Python library introduction

August 25, 2014

Installation

- Reminder: Installable python module on github:

  - https://github.com/AllenBrainAtlas/friday-harbor

- Install via "python setup.py install"

- This code can manipulate data from the data directories

- Mesoscale connectivity code and data are in the linear_model subdirectory

Data Sets:

- Voxelized connectivity projection (per experiment)

  - Cre and wildtype

  - Python package to access and manipulate

- Linear model connectivity

  - Wildtype only

  - .mat file of 213 connected regions (Oh et al. 2014)

- Fast-marching fiber tracts (per experiment)

  - Cre and wildtype

  - Very large data set. Visualized in Brain Explorer

Getting the data:

- We have two external HD's with data, broken into several smaller chunks

  - ./data_wild_cortex: wild-type voxel data, cortex only, 1.3 GB

  - ./data_wild: wild-type voxel data, cortex only, 4.6 GB

  - ./data_cortex: all mouse lines, cortex only, 6.3 GB

  - ./data_cre_subcortex: subcortical, only cre lines, 7.3 GB

  - ./data_all: all injection experiment voxels, 18 GB

  - ./data_lines: everything, including "virtual tractography" 63 GB

- This will be the directory you point to with the keyword argument "data_dir" in the code, when you create an Ontology or ExperimentManager (More on this later)

Getting the data:

- This data is also available via afp (Mac) or smb (Linux/Windows) download across the network:

  - afp://ocean3.fhl.washington.edu

  - smb://ocean3.fhl.washington.edu

- login: fhlguest pass: fhlguest

- Data is in: ~/Public

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Examples:

- I will be using the Eclipse IDE (with pydev module) to demo examples

- Spyder, IPython Notebook, emacs, vim, ect. are good alternatives

- Examples are In the "examples" subdirectory

- If your install isn't working perfectly, just follow along up here; we have the rest of the day to get you started

Examples:

Two main data structures; both have the kwarg "data_dir", pointing to the directory that contains your selected voxel data.

- ExperimentManager:

  - Organizes all members of the experiment class (from the data set)

  - Facilitates access to voxel-based projection density (PD), and masks of the injection site.

- Ontology:

  - Organizes all members of the structure class (annotated regions)

  - Facilitates access to structure masks (left and right hemisphere, and combined)

- Lines

  - Simple accessors for the binary line files.

  - Facilitates extracting experiment-voxel info, and the tract coordinates