

1. Environment Setup

There are two ways to set up your environment:

Option1

```
conda env create -f environment.yml
```

Option2

create an Anaconda environment with the name you want:

```
conda create --name <your name>
```

then, install the packages required:

```
pip install -r requirements.txt
```

as we tested with Intel Macbook Pro 2020, xlswriter also needed to be installed:

```
conda install -c conda-forge xlswriter
```

2. Prepare the data you want to analyze

2.1 Organize your folders

Image sequences from each experiment should be collected into one folder. These images, should have the same name format.

for example:

exp1 242en435-CF N1303K 20220921timeseries-01_s01t01.tif

exp1 242en435-CF N1303K 20220921timeseries-01_s01t02.tif

exp1 242en435-CF N1303K 20220921timeseries-01_s01t03.tif

exp1 242en435-CF N1303K 20220921timeseries-01_s01t04.tif

And for this experiment, " **exp1 242en435-CF N1303K 20220921timeseries-01** " will be the *"prefix"*

Then, put these experiment data folders into **one folder**, for example: `"/Input"`

In the `/Input` there are 3 folders: *exp1, exp 2, exp 3*

```
Image
|
|__exp1
|
|__exp2
|
|__exp3
```

2.2 Organize your image name format

The test image names are following the format from ZEISS software, and with the experiment time of **2h**; Therefore, the names are with suffix *s...t01* to *s...t13*

!!!Important The dynamic morphological changes are based on the detection of dynamic morphological changes from the **t02** to

Operations under */cfanalyzer* folder:

3. Modify the codes

- In the `bayersian/detect_1.py`, modify the paths of your *Image* folder described in 2.1 (line 11~38, indicated in the comments):

```
folder_images = <your iamge path>
```

load the trained model to count the total number, we put the model in the directory */trained_models/bayersian/best_model.pth*. Copy and paste the location of this file into the path:

```
model_baylos = <the path of trained VGG19 model>
```

Output folder you want:

```
output_folder = <out path your want>
```

- In the `yolov7/detect_2.py`, copy and paste the paths of your *Output* folder:

```
output_folder = <same as in detect_1.py>
```

load the trained model to count the swelling organoids, which is an yolov7 model, we put the model in the directory */trained_models/yolov7/last.pt*. Copy and paste the location of this file into the path:

```
model_yolov7 = <the path of trained yolov7 model>
```

Now, the modifications are completed.

4. Run the codes

Option1

Run script directly (Test version)

```
sudo sh run.sh
```

Option2

Run on terminal:

open terminal in this folder and

```
cd bayersian
```

Then, run the code:

```
python detect_1.py
```

Then go to the directory */yolov7*

```
cd .. && cd yolov7
```

Run the code:

```
python detect_2.py
```

The indications are shown on the terminal.