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

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. info_ucf 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