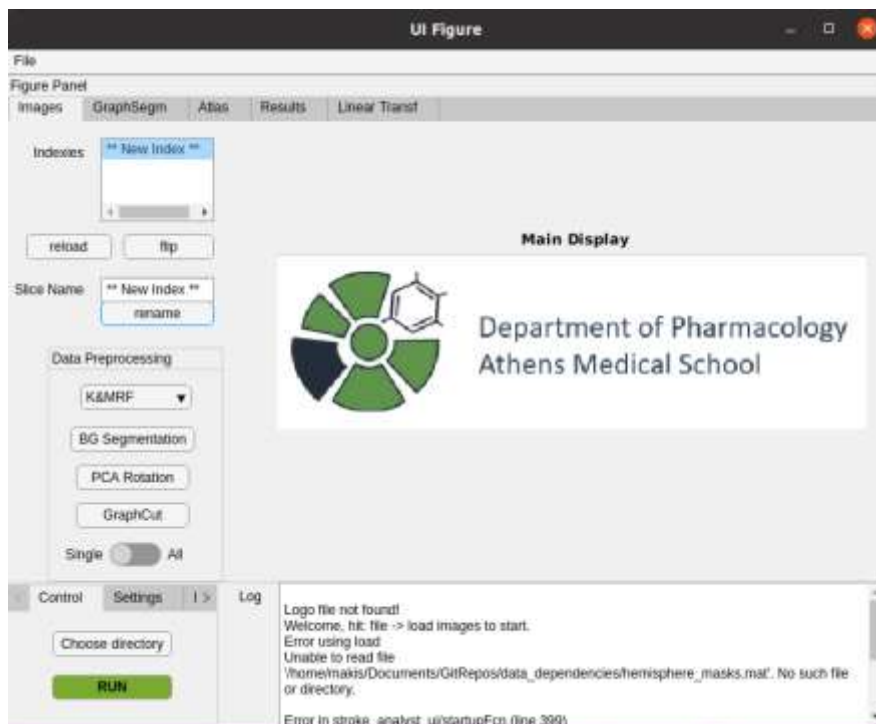# Stroke Analyst Operator Guide

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Launch Stroke Analyst

1. Go to the directory that Stroke Analyst (SA) resides and open a terminal (right click and press "**Open in terminal**")
2. Type: ./run_stroke_analyst.sh <Matlab runtime location>

    <Matlab Runtime location > is the location where Matlab runtime is installed.

3. This is the stroke analyst launch instance

Load dependencies & set absolute paths

Before performing analysis with SA certain dependencies must be complied (e.g. machine learning model, etc.). The above dependencies consist of 1) model path, 2) subject path, 3) dependencies directory, 4) drams directory.

1. On the left upper corner press the **File** button.
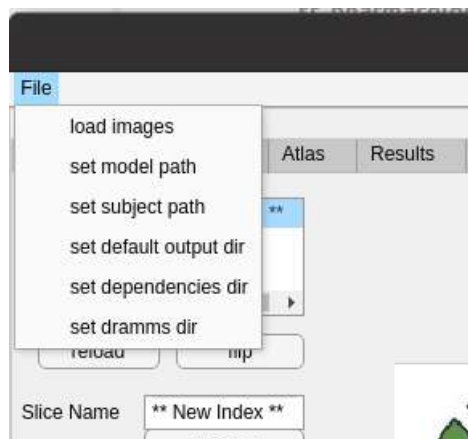
2. Set model path. This is the absolute path for the machine learning model provided with the SA software.

3. Set subject and default output directory paths. Subject path is where SA will try and locate brain images. Output directory is the default location where SA will save the analysis data.
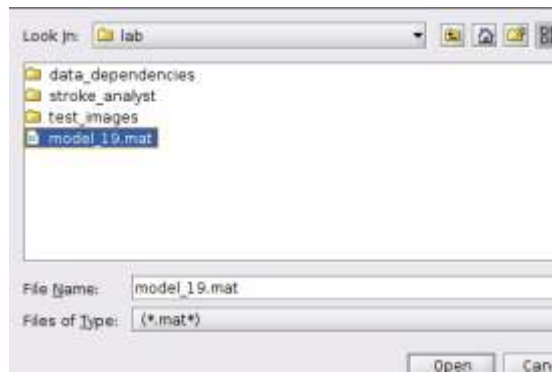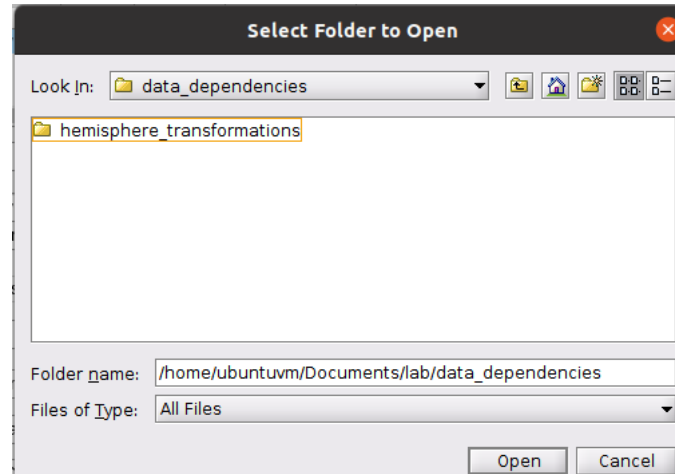
4. Set dependencies directory. Dependencies directory is a folder containing additional files needed for the analysis (e.g. TTC atlas, Allen anatomical masks, etc.) and it is provided with the SA software. Select the absolute path:

