\_subj\_stats2.fsf to create a stats folder for a specific subject number, MRI parameter and skip number

$0 <sourcedata folder> <SubjectNumber> <MRIParameter> e.g [default] [options] (default,paramA,paramB) Output: .Feat Full analysis folder stats folder is copied to derivatives/StatsOutput/SubjNo/SubjNo\_MRIParam. e.g. ./multi\_subj\_stats\_test.sh /Users/colette/sourcedata/ sub-01 paramA 060

**Scripts/ inputs required:**

template\_one\_subj\_stats2.fsf

Full analysis feat folder e.g sub-01\_FullparamA.feat (run multi\_subj.sh - run to create the .feat folder)

**Output:** Stats folder for a specific subject number, MRI parameter and skip number:

{subject number}\_{MRI Parameter}\_{Skip Number}

CVRmaps and folder

Zstats2 folder

**Other Info:**

Prints arguments (sourcedata folder, subject number, MRIparameter)

Creates & runs feat stats design file using a copy of the template ==> designStats{MRI Parameter}.fsf - is not required once the script has completed

Moves the stats folder and renames it from {Souredata folder} /{subject number}\_Full{MRI Parameter}.feat/stats to:

{Souredata folder}/derivatives/StatsOutput/{subject number}/ {subject number}\_{MRIParam}

Renames all the files in the {subject number}\_{MRI Parameter}\_{Skip Number} folder to have the extension {subject number}\_{MRI Parameter}\_{Skip Number}.nii.gz

Creates a CVRmap folder CVRmaps\_{subject number}\_{MRI Parameter} and moves the CVRmaps into this folder.

Uses fslmaths cope2\_{subject number}\_{MRI Parameter}\_{Skip Number} -div cope6\_ {subject number}\_{MRI Parameter}\_{Skip Number} to Create CVRmaps CVRmap\_{subject number}\_{MRI Parameter}\_{Skip Number}

Creates a folder Zstat2\_{subject number}\_{MRI Parameter} and moves the zstat2 files into it.

## ~~~ run\_multi\_subj\_stats.sh ~~~

**Script Name:** run\_multi\_subj\_stats.sh

**Usage:** Runs loop through multi\_subj\_stats.sh for skip numbers 000 to 120 in steps of 4seconds and outputs these in the StatsOuput\_{subject number} folder

Usage: $0 <sourcedata folder> <subjectnumber> <MRIParam> Output: Feat Stats folders for one subject, skip numbers 000 to 120, 4sec intervals e.g. ./run\_multi\_subj\_stats.sh /Users/colette/sourcedata sub-02 paramA

**Scripts/ inputs required:**

template\_one\_subj\_stats2.fsf

Full analysis feat folder e.g sub-01\_FullparamA.feat (run multi\_subj.sh - run to create the .feat folder)

multi\_subj\_stats.sh

**Output:** {sourcedata folder}/derivatives/StatsOutput/{subject number}/{subject number}\_{MRI Parameter}/{subject number}\_{MRI Parameter}\_{Skip Number} for skip number 000 to 120 in intervals of 4 seconds.

Creates a file with all of the zstat2 files combined called zstat2\_concat\_ {subject number}\_{MRI Parameter}

**Other Info:**

Prints input arguments subject number, MRI Parameter

All the above for multi\_subj\_stats.sh but creates 30 stats folders, CVRmaps, zstats2 files (\_000 to \_120)

Uses fslmerge to merge all the zstat2 files for that subject into one files called {sourcedata folder}/derivatives/StatsOutput/{subject number}/{subject number}\_{MRI Parameter}/Zstat2\_ {subject number}\_{MRI Parameter} /zstat2\_concat\_ {subject number}\_{MRI Parameter}

## ~~~ run\_multi\_subj.sh ~~~

**Script Name:** run\_multi\_subj.sh

**Usage:** For the range of subject 1 to 6 - full feat analysis for each subject, creates a stats folder for each subject for each skip number and their associated CVRmaps & concat zstat2 file.

