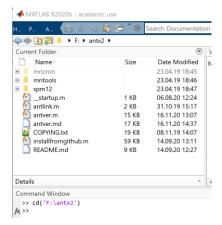
BrukerImport

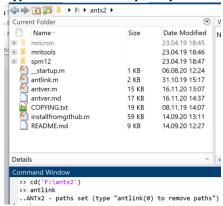
This tutorial shows how to import Bruker data:

Set Matlab's current to antx2-TBX

Example: cd('F:\antx2')

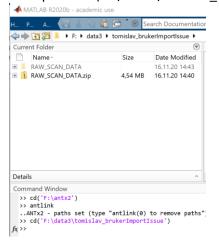


Type 'antlink' to temporary set the antx2'-paths



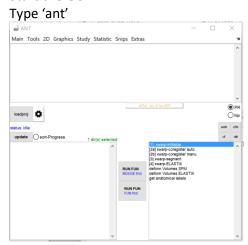
Go to project-folder

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



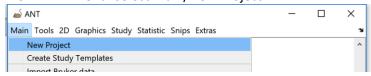
NOTE: I just created a folder 'tomislav_brukerImportIssue'. This folder contain a folder with the unzipped raw-bruker data ('RAW_SCAN_DATA')

Start the GUI:

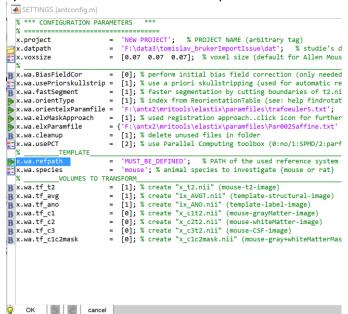


CREATE NEW PROJECT:

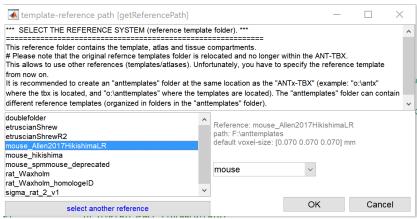
From ANT-menu: select Main/New Project



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

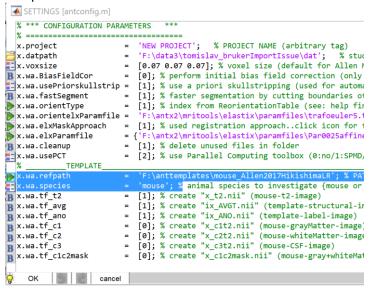


For this, select the green icon left to the 'refpath'-parameter.



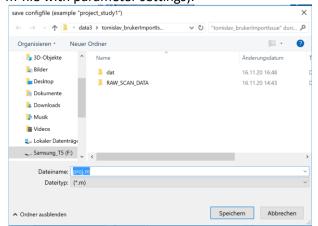
Select the reference system from left listbox. Here, I selected the Allen Mouse atlas with Hikishima TPMs (highlighted). Hit [OK]. Note that the left listbox contains only templates that have been already downloaded (To download the templates use either ANT-Menu: EXTRAS/ get templates from googledrive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

The parameter window should now look as follows:

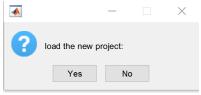


I.E: the reference system and the animal species are defined. Hit [OK].

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_brukerImportIssue). 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_brukerImportIssue" now contains:

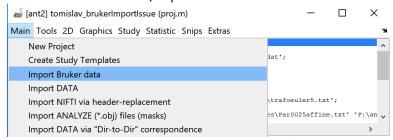
RAW_SCAN_DAT: Folder with Bruker-raw data (btw. The data can be stored somewhere else ... it's more convenient for now)

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

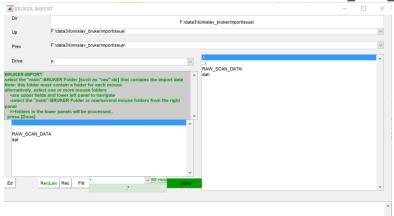
proj.m : parameter file (project file).

BRUKER IMPORT

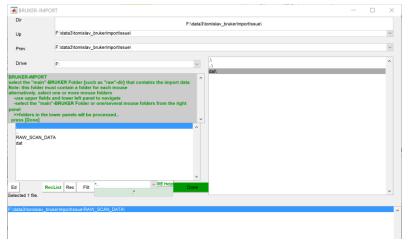
Go to ANT-MENU: Main/import Bruker data



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

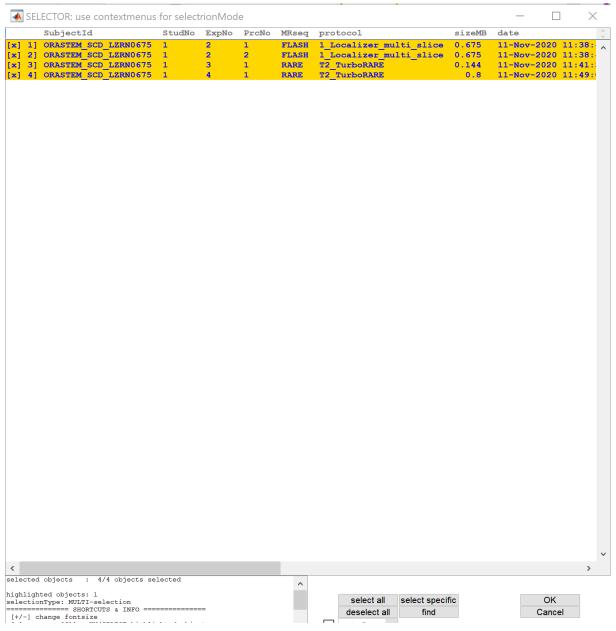


NOTE: The item(s) disappear(s) and reappear(s) in the lower listbox when selecting from the right listbox.



