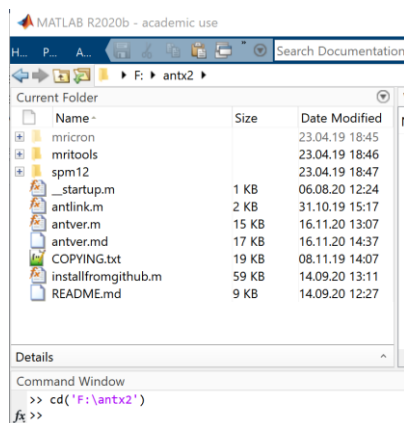


BrukerImport

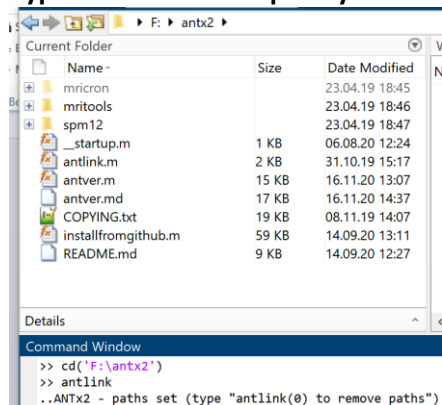
This tutorial shows how to import Bruker data:

Set Matlab's current to antx2-TBX

Example: `cd('F:\antx2')`

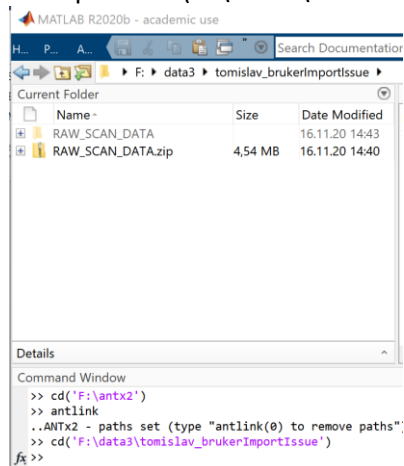


Type 'antlink' to temporary set the antx2'-paths



Go to project-folder

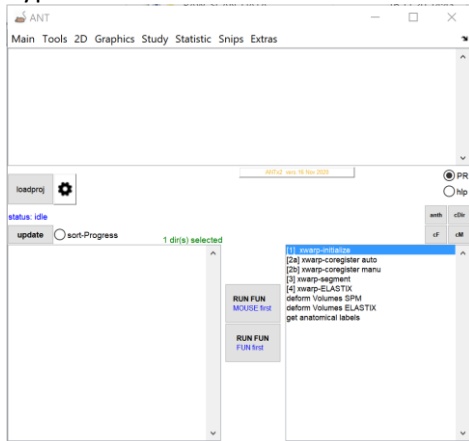
Example `>> cd('F:\data3\tomislav_brukerImportIssue')`



NOTE: I just created a folder 'tomislav_bruckerImportIssue'. This folder contain a folder with the unzipped raw-brucker data ('RAW_SCAN_DATA')

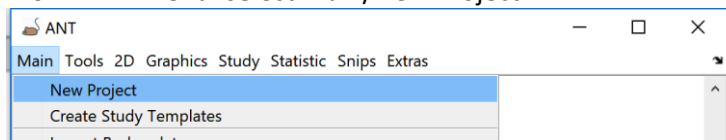
Start the GUI:

Type 'ant'

