Tutorial: Running ANTx on machines without graphic support "working without graphical user interfaces, GUIs"

This tutorial shows how to perform some basic steps without GUIs, for instance when running on a HPC-machine.

CONTENTS

1) OPTIONAL: How to set the paths of ELASTIX in UNIX (LINUX)-systems:

```
MAKE ELASTIX RUNNING ON UNIX/LINUX-Systems
=========================================
 1) SET PATH OF ELASTIC IN .bashrc-FILE
=========================================
FOR INFORMATION:
see: Elastix-manual (section 3.2)
see: https://usermanual.wiki/Document/elastix490manual.1389615963/html#pf17

Linux: Add the following lines to your .bashrc file:
-----------------------------------------------------
export PATH=folder/bin:$PATHexport
LD_LIBRARY_PATH=folder/lib:$LD_LIBRARY_PATH
-----------
...where "folder" is the path to the linux-Elastix-folder (which is located in the antx2-
folder): YOUR-DRIVE\antx2\mritools\elastix\elastix linux64 v4.7

EXAMPLE:
My linux-elastix-folder is "/sc-projects/sc-proj-agtiermrt/Daten-
2/ressources/antx2/mritools/elastix/elastix linux64 v4.7/". Thus, my bahrc-file it modified as
follows:
#-------------------------[ELASTIX-PATH in bashrc]--------------------------------------
export PATH=/sc-projects/sc-proj-agtiermrt/Daten-
2/ressources/antx2/mritools/elastix/elastix_linux64_v4.7/bin:$PATH
export LD LIBRARY PATH=/sc-projects/sc-proj-agtiermrt/Daten-
2/ressources/antx2/mritools/elastix/elastix linux64 v4.7/lib:$LD LIBRARY PATH
#-----------------------------------------------------------------------------------------

=======================================
 2) RELOAD .bashrc-FILE & TEST ELASTIX
=======================================
- save .bashrc-file, exit editor, than type the following to reload the .bashrc-file again:
source .bashrc

- check installation, by typing:
elastix
 - if successful, a message is displayed:
Use "elastix --help" for information about elastix-usage.
```

2) OPTIONAL: Open interactive session on HPC and start Matlab

OPEN INTERACTIVE JOB on HPC (optional)

```
srun --time 7-00 --mem=64G --ntasks=8 --pty bash -i
```

-Please check the parameters, here for 7 days, 64 Gb Ram, 8 cores

LOAD MATLAB-MODULE AND START MATLAB (optional)

```
module load scientific/matlab/R2021b
matlab
```

-to access Matlab might be different on another machine!

3) BASICS

FROM NOW ON type in the MATLAB CMD-WINDOW…

ADD ANTx-PATHS

Go to the ANTx-patd and link all necessary paths using "**antlink**"-command:

```
cd /sc-projects/sc-proj-agtiermrt/Daten-2/ressources/antx2/
antlink
```

GO TO STUDY-FOLDER

Create an empty study folder (here "groeschel"). The study-folder is the folder where the registration of several animals of a study is performed.

```
cd /sc-projects/sc-proj-agtiermrt/Daten-2/mri/projects/groeschel/
```

UPDATE ANT-TOOLBOX

This is not mandatory... just type **updateantx(2)** to update the toolbox, i.e. obtain the latest version from GitHub. For more info type help updateantx.

```
updateantx(2)
```

CREATE AN ANTx-PROJECT-FILE:

```
makeproject('projectname',fullfile(pwd,'proj.m'), 'voxsize',[.07 .07 .07],'wa_refpath','/sc-projects/sc-proj-agtiermrt/Daten-2/ressources/anttemplates/mouse_Allen2017HikishimaLR','wa_species','mouse');
```

-here the project-file "**proj.m**" is created using a target voxel size of 0.07 x 0.07 x 0.07 mm, the **animal template** is "**mouse_Allen2017HikishimaLR**", with the species **'mouse'**.

- a suitable template has to be downloaded from google-drive :

https://drive.google.com/drive/folders/1q5XOOVLvUYLqYsQJLqNRF7OK8fNwYhI9

The template should be unzipped and stored where it could be reached (do not save the downloaded template in the current project-folder!). Creating a project-file has to be done only once!

