Assessing Drosophila neurons types based on topology and connectomics with GNNs

An increase in the speed and quality of modern neuroimaging techniques allows for large-scale connectomics studies of invertebrates, i.e. Drosophila. Connectomics is useful in generating biological insights about ensembles of neurons with interesting behavioural functions. New computational tools are needed to search and organise these data. For instance, one important question is how similar are neurons between two hemispheres of the fruit fly brain. To answer these questions a heuristic NBLAST algorithm is used. It considers both position and local geometry by decomposing neurons into short segments; matched segments are scored using a probabilistic scoring matrix. However, NBLAST ignores the topology of a neuron and its connectomics. On the other hand, neuronal connections in the brain can be represented as a graph. Graph Neural Networks have been shown to account both for local node features and adjacency matrix in the classification task. The aim of this project is to create classification model that would allow to determine the types of neuronal cells in order to improve neurons taxonomy.

Fixing neuronal morphology with graph generative models

An increase in the speed and quality of modern neuroimaging techniques allows for imaging individual neuