Directory

Installation

The sections below explain how to download and install app on your computer.

- Create a Conda environment: Use the following command to create a Conda environment named name with Python version 3.9:

```Bash
conda create -n name python=3.9.19
```

- Activate the environment: Activate the newly created Conda environment using the following command:

```Bash
conda activate name
```

- After activating the Conda environment, run the following command to install necessary scientific computing and image processing libraries listed in the `requirements.txt` file.

```Bash
python -m pip install -r requirements.txt
```

Download Node.js and npm; Node.js version 18.20.3 has been verified to be usable. The relevant paths need to be configured for global access.

Introduction

This tutorial introduces how to use the app to assess mitochondrial health. It covers the entire mitochondrial health assessment process within the app: mitochondrial image evaluation classification, segmentation, post-processing, and precise calculation.

This tutorial uses mitochondria from myocardial tissue provided by Southern University of Science and Technology as the test dataset. This dataset was collected using FIB-SEM electron microscopy.

The system is divided into three main sections: classification assessment, image segmentation and precise calculation.
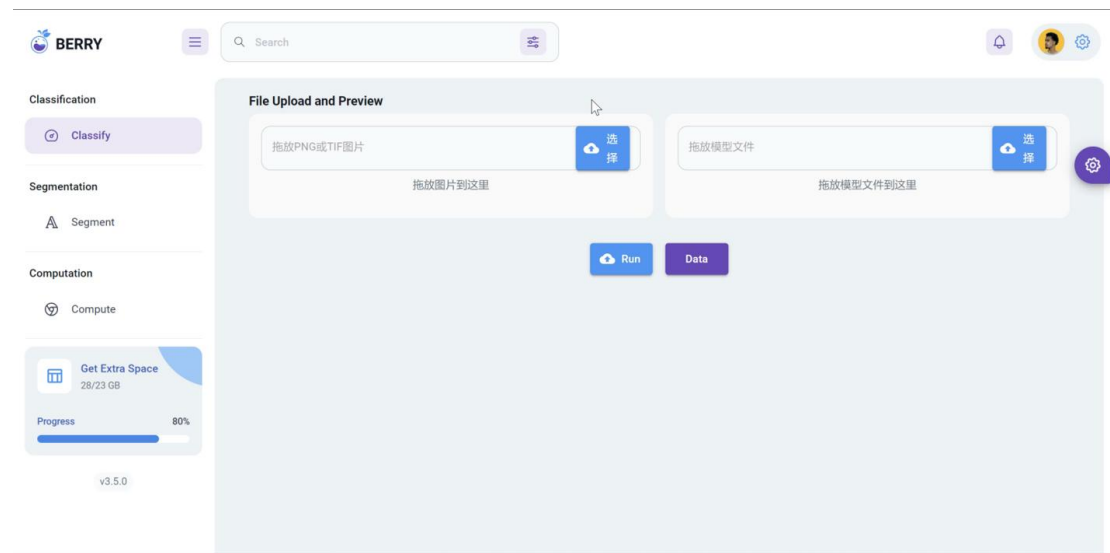
Classify

We will start by launching the app GUI. First, open the software package and navigate to the scripts directory. Open a terminal at this location and enter the command conda activate name to activate the previously created conda virtual environment named 'name'. Next, open an Administrator Command Prompt and use the cd command to navigate to the AMM-Seg/vite/ directory of your project. Then, type npm start to run the project. This will open a browser and navigate to http://localhost:3000/free.
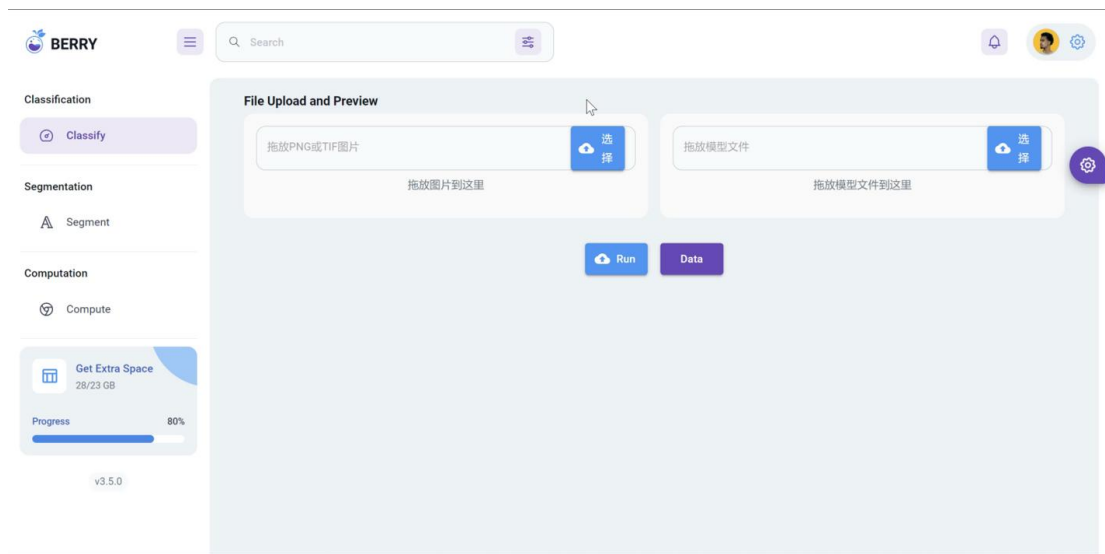
First, you need to upload the image and weight files. Fill in the following parameters in the 'Segment' tab:

