

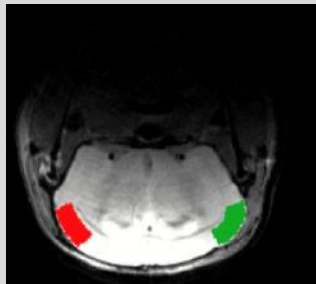
Tutorial mask-based parameter extraction from images in native space

Scenario:

A mask was generated for each animal in native space. The mask contains two ROIs: ROI-1 with ID-1 (value is 1) and ROI-2 with ID-2 (value is 2).

For a specific image in native space, we want to extract basic parameters such as mean/min/max/number of voxels and volume for each ROI of the mask.

Example: t2.nii-image overlayed with the mask 'EMS.nii', both images in Native space. The mask contains two ROIs.



Content

- 1) Prerequisite
- 2) Steps to perform the parameter extraction
 - 2.1) Readout-file selection
 - 2.2) Mask-file selection
 - 2.3) Select a filename-prefix for resulting excel-file
- 3) The output: Excel-file
- 4) Batch

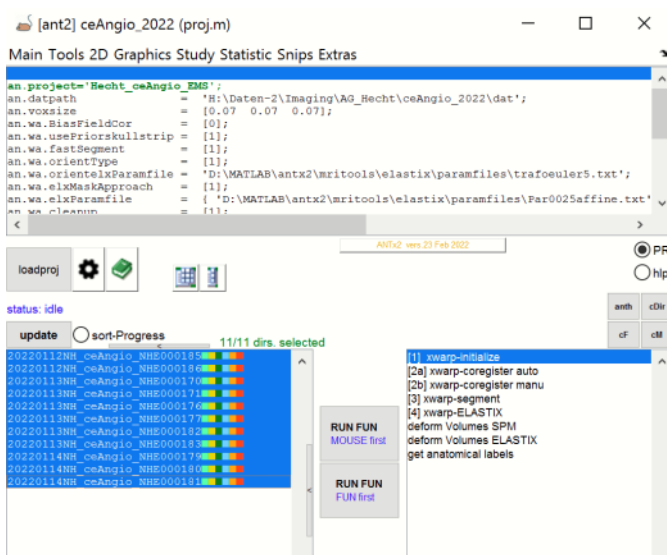
1) Prerequisite

For all animals the mask file (here: 'EMS.nii') and the readout-file for parameter-extraction (here: 'rc_rCBV.nii') exist. Mask-file and readout-file should meet the following criteria:

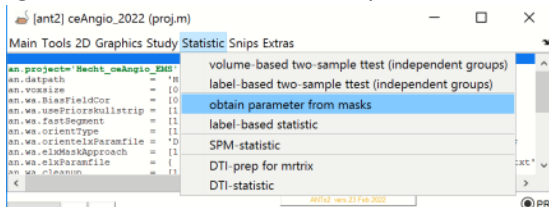
- share same space (here: native space)
- In register to each other
- Ideally same voxel-size and identical header-matrix

2) Steps to perform the parameter extraction

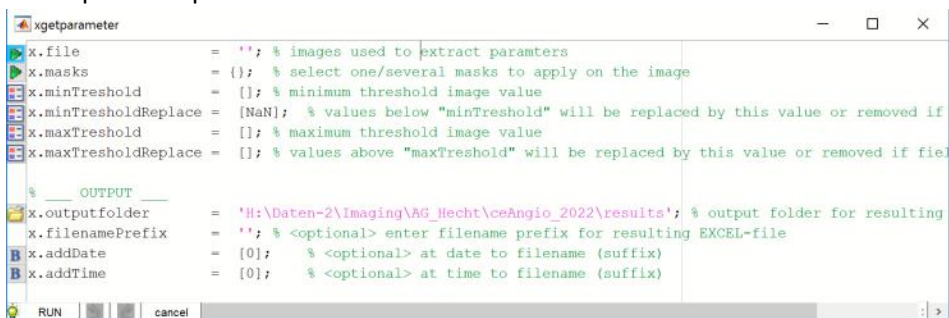
- Select all animals from the left animal list box