LOAD THE PROJECT-FILE "proj.m"

Here we load the created project-file **"proj.m":**

```
loadconfig(fullfile(pwd,'proj.m'));
```

CHECK WHETHER THE PROJECT-FILE IS LOADED

```
global an;
 an
```

The global variable "an" (struct) contains the basic information for this study. In the CMD-window you should the following:

```
  project: 'NEW PROJECT'
  datpath: '/sc-projects/sc-proj-agtiermrt/Daten-2/mri/projects/groeschel/dat'
  voxsize: [0.0700 0.0700 0.0700]
     wa: [1x1 struct]
```

4) IMPORT BRUKER-DATA

Before doing this step, I just created the 'raw'-folder within the study's folder and copied the datasets of two animals into the '**raw'**-folder. First we just read the file-information of the Bruker raw-data from the "raw"-folder (fullfile(pwd,'raw')) which is located in the current study folder.

The file-information will be stored in the resulting w-struct.

```
w=xbruker2nifti(fullfile(pwd,'raw'),0,[],[],'gui',0,'show',1); % first read all data and show it
```

The w-struct contains the file-information table "d" with header "hd". This table is listed in the CMD-window when running this command. You could save & reload the struct and import some data later on (advantage: loading time is reduced). To show the table again just type:

```
w.showtable(w) ; %to show the table in CMD-window
```

If graphic is supported you could also visualize the table in an extra window via w.showtable2(w) .

Here, the raw-data folder contains two data-sets (i.e. the data from two animals):

```
    BRUKER DATA
set SubjectId                          StudNo ExpNo PrcNo MRseq       protocol                  sizeMB   date                  file
1   20200925MG_LAERMRT_MGR000025 1     1      1     FLASH       01_1_Localizer_CRP            0.393216 20-Oct-2020 15:07:20 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     10     1     SINGLEPULSE 02_6_freqAdj_SINGLEPULSE      0.004096 20-Oct-2020 15:05:32 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     11     1     DtiEpi      02_7_DTI_EPI_seg_b2500_37dir  112.0666 20-Oct-2020 15:06:12 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     11     2     DtiEpi      nan                           129.7613 20-Oct-2020 15:06:59 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     13     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:07:11 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     16     1     STEAM       04_3_Localized_shim_MGB       0.004096 20-Oct-2020 15:03:38 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     17     1     STEAM       04_3_STEAM_1H_MGB             0.004096 20-Oct-2020 15:05:13 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     19     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:08:29 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     2      1     FLASH       01_2_Localizer_multi_slice     1.10592 20-Oct-2020 15:09:05 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     20     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:05:33 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     21     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:04:55 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     22     1     FieldMap    B0Map-ADJ_B0MAP               1.048576 20-Oct-2020 15:05:31 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     23     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:05:32 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     24     1     FLASH       01_2_Localizer_multi_slice     1.10592 20-Oct-2020 15:03:47 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     25     1     RARE        03_T2_TurboRARE_CRP_MapShim    2.94912 20-Oct-2020 15:08:28 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     26     1     FieldMap    B0Map-ADJ_B0MAP               1.048576 20-Oct-2020 15:03:51 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     27     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:04:48 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     28     1     STEAM       04_2_STEAM_1H_IC_single       0.004096 20-Oct-2020 15:05:25 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     29     1     STEAM       04_3_Localized_shim_MGB       0.004096 20-Oct-2020 15:03:52 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     3      1     RARE        03_T2_TurboRARE_CRP             6.5536 20-Oct-2020 15:05:38 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     31     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:05:39 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     33     1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 15:08:23 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     35     1     STEAM       04_2_STEAM_1H_IC_single       0.004096 20-Oct-2020 15:07:33 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     4      1     DtiEpi      02_1_DTI_EPI_seg_b100_6dir    20.64384 20-Oct-2020 15:08:11 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     4      2     DtiEpi      nan                           129.7613 20-Oct-2020 15:08:24 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     5      1     FieldMap    B0Map-ADJ_B0MAP               1.048576 20-Oct-2020 15:03:53 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     6      1     SINGLEPULSE 02_2_freqAdj_SINGLEPULSE      0.004096 20-Oct-2020 15:05:00 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1     7      1     DtiEpi      02_3_DTI_EPI_seg_b900_13dir   41.28768 20-Oct-2020 15:08:40 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
```

```
1   20200925MG_LAERMRT_MGR000025 1      7     2     DtiEpi      nan                          129.7613 20-Oct-2020 15:09:00 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1      8     1     SINGLEPULSE 02_4_freqAdj_SINGLEPULSE     0.004096 20-Oct-2020 15:08:25 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1      9     1     DtiEpi      02_5_DTI_EPI_seg_b1600_25dir 76.67712 20-Oct-2020 15:04:13 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
1   20200925MG_LAERMRT_MGR000025 1      9     2     DtiEpi      nan                          129.7613 20-Oct-2020 15:04:41 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      1     1     FLASH       01_1_Localizer_CRP           0.393216 20-Oct-2020 14:57:50 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      10    1     DtiEpi      02_7_DTI_EPI_seg_b2500_37dir 112.0666 20-Oct-2020 14:56:04 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      10    2     DtiEpi      nan                          129.7613 20-Oct-2020 14:56:29 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      11    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:57:36 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      12    1     STEAM       04_2_STEAM_1H_IC_single      0.004096 20-Oct-2020 14:54:36 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      13    1     STEAM       04_3_Localized_shim_MGB      0.004096 20-Oct-2020 14:57:43 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      14    1     STEAM       04_3_STEAM_1H_MGB            0.004096 20-Oct-2020 14:57:16 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      15    1     FieldMap    B0Map-ADJ_B0MAP              1.048576 20-Oct-2020 14:59:45 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      16    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:54:32 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      17    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:55:28 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      18    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:56:48 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      19    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:59:15 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      2     1     FLASH       01_2_Localizer_multi_slice    1.10592 20-Oct-2020 14:59:33 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      20    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:56:38 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      21    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:54:36 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      23    1     STEAM       04_2_Localized_shim_IC_single 0.004096 20-Oct-2020 14:55:32 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      3     1     RARE        03_T2_TurboRARE_CRP             6.5536 20-Oct-2020 14:57:06 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      4     1     DtiEpi      02_1_DTI_EPI_seg_b100_6dir   20.64384 20-Oct-2020 14:58:07 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      4     2     DtiEpi      nan                          129.7613 20-Oct-2020 14:58:30 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      5     1     SINGLEPULSE 02_2_freqAdj_SINGLEPULSE     0.004096 20-Oct-2020 14:54:33 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      6     1     DtiEpi      02_3_DTI_EPI_seg_b900_13dir  41.28768 20-Oct-2020 14:54:49 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      6     2     DtiEpi      nan                          129.7613 20-Oct-2020 14:55:18 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      7     1     SINGLEPULSE 02_4_freqAdj_SINGLEPULSE     0.004096 20-Oct-2020 14:59:22 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      8     1     DtiEpi      02_5_DTI_EPI_seg_b1600_25dir 76.67712 20-Oct-2020 14:58:47 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      8     2     DtiEpi      nan                          129.7613 20-Oct-2020 14:59:07 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
2   20200925MG_LAERMRT_MGR000027 1      9     1     SINGLEPULSE 02_6_freqAdj_SINGLEPULSE     0.004096 20-Oct-2020 14:54:33 /sc-projects/sc-proj-agtiermrt/Daten-2/mri/proje
```

