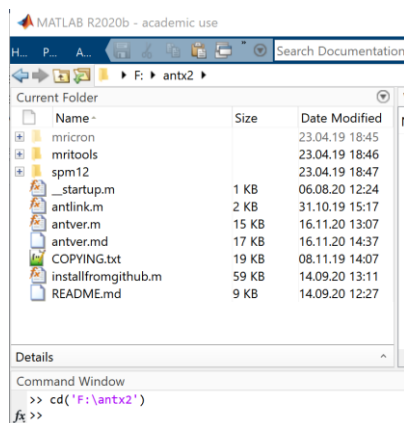


# BrukerImport

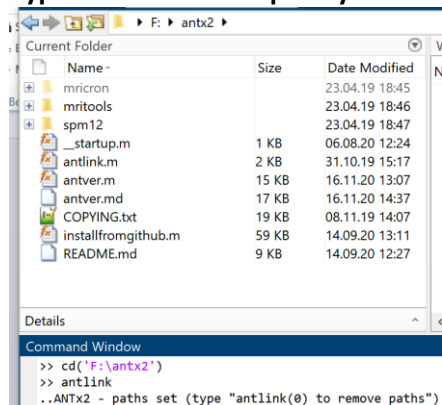
This tutorial shows how to import Bruker data:

Set Matlab's current to antx2-TBX

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

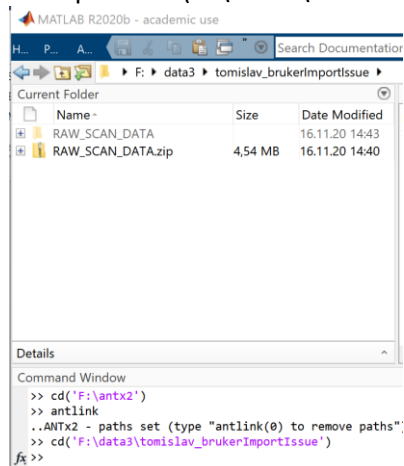


Type 'antlink' to temporary set the antx2'-paths



Go to project-folder

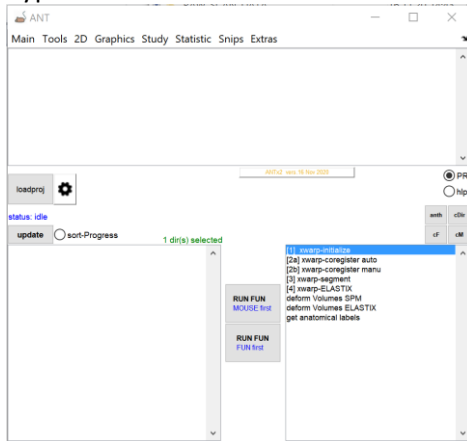
Example `>> cd('F:\data3\tomislav_brukerImportIssue')`



**NOTE:** I just created a folder 'tomislav\_bruckerImportIssue'. This folder contain a folder with the unzipped raw-brucker data ('RAW\_SCAN\_DATA')

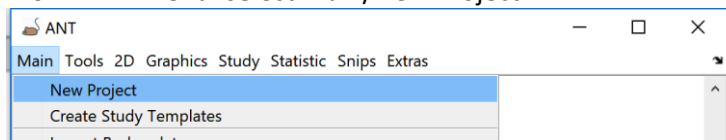
## Start the GUI:

Type 'ant'

