## **VL Python GUI Protocol**

This document describes installation instructions and standard operating protocol for the VL Python GUI. The GUI has only been tested on Windows but should also work on Linux and is built in Python using Napari, PyQT, and Pytorch. The GUI requires an NVIDIA GPU as CUDA is used.

If you have any questions, please contact us at the emails listed in VL\_CSA\_documentation\_v2.pdf

## Installation

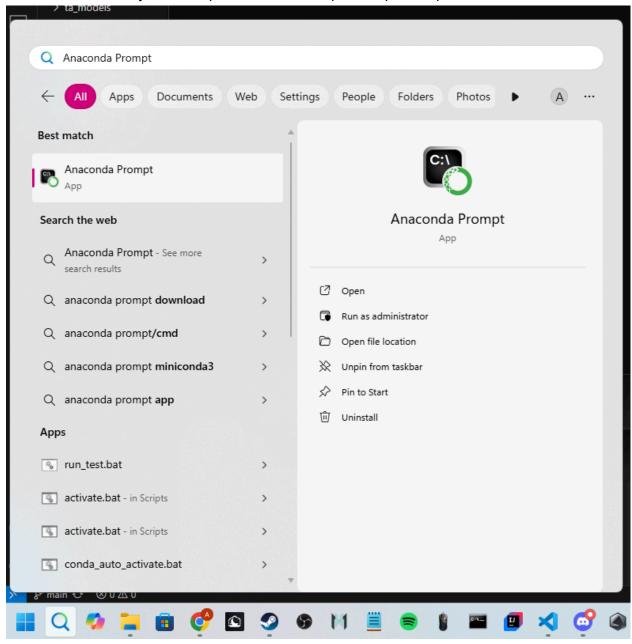
This GUI has only been tested on Windows but following these instructions should also work on Linux.

- 1) Make sure NVIDIA Drivers are installed and preferably up to date. This can be done through the NVIDIA app.
- 2) Sign up for Anaconda and download Miniconda at: <a href="https://www.anaconda.com/download">https://www.anaconda.com/download</a>
- 3) Now that Miniconda has been installed, press windows and search for "Anaconda Prompt". Open it up and let it set up.
- 4) Download this Github Repo either as a zip and extract it or through git clone.
- 5) In the Anaconda Prompt, navigate to this Github repository using:
  - a) cd PATH\_TO\_GITHUB\_REPO/NAPARI\_DCM\_GUI Replacing PATH\_TO\_GITHUB\_REPO with your path to this Github repository
- 6) Run the following commands to set up the environment
  - a) conda create -n napari python=3.10
  - b) conda activate napari
  - c) pip install -r requirements.txt
- 7) Download the model at <a href="https://huggingface.co/kenziew/ultrasound\_vl\_csa\_and\_ei/blob/main/model\_trace.pt">https://huggingface.co/kenziew/ultrasound\_vl\_csa\_and\_ei/blob/main/model\_trace.pt</a> and copy it into the vl models folder within NAPARI DCM GUI.

## **Standard Operating Protocol**

 If you are continuing analysis from a previous session, disregard this step. Make sure vl\_output DOES NOT exist as a folder within NAPARI\_DCM\_GUI. Otherwise, previous sessions of the muscle group specific GUI will be remembered.

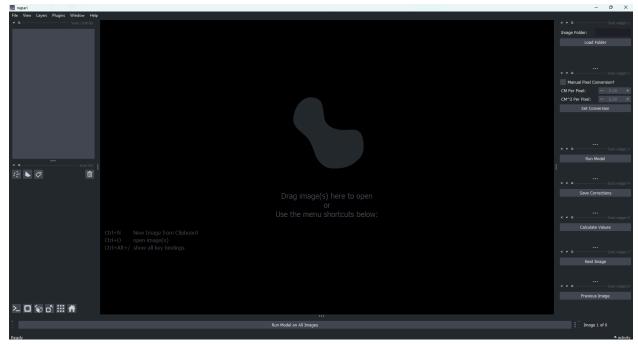
2) Press the window key, search up "Anaconda Prompt", and press Open.