1. **Tomogram path**: Click the "choose" button to select the file path. Supported file formats include png, tif, and mrc.

2. **Net weights path**: Click the " choose " button to select the file path. Supported file format is pt.

Then, click the "Run" button. After the image processing is completed, clicking the "data" button will navigate to the data display interface. On the left is the original image, in the center is the classified image, and on the right is the data statistics pie chart.
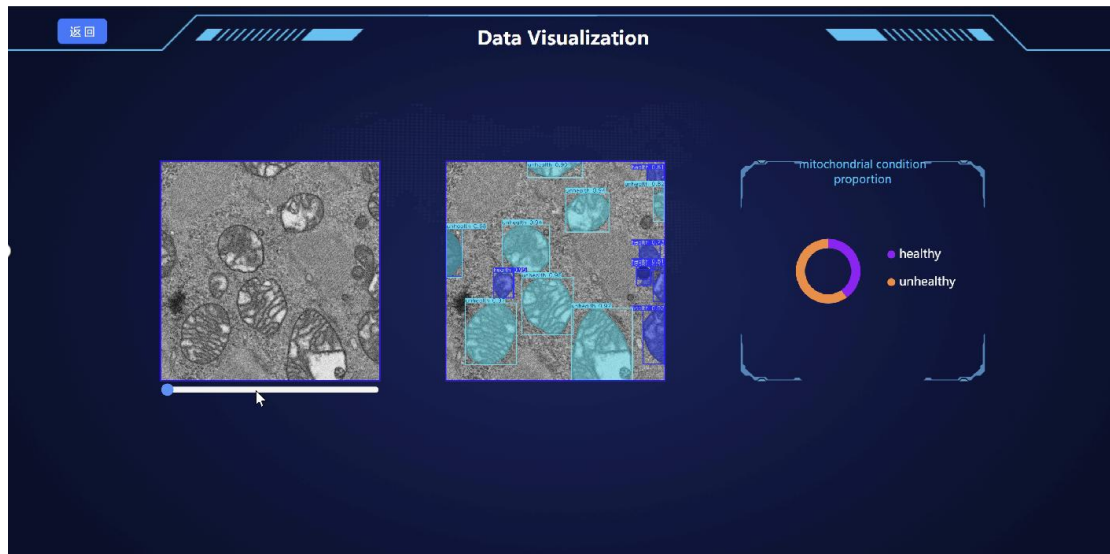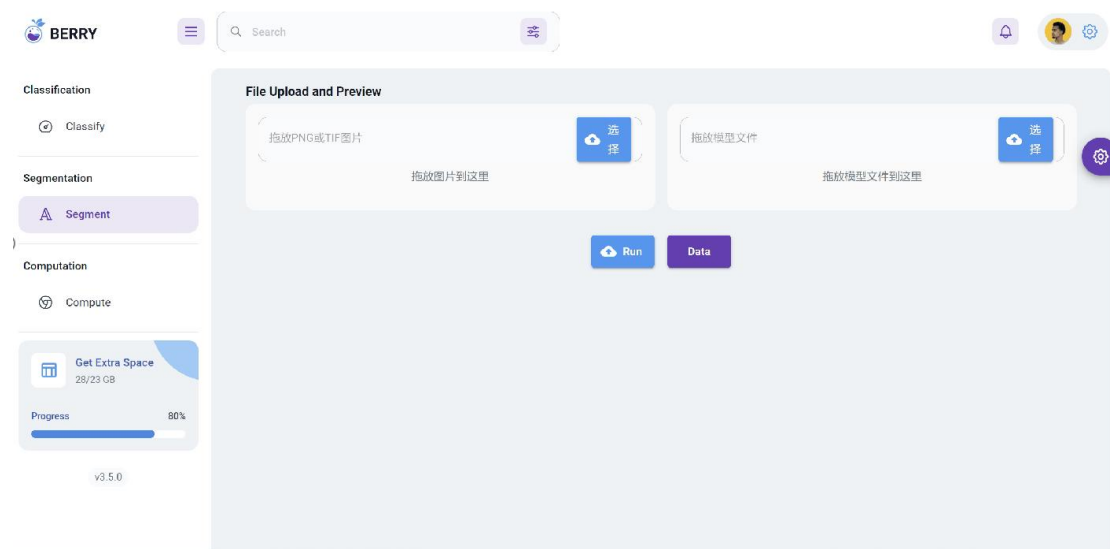
Ultimately, the generated category label images will be saved in the directory: `/AMM-Seg/vite/public/class_predict`.