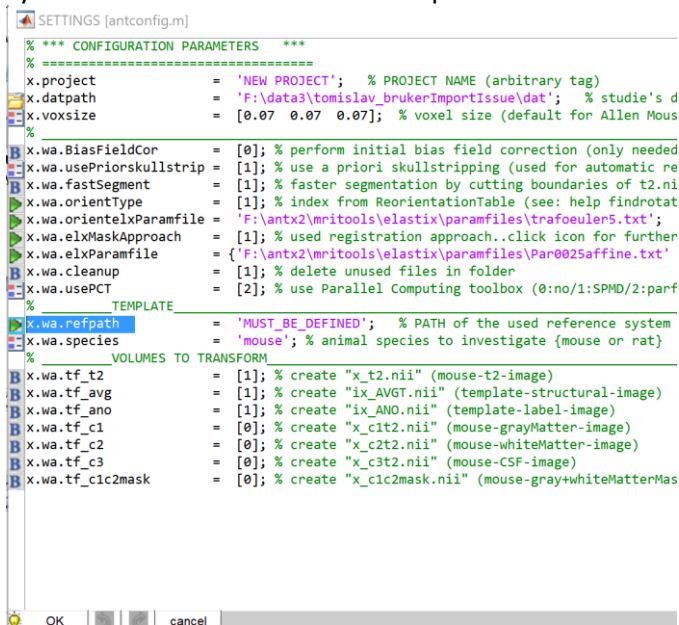


CREATE NEW PROJECT:

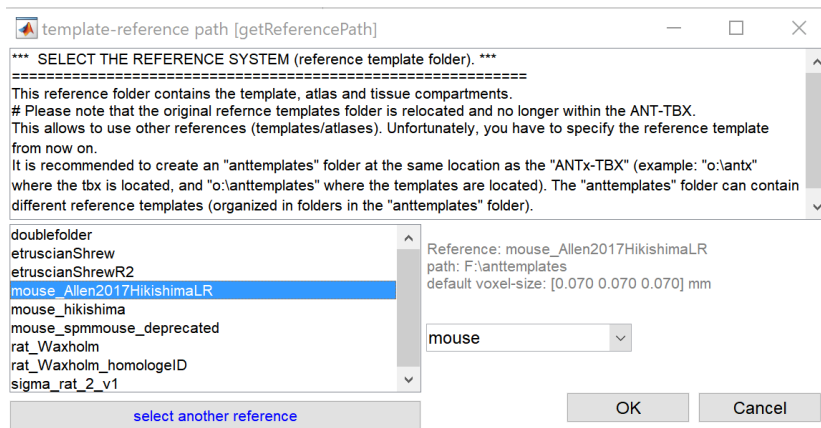
From ANT-menu: select Main/New Project



In the parameter window define the reference system (templates). This is important. The reference system defines the animal-related space and Atlas

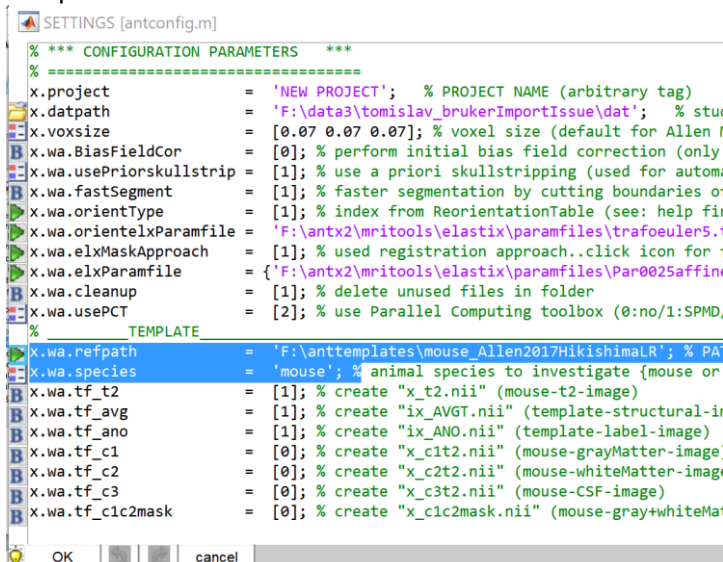


For this, select the green icon left to the 'refpath'-parameter.



