20260525_hello_flywire2024_single_neuron_swc_morphology

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Dataset

Single fruit fly wiring diagram from Dorkenwald, et al Nature 2024:
https://www.nature.com/articles/s41586-024-07558-y

FAFB v783, ~140K neurons total

Contains a number of objects, including synaptic connectivities and morphologies.

Morphology data is in SWC format for each cell, corresponding to neuronal “skeleton”. These are ASCII files and can be opened with a text editor. More info on SWC (not necessary for this hello_signal file) here:
http://www.neuronland.org/NLMorphologyConverter/MorphologyFormats/SWC/Spec.html

Individual SWC size ~100Kb (small cell) - ~20Mb (large cell)

All ~140K SWCs ~ about 13Gb zipped, 21 Gb unzipped.

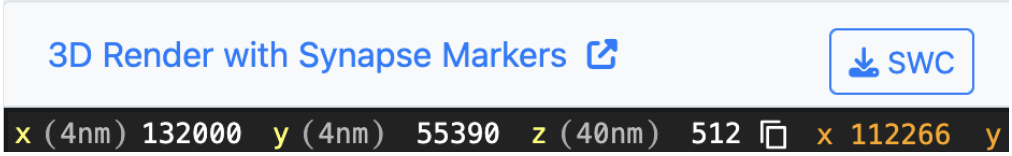
Accessing data

SWCs can be downloaded one-at-a-time or in bulk.
Here we will download the right APL neuron, a large identified neuron in the mushroom body.

NOTE: Units in SWC are in nm, even though the bulk download link in the GUI may say they are microns. The header of each SWC file confirms that units are nm.

To download a individual SWCs

- Make a directory called `sk_lod1_783_healed`
    - This is specifies the connectome version to use
- Navigate to https://codex.flywire.ai/?dataset=fafb
    - NOTE: You will likely need to login e.g. via a Google account
    - NOTE: Safari sometimes has issues with the GUI.
- Use GUI to find the right APL neuron:
    - Enter APL into the search query
    - Find the APL neuron whose “soma side” is “right”
        - Its ID should be 720575940613583001
    - Click on the image of the brain with right APL highlighted to view the neuron
    - Click the download SWC button and save the SWC file within `sk_lod1_783_healed`



SWCs can also be downloaded in bulk (not needed for this hello_signal file):

- Navigate to https://codex.flywire.ai/api/download?dataset=fafb
    - You will likely need to login e.g. via a Google account
- Select “Neuronal Skeletons (13 Gb)” and click on “sk_lod1_783_healed.zip”
- Unzip into folder `sk_lod1_783_healed`

Software used below

Python version 3.12.12, with the following packages

- Numpy version 2.3.5
- Matplotlib version 2.10.6

Code

Copy the following code into a python file, e.g. view_swc.py, in the same directory as as sk_lod1_783_healed, i.e. the directory structure should be

```
my_project
  - view_swc.py
  - sk_lod1_783_healed
    - 720575940613583001.swc
```

Python code:

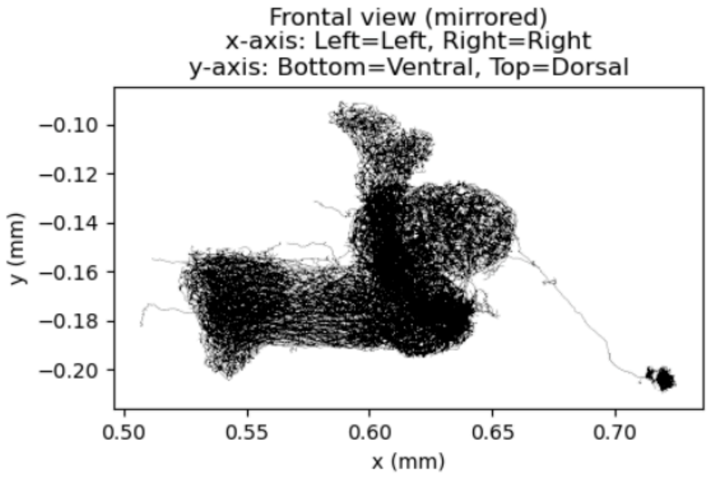
```
import matplotlib.pyplot as plt
import numpy as np
import os

SWC_DIR = 'sk_lod1_783_healed'  # directory where SWC files live
APL_R_ID = 720575940613583001  # neuron ID for right APL

def load_swc(neuron_id):
    # load an SWC given the neuron ID
    fpath = os.path.join(SWC_DIR, f'{neuron_id}.swc')
    return np.loadtxt(fpath, comments='#')

# for SWC plotting
def get_nan_curve(segs):
    """
    Convert collection of line segments to single
    curve broken by nans (for fast plotting).
    """
    temp_x = np.concatenate(
        [segs[:, :, 0], np.nan*np.zeros((len(segs), 1))], axis=1)
    x_curve = temp_x.flatten()

    temp_y = np.concatenate(
        [segs[:, :, 1], np.nan*np.zeros((len(segs), 1))], axis=1)
    y_curve = temp_y.flatten()

    temp_z = np.concatenate(
        [segs[:, :, 2], np.nan*np.zeros((len(segs), 1))], axis=1)
    z_curve = temp_z.flatten()
```