Here we want to import the turboRARE-image **("03_T2_TurboRARE_CRP.nii")** and the image **"DTI_EPI_seg_b100_6dir"**.
To visualize the filtered table run the following command (note that the w-struct is used as 1st argument):

```
w2=xbruker2nifti(w,0,[],[],'gui',0,'show',1,'flt',{'pro','03_T2_TurboRARE_CRP|EPI_seg_b100' } );
```

the table now looks as follows:

```
    BRUKER DATA

set SubjectId                  StudNo ExpNo PrcNo MRseq  protocol                  sizeMB   date                  file
1   20200925MG_LAERMRT_MGR000025 1      3     1     RARE   03_T2_TurboRARE_CRP         6.5536 20-Oct-2020 15:05:38 /sc-projects/sc-
1   20200925MG_LAERMRT_MGR000025 1      4     1     DtiEpi 02_1_DTI_EPI_seg_b100_6dir 20.64384 20-Oct-2020 15:08:11 /sc-projects/sc-
2   20200925MG_LAERMRT_MGR000027 1      3     1     RARE   03_T2_TurboRARE_CRP         6.5536 20-Oct-2020 14:57:06 /sc-projects/sc-
2   20200925MG_LAERMRT_MGR000027 1      4     1     DtiEpi 02_1_DTI_EPI_seg_b100_6dir 20.64384 20-Oct-2020 14:58:07 /sc-projects/sc-
```

Now let's import these data. For this just set the 'show'-parameter to 0:

```
w2=xbruker2nifti(w,0,[],[],'gui',0,'show',0,'flt',{'pro','03_T2_TurboRARE_CRP|EPI_seg_b100' } );
```