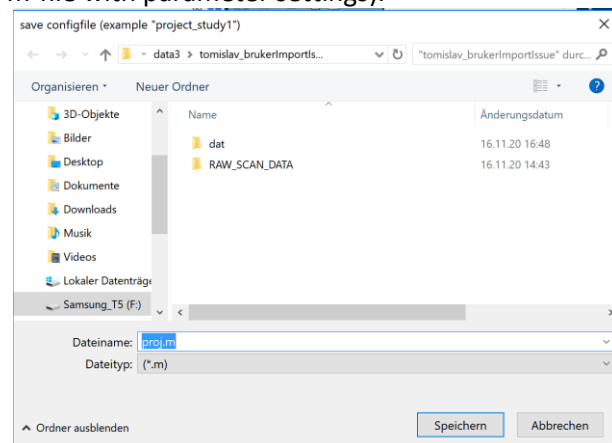
Select the reference system from left listbox. Here, I selected the Allen Mouse atlas with Hikishima TPMs (highlighted). Hit **[OK]**. Note that the left listbox contains only templates that have been already downloaded (To download the templates use either ANT-Menu: EXTRAS/ get templates from googledrive or EXTRAS/ download templates).

The parameter window should now look as follows:

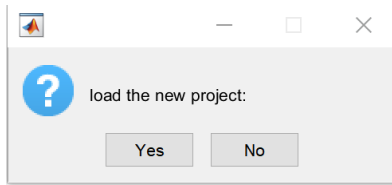


I.E: the reference system and the animal species are defined. Hit **[OK]**.

When hitting [OK], the user is prompted to save the project-file name (the project file is just a Matlab m-file with parameter settings).



Please save this file in the study folder. (Example: F:\data3\tomislav_bruckerImportIssue). Hit **[SAVE]** (german: 'Speichern'). If so, another window pops up and ask whether to load the project.



Hit [YES].

NOTE: In the next session just open the ANT GUI and select [loadproj]-button from the main GUI to load the studie's project file (aka parameter file).

The Study-folder “tomislav_bruckerImportIssue” now contains:

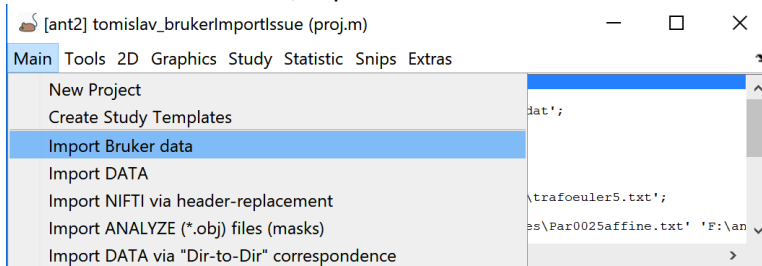
RAW_SCAN_DAT : Folder with Bruker-raw data (btw. The data can be stored somewhere else ... it's more convenient for now)

Dat: Folder, that is created when setup a new project. Later this folder will contain the data for all animals

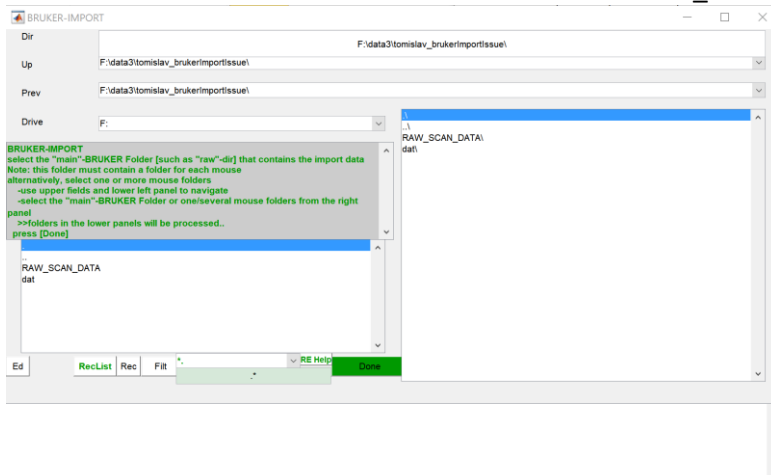
proj.m : parameter file (project file).

