

# 2020.05

Thursday, May 14, 2020

16:16

## May 1- May 7:

1. Setup the portforwarding, neuroglancer, JupyterLab
  - a. Create a new conda environment to install neuroglancer
    - i. Pip install neuroglancer (ng=1.1.6)
  - b. `conda install -c conda-forge jupyterlab`
  - c. Two ways to portforward ng and JupyterLab:
    - i. First choice:
      - 1) In local PC: `ssh -L portnumber:localhost:portnumber useraccount`  
For example: `ssh -L 12306:localhost:12306 silin@login.rc.fas.harvard.edu`
      - 2) In login node: `ssh -L portnumber:localhost:portnumber worknode`  
For example: `ssh -L 12306:localhost:12306 coxgpu01`
      - 3) Enter environment, open ng, and set the port number to 12306
      - 4) Open the link in browser
    - ii. Second choice:
      - 1) Login the cluster from local PC without port
      - 2) Using "srun" to log in work node
      - 3) Enter environment and select an idle port:

```
for myport in {6818..11845}; do ! nc -z localhost ${myport} && break; done; echo "ssh -NL $myport:$(hostname):$myport $USER@login.rc.fas.harvard.edu"
```

Save the command printed in terminal.
      - 4) Open jupyter lab using selected port:

```
jupyter lab --no-browser --ip=0.0.0.0 --port=${myport}
```
      - 5) In a new terminal, run the saved command
      - 6) Open the Jupyter Lab link in browser

## May 12-14:

1. Setup the environment of **kimimaro**:
  - a. module load gcc or module load g++
  - b. Pip install kimimaro
  - c. Install matplotlib
2. Run skeletonize package kimimaro.
  - a. Run `run_kimimaro.py` to get the skeleton of mitochondria
    - i. Useful features: `skels[12].viewer()`
    - ☒ ii. Problem: can not run "label\_skeleton" attribute (Solved: `import mesh`)
  - b. Show the mitochondria in neuroglancer
    - ☒ i. Not sure it is right to load all mitos (Solved: `res=[64,64,60]` for data: `/n/pfister_lab2/Lab/donglai/mito/db/30um_rat/mito_64nm.h5`)
    - ☒ ii. Not sure how to load one mitos given vertices. (Solved: downgrade the version of ng: `ng=1.1.6`; scale: `[1/30, 1/32, 1/32]`)

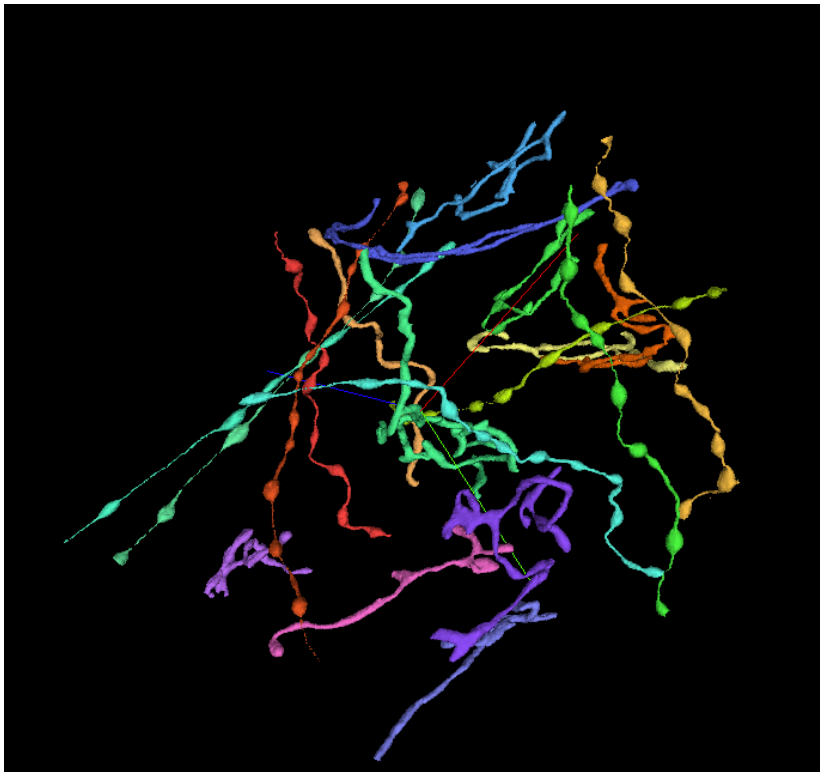
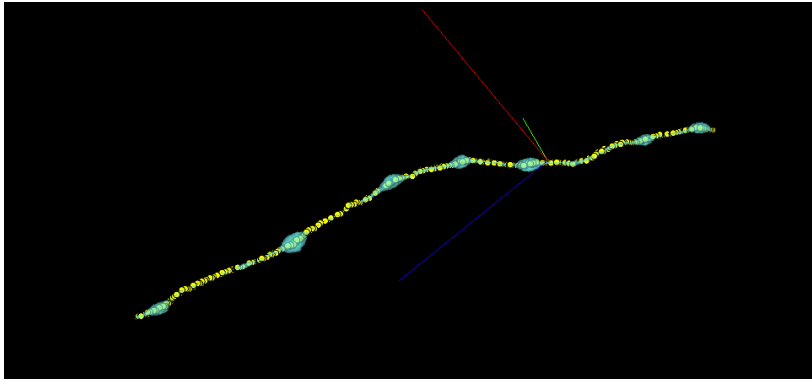
## May 15:

1. The relationship between `skels.vertices` and ng **coordinates**
  - a. found the range of the coordinates in neuroglancer is (500,256,512), but the coordinates generated by `skels.vertices` have numbers up to 15000. So I calculate the relationship of the two coordinates: the coordinate from *vertices* attribute  $/(64 \text{ for } x,y; 60 \text{ for } z) * 2 =$  coordinate in neuroglancer.

## May 16-17:

1. Show skeleton adequately





# Toy example:

Yesterday ▾

```
>>> a = segpred['main']
>>> a.shape
(500, 256, 512)
>>> ui = np.unique(a)
>>> ui.shape
(14330,)
>>> ui, uc = np.unique(a, return_counts=True)
>>> ui[1]
1
>>> uc[1]
985
>>> ui.shape
(14330,)
>>> uc.shape
(14330,)
>>>
```

```
///  
>>> ui[uc>1000].shape  
(908,)  
>>> ui[uc>10000].shape  
(20,)  
>>> ui[uc>10000]  
array([    0,   140,   335, 2666, 2764, 3151, 4011, 5168, 5338,  
       7332, 7586, 7653, 8637, 9817, 9879, 10896, 11001, 12813,  
       13232, 15838], dtype=uint32)  
>>>
```

2. Analysis - see ppt.

**bump : fusion ; function**

**Questions : length ; thickness ; description on shape**