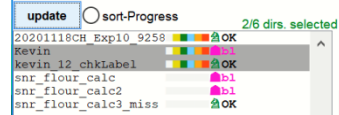


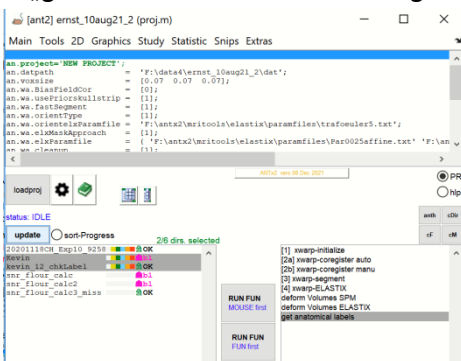
# Regionwise read-out in Native Space (NS)

- 1 -start ANT-gui: type „ant“  
-go to study-folder: use cd... or use matlab-path edit box or matlab's browse  
-to-folder-icon : ..example: cd F:\data4\ernst\_10aug21\_2  
-load project: via [loadproj]-button and select your project (m-file)

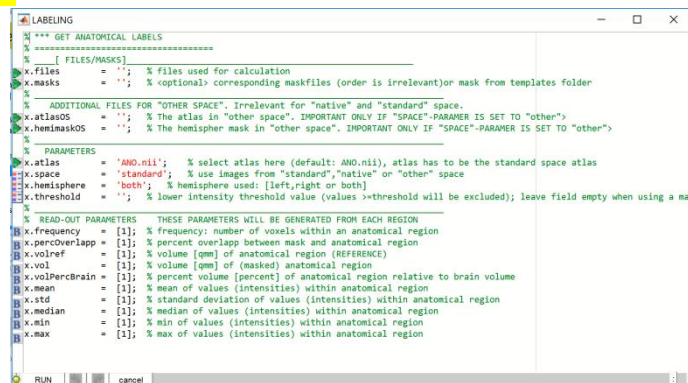
- 2 Select animals in the **left listbox**: ..here I selected two animals  
**Prerequisite: It is assumed here that the selected animals are already registered to standard space (template-space)...this is also mandatory im image paramter are extracted from NS**



- 3 Select „get anatomical labels“ from the **right listbox**:

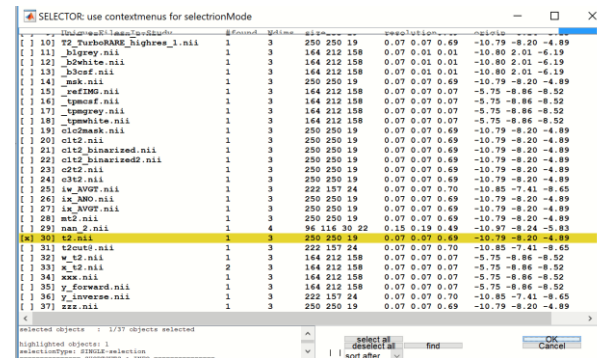


- 4 Hit **lower [RUN FUN]** -button..The parameter window will pop-up.

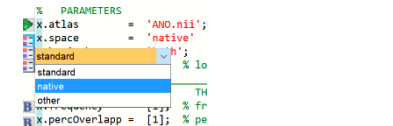


- 5 Click [green icon] left to „x-files“...to open the file selector window...

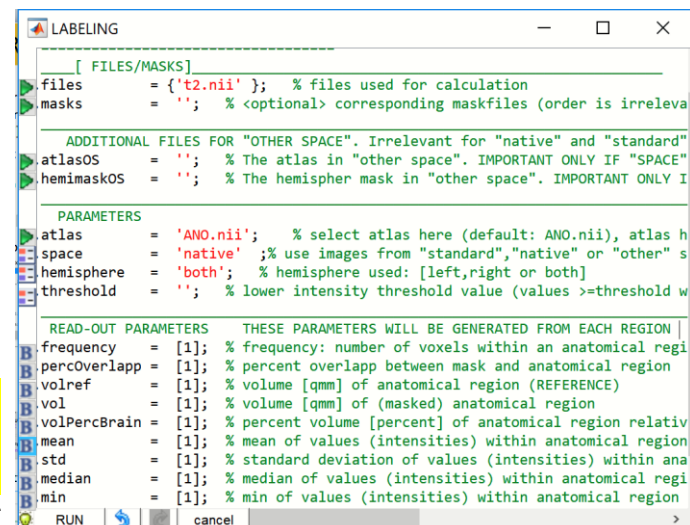
- 6 In the file selector window select the „t2.nii“ -image. The t2.nii-file is in the animal's native space, and we want to extract region-wise parameter here. Hit [OK]