-go to MENU: **Statistic/obtain parameter from masks**



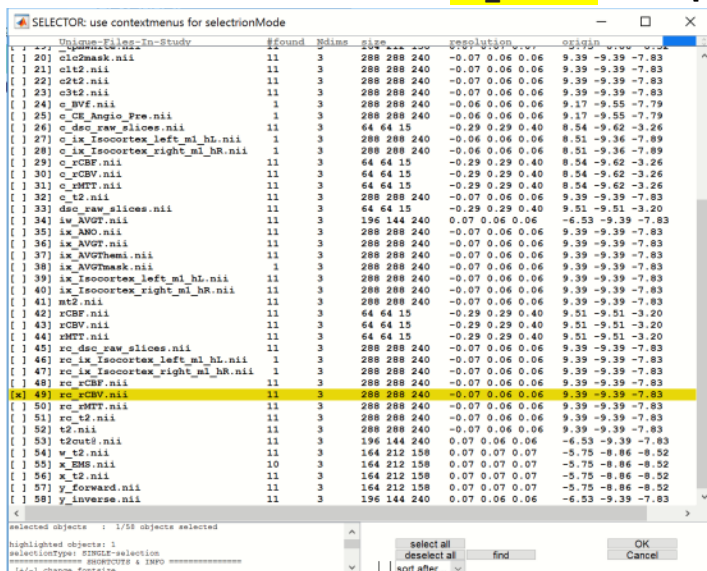
-this opens the parameter-GUI



Now do the following steps:

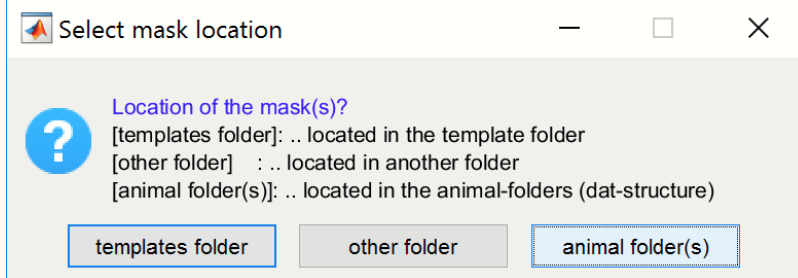
2.1) Readout-file selection

- select green icon left to the **x.file**-parameter
- from the file-section window select **"rc_rCBV.nii"** → hit [OK].



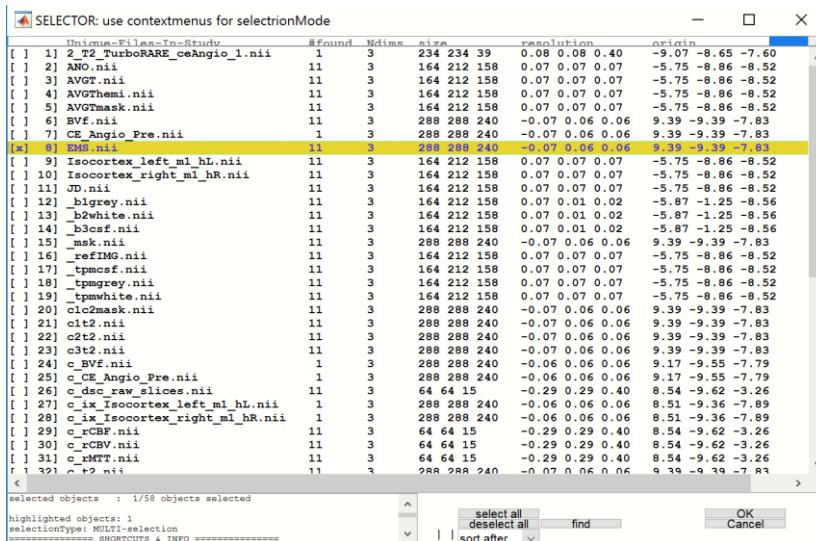
2.2) Mask-file selection

- select green icon left to the **x.masks**-parameter ...this opens a dialog...



-select [animal folder(s)] from the question-dialog

Reason: In this example each animal has it's own mask (native space), stored in the respective animal-folder (within the "dat"-folder).



- from the file-section window select the "EMS.nii"-file → hit [OK].

Remember: the "EMS.nii"-file is a mask-file containing 2 ROIs.

Important-1: selection of multiple masks possible here

You can also select more than one mask-image in this step. The numeric-Ids (values) in each mask-file do not interfere with the numeric ids of other selected masks during read-out and creation of the excel-file.