BRUKER IMPORT

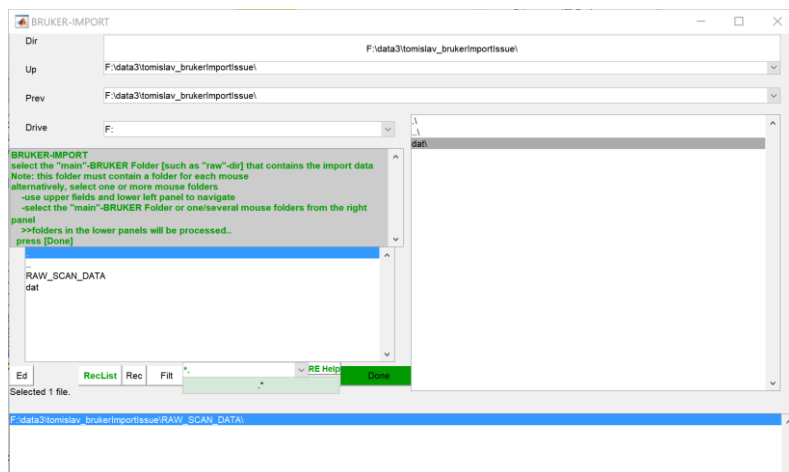
Go to ANT-MENU: Main/import Bruker data



In the Selection window select the Bruker raw data “RAW_SCAN_DATA” from the right listbox