- 7 **IMPORTANT:**  
-here we do not use additional masks,...leave x.masks empty  
- now the input image is in native space. DO not change the ATLAS (keep „ANO.nii“ for x.atlas)!  
**-change x.space to „native“ via left icon (because the image is in NS)**  
-extract paramter from both hemispheres together: thus, keep x.hemispheres=„both“



- 8 The parameter window should now look as follows:



Hit the „bulb“-  
icon to get  
further help

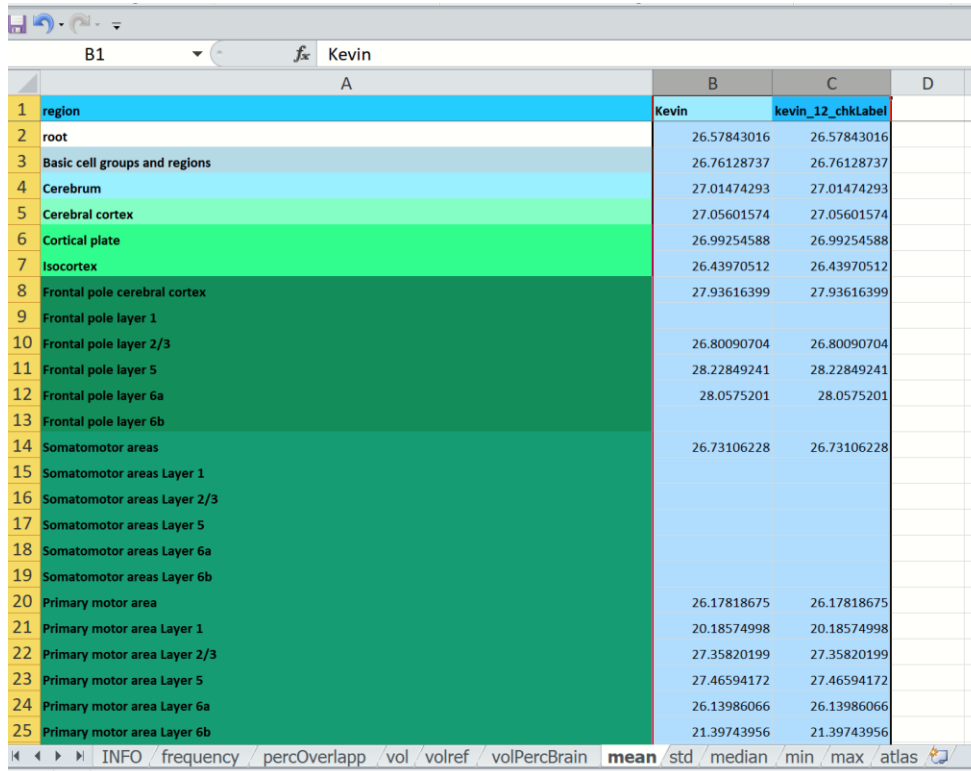
Hit [RUN]

9

When done...Matlab's comand window should show a **hyperlink** to open the Exelfile or open the explorer and highlight the file in the results-folder

```
..creating XLSfile: F:\data4\ernst_10aug21_2\results\labels_native_both_20Dec2021_12-43
new file [labels_native_both_20Dec2021_12-43-21.xlsx]: Explorer or open
>>
```