5) VISUALIZE FILES AND FOLDERS

-type **dispfiles** to see a file-by-folder matrix in the command-window (see dispfiles for further help):

```
dispfiles
```

The following is displayed in the CMD-window:

```
    FILE x FOLDER

                              20200925MG_LAERMRT_MGR000025 20200925MG_LAERMRT_MGR000027 counts
                              ============================ ============================ ======
02_1_DTI_EPI_seg_b100_6dir_1.nii +                          +                            2/2
03_T2_TurboRARE_CRP_1.nii     +                            +                            2/2
counts                        2/2                          2/2
```

Here we see that the study's "**dat"**-folder now contains two animal-folders ("**20200925MG_LAERMRT_MGR000025**" and "**20200925MG_LAERMRT_MGR000027**"). Each Folder contains the two imported files (**"02_1_DTI_EPI_seg_b100_6dir_1.nii"** and **"03_T2_TurboRARE_CRP_1.nii").**

6) SELECTION OF ANIMALS

Before renaming the files let's first select the animals we want to process.
Here we will select all animals:

```
mdirs=antcb('getallsubjects')
```

Note that the variable "**mdirs**" contains the full paths names of the selected animals:

```
    {'/sc-projects/sc-proj-agtiermrt/Daten-2/mri/projects/groeschel/dat/20200925MG_LAERMRT_MGR000025'}
    {'/sc-projects/sc-proj-agtiermrt/Daten-2/mri/projects/groeschel/dat/20200925MG_LAERMRT_MGR000027'}
```

Alternative selection of all animals:

```
mdirs =antcb('selectdirs',[1:2 ])
mdirs=antcb('selectdirs','all')
```

7) RENAME FILES

Here we rename the file **'03_T2_TurboRARE_CRP_1.nii'** to 't2.nii'. Note that the name convention of **"t2.nii"** is mandatory, because this file is used for registration to standard space. I.e., the registration relies on the name 't2.nii'!
The renaming of the file **'03_T2_TurboRARE_CRP_1.nii'** is just because I hate long names.
Let's rename '03_T2_TurboRARE_CRP_1.nii' to t2.nii':

```
xrename(0,'03_T2_TurboRARE_CRP_1.nii','t2.nii',':','dirs',mdirs);
```

and rename '02_1_DTI_EPI_seg_b100_6dir_1.nii' to 'dti_b100.nii':

```
xrename(0,'02_1_DTI_EPI_seg_b100_6dir_1.nii','dti_b100.nii',':','dirs',mdirs);
```

Here for safety reasons, we make a copy of the original file and rename the copied file. Note that copying and renaming of the copied version is defined via the colon-symbol (:); the 4th input arg). Alternatively, to rename the original files just keep the 4th arg empty.

Now, we check whether the new files exist via dispfiles:

```
dispfiles
```

```
    FILE x FOLDER
                                20200925MG_LAERMRT_MGR000025 20200925MG_LAERMRT_MGR000027 counts
                                ============================ ============================ ======
02_1_DTI_EPI_seg_b100_6dir_1.nii +                            +                            2/2
03_T2_TurboRARE_CRP_1.nii        +                            +                            2/2
dti_b100.nii                     +                            +                            2/2
t2.nii                           +                            +                            2/2
counts                           4/4                          4/4
```

8) REGISTER "t2.nii" TO TEMPLATE SPACE (STANDARD SPACE)

Registration of **"t2.nii"** to standard space is done in 4 steps: [1] initialization, [2] rough rigid registration, [3] segmentation and [4] warping. You can perform these steps ('task') isolated & sequentially or combined,. Note however, that task '2' can be only performed when task '1' has been already performed. Here the rough registration is done automatically (autoreg', 1). We also use parallel processing across animals ('parfor',1); Please check the memory and number of cores when using parallel processing:

```
xwarp3('batch','task',[1:4 ],'autoreg',1,'parfor',1, 'mdirs',mdirs(:) );
```

Now let's check whether the **"t2.nii"** is transformed to standard-space (new name is: **"x_t2.nii")** and the template **("AVGT.nii")** and atlas (**"ANO.nii")** is back-transformed to native-space (new names: **"ix_ANO.nii"** & **"ix_AVGT.nii")** via:

```
dispfiles('flt','^x.*.nii|^ix.*.nii');
```

```
    FILE x FOLDER
           20200925MG_LAERMRT_MGR000025 20200925MG_LAERMRT_MGR000027 counts
           ============================ ============================ ======
ix_ANO.nii  +                           +                            2/2
ix_AVGT.nii +                           +                            2/2
x_t2.nii    +                           +                            2/2
counts      3/3                         3/3
```

