First, download the python codes:
git clone https://github.com/QibingJiang/cell_process_moffitt_py_2023.git

Second, run the following command,
cd cell_process_moffitt_py

First, there are some package need to be installed:
pip install opencv_python
pip install scipy
pip install astropy
pip install astropy
pip install shutil

Now, you can run the python codes:
python3 ./cell_process.py configure.txt input_dir
input_dir is the directory where the images are. For example,
python3 ./cell_process.py configure.txt /home/qibing/disk_t/Pt204/RawData/Beacon-2

You do not need to specify output directory. The result would be put into the TimeLapseVideos_cbb folder under each patient folder. For example: "/home/qibing/disk_t/Pt204/TimeLapseVideos/"

In the TimeLapseVideos cbb folder,

- 1. Results contains files Results *.csv, each of which is the live cell area for one Beacon.
- 2. In the video, the cells in blue circles are live, and yellow for dead.
- 3. Cell_tracks contains other information. The file named Beacon_*_cell_tracks.txt contains the information for each cell track. In this file, each row represents one image (one time point). the 5 columns are track-id, x-coordinate, y-coordinate, cell area, cell core brightness average, eccentricity. The coordinates origin is at the top left corner of the image. Image size is 1328(width)x1048(height). x-coordinate is horizontaly, and always positive. y-coordinate is vertically, and always positive.
- 4. In the file named Beacon_*_live_dead_table.txt, each row represents one image (one time point). The 4 columns are the number of live cells, the number of dead cells, the area sum of live cells, the area sum of dead cells.

If you want to compile the python codes to executable file, then install the package: pip install pyinstaller

Now you can run the command: pyinstaller ./cell_process.py

The executable file is here ./dist/cell process/cell process