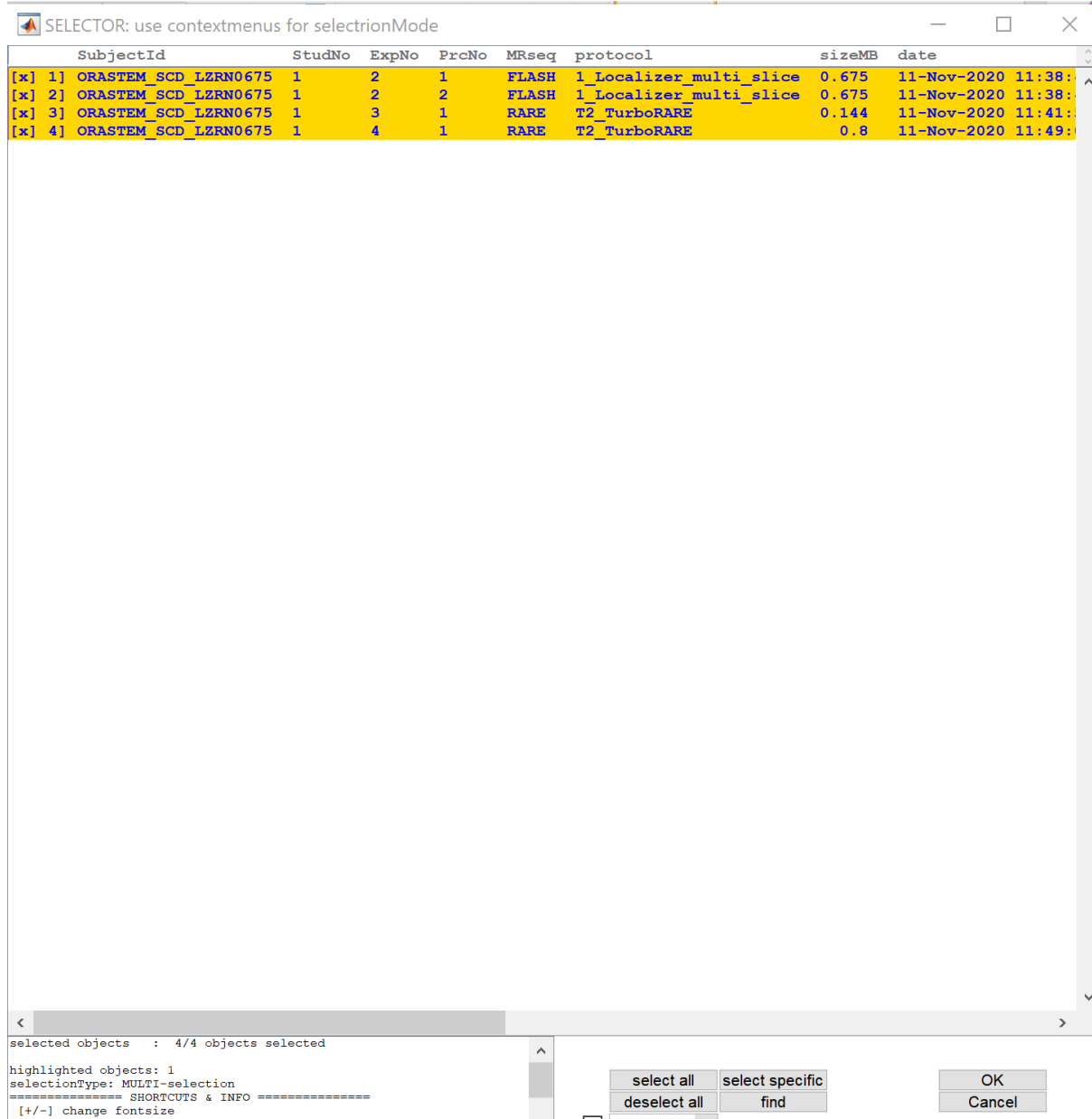


NOTE: The item(s) disappear(s) and reappear(s) in the lower listbox when selecting from the right listbox.



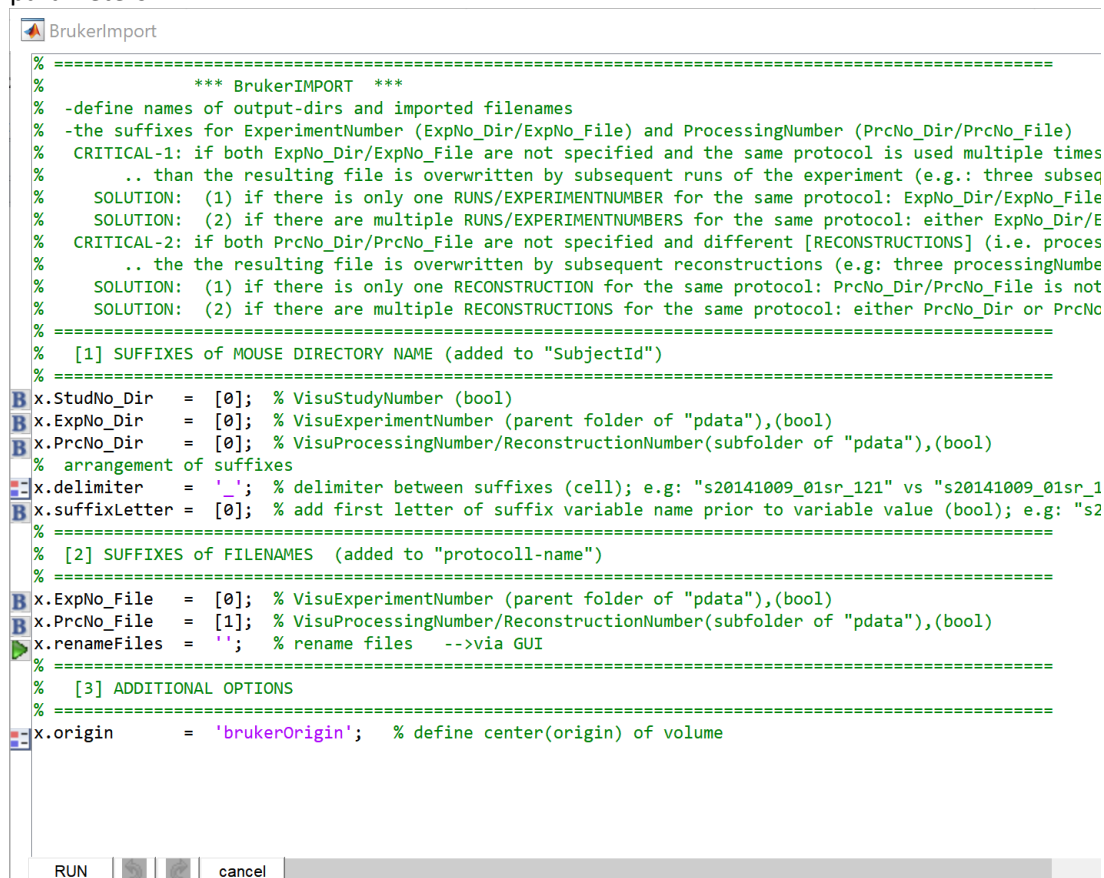
Hit **[Done]**.