Here we see that all three files were created for each data set

9) Extract the first 3d-volume from the 4D-vlume 'dti_b100.nii'

Use the following command to extract the 1st volume (4th input arg: 1) of **'dti_b100.nii'** and save it as **'dti_b100_1stIMG.nii'** for all animals (mdirs):

```
xrename(0,'dti_b100.nii' ,'dti_b100_1stIMG.nii' ,'1','dirs', mdirs );
```

Again, check the existence of the new files via:

```
dispfiles('flt','^dt')
```

```
    FILE x FOLDER
                   20200925MG_LAERMRT_MGR000025 20200925MG_LAERMRT_MGR000027 counts
                   ============================ ============================ ======
dti_b100.nii       +                            +                            2/2
dti_b100_1stIMG.nii +                           +                            2/2
counts             2/2                          2/2
```

10) COREGISTER 'dti_b100_1stIMG.nii' to 't2.nii'

Now let's coregister the **file 'dti_b100_1stIMG.nii'** (moving image) to the **'t2.nii'**-image (fixed image):

```
z=[];
z.TASK={ '[2]' };                          ;% flag 2 (or '2') signals to perform coregistration via SPM
z.targetImg1={ 't2.nii'  };                ;% TARGET-IMAGE
z.sourceImg1={ 'dti_b100_1stIMG.nii'  }; ;% SOURCE-IMAGE
z.sourceImgNum1=[1];                        ;% IN CASE OF 4D-vol use 1st 3d-volume of SOURCE
z.applyImg1=   ''                           ; % HERE, THE TRAFO IS NOT APPLIED TO OTHER IMAGES
z.cost_fun='nmi';
z.sep=[7  2  1  0.5  0.1  0.05];
z.tol=[0.01  0.01  0.01  0.001  0.001  0.001];
```

```
z.fwhm=[4 4];
z.centerering=[0];
z.reslicing=[1];                    ;% OUTPUT-IMAGE IS RESLICED TO MATCH WITH TARGET
z.interpOrder='auto';
z.prefix='r3';                      ;% OUTPUT  FILE-PREFIX
z.warping=[0]; %WARPING IS "OFF"
z.isparallel=1;                     ;% PARALLEL PROCESSING ENABLED
xcoreg(0,z, mdirs);
```

Again, check existence of the registered file:

```
dispfiles('flt','^r3')
```

```
-------------------------------------------------------------------------------
    FILE x FOLDER
-------------------------------------------------------------------------------
                      20200925MG_LAERMRT_MGR000025 20200925MG_LAERMRT_MGR000027 counts
                      ============================ ============================ ======
r3c_dti_b100_1stIMG.nii +                          +                            2/2
r3c_t2.nii            +                          +                            2/2
counts                2/2                        2/2
-------------------------------------------------------------------------------
```

Here we see that that the file **'r3c_dti_b100_1stIMG.nii'** exists for each animal. The file **"r3c_t2.nii**" is just a copy of the unchanged target-file ('t2.nii', fixed image).

11) TRANSFORM ANOTHER IMAGE TO STANDARD-SPACE

Now, we want to transform the image **"r3c_dti_b100_1stIMG.nii"** to standard-space (1st arg: 1) for all selected animals (mdirs), using b-spline interpolation (4th arg: 4), using the local reorientation information estimated from the rough rigid registration step (5th arg: 'local') and indicate that the input-file is located in the animal folder (6th arg: struct('source','intern') . This will create the file **"x_r3c_dti_b100_1stIMG.nii"** in standard-space:

```
fis=doelastix(1, mdirs,{'r3c_dti_b100_1stIMG.nii'},4,'local' ,struct('source','intern'));
```

Let's check the existence of the file **"x_r3c_dti_b100_1stIMG.nii":**

```
dispfiles('flt','x_.*')
```

```
-------------------------------------------------------------------------------
    FILE x FOLDER
-------------------------------------------------------------------------------
                      20200925MG_LAERMRT_MGR000025 20200925MG_LAERMRT_MGR000027 counts
                      ============================ ============================ ======
ix_ANO.nii            +                            +                            2/2
ix_AVGT.nii           +                            +                            2/2
ix_AVGThemi.nii       +                            +                            2/2
x_r3c_dti_b100_1stIMG.nii +                        +                            2/2
x_t2.nii              +                            +                            2/2
counts                5/5                          5/5
-------------------------------------------------------------------------------
```