5. Set dramms directory. For Dramms software to integrate with SA you must set the absolute path the dramms **bin** folder. "bin" folder is located under the dramms installation directory.
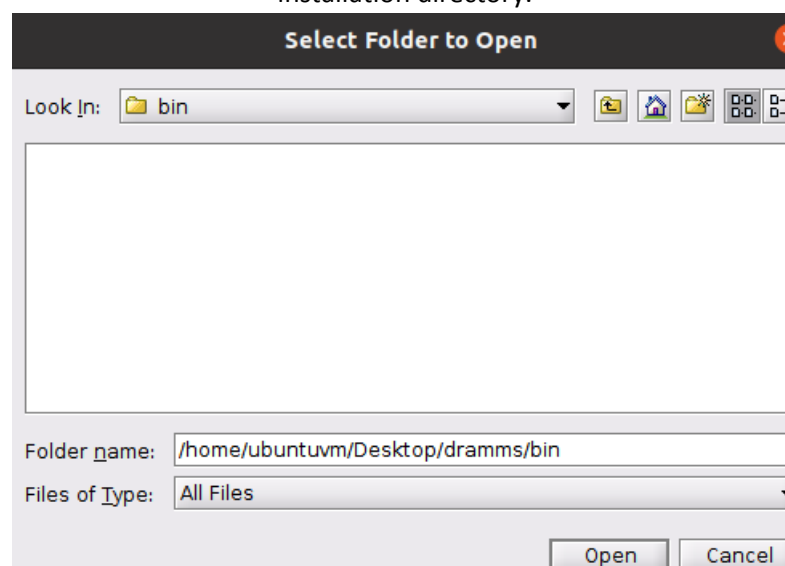
With that step the Dependencies & set absolute paths part is completed and does not need to be repeated unless the location of any of the above dependency data changes.

Basic analysis routes

SA offers multiple analysis tools that can be used in separately or together for the analysis of an ischemic stroke. For a correct analysis to be performed 2 mandatory conditions must be met. 1) Background segmentation must be performed to every not preprocessed brain image and each brain image must be indexed with a location relative to bregma point. The indexing follows a simple number to character convention, e.g. for a brain image/slice presenting at 0,02 (bregma positive) the naming convention should be "bp0_02". Respectively for a brain image/slice located at -0.10 the naming convention follows the same rule, "bn0_10". Note that both decimal points are important and for the previous example you shouldn't use "bn0_1".

Often analysis routes

1. *Load images -> background segmentation (either automatically or semi automatically) -> PCA rotation -> Brain Slice naming -> Lesion Prediction.*
2. *Load images -> background segmentation (either automatically or semi automatically) -> PCA rotation -> Linear registration (verify indexing accuracy) - Brain Slice naming -> Lesion Prediction.*

From the above parent pipelines, several steps that are not needed can be excluded, e.g. Background segmentation, if the image background has been previously removed, or PCA rotation If the brain image alignment Is correct.

Second route, deep dive (step by step)

1. **Load images**. On the left right cornet click on File and then on load images button.
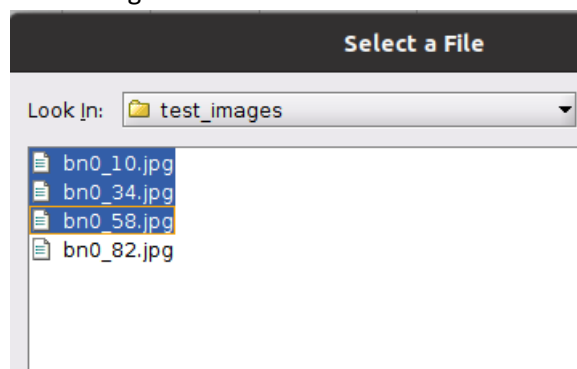

Brain images will be loaded to SA and are going to be presented at the **images tab**.

Different images can be selected from the list element.

2. **Background segmentation** can be performed (fully automatically) using two algorithms presented in under the Data Preprocessing panel at the drop down select list (options**: K&MRF, K&SUPER**); then press the "**BG Segmentation**" button. Results might vary due to different backgrounds and artifacts (e.g. leaks). Either select each separate image from the list or select the "All" (Single - All) option at the bottom of the Data preprocessing panel.
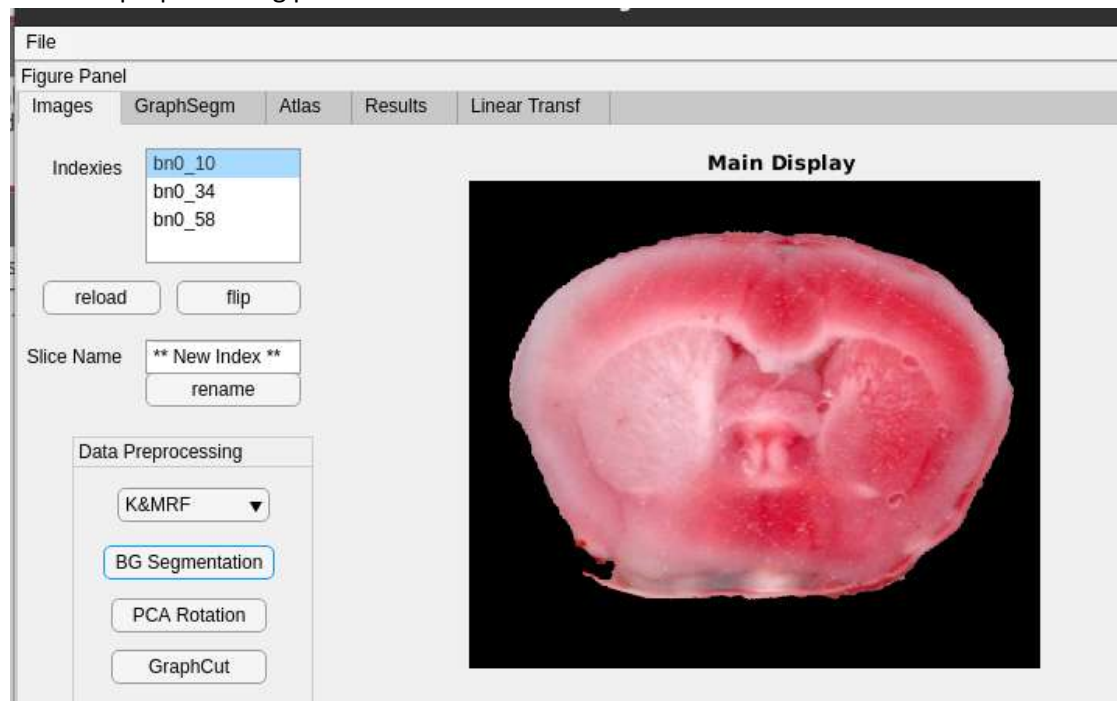
If the result does not satisfy you (i.e. background is not optimaly removed) you can either press the **reload** button or increase the accuraccy of the BG by using the Graph Cut algorithm.

