HYPHAEdelity User Guide

Prepared by: Lisa Rogers, PhD and Scott Britton

Last Edit: October 21, 2022

INTRODUCTION

HYPHAEdelity is an application created by Dr. Lisa Rogers and Scott Britton to automate the assessment of two-dimensional whole colony images and quantify the magnitude of peripheral whole colony yeast filamentation. The software application functions by determining the total area of filamentous growth, referred to as the f-measure, utilizing image analysis tools intrinsic to the OpenCV Python library. The data from this analysis is output as a set of binary files and a single statistics-containing csv file.

This guide provides instructions for downloading and using HYPHAEdelity. The full explanation of the methods used to analyze the images and produce statistics is given in Britton, S., Rogers, L., White, J., and Maskell, D. (2022). There are five sample images available on Github for additional software verification.

HYPHAEdelity is freely available for download at https://github.com/unstablelimitcycle/hyphaeDetection/tree/main/hyphaeDelityGUI.app/Contents. Bug reports should be submitted to dr.lisa.j.rogers@gmail.com.
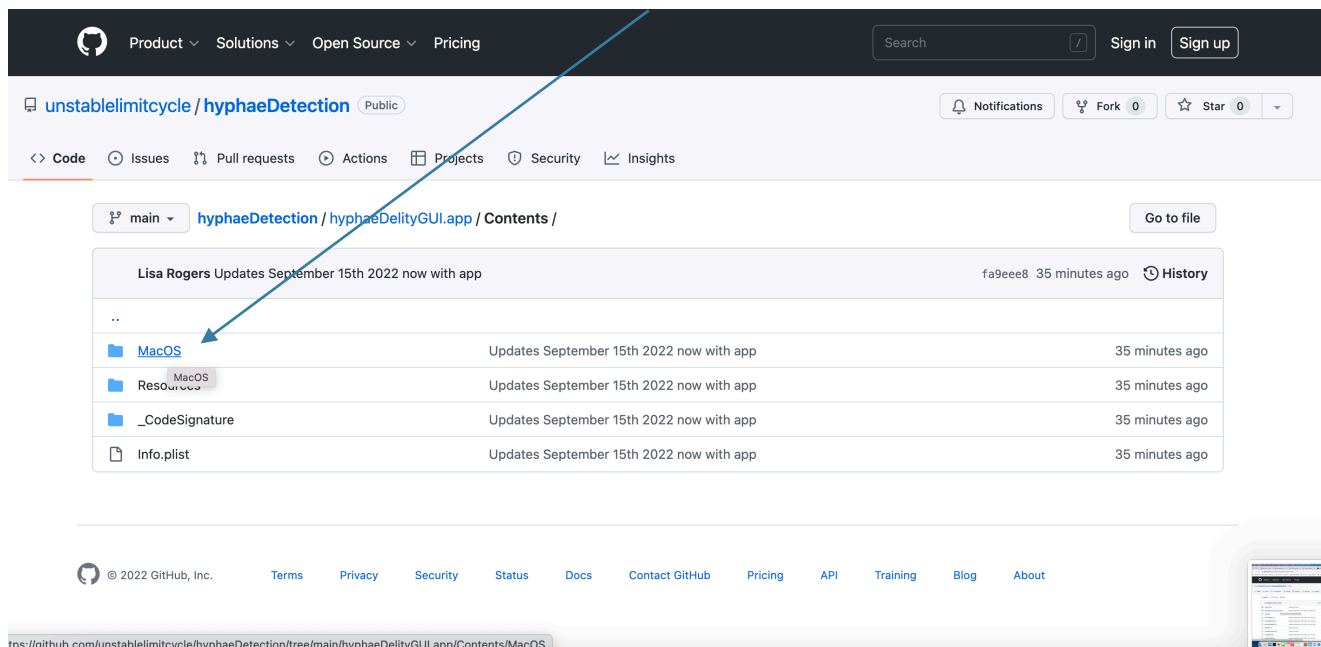
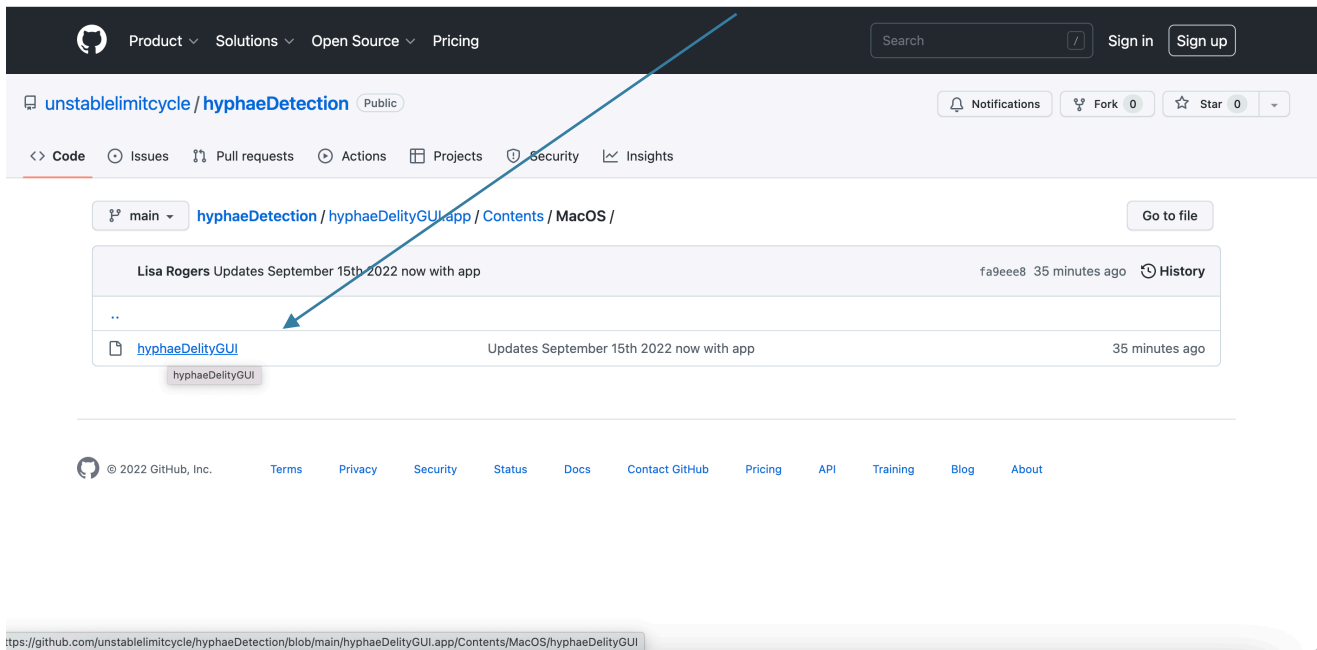# INSTALLATION