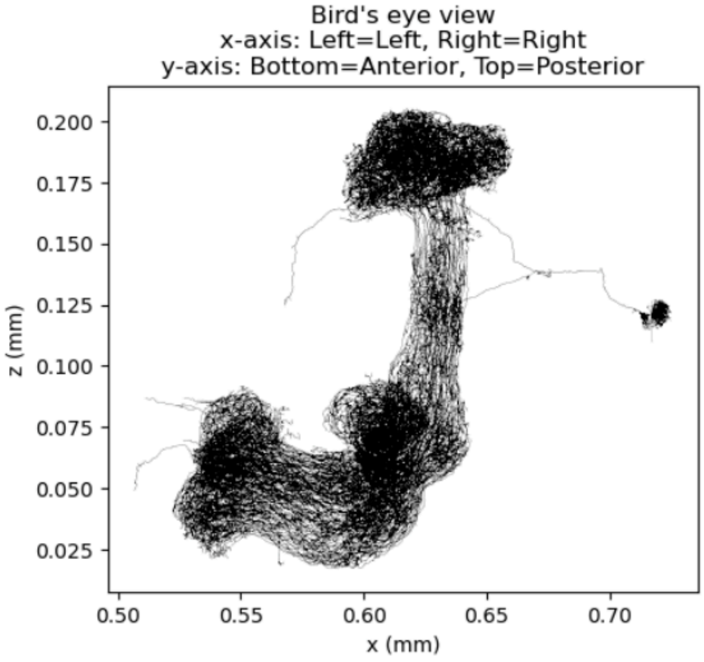
```
    return x_curve, y_curve, z_curve


def plot_swcs(
        swc_datas, axs, color='k', z_order=0,
        lw=.5, alpha=1, x_lims=None, y_lims=None):
    """Plot one or more SWC files in the specified color."""

    for swc_data in swc_datas:

        # extract the SWC data (in nm)
        x, y, z = swc_data[:, 2], -swc_data[:, 3], swc_data[:, 4]

        # convert from nm to mm
        x /= 1e6
        y /= 1e6
        z /= 1e6
        parent = swc_data[:, 6].astype(int)

        mask = parent > 0

        p0 = np.column_stack([x[mask], y[mask], z[mask]])
        p1 = np.column_stack([
            x[parent[mask] - 1],
            y[parent[mask] - 1],
            z[parent[mask] - 1]
        ])

        segments = np.stack([p0, p1], axis=1)

        x_curve, y_curve, z_curve = get_nan_curve(segments)

        axs[0].plot(x_curve, y_curve, c=color, lw=.1, zorder=z_order, alpha=alpha)
        axs[1].plot(x_curve, z_curve, c=color, lw=.1, zorder=z_order, alpha=alpha)

    # format plot
    axs[0].set_aspect('equal')
    axs[0].set_xlabel('x (mm)')
    axs[0].set_ylabel('y (mm)')
    axs[0].set_title(
        'Frontal view (mirrored)\n'
        'x-axis: Left=Left, Right=Right\n'
        'y-axis: Bottom=Ventral, Top=Dorsal')

    axs[1].set_aspect('equal')
    axs[1].set_xlabel('x (mm)')
    axs[1].set_ylabel('z (mm)')
    axs[1].set_title(
        'Bird\'s eye view\n'
        'x-axis: Left=Left, Right=Right\n'
        'y-axis: Bottom=Anterior, Top=Posterior')

# plot
fig, axs = plt.subplots(1, 2, figsize=(10, 5), tight_layout=True)
```

```
swc_data = load_swc(APL_R_ID)
swc_datas = [swc_data]  # can add multiple SWCs if desired
plot_swcs(swc_datas, axs, color='k')
plt.show()
```

Outputs

Plot of the APL neuron on the right side of the brain.





Notes

The SWC coordinates are mirrored about the frontal axis of the fly, like you are the fly looking in the mirror.

Neuron IDs can found via the flywire GUI or programmatically accessed by cell type or classification via the CSV files available at https://codex.flywire.ai/api/download?dataset=fafb under the “Cell Types” and “Classification / Hierarchical Annotation” tabs.