Graph Cut, Semi-Automated background segmentation

To access the Graph Cut (GC) functionality, first select from the image list the image that you want to optimize its BG segmentation and press the "GraphCut" button. Then, from the *Figure Panel*, select the "**GraphSegm**" tab.
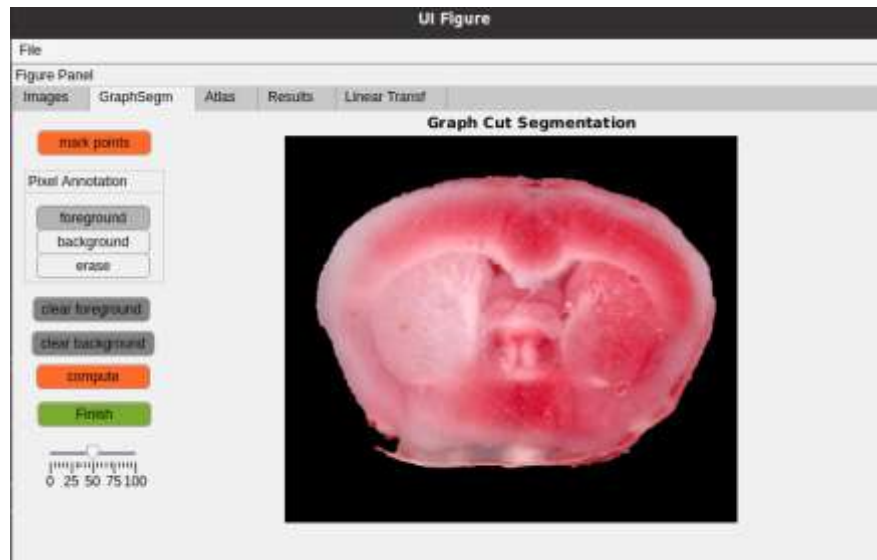

GC operation logic: Annotate (mark points button) some areas that represent the foreground and some that represent the background of the brain image, press the "**compute**" button, and view the resulting BG segmentation. If the outcome is desirable, press "**Finish**" and switch to the *Images tab* to continue the processing of other brain images.

e.g.
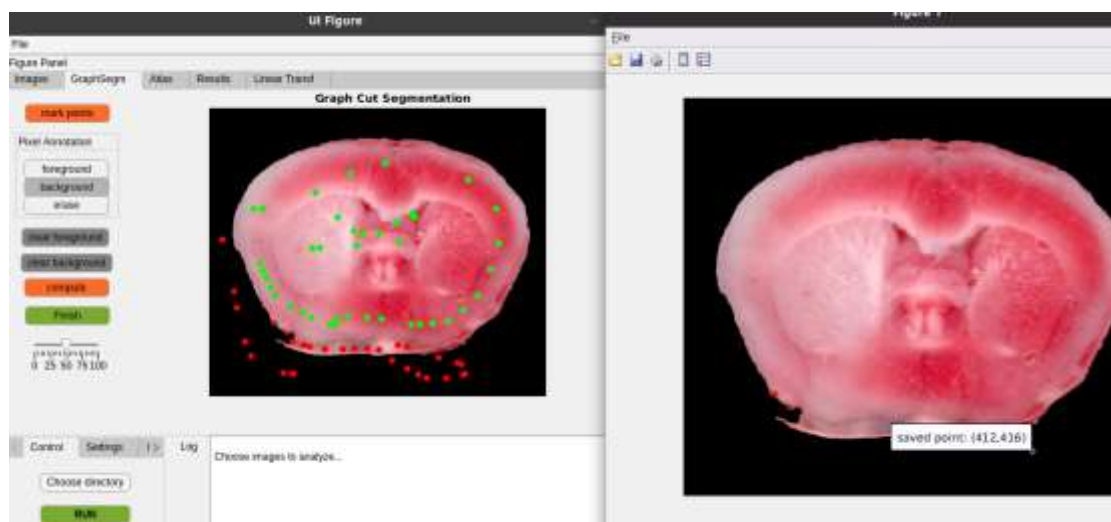
Note: "mark points" button will launch a second interactive display (which you can close when you finish the processing) where you can left click to mark points (or drag your mouse while pressing the left click). You can select to either mark foreground or background points by using the select button (foreground – background) under the Pixel *Annotation tab*.