12) TRANSFORM ANOTHER IMAGE TO NATIVE-SPACE

In the same way we could also transform an image from standard-space to the the template space (for instance the Atlas). Here we transform the template's hemispheric mask **('AVGThemi.nii')** to native space (new name: **'ix_AVGThemi.nii'**). For transformation to native space the 1st arg is -1, we use NN-interpolation to preserve numbers/hemispheric-IDs (4th arg: 0):

```
fis2=doelastix(-1, mdirs,{'AVGThemi.nii'},0,'local' ,struct('source','intern'));
```

Let's check the existence of the file **'ix_AVGThemi.nii'**:

```
dispfiles('flt','ix_.*')
```

```
-------------------------------------------------------------------------------
    FILE x FOLDER
-------------------------------------------------------------------------------
                20200925MG_LAERMRT_MGR000025 20200925MG_LAERMRT_MGR000027 counts
                ============================ ============================ ======
ix_ANO.nii      +                            +                            2/2
ix_AVGT.nii     +                            +                            2/2
ix_AVGThemi.nii +                            +                            2/2
counts          3/3                          3/3
```

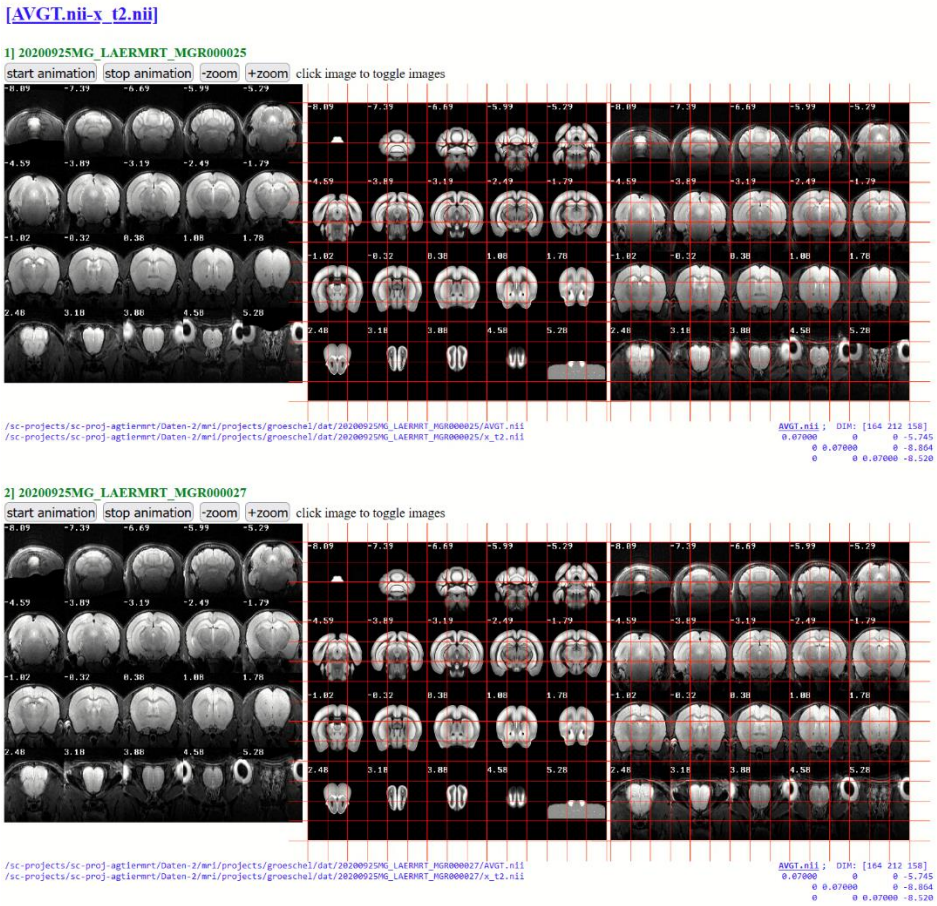
13) CHECK REGISTRATION in STANDARD-SPACE - CREATE HTML-FILE

Next, we will create an HTML-file to visualize the overlay of the template **"AVGT.nii"** and **"x_t2.nii"** (animal in standard-space). The 3rd arg defines the output-folder, the 4th input, defines the size of the images and the number of slices to visualize:

```
checkreghtml(mdirs,{'AVGT.nii','x_t2.nii' },fullfile(pwd,'checks'),struct('size',300,'slices','n20'))
```