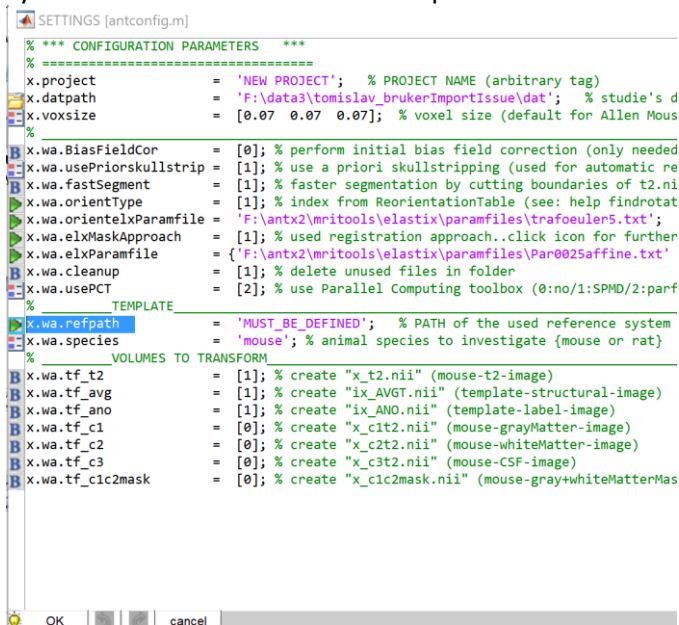


## CREATE NEW PROJECT:

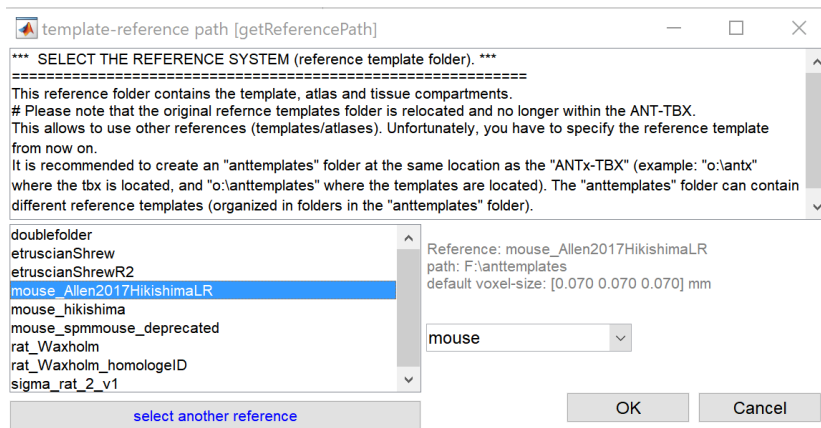
From ANT-menu: select Main/New Project



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

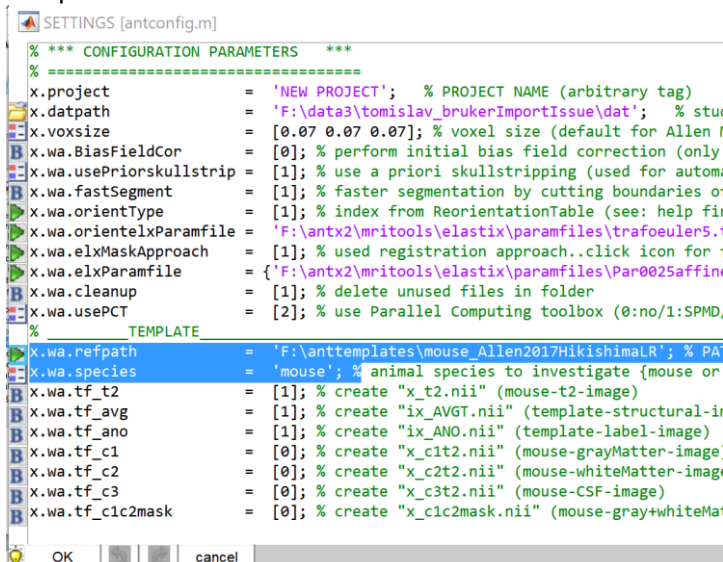


For this, select the green icon left to the 'refpath'-parameter.



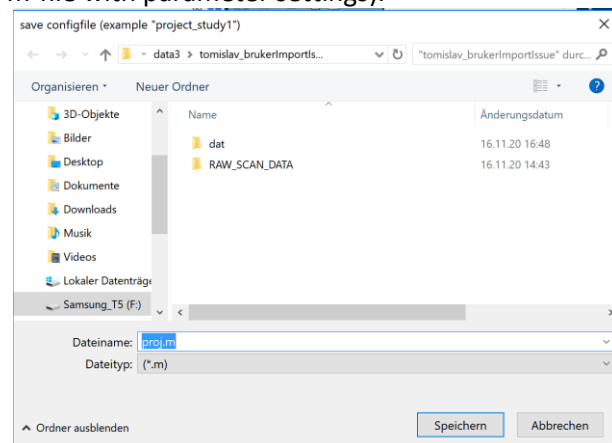
Select the reference system from left listbox. Here, I selected the Allen Mouse atlas with Hikishima TPMs (highlighted). Hit **[OK]**. Note that the left listbox contains only templates that have been already downloaded (To download the templates use either ANT-Menu: EXTRAS/ get templates from googledrive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

The parameter window should now look as follows:

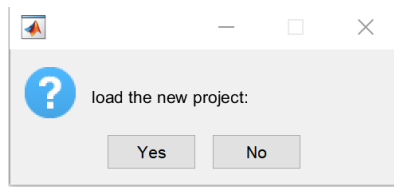


I.E: the reference system and the animal species are defined. Hit **[OK]**.