The Bruker-File selection window lists all available Bruker data.



Select the files you want to convert. Here I selected all files. Hit **[OK]**.

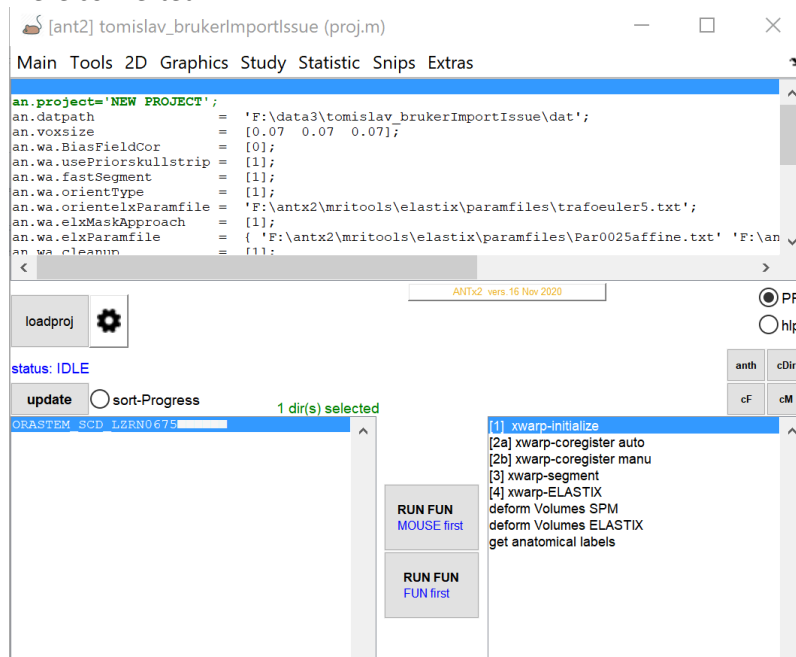
Now the Bruker-parameter window pops up. This window shows all available and changeable parameters:



Here, use the default parameter setting. Hit [RUN].

At this step, all selected Bruker files should be converted to NIFTI-files and stored in the study's 'dat'-folder.

The main gui shows a new folder (i.a. one animal) in the left list-box. Here data of only one animal were converted.