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].

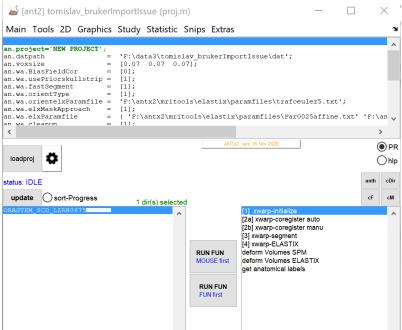
Now the Bruker-parameter window pops up. This window shows all available and changeable parameters:

```
▲ BrukerImport
                                *** BrukerIMPORT ***
         -define names of output-dirs and imported filenames
          -the suffixes for ExperimentNumber (ExpNo_Dir/ExpNo_File) and ProcessingNumber (PrcNo_Dir/PrcNo_File)
          CRITICAL-1: if both ExpNo_Dir/ExpNo_File are not specified and the same protocol is used multiple times
                      . than the resulting file is overwritten by subsequent runs of the experiment (e.g.: three subseq
              SOLUTION: (1) if there is only one RUNS/EXPERIMENTNUMBER for the same protocol: ExpNo_Dir/ExpNo_File
   %
              SOLUTION: (2) if there are multiple RUNS/EXPERIMENTNUMBERS for the same protocol: either ExpNo_Dir/E
          CRITICAL-2: if both PrcNo_Dir/PrcNo_File are not specified and different [RECONSTRUCTIONS] (i.e. proces
                     .. the the resulting file is overwritten by subsequent reconstructions (e.g: three processingNumbe
              SOLUTION: (1) if there is only one RECONSTRUCTION for the same protocol: PrcNo_Dir/PrcNo_File is not
              SOLUTION: (2) if there are multiple RECONSTRUCTIONS for the same protocol: either PrcNo_Dir or PrcNo
          [1] SUFFIXES of MOUSE DIRECTORY NAME (added to "SubjectId")
\mathbf{B}x.StudNo_Dir = [0]; % VisuStudyNumber (bool)
                             = [0]; % VisuExperimentNumber (parent folder of "pdata"),(bool)
= [0]; % VisuProcessingNumber/ReconstructionNumber(subfolder of
B x.ExpNo_Dir
Bx.PrcNo_Dir
                                             % VisuProcessingNumber/ReconstructionNumber(subfolder of "pdata"),(bool)
   %.refue_bi
% arrangement of suffixes
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_121" vs "s20141009_01sr_1
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_121" vs "s20141009_01sr_1"
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell); e.g: "s20141009_01sr_109."
x.delimiter = '_'; % delimiter between suffixes (cell)
x.delimiter
x.suffixLetter = [0]; % add first letter of suffix variable name prior to variable value (bool); e.g: "s2
   % [2] SUFFIXES of FILENAMES (added to "protocoll-name")
   x.ExpNo_File = [0]; % VisuExperimentNumber (parent folder of "pdata"),(bool)
Bx.PrcNo_File = [1]; % VisuProcessingNumber/Recor
x.renameFiles = ''; % rename files -->via GUI
                                             % VisuProcessingNumber/ReconstructionNumber(subfolder of "pdata"),(bool)
    [3] ADDITIONAL OPTIONS
   % -------
                              = 'brukerOrigin'; % define center(origin) of volume
x.origin
       RUN Cancel
```

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^{st} "T2_TurboRARE" file the 2^{nd} "T2_TurboRARE" file overwrites the 1^{st} 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
 9
            *** BrukerIMPORT ***
 %
   -define names of output-dirs and imported filenam
   -the suffixes for ExperimentNumber (ExpNo Dir/Exp
   CRITICAL-1: if both ExpNo Dir/ExpNo File are not
        .. than the resulting file is overwritten b
 %
    SOLUTION: (1) if there is only one RUNS/EXPER
    SOLUTION: (2) if there are multiple RUNS/EXPE
   CRITICAL-2: if both PrcNo_Dir/PrcNo_File are not
 %
        .. the the resulting file is overwritten by
     SOLUTION: (1) if there is only one RECONSTRUC
 %
    SOLUTION: (2) if there are multiple RECONSTRU
 [1] SUFFIXES of MOUSE DIRECTORY NAME (added to '
 Bx.StudNo_Dir = [0]; % VisuStudyNumber (bool)
            = [0]; % VisuExperimentNumber (pare
R x.ExpNo_Dir
x.PrcNo_Dir = [0]; % VisuProcessingNumber/Recor
 % arrangement of suffixes
x.delimiter = '_'; % delimiter between suffixes
x.suffixLetter = [0]; % add first letter of suffix
 % [2] SUFFIXES of FILENAMES (added to "protocoll-r
 B x.ExpNo_File = [1]; % VisuExperimentNumber (pare
\mathbf{R}x.PrcNo_File = [1]; % VisuProcessingNumber/Recor
x.renameFiles = ''; % rename files -->via GUI
 [3] ADDITIONAL OPTIONS
 x.origin
          = 'brukerOrigin'; % define center(
       Sancel Sancel
```

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

```
'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"