Compute output:
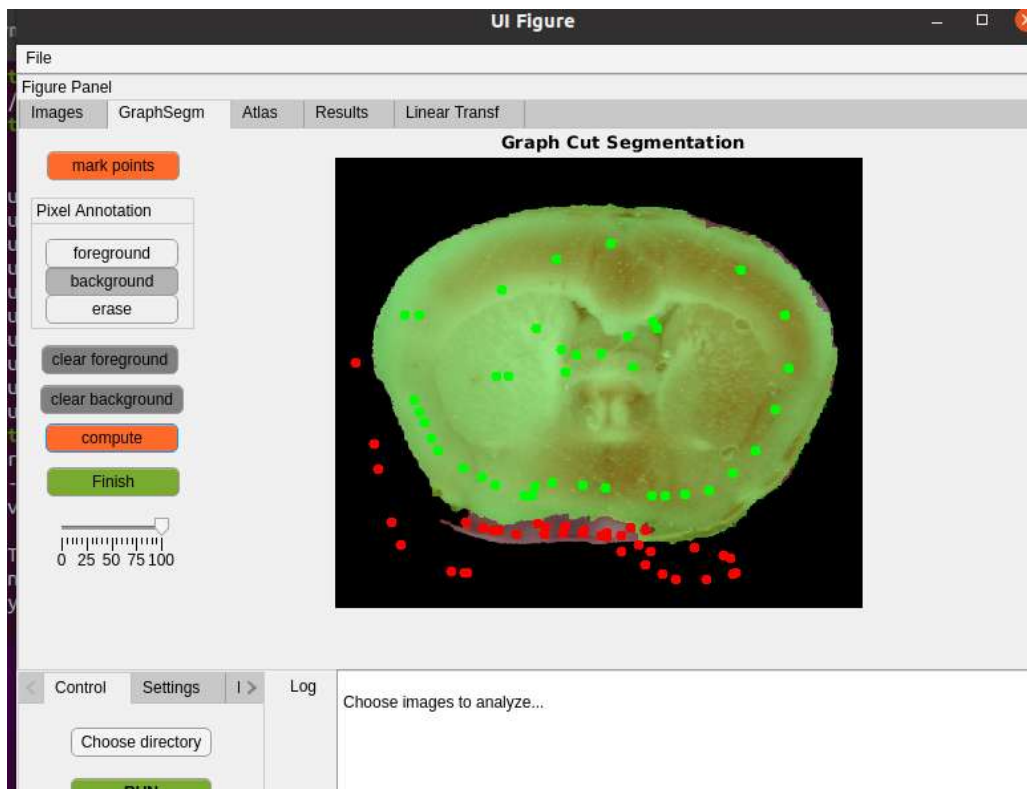
Additional control is provided to the user with the rest of the control buttons (under *Pixel Annotation* panel).

- Clear Background button: Clears all the BG points.
- Clear Background button: Clears all the FG points.
- Drag bar (0-100): Controls the superpixel density of the algorithm [ref:] (Preferred value 100).

3. PCA rotation

PCA rotation is essential in case of large rotational misalignments. Rotational misalignments need to be addressed as, in some cases, might result to failed registration step [ref]. Press the PCA rotation button address for rotation alignments. Note this step can be excluded if brain slices do not present significant rotation misalignments.
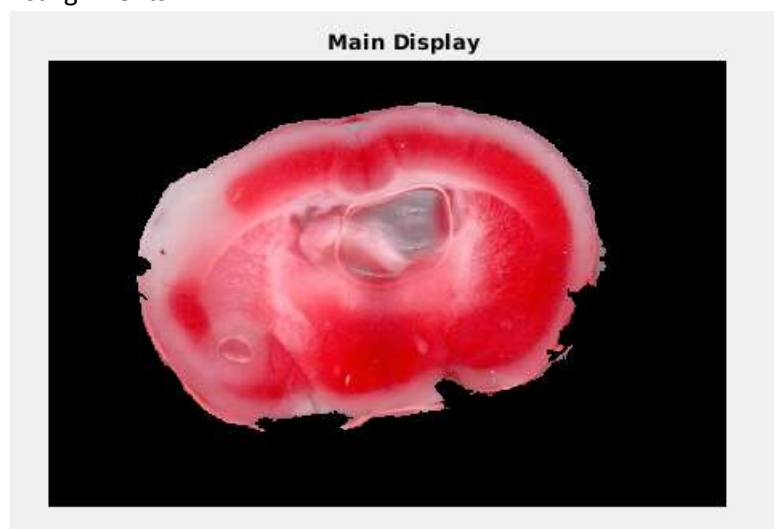
After PCA rotation
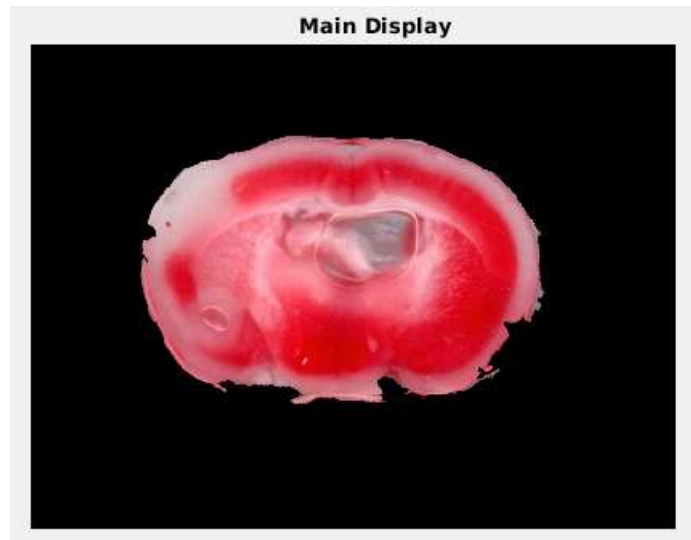
4. **Brain slice naming/indexing – Linear Registration**