Now you can visualize the registration with your Web-browser. The 1st image is an animated gif, showing the overlay of the **'AVGT.nii'** and **'x_t2.nii'** images. Click onto the image to toggle between

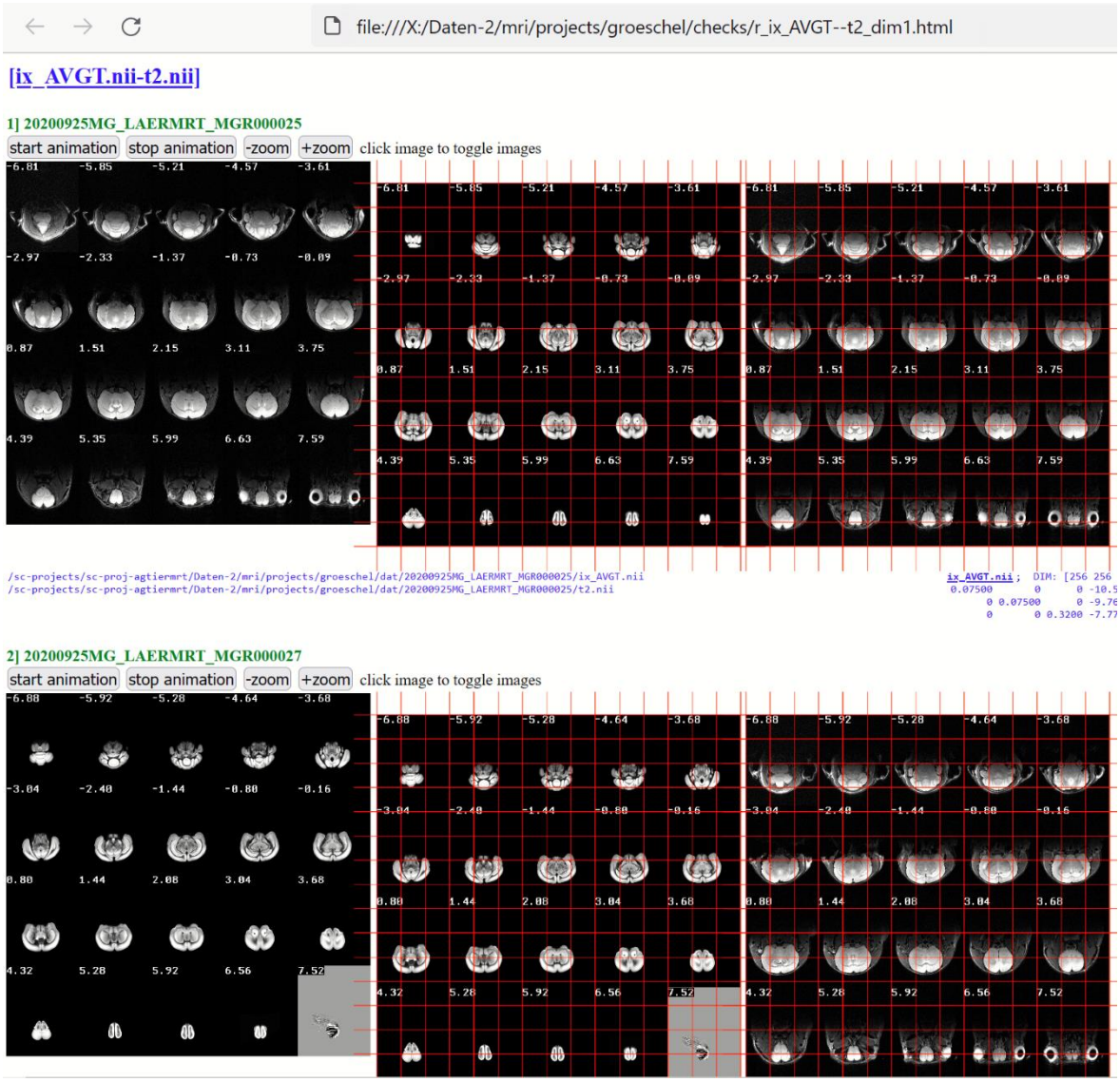
the two images, or hit ‘start animation’-button to see the animated gif. The 2nd ('AVGT.nii') and 3rd image ('x_t2.nii') shows the two images side-by-side.