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:**

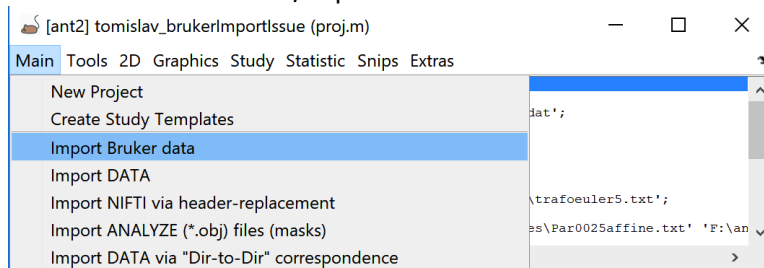
**RAW\_SCAN\_DAT :** Folder with Bruker-raw data (btw. The data can be stored somewhere else ... it's more convenient for now)

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

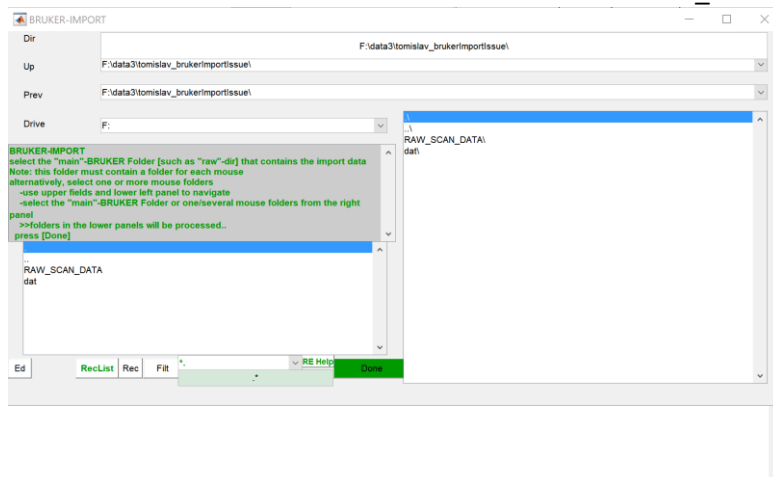
**proj.m :** parameter file (project file).

## BRUKER IMPORT

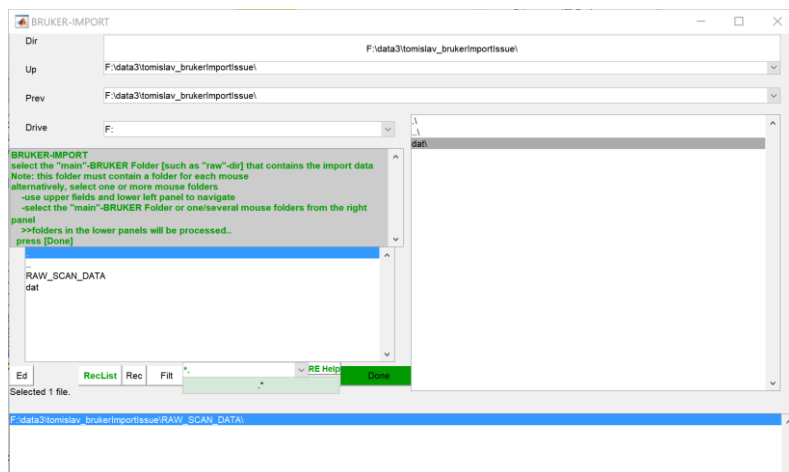
Go to ANT-MENU: Main/import Bruker data



In the Selection window select the Bruker raw data “RAW\_SCAN\_DATA” from the right listbox