Stroke analysis in SA is based in outlier and machine learning techniques. One od the most important aspects of our methodology is to compare a new sample to normal statistics (TTC atlas). SA presents a newly created TTC atlas. Our TTC atlas is provided separately from the SW as well as in it. Access the TTC atlas at the atlas Tab of the *Figure panel*.
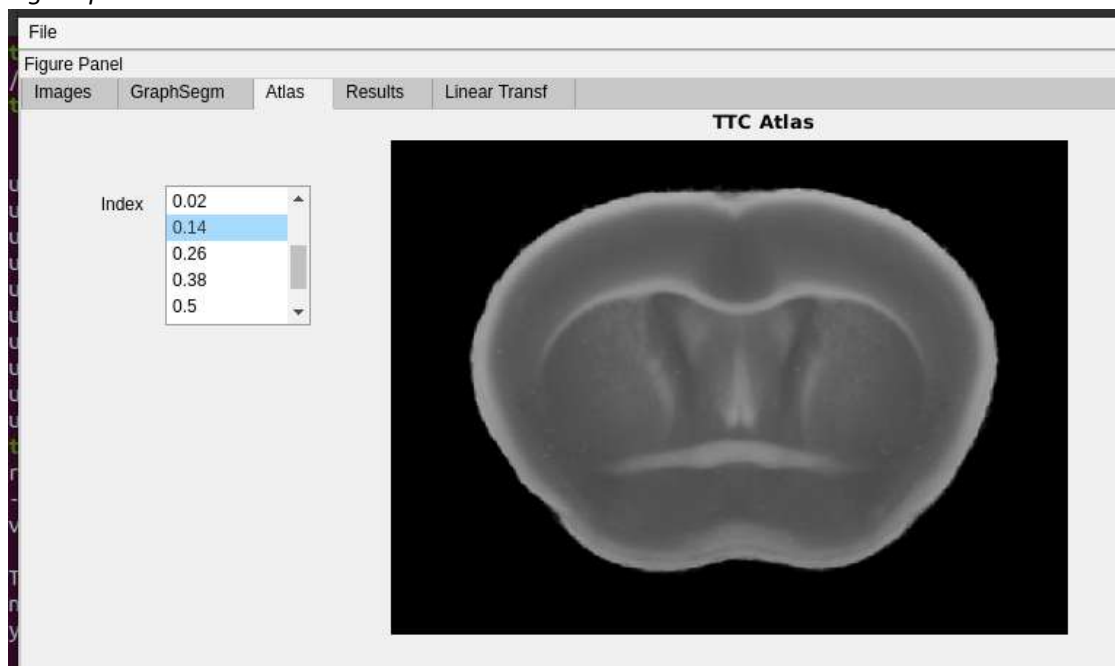

