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Additional info for worm project

Heather Berlin <heathermberlin@gmail.com>   Mon, Mar 13, 2017 at 5:06 PM
To: rparvat@mit.edu
Cc: Yaron Meirovitch <yaron.mr@gmail.com>

Hi Rajeev,

Thanks so much for helping us with this project! I've created a directory for you on the connectomix server that should contain all relevant files: `/home/heather/worm`

```
connectomix:
|
|---/home/heather/worm
   |
   |----probs
   |
   |----probs_by_z
   |
   |----skeleton
   |
   |-----EM
```

Each of the directories in /home/heather/worm/ contains x,y,z values stored in various file formats which must be mapped to absolute coordinate values. We'll call these absolute coordinates X_i, Y_i, and Z_i (zero-based). Z_i corresponds to a specific slice of the worm along the z-axis.
Ranges of absolute coordinates:
      Z_i : 0-1051
      X_i: 0-101631
      Y_i: 0-45567

For each directory listed below, I've included the conversion needed to map the x,y,z coordinates from each of the file formats to the desired absolute coordinates, X_i, Y_i, and Z_i.

EM directory

- contains directories of EM images for each Z_i
- within a given Z_em directory, files are labeled as:
  - Yem_Xem_1.jpg where 1 corresponds to the resolution

- Z_i = Z_em
- Y_i = [Yem*512, (Yem+1)*512-1]
- X_i = [Xem*512, (Xem+1)*512-1]

probs directory
    - contains directories labeled Block_Zsection_Ysection_Xsection (Zsection is zero-based, Ysection and Xsection are not)
    - within each Block_Zsection_Ysection_Xsection directory, membrane probability outputs are labeled as:

        Depth_id-xnn-out-ch-01.png   (Depth_id is zero-based)

- Z_i = 100*Zsection + Depth_id
- Y_i = [(Ysection-1)*1024, (Ysection*1024)-1]
- X_i = [(Xsection-1)*1024, (Xsection*1024)-1]

For example, the file `/home/heather/worm/probs/Block_000004_000009_000028/forward/0034-xnn-out-ch-01.png`

contains membrane probability outputs for:

- $Z\_i = 434$
- $Y\_i = [8*1024, 9*1024-1]$
- $X\_i = [27*1024, 28*1024-1]$

<u>skeleton directory</u>

- contains txt files containing seed locations for each skeleton ID
- filename corresponds to the skeleton ID
- each row of a skeleton ID .txt file corresponds to X_catmaid Y_catmaid Z_catmaid   (zero-based)
- To map the seeds to our images, our index values are found by:

  - $X\_i = X\_catmaid / 2$
  - $Y\_i = Y\_catmaid / 2$
  - $Z\_i = Z\_catmaid / 30$

<u>probs_by_z directory</u>

You might find it easier to access full membrane probability outputs for a specific slice on the z axis. We have outputs for 200 slices located at /home/heather/worm/probs_by_z

- each .mat file is a matrix of the entire membrane probability map for the z id corresponding to the filename
- z=400-699

Please let me know if you have any questions! I will be at MIT tomorrow; assuming classes are canceled, I will be free to meet anytime during the day. Otherwise, I'm available 11-2 or after 5pm.

Best,

Heather