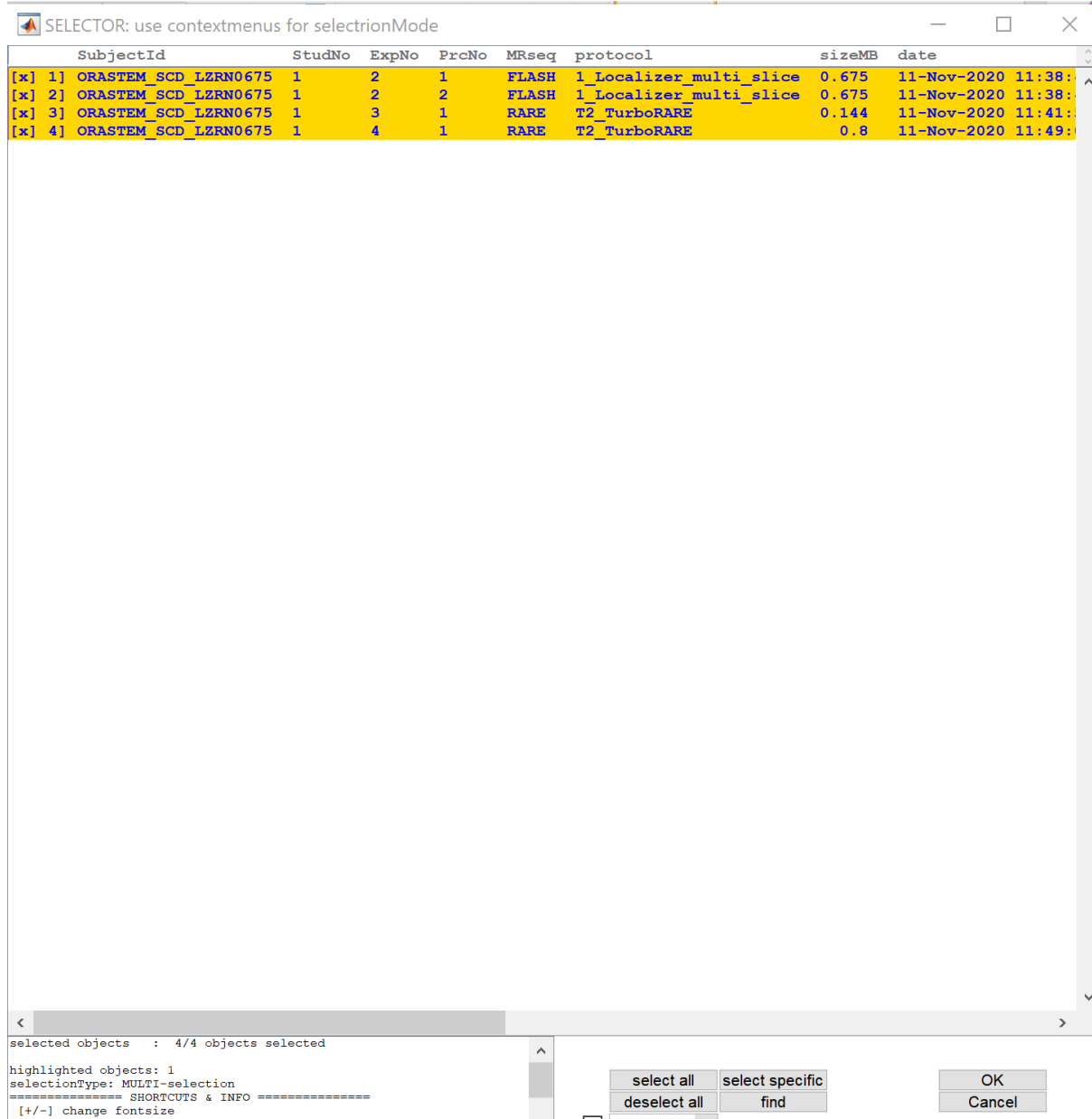


NOTE: The item(s) disappear(s) and reappear(s) in the lower listbox when selecting from the right listbox.