At this step you must index each brain image according to our TTC atlas, this is essential in order to be able to perform comparisons across the correct corresponding brain slices (correct indexing). To evaluate the accuracy of your indexing you could, optionally view the output of a linear registration between the considered brain slice for analysis and its corresponding TTC atlas brain slice. Note that this step is not mandatory (as it is automatically triggered during the analysis) but this visualization it has shown to be very helpful in terms of brain slice indexing, also you can confidently choose between different linear registrations, were this choice is carried out to the automation analysis too.
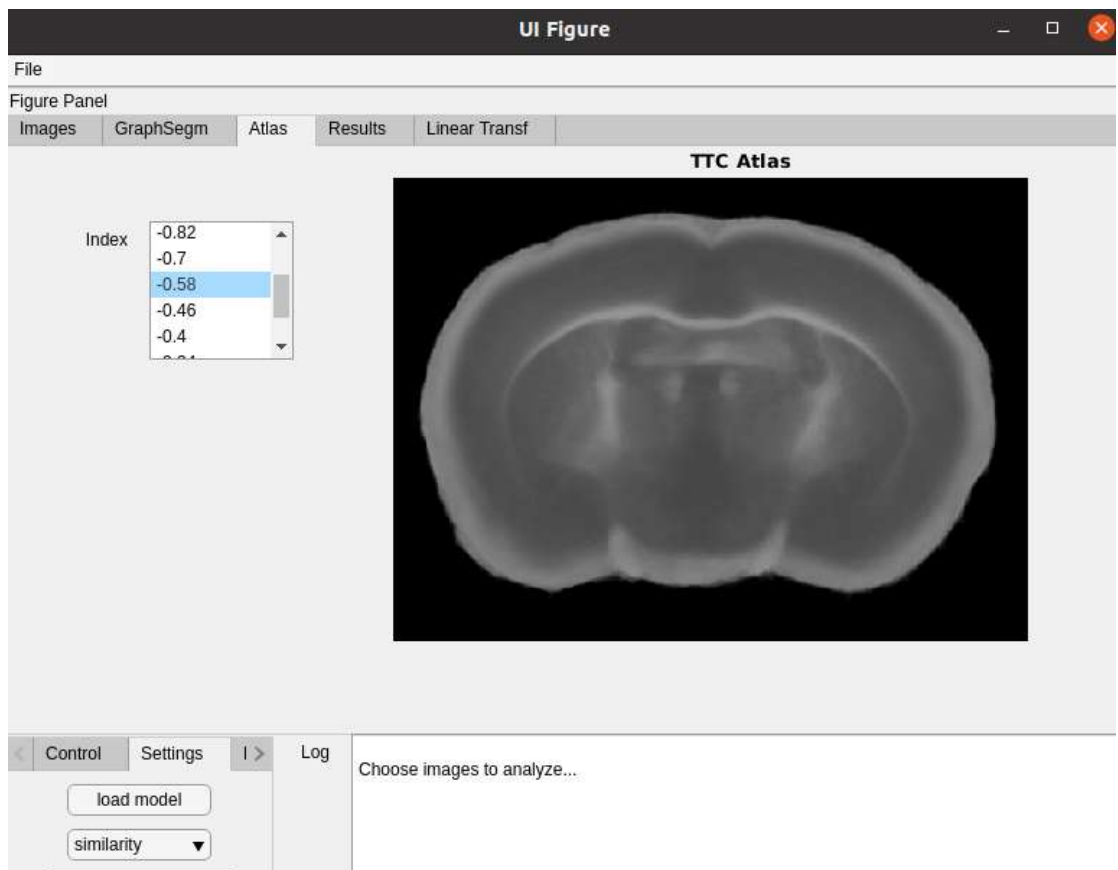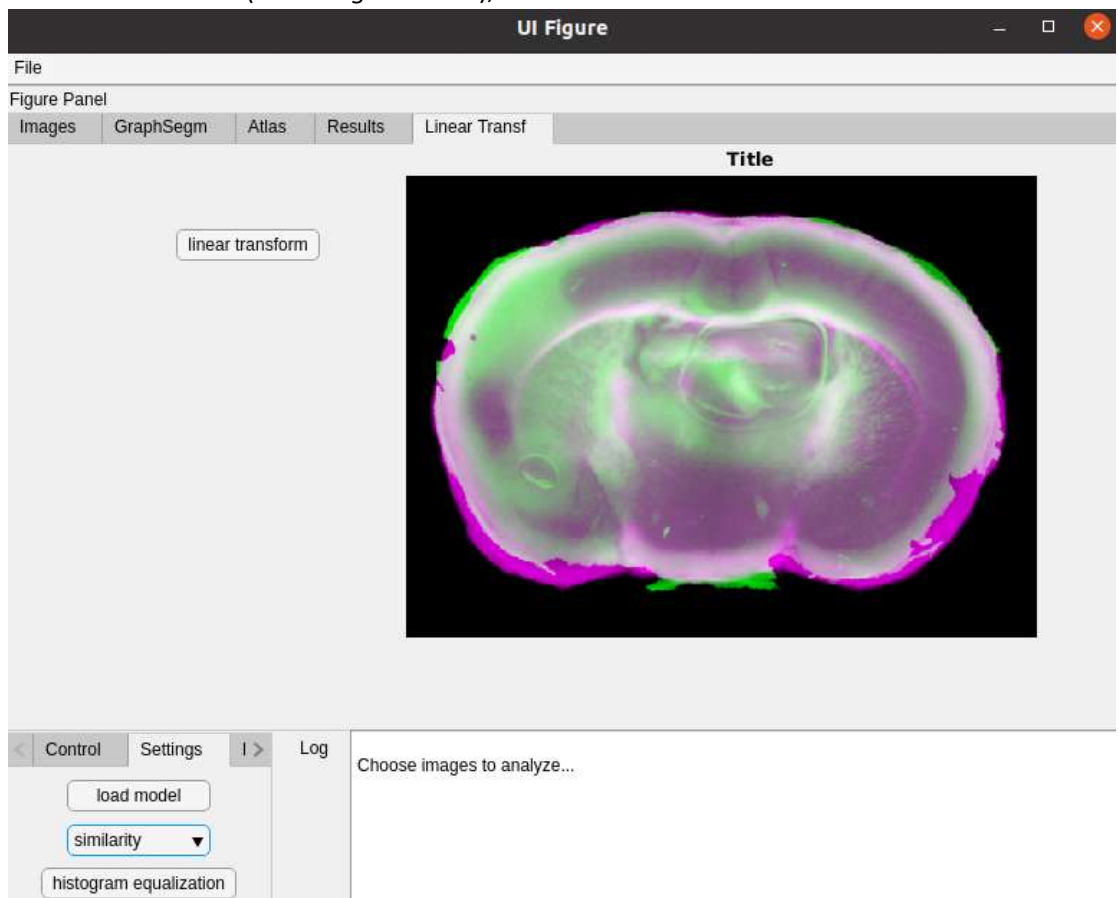
e.g.