Open the document and select the „**mean**“-sheet. This sheet shows you the mean value for each region (rows) and each animal. **Note here that the dataset of the 2nd Animal was just copied thus from the first animal...thus the values are identical!**



	A	B	C	D
1	region	Kevin	kevin_12_chkLabel	
2	root	26.57843016	26.57843016	
3	Basic cell groups and regions	26.76128737	26.76128737	
4	Cerebrum	27.01474293	27.01474293	
5	Cerebral cortex	27.05601574	27.05601574	
6	Cortical plate	26.99254588	26.99254588	
7	Isocortex	26.43970512	26.43970512	
8	Frontal pole cerebral cortex	27.93616399	27.93616399	
9	Frontal pole layer 1			
10	Frontal pole layer 2/3	26.80090704	26.80090704	
11	Frontal pole layer 5	28.22849241	28.22849241	
12	Frontal pole layer 6a	28.0575201	28.0575201	
13	Frontal pole layer 6b			
14	Somatomotor areas	26.73106228	26.73106228	
15	Somatomotor areas Layer 1			
16	Somatomotor areas Layer 2/3			
17	Somatomotor areas Layer 5			
18	Somatomotor areas Layer 6a			
19	Somatomotor areas Layer 6b			
20	Primary motor area	26.17818675	26.17818675	
21	Primary motor area Layer 1	20.18574998	20.18574998	
22	Primary motor area Layer 2/3	27.35820199	27.35820199	
23	Primary motor area Layer 5	27.46594172	27.46594172	
24	Primary motor area Layer 6a	26.13986066	26.13986066	
25	Primary motor area Layer 6b	21.39743956	21.39743956	

Please inspect the info-sheet to obtain information about the document and sheets

Use also the bulb-icon to obtain help for the paramter-window or type „uhelp xgetlabels4“ in the command window

# Get the code

Type „char(anth)“ in the matlab command window or click [anth]-icon or type „uhelp anth“ to obtain the latest function-  
**Related code**  
**-you may rerun/modify+rerun the code for same/other animals**  
**(don't forget to select them in the left listbox)**

```
% % =====  
% % #g FUNCTION:      [xgetlabels4.m]  
% % #b info :         #yk xgetlabels4: get regionwise parameter for an image  
% % =====  
z=[];  
z.files      = { 't2.nii' };      % % files used for calculation  
z.masks      = '';               % % <optional> corresponding maskfiles (order is irrelevant)or mask from templates folder  
z.atlasOS     = '';               % % The atlas in "other space". IMPORTANT ONLY IF "SPACE"-PARAMER IS SET TO "other">  
z.hemimaskOS  = '';               % % The hemisphere mask in "other space". IMPORTANT ONLY IF "SPACE"-PARAMER IS SET TO "other">  
z.atlas       = 'ANO.nii';        % % select atlas here (default: ANO.nii), atlas has to be the standard space atlas  
z.space       = 'native';         % % use images from "standard","native" or "other" space  
z.hemisphere  = 'both';           % % hemisphere used: [left,right or both]  
z.threshold   = '';               % % lower intensity threshold value (values >=threshold will be excluded); leave field empty when using a mask  
z.frequency   = [1];              % % frequency: number of voxels within an anatomical region  
z.percOverlapp = [1];              % % percent overlapp between mask and anatomical region  
z.volref      = [1];              % % volume [qmm] of anatomical region (REFERENCE)  
z.vol         = [1];              % % volume [qmm] of (masked) anatomical region  
z.volPercBrain = [1];             % % percent volume [percent] of anatomical region relative to brain volume  
z.mean        = [1];              % % mean of values (intensities) within anatomical region  
z.std         = [1];              % % standard deviation of values (intensities) within anatomical region  
z.median      = [1];              % % median of values (intensities) within anatomical region  
z.min         = [1];              % % min of values (intensities) within anatomical region  
z.max         = [1];              % % max of values (intensities) within anatomical region  
xgetlabels4(1,z);
```

Obtain  
history/code via  
button