Segmentation of 2D Images

(1) Tomogram path: Click the Browse button to select the file path. Supported file formats include png,tif and mrc.

(2) Net weights path: Click the Browse button to select the file path. Supported file format is ckpt.

Click click the "Run" button. The system will perform segmentation based on the data and weight files uploaded by the user . After the image processing is completed, clicking the "data" button will navigate to the data display interface. On the left is the original image, in the center is the overlaid image of the segmented image and the original image, and on the right is the segmented image.
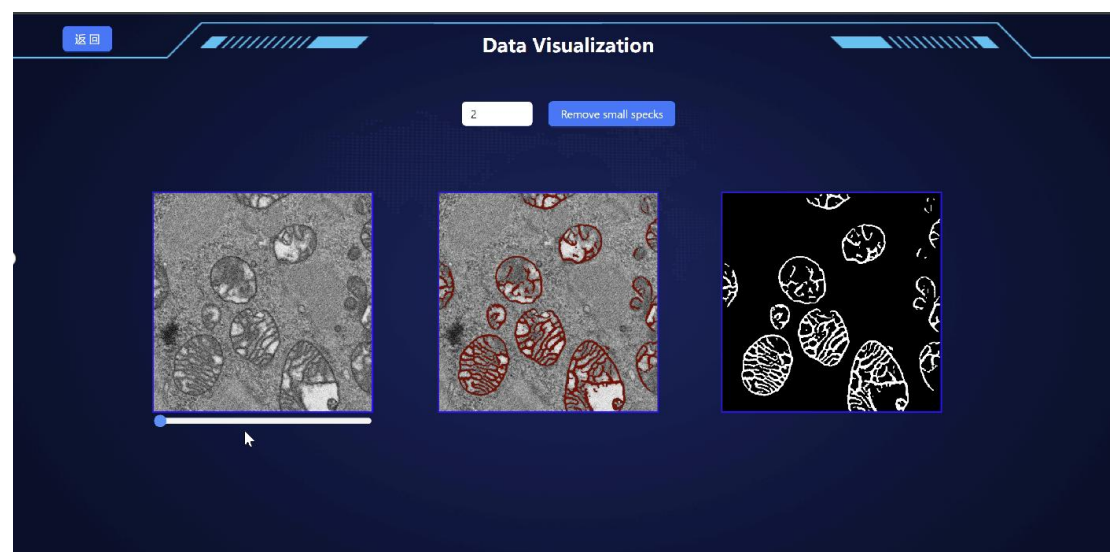
In addition, users can customize parameters by clicking on the "Morphological Opening" tab in the functional tabs, to perform post-processing on the segmentation results, removing small dots from the image to ensure accuracy and correctness of the final result. The final result will be saved in the directory: `/AMM-Seg/vite/public/postP`.

The final generated highlight images and segmentation images will be saved in the directory: `/AMM-Seg/vite/public/seg`.