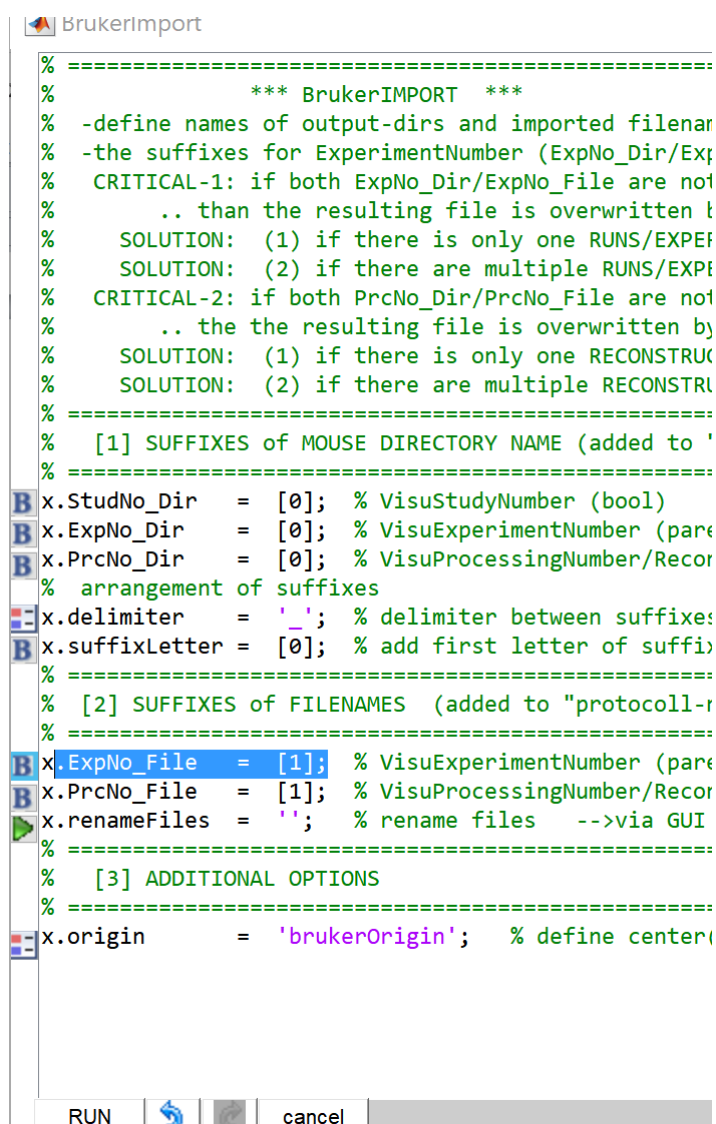


The animal folder 'ORASTEM_SCD_LZRN0675' was created in the 'dat'-folder and contains the following files:

"1_Localizer_multi_slice_1.nii"
"1_Localizer_multi_slice_2.nii"
"T2_TurboRARE_1.nii"

IMPORTANT:

In fact, 4 Bruker files were selected in the Bruker file-selection window (see above),. However, only 3 files were converted. This issue arises if Bruker files have identical "VisuProcessingNumber or ReconstructionNumbers for different scans (happens for instance if the MR sequence was repeated). Here, the "T2_TurboRARE" protocols were repeated (2x). After conversion of the 1st "T2_TurboRARE" file the 2nd "T2_TurboRARE" file overwrites the 1st one. To obtain all files you have to set the Experiment-Number in the Bruker-Parameter window to [1]. (i.e : x.ExpNo_File = [1]).



```
% =====  
% *** BrukerIMPORT ***  
% -define names of output-dirs and imported filenames  
% -the suffixes for ExperimentNumber (ExpNo_Dir/ExpNo_File)  
% CRITICAL-1: if both ExpNo_Dir/ExpNo_File are not  
% .. than the resulting file is overwritten by  
% SOLUTION: (1) if there is only one RUNS/EXPERIMENT  
% SOLUTION: (2) if there are multiple RUNS/EXPERIMENT  
% CRITICAL-2: if both PrcNo_Dir/PrcNo_File are not  
% .. the the resulting file is overwritten by  
% SOLUTION: (1) if there is only one RECONSTRUCTION  
% SOLUTION: (2) if there are multiple RECONSTRUCTIONS  
% =====  
% [1] SUFFIXES of MOUSE DIRECTORY NAME (added to 'mouse')  
% =====  
B x.StudNo_Dir = [0]; % VisuStudyNumber (bool)  
B x.ExpNo_Dir = [0]; % VisuExperimentNumber (para)  
B x.PrcNo_Dir = [0]; % VisuProcessingNumber/Reconstr  
% arrangement of suffixes  
x.delimiter = '_'; % delimiter between suffixes  
B x.suffixLetter = [0]; % add first letter of suffix  
% =====  
% [2] SUFFIXES of FILENAMES (added to "protocol-")  
% =====  
B x.ExpNo_File = [1]; % VisuExperimentNumber (para)  
B x.PrcNo_File = [1]; % VisuProcessingNumber/Reconstr  
x.renameFiles = ''; % rename files -->via GUI  
% =====  
% [3] ADDITIONAL OPTIONS  
% =====  
x.origin = 'brukerOrigin'; % define center of mass
```

This option adds the experiment number to the converted Nifti filename and prevents overwriting scans with the same protocol name.

Now the animal folder 'ORASTEM_SCD_LZRN0675' in the 'dat'-folder contains the following files:

'1_Localizer_multi_slice_2_1.nii'
'1_Localizer_multi_slice_2_2.nii'
'T2_TurboRARE_3_1.nii'
'T2_TurboRARE_4_1.nii'

*Filename construction: “**protocolName+ExperimentNumber+ExperimentNumber**”*

For other information

→ ANT-MENU: EXTRAS/documentation (docs)

What could be read next?: “**tutorial_orientation_and_manucoreg.doc**”