“Session” is a cell of structures.

Each line of “Session” is a subject.

Several columns are for different resolutions detected.

(If there are several lines, there are several subjects, but this shouldn’t be the case in our situation as the pipeline will be run for each subject separately.)

Within each cell, you can see something like this :

Phase: {[1x138 char]}

Magnitude: {[1x145 char]}

Struct: {[1x141 char]}

EPI: {{176x1 cell}}

EPIresolution: {'1pt5mm'}

PMdefaultfile: {[1x116 char]}

Session{1}.Phase is a cell of string indicating the path to the phase image of the B0 maps for EPI image distortion correction. Session{1}.Magnitude is similar and indicates the path to the magnitude image of the B0 maps, also used for EPI image distortion correction.

If Session{1}.Phase is empty, Session{1}.Magnitude is empty, and no EPI image distortion is performed.

Session{1}.Struct is a cell of string indicating the path to the anatomical image.

Session{1}.EPI is either a cell of string indicating the path to the unique fMRI run, either, if there are several runs (and the resolution of fMRI is identical among those), a cell of cell of strings. In the latter case the number of columns in the cell indicates the number of runs.

Session{1}.EPIresolution is a cell of string indicating the resolution of the fMRI. It is simply detected as the part of the folder name containing the token “mm”. It is not very useful to choose the correct file for EPI image distortion but rather to know “how many *different* resolutions there are” (there could potentially be two runs at 2 mm and 1 run at 3 mm).

Session{1}. PMdefaultfile indicates the file that should be used for EPI image distortion correction. The files are found in “…\fMRI\_automatedPipeline\FieldMap\_defaults\” and this folder should be updated each time there is a new fMRI sequence added. Antoine knows how to construct such a file but there is also a coarse description within that folder.

If no B0 maps are found, the string of the cell of this field is equal to : 'No B0 maps found, no EPI image distortion correction'.

“Session” is actually the output of “reshapeSession.m”, which organizes “Sessions” (output of “prepare\_fMRI\_session\_coregFun2Str.m”) such that datasets with multiple resolutions are processed correctly by SPM. Therefore :

Within “fMRI\_automated\_preproc.m” (and “prepare\_fMRI\_session\_coregFun2Str.m”) this variable “Sessions” is a structure, not a cell of structures. It will become a cell of structures with “Session”, which contains information of all subjects. This “Session” is what is saved in the “Log\_... .mat” file. You can see examples of this on the LAB01655 here :

C:\TEMP\test\_fMRI\_pipeline

(I just here saved the jobs that would have been performed by SPM, but I didn’t run them.)

The other outputs of “prepare\_fMRI\_session\_coregFun2Str.m” are :

uniqueRes

&

uniqueResIdx

🡺 These two both comes from :

[uniqueRes, m1, uniqueResIdx] = unique(Sessions.EPIresolution);

block 🡺 if preliminary jobs are needed (such as computing MPMs using VBQ), this will not be empty and will be added prior to other fMRI preprocessing jobs. See line 364 of fMRI\_automated\_preproc.m

CheckValid 🡺 in case no anatomical data is found this will not be empty and will prevent to run invalid SPM jobs (the pipeline will then give an error message and save a .mat file containing this error).