Membrane Structure Calculation

After completing the image segmentation and post-processing operations, navigate to the "Compute" tab of this system. Simply click on the "Run" button under this tab to calculate the lengths of each mitochondrial outer membrane and cristae in a single image, as well as the total sum of outer membrane and cristae lengths across all images.
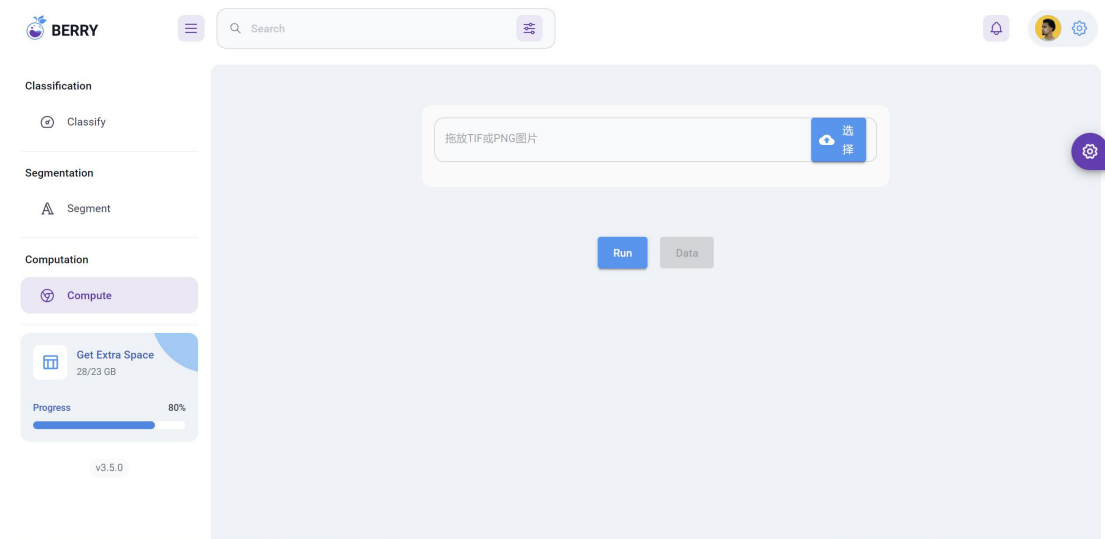
After the image processing is completed, clicking the "data" button will navigate to the data display interface.
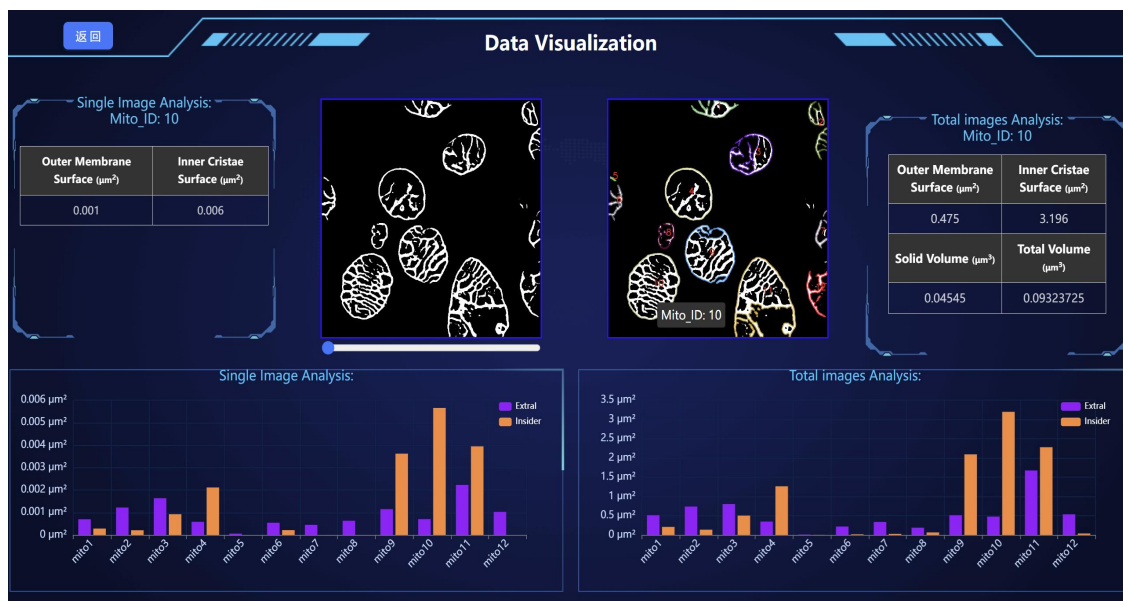
At the same time, when the user hovers the mouse over a mitochondrion, the label number of that mitochondrion will automatically appear to the upper right of the mouse cursor. If a user selects a mitochondrion with a left-click, the system will automatically perform both single and multiple analyses on that mitochondrion, with corresponding data being displayed in real-time in the "Single Image Analysis" and " Total Image Analysis" areas.

The final computed data will be saved in the following files under the directory: ` /AMM-Seg/vite/public/outputs`:

- `single_info.csv`
- `total_info.csv`