Example: Theoretical scenario: You have 2 masks:

-Mask1: "mask-1.nii" with 4 ROIs and respective ids: 1,2,3,4 and

-Mask2: "mask-2.nii" with 3 ROIs and respective ids: 1,2,3

→ You can select the two mask "mask-1.nii" and "mask-2.nii" in one step here

→ The resulting excel-file will contain the mask-file name and the respective ID of the two masks.

Example in the output-file:

mask-1__ID_1 .. with parameter extraction here

mask-1__ID_2 .. with parameter extraction here

mask-1__ID_3 .. with parameter extraction here

mask-1__ID_4 .. with parameter extraction here

mask-2__ID_1 .. with parameter extraction here

mask-2__ID_2 .. with parameter extraction here

mask-2__ID_3 .. with parameter extraction here

Important-2: A text-file with specific labels can be used in combination with the mask

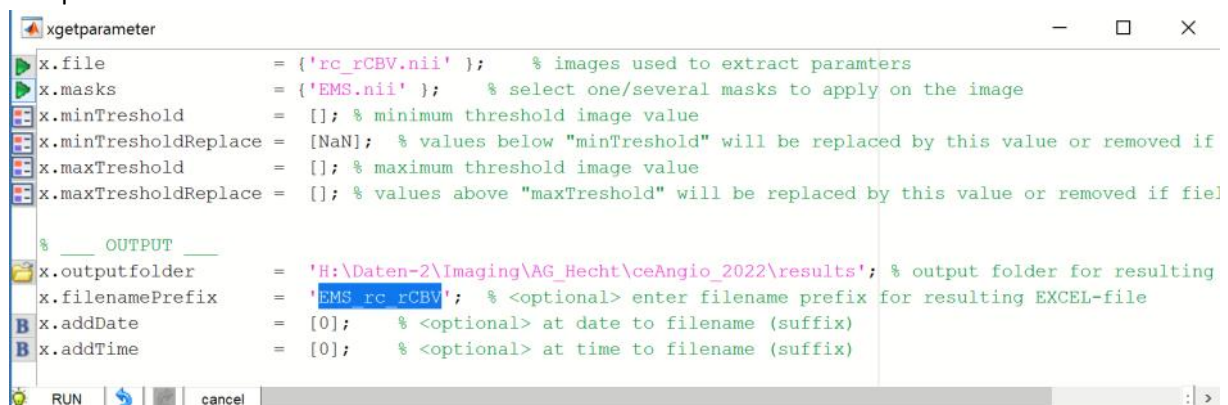
If a text-file with IDs and label is provided, the labels will be used in the resulting excel-file
To following is mandatory when using a text-file:

- text-file must have the same name as the mask-file
 - example: for “EMS.nii” the text-file would by “EMS.txt”
- text-file and mask-file must be in the same folder
 - in this example both files would be in the animal folders
- the text-file contains: the id (value) and the label for each ROI in the mask (row-wise)
 - for example, for this tutorial the text-file would contain:
1 L_somat_Cortex
2 R_somat_Cortex

2.3) Select a filename-prefix for resulting excel-file

- for the parameter: **filenamePrefix** type an arbitrary string that is used as prefix in the resulting filename. Here, I used “EMS_rc_rCBV” (here a combination of mask- and readout-filename) as prefix

The parameter window should now look as follows:



Optional Settings

- 1) minTreshhold: set a min-threshold for the readout-image ..., in this case: values below this values will by replace by the value defined by minTreshholdReplace (here NAN-values).
The latter can be changed via “minTreshholdReplace”-parameter.
→ example: minTreshhold =3 and minTreshholdReplace=3: In this case values below 3 will be replaced by the value 3
- 2) maxTreshhold/TreshholdReplace: ...same logic ...
- 3) outputfolder: change output-folder ...default: “results”-folder in the study-folder
- 4) addDate & addTime : add date & time to the filename of the new excel-file

-finally hit [RUN]

3. The output: Excel-file

- When the parameter “outputfolder” is not changed the resulting excel-file will be stored in the “results”-folder of the current study (aka project).
- Here the name of the **Excel-file** is “res_EMS_rc_rCBV_maskParameter.xlsx” (“res”+filenamePrefix + “_maskParameter.xlsx”)

-The Excel-file contains the following sheets:

'info' basic information: date/mask-name/animals/ missing animals (due to missing files)
 'frequencyMsk' : number of voxels for each ROI (real ROI-size , readout-image independent, true size of the ROI)
 'volMsk' : volume of the ROI (real ROI-size , readout-image independent, true size of the ROI)
 'frequency' : number of voxels for each ROI (readout-image dependent, NaN/threshold dependent→thus can be smaller than 'frequencyMsk')
 'vol' : volume of the ROI (readout-image dependent (Nan-values!)) NaN/threshold dependent→thus can be smaller than 'volMsk')
 'mean' : mean intensity value of readout-image within ROI
 'std' : standard deviation over intensities of readout-image within ROI
 'median' : median intensity value of readout-image within ROI
 'integrDens' : product of number voxels and mean intensity of readout-image within ROI
 'min' : min intensity value of readout-image within ROI
 'max' : max intensity value of readout-image within ROI

- The parameter-sheets have the following structure:

-ROWS: ...ROI-MASK , i.e., each row represents the parameter readout for a specific ROI

-COLUMNS:...ANIMALS, i.e. each column contains the data of one animal

Example: mean-parameter (sheet: “mean”): Here we have two ROIs from one mask-image (represented in rows) and a number of animals (columns).

	A	B	C	D	E	F	G	
1	Region	20220112NH_ceAngio_NHE000185	20220112NH_ceAngio_NHE000186	20220113NH_ceAngio_NHE000170	20220113NH_ceAngio_NHE000171	20220113NH_ceAngio_NHE000176	20220113NH_ceAngio_NHE000177	202
2	EMS_1_ID_1	2721.263509	3225.162436	4042.199138	1800.53239	4863.803108	4852.100298	
3	EMS_2_ID_2	3496.009106	4543.16769	4013.795715	2156.445782	4328.689987	4669.272042	
4								
5								
6								
7								
8								
9								
10								

4. Batch

-type **anth** to obtain the code... alternatively you could type: **uhelp(anth)** or hit the [anth]-button from the ANT-GUI.

- you can then copy and modify the code

```
%
=====
% FUNCTION: [xgetparameter.m]
% info : [xgetparameter.m] obtain mask-based parameter from images (multi-masks & masks can be mulinary)
%
z=[];
z.file = ('rc_rCBV.nii' ); % images used to extract parameters
z.masks = ('EMS.nii' ); % select one/several masks to apply on the image
z.minThreshold = []; % minimum threshold image value
z.minThresholdReplace = [NaN]; % values below "minThreshold" will be replaced by this
z.maxThreshold = []; % maximum threshold image value
z.maxThresholdReplace = []; % values above "maxThreshold" will be replaced by this
z.outputfolder = ('H:\Daten-2\Imaging\AG_Hecht\ceAngio_2022\results'); % output folder for resulting EXCEL-file
z.filenamePrefix = ('EMS_rc_rCBV'); % enter filename prefix for resulting EXCEL-file
z.addDate = [0]; % at date to filename (suffix)
z.addTime = [0]; % at time to filename (suffix)
xgetparameter(1,z);
%
=====
```

Here is the code to rerun the task:

```
% %
% % =====
% % #g FUNCTION: [xgetparameter.m]
% % #b obtain mask-based parameter from images (multi-masks & masks can be mulinary)
% % =====
```

```

z=[];
z.file           = { 'rc_rCEV.nii' };           % % images used to extract paramters
z.masks          = { 'EMS.nii' };               % % select one/several masks to apply on the
image                                                    %
z.minTreshold    = [0];                         % % minimum threshold image value
z.minTresholdReplace = [NaN];                   % % values below "minTreshold" will be
replaced by this value or removed if field is empty
z.maxTreshold     = [];                         % % maximum threshold image value
z.maxTresholdReplace = [];                     % % values above "maxTreshold" will be
replaced by this value or removed if field is empty
z.outputfolder    = 'H:\Daten-2\Imaging\AG_Hecht\ceAngio_2022\results'; % % output folder for resulting EXCEL-file
z.filenamePrefix  = '_test';                   % % <optional> enter filename prefix for
resulting EXCEL-file
z.addDate         = [1];                       % % <optional> at date to filename (suffix)
z.addTime         = [1];                       % % <optional> at time to filename (suffix)
xgetparameter(1,z);

```