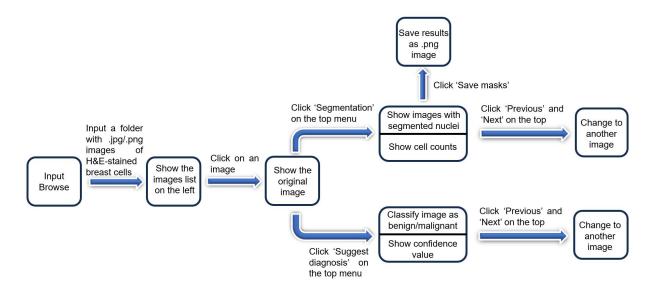
Documentation of Brachistools

Welcome to using our software Brachistools!

Our software is designed to segment nuclei from histopathology breast cancer images and is aimed at diagnosing the cancer type (malignant / benign). Here is an overview of the basic workflow of our software.



Instructions of usage

1. Download the software

The instructions are uploaded to GitHub: https://github.com/tony-yuan33/brachistools. You can follow the command lines to download our software.

Once you have entered our GitHub, you can open README.md from the file list.

1) Go to the *Installation* section for basic installation of our software.

Open your terminal. Enter a directory for cloning the repo.

Clone the repo through git clone https://github.com/tony-yuan33/brachistools.git.

Enter the repo through cd brachistools.

Install GUI through python -m pip install .[gui].

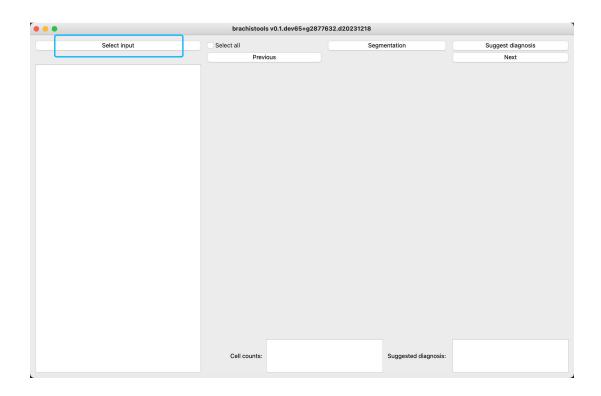
2) Check the *Running locally* section to run the software.

Open the GUI through python -m brachistools gui.

For more details, please refer to README.md.

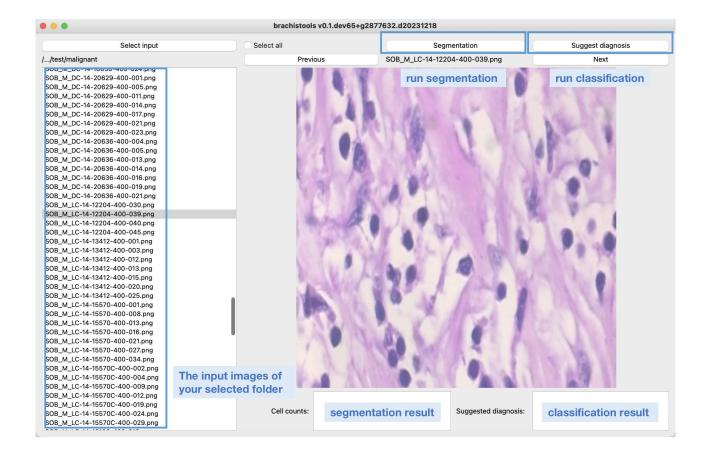
2. Upload the file

Once you have successfully opened our GUI interface, you should upload the image folders first for analysis. Click Select input to upload your folder.



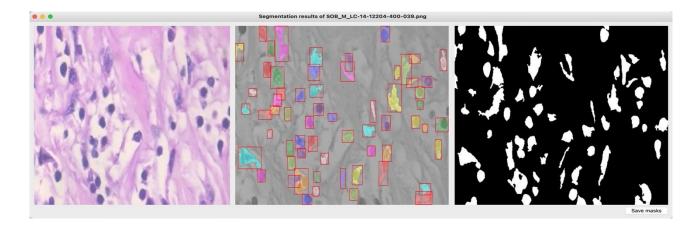
3. An overview of the software interface

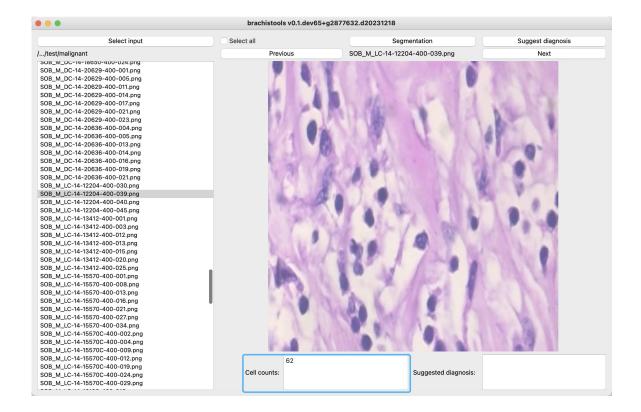
The screenshot provided here shows the interface of our software. Once you have uploaded the image folder, you can try with the buttons Segmentation and Suggest diagnosis to run segmentation and classification tasks. Additionally, the Previous and Next buttons allow you to conveniently navigate through the images.



4. Segmentation results

Click the Segmentation button to run segmentation. Here are the results integrated with the original image (left), segmented nuclei with bounding boxes (middle), and the mask generated (right). You can click the Save masks button on the bottom right corner to save the results. The number of nuclei separated is also shown on the main interface.





5. Classification results

After performing the classification, the predicted diagnosis result with its confidence is shown.