14) CHECK REGISTRATION in NATIVE-SPACE - CREATE HTML-FILE

In the same, we can create an overlay of images in native-space. Here we compare the images **“t2.nii”** and **“ix_AVGT.nii”** for all animals and save the output as HTML-file.
Note that the slicing is now done from the 1st-dimension (‘dim’: 1)

```
checkreghtml(mdirs,{'ix_AVGT.nii','t2.nii' },fullfile(pwd,'checks'),struct('size',300,'slices','n20','dim',1))
```



15) Regionwise parameter-extraction

We now extract parameters such as volume, mean, median etc. for each region using the image "t2.nii" and the standard atlas (z.atlas= 'ANO.nii'). Here, from the image in native space (z.space= 'native') the parameters are aggregated over the left and right hemisphere (z.hemisphere= 'both'). The resulting Excelfile 'regwise_t2' is stored in the 'results'-folder (subfolder of the study-folder).

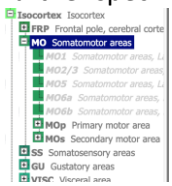
```
z=[];
z.files          = 't2.nii';        % file used for parameter extraction
z.atlas          = 'ANO.nii';       % selected atlas name, atlas has to be the standard space atlas name
z.space          = 'native';        % use images from "native" space
z.hemisphere     = 'both';          % hemisphere used: [left,right or both]
z.fileNameOut    = 'regwise_t2' ; % <optional> name of the output-file.
xgetlabels4(0,z,mdirs);
```

The resulting excel-file contains a sheet for each parameter. Here see the volume-sheet ("vol") with region-wise volume in mm3 for each region (rows) and each animal (columns). See "info"-sheet & xgetlabels4.m **for more information:**

	region	20200925MG_LAERMRT_MGR000025	20200925MG_LAERMRT_MGR000027
2	root	494.8288316	483.2800356
3	Basic cell groups and regions	439.7092504	430.7632534
4	Cerebrum	261.3599111	260.6777113
5	Cerebral cortex	209.5541287	207.7019293
6	Cortical plate	200.5649318	198.6353324
7	Isocortex	112.9841616	113.9579612
8	Frontal pole cerebral cortex	0.883799699	0.854999709
9	Frontal pole layer 1	0.131399955	0.17639994
10	Frontal pole layer 2/3	0.363599876	0.280799904
11	Frontal pole layer 5	0.313199893	0.320399891
12	Frontal pole layer 6a	0.075599974	0.077399974
13	Frontal pole layer 6b	0	0
14	Somatomotor areas	23.08859214	22.43699237
15	Somatomotor areas Layer 1	0	0
16	Somatomotor areas Layer 2/3	0	0
17	Somatomotor areas Layer 5	0	0
18	Somatomotor areas Layer 6a	0	0
19	Somatomotor areas Layer 6b	0	0
20	Primary motor area	10.50299643	10.2779965
21	Primary motor area Layer 1	1.349999541	1.274399566
22	Primary motor area Layer 2/3	3.648598759	3.639598762

INFO | frequency | percOverlapp | vol | volref | volPercBrain | mean | std | median | min | max | atlas ...

Note: Zero volume entries as for the “somatomotor areas” is because the region-IDs are not defined/exist in the Allen brain Atlas (see also: **http://atlas.brain-map.org/atlas#atlas=1&plate=100960428&structure=500&x=5245.5&y=3833.5&zoom=-4&resolution=33.45&z=6)** Here we see that the layers of “somatomotor areas” are grayed, i.e. not further specified



Of course you could extract parameters from images in standard space as well:
Example: Just change the following from the above example:
z.files = **'x_t2.nii'**; i.e. the t2w-image in standard space is use
z.space = **'standard'**; this indicated that the image is in standard space
z.fileNameOut = **'regwise_x_t2'** just another name for the resulting Excelfile:

EXAMPLE: PARAMTER EXTRACTION FROM STANDARD SPACE

```
z=[];
z.files          = 'x_t2.nii';        % file used for parameter extraction
z.atlas          = 'ANO.nii';     % selected atlas name, atlas has to be the standard space atlas name
z.space          = 'standard';        % use images from "standard” space
z.hemisphere     = 'both';          % hemisphere used: [left,right or both]
z.fileNameOut    = 'regwise_x_t2' ; % <optional> name of the output-file.
xgetlabels4(0,z,mdirs);
```

…End of this tutorial. More progress is hopefully coming soon.