For an brain slice under analysis we have chosen the index of "bn0_18", after looking the TTC atlas, we verify that our indexing is correct by performing a linear registration.
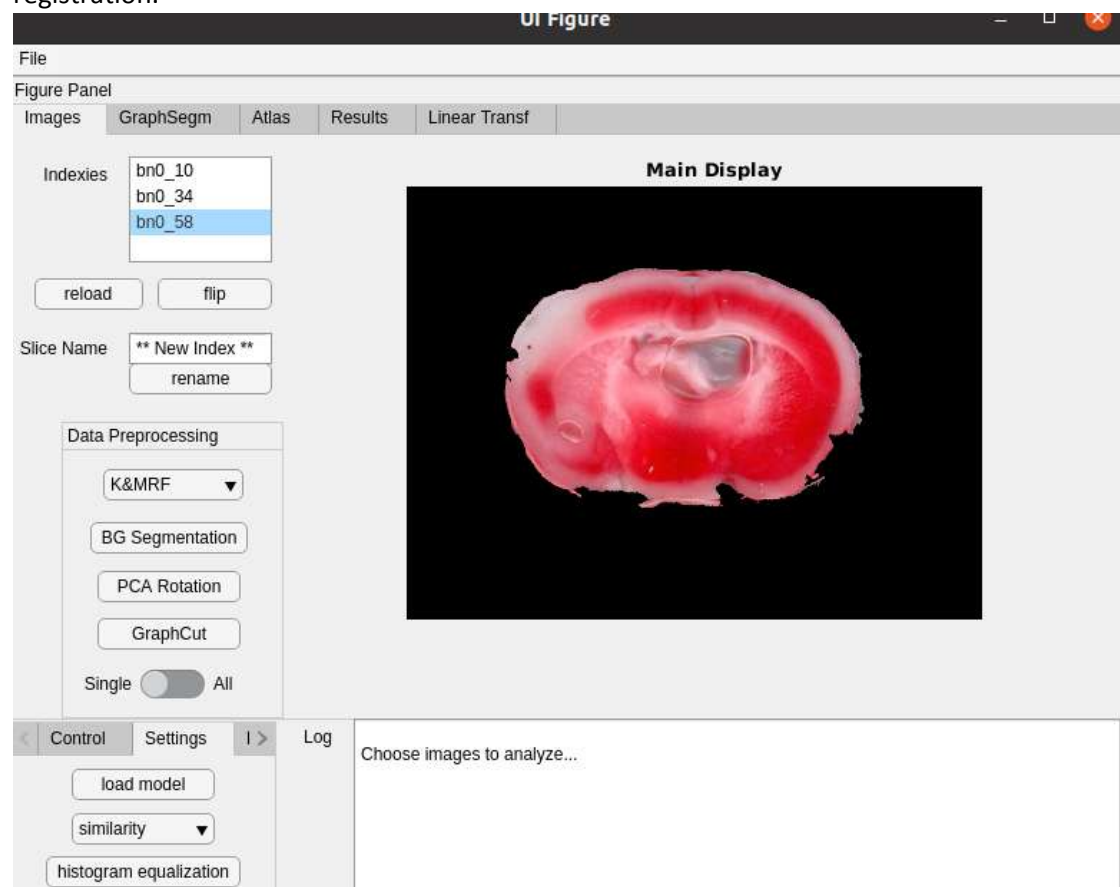
TTC atlas slice

Go to **Linear Transf** (at the *Figure Panel*), and click the **linear Transform** button.

At the display panel you can see the two overlayed brain slices. Gray color indicates small intensity differences, while green color indicates large intensity differences. Different linear registration algorithms can be selected from the panel located at the lower left corner of the SA interface. Possible options are:
- Similarity transformation (**Default**)
- Rigid transformation
- Translation transformation
- Affine Transformation

Where different transformations introduce more degrees of freedom. This linear transformation option that you make will be also transferred to the Automated analysis.

Suggestion: Take some time to experiment with the slice naming procedure, linear registration process time is limited (1-2 secs). Due to TTC slicing procedure, brain slices might present significant deformations, it is important to choose an optimal index.

5. Run analysis:
Prerequisite: Machine learning model must be loaded. Look at figure xx, at the panel located at the lower left corner, press the load model button.
Before running the analysis you have some additional options as a user. 1) Perform analysis for "All" loaded slices or perform analysis for a "Single" slice. 2) Choose a specific output directory (if you don't use this option this will be automatically select the default output directory). Then press the **RUN** button and wait for the results. Analysis time varies depending on the computer hardware (usually 1 – 5 mins).

6. View Results
View Result tab is also located under the *Figure Panel.* Here you can view different results in two side by side displays. If you had previously selected to analyze all load brain slices you could also select different brain slices from the list at the mid-upper left corner. Display options can be selected from two drop down buttons and the available items are:
- Z-score map: indicates deviation from normality (deviations from the registered healthy TTC atlas slice).
- Lesion: is the lesion prediction of the automated analysis presented as a binary image.
- Lesion overlay: Lesion prediction overlayed over the original brain image.
- Reference: is the selected TTC Atlas slice.
- Subject: is the brain slice that has been analyzed.
- Left and Right hemisphere masks: Are the hemisphere masks overlayed to the original brain image.
- Registered: is the original brain slice after being linearly and deformably transformed to the selected TTC atlas slice.