This process should look like the above

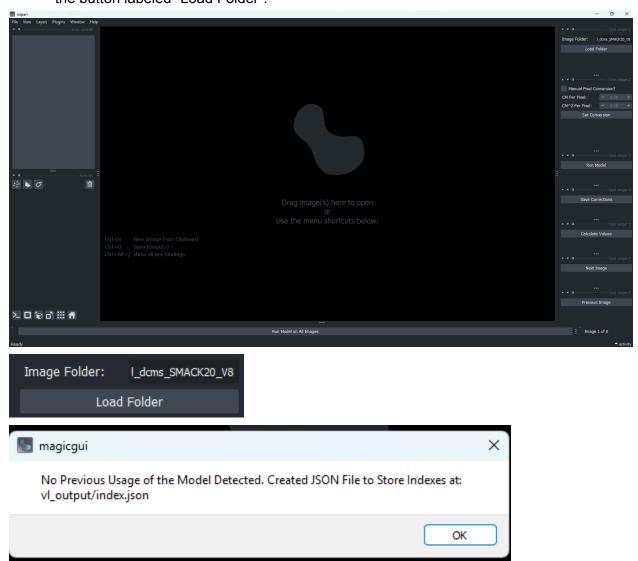
- 3) Navigate to the directory this repository is in using:
  - a) cd PATH\_TO\_GITHUB\_REPO/NAPARI\_DCM\_GUI
    Replacing PATH\_TO\_GITHUB\_REPO with your path to this Github repository
- 4) Run the following commands:
  - a) conda activate napari
  - b) python napari\_gui.py

Now the GUI should pop up which looks similar to below.

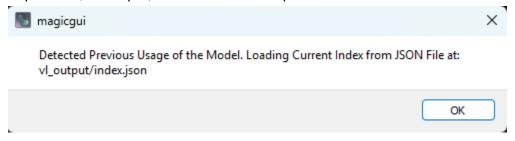


5) Find the path for the study folder on which you wish to run the model. Make sure the folder **ONLY** has ultrasounds in **DICOM** format of the **VL** and no other images or files. Note that all sub-folders will be accessed and the study subfolder structure will be copied in the output for easy navigation.

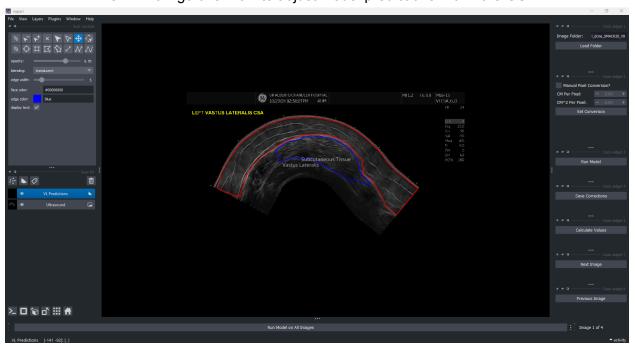
6) Copy the study folder path into the top right textbox labeled "Image Folder:" and press the button labeled "Load Folder".



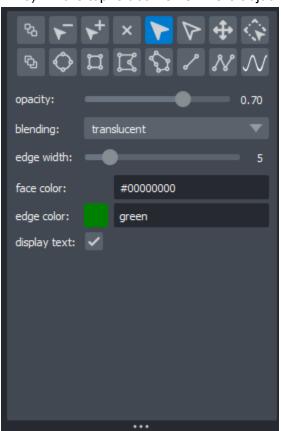
You should get a popup message similar to the above. However, if instead it states that there has been previous usage of the model like below, this means that the GUI will continue on from a previous session and unless you are continuing analysis from a previous session, close the Napari GUI, do step 1, and restart from step 4.