1. Download hyphaeDelityGUI.app from GitHub.

It's freely available at https://github.com/unstablelimitcycle/hyphaeDetection. Once you navigate to the website, click the hyphaeDelityGUI.app/Contents folder.
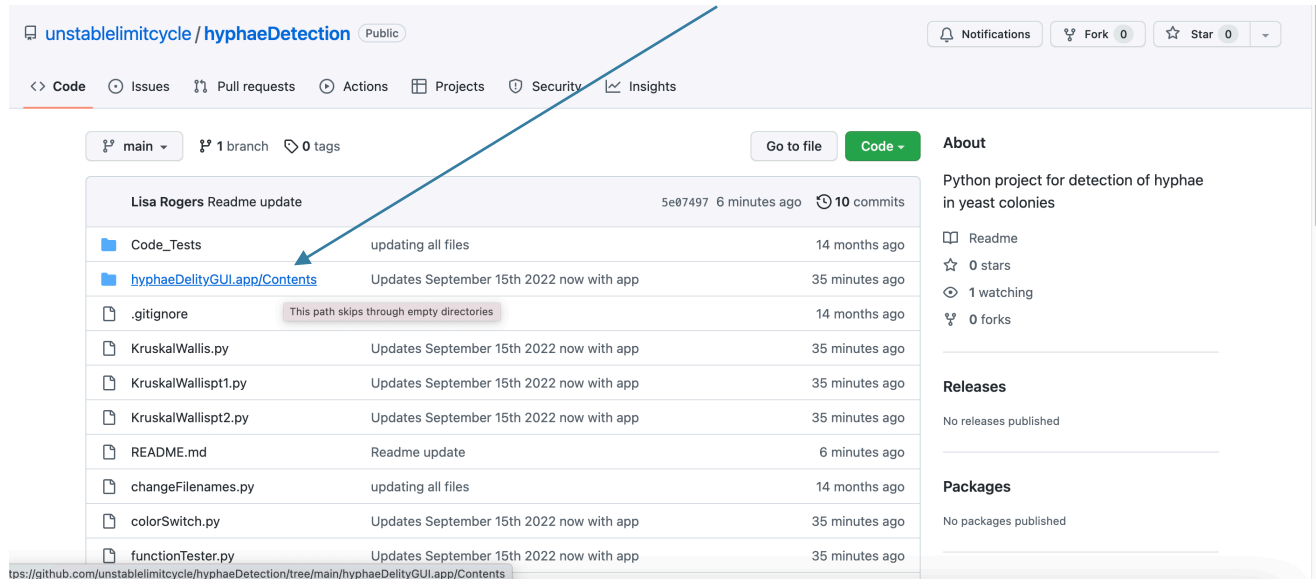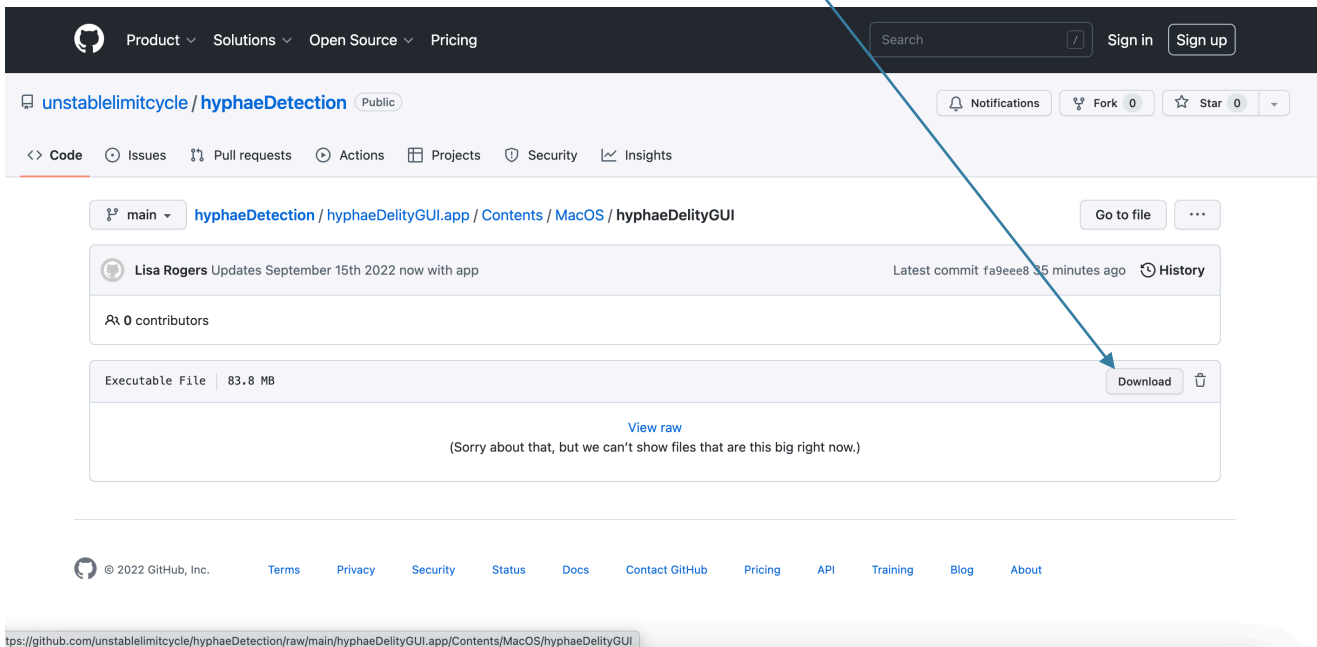

2. Once in the Contents folder, click the MacOS folder.

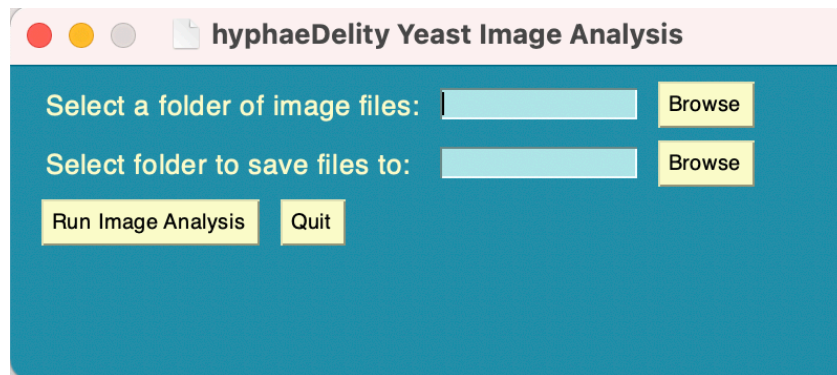3. Once in the MacOS folder, click the hyphaeDelityGUI link.