e.g.
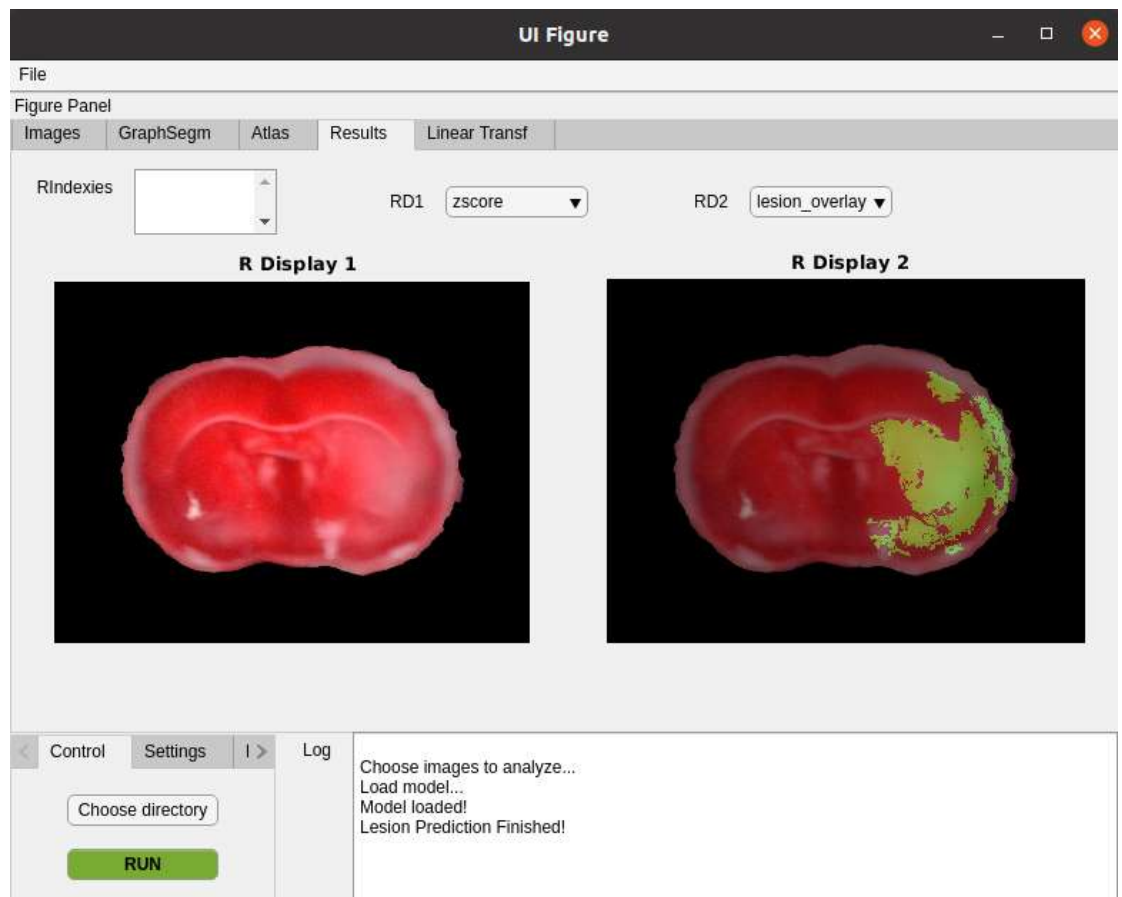
7. Data analysis results (Volumetry and Region Identification)
   Stroke Analyst generates various result data. All result data are generated in their own separate folder. Folder name follows a name convention: <date>_<bregma index>. Inside this folder various metadata are generated alongside a folder containing the analysis results. Said results are:
   - Affected Regions (txt file)
   - Volumetry Data (excel file)
   - Lesion prediction image
   - Hemisphere detection images
   - Reference image (TTC atlas corresponding brain slice)
   - Registered image

8. Manual Lesion Correction. SA presents a manual lesion correction functionality (to address for challenging brain slices/regions) where the user is capable of manually removing or adding lesion areas.
   e.g.
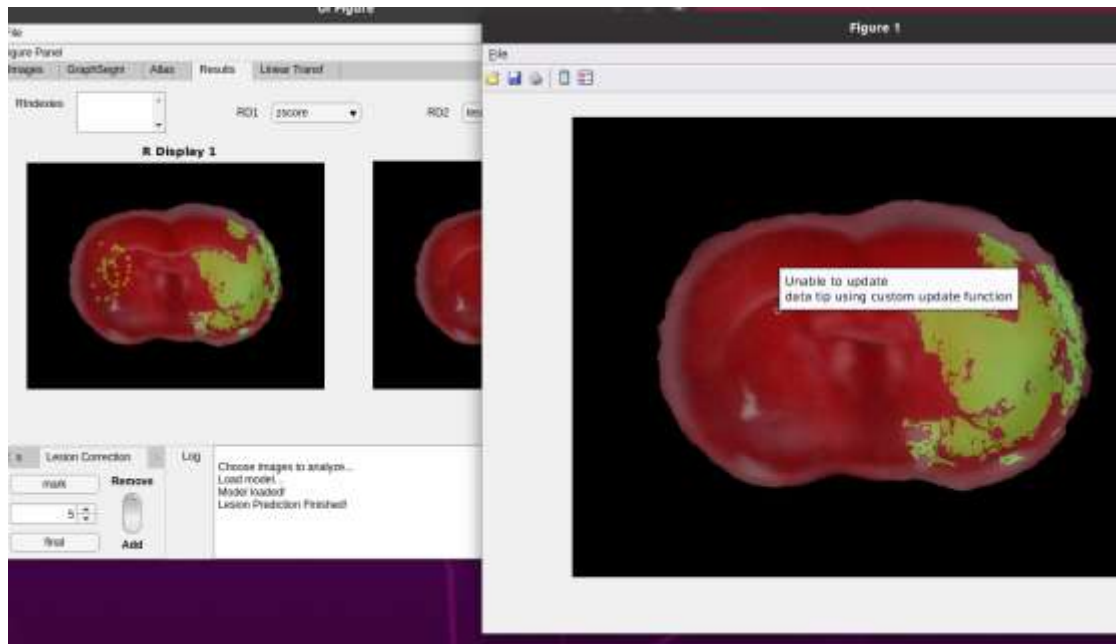
Using the bottom left panel, select *Lesion Correction.* Here you can either add or remove areas with a brush-like tool. Furthermore, you can select the size (radius) of the brush tool. Upon finishing the lesion correction, press final, this will also update all the result data.