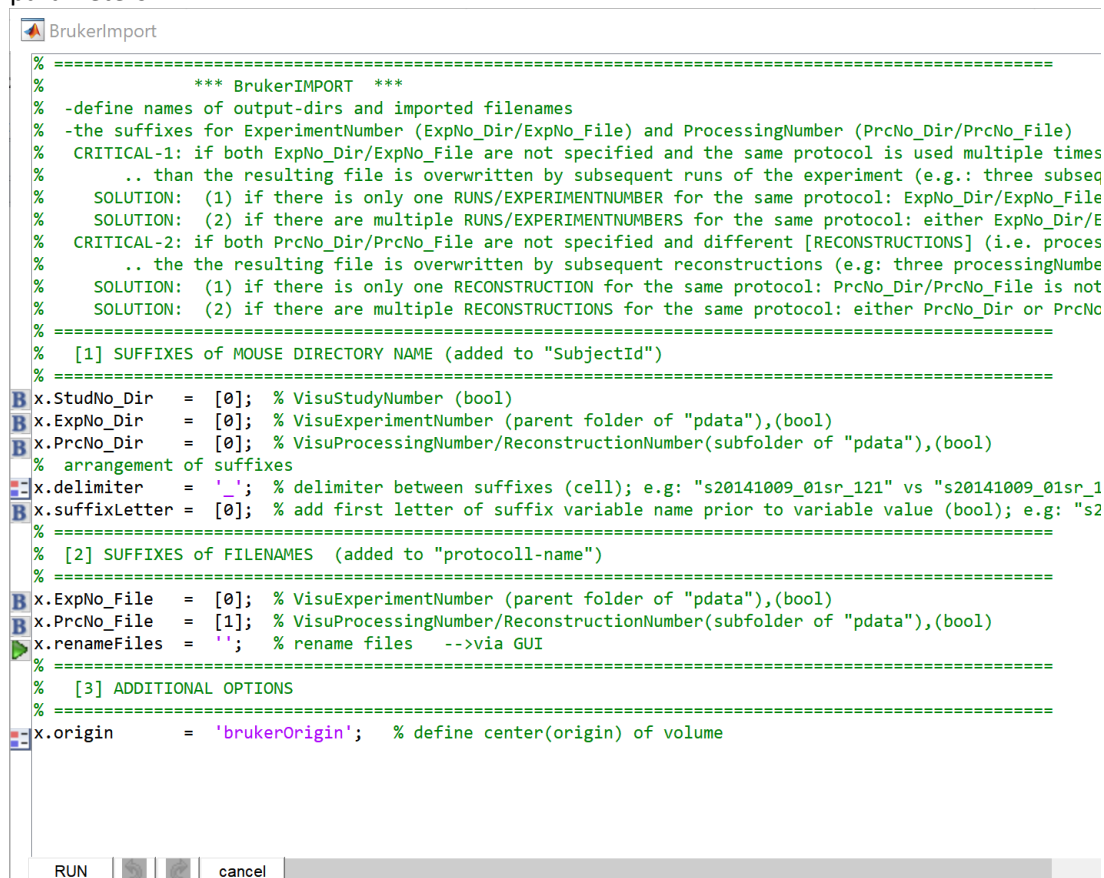
Hit [Done].

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



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

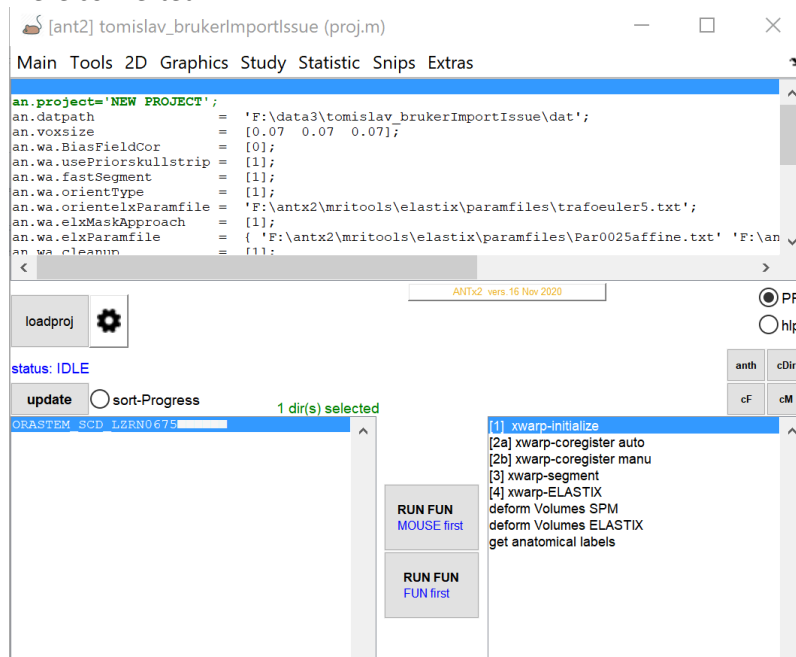
Now the Bruker-parameter window pops up. This window shows all available and changeable parameters:



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 1<sup>st</sup> "T2\_TurboRARE" file the 2<sup>nd</sup> "T2\_TurboRARE" file overwrites the 1<sup>st</sup> 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] ).

```
BruckerImport
% =====
% *** 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 empty
% .. then the resulting file is overwritten by the 1st one
% 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 empty
% .. then the resulting file is overwritten by the 1st one
% 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/ReconstructionNumber
% 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/ReconstructionNumber
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**”