4. In the hyphaeDelityGUI folder, click download.

INPUT

1. Once downloaded, double click the hyphaeDelityGUI.app file. It takes approximately 15 seconds to load, so if you see the icon pop up and disappear, don't fret! HYPHAEdelity is loading!


2. Once the app opens, you will see the above window. Click the first Browse button to select a folder of image files to analyze. A Finder window will open with your files. Select the desired folder of images.
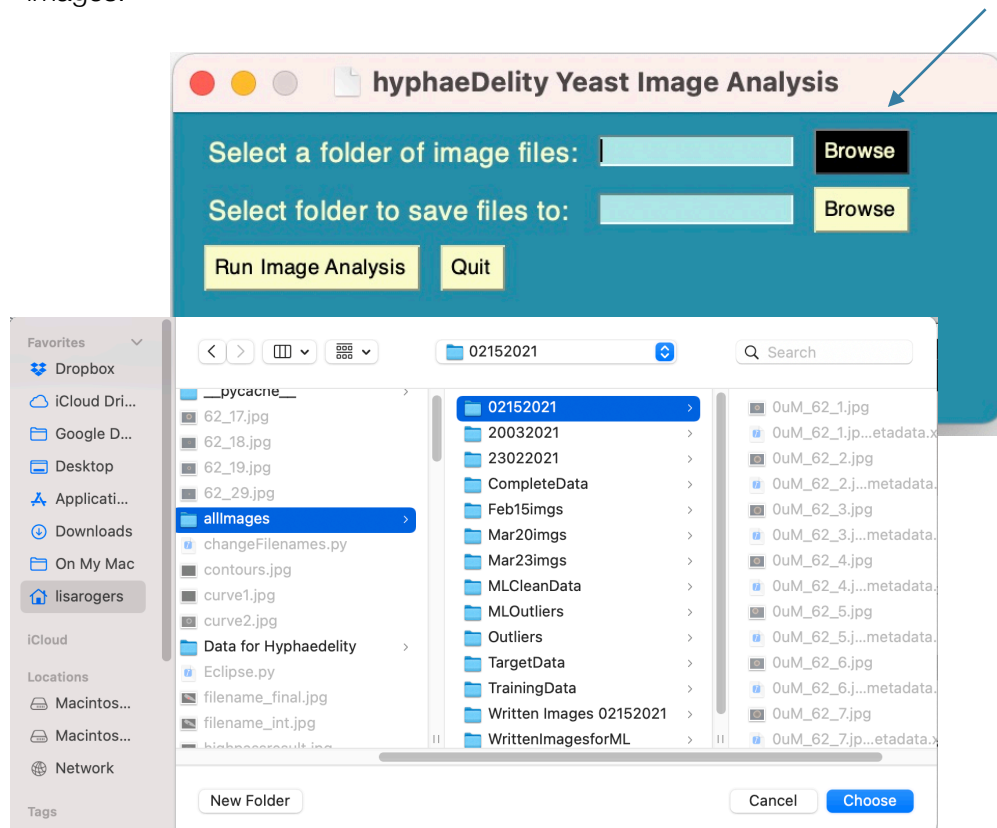
3. Once you have designated a folder of images to open, use the second Browse button to select a folder to save the analyzed output files in. A Finder window will open with your files. Select the desired folder to save your output files.
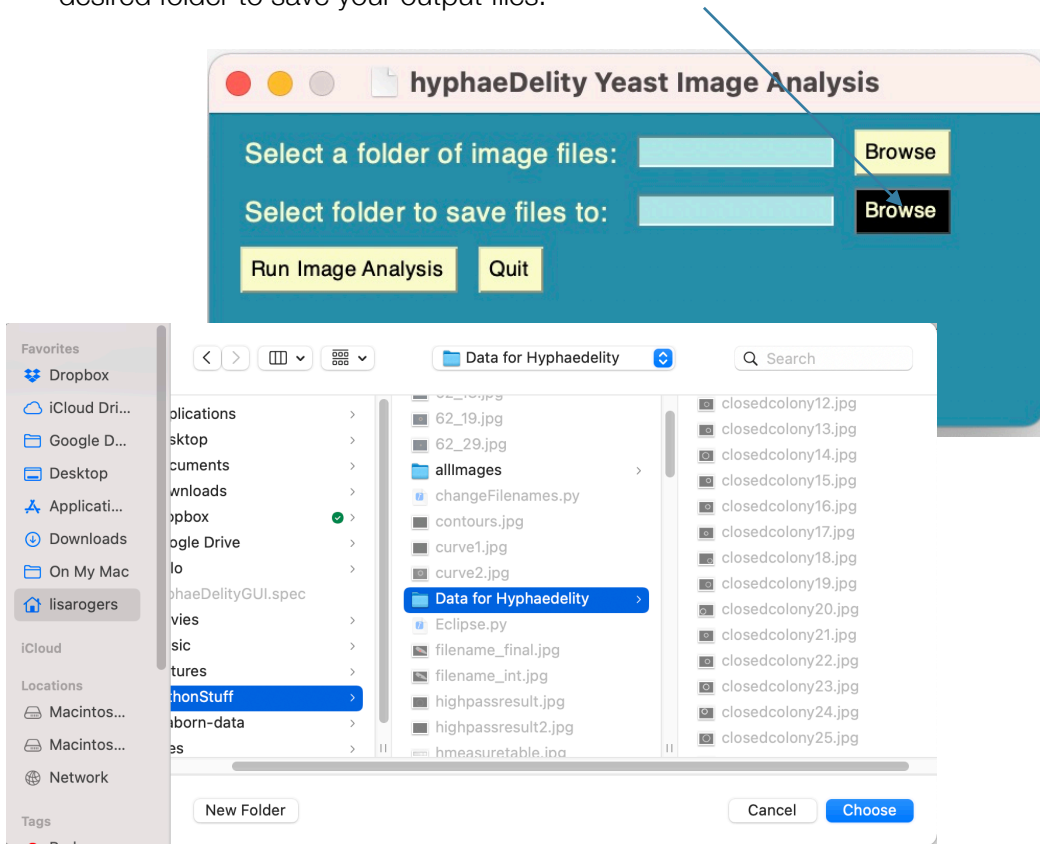
4. Once all folders have been chosen, click the Run Image Analysis Button. The window will automatically close when the analysis is done.
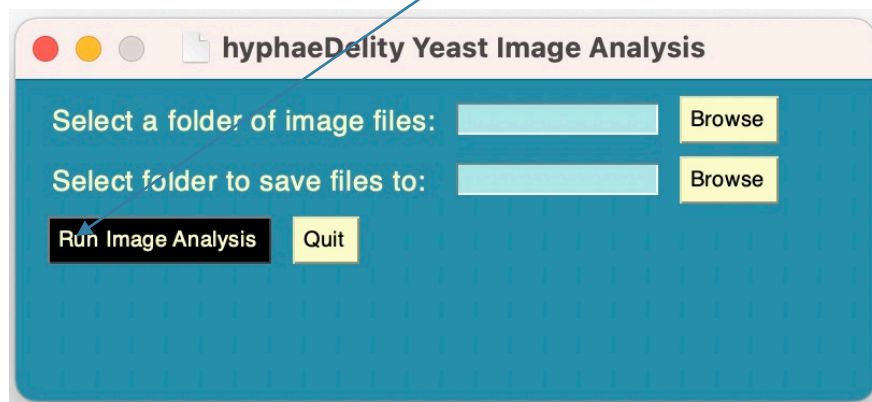
OUTPUT

1. **Statistics**

   The statistics are saved as a .csv labeled "Test Data Output.csv" in the folder you designated to save analyzed output files. The first column of the .csv contains the image name, the second column contains the inner contour area, the third column contains the outer contour area, and the fourth column contains the f-measure.

2. **Binary Files**

   The following three sets of binary files are output to the folder that you designated when running hyphaeDelity:

   - **binarycolony[number].jpg:** The initial binarized colony file - just the image converted to black and white.

   - **closedcolony[number].jpg:** The binarized colony image file with all morphological changes required for accurate OpenCV analysis.

   - **allContours[number].jpg:** The binary file of the two main drawn contours - the inner colony ring and the hyphal projections.

REFERENCES

Britton, S., Rogers, L., White, J., and Maskell, D. (2022), HYPHAEdelity: A quantitative image analysis tool for assessing whole peripheral colony filamentation. Under review at FEMS Yeast Research.