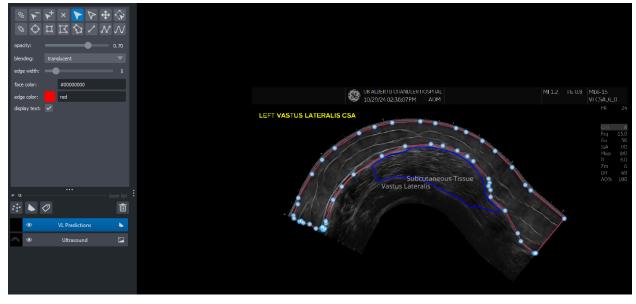
- 7) There are two manners in which the VL model can be used within this GUI. These can be mixed and matched, however, using the method described below in a) will overwrite all previous progress made on a study so make sure to do a) before b) if mixing approaches.
  - a) If you would like the model to run on all the images without human adjudication, simply press the button on the bottom labeled "Run Model on All Images". A popup message will appear once analysis is over and visualizations and clinical value estimations will be put into the output folder, vl\_output. More information on the output can be found by skipping ahead to Step 12.
  - b) If you would like to adjudicate the model's predictions, one image at a time, the first ultrasound in the image folder should have popped up already like below and we will now go over how to adjust model predictions within the GUI.



8) In the top left corner is where adjudications to the predictions can be made.



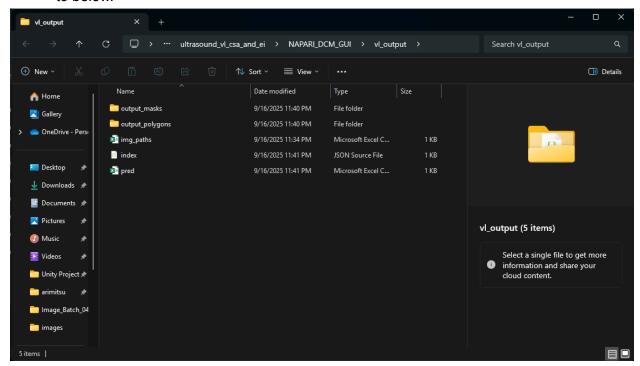
The button in the first row, second column can be used to remove points in the outline of the mask and the button in the first row, third column can be used to add points in the outline of the mask. The button in the first row, fifth column (the button selected/highlighted in the image), can be used to select and edit a prediction. The button in the first row, seventh column can be used to move around the image. Below are a few images showcasing how editing works.



Above, the prediction of the subcutaneous tissue has been selected. Now, these points can be moved around or more points can be added. Play around and get familiar with the interface. One thing to note is that the labels (the grey text) are placed in the center of the mask, regardless of whether that overlaps with another one (please let us know if there is any way to avoid this). Thus, it is important to remember that the vastus lateralis is blue and the subcutaneous tissue is red.

- 9) Once you have determined the model predictions are adequate, you may click the "Next Image" button to move to the next image in the study. This button will automatically save the current state of the predictions in the GUI and save clinical values based on the predictions. You may also manually save these by pressing the "Save Corrections" and "Calculate Values" respectively. You may view the previous image before the current one in the GUI by pressing the "Previous Image" button and you may rerun the model on an image by pressing the "Run Model" button.
- 10) SPECIAL CASES: There may be some images which have various problems with them. Perhaps the model is unable to predict any region in the image to be a part of the vastus lateralis, or the cm per pixel conversions may not be read correctly automatically from the DICOM metadata.
  - a) In the first cases, a fallback mechanism has been put in place where a square mask will appear if the vastus lateralis or subcutaneous tissue has not been predicted. Please adjust this mask to the correct region on the ultrasound.
  - b) In the second case, you may check the box called "Manual Pixel Conversion?" and input the conversions of centimeters and centimeters^2 per pixel into the textboxes called "CM Per Pixel:" and "CM^2 Per Pixel:" and press the "Set Conversion" button. Then, you may press the "Calculate Values" button to get clinical values.
- 11) You may take breaks or even close the GUI. The current image you were on before closing the GUI will be saved and the next time you open up the GUI and follow steps 1-6, it should open up to the last viewed image.

12) Once you have finished with all the images, you will end up with an output folder similar to below.



The folder "output\_masks" will contain visualizations of the model predicted/human adjudicated predictions, which may be useful for figures in your research and to check the quality of ultrasound annotations. The csv "pred" contains all clinical values needed for research purposes such as muscle thickness, cross-sectional area, and echo intensity. The other files are simply used by the GUI for various utility purposes.

13) Remember to copy this output folder to another location for safekeeping and delete the output folder (vl\_output) once you are finished.