$0 <sourcedata folder> <MRIParam> e.g. ./run\_multi\_subj.sh /Users/colette/sourcedata/ paramA

**Scripts/ inputs required:**

datasets in the bids format e.g. sourcedata/sub-01/func/sub-01\_task-hyper\_acq-default\_asl.nii.gz

template\_one\_subj2.fsf

template\_one\_subj\_stats2.fsf

Multi\_subj.sh

Multi\_subj\_stats.sh

Run\_multi\_subj.sh

**Output:**

4.11GB data for subjects 1-6, all three MRI parameters

Full feat analysis with the input file name followed by extension .feat e.g sub-01\_FullparamA.feat

Output directory: {sourcedata folder} /design{MRI Parameter}.fsf

Stats folder for a specific subject number, MRI parameter and skip number from subjects 01 to 06:

{subject number}\_{MRI Parameter}\_{Skip Number}

CVRmaps and folder

Zstats2 folder

**Other Info:**

Runs run\_multi\_subj\_stats.sh

Runs multi\_subj.sh

So this creates the full feat analysis and then runs the stats feat through the subjects 01 to 06 for the MRI parameter selected.

## ~~~ run\_all\_multi\_subj.sh ~~~

**Script Name:** run\_all\_multi\_subj.sh

**Usage:** Runs through each subject 1-6 for MRI parameters default, paramA, paramB and creates everything from run\_multi\_subj.sh

$0 <sourcedata folder> e.g. ./run\_all\_multi\_subj.sh /Users/colette/sourcedata/

**Scripts/ inputs required:**

datasets in the bids format e.g. sourcedata/sub-01/func/sub-01\_task-hyper\_acq-default\_asl.nii.gz

template\_one\_subj2.fsf

template\_one\_subj\_stats2.fsf

Multi\_subj.sh

Multi\_subj\_stats.sh

Run\_multi\_subj.sh

**Output:**

Runs through all of the above for each of the three MRI parameters in one go.

4.11GB data for subjects 1-6, all three MRI parameters

Full feat analysis with the input file name followed by extension .feat e.g sub-01\_FullparamA.feat

Output directory: {sourcedata folder} /design{MRI Parameter}.fsf

Stats folder for a specific subject number, MRI parameter and skip number from subjects 01 to 06:

{subject number}\_{MRI Parameter}\_{Skip Number}

CVRmaps and folder

Zstats2 folder

**Other Info:**

Prints as it runs run\_multi\_subj.sh for each MRI parameter.

# Error codes

**Error:** -bash <scriptname.sh> not found

**Reason:** terminal is not in the folder with that script in it

**Solution:** use ‘pwd’ to check which directory you are in and ‘ls’ to see if the script is in that folder, then ‘cd’ to the correct folder if needed

**Alternatively:** run the command with the fullpath to that script so that it can find it

**Error:** -bash <file.nii.gz> not found

**Reason:** the script does not have the full path to the file if copying

There maybe a typo in the script input arguments so that the file printed on screen is not what you are expecting

**Solution:** check paths to these and associated files, scripts and also for typos in the inputs.

## Terminal

Script not found – expecting to run the script from the directory they are in.

**Error: terminal:** -bash <scriptname>.sh /bin/bash: bad interpreter: Operation not permitted

**Reason:** weird bbedit mac security thing.

**Solution:**

$ ls -l@ filepath/script.sh If it says it's got **com.apple.quarantine**, that's the problem. Run one of these on it, from least dangerous to most:

$ xattr -d com.apple.quarantine filepath/script.sh # delete that attr  
$ xattr -c filepath/script.sh # delete ALL the attrs on file  
$ xattr -c \* # on every file in this dir  
$ xattr -cr . # and all subdirectories

## Feat design files:

**Error:** sed -i -e "s|OUTPUTDIR|${srcout}|" ${srcout}/designStats.fsf #in the designDefault.fsf file find and replace 'OUTPUTDIR' with the outputdata file above <- does not work

**Reason:** Note this does not work – feat over-rides any attempt to output the stats folder to anywhere other than the original Full{MRI Parameter}.feat folder

**Solution:** multi\_subj\_stats.sh moves and renames this folder to be in the subject number and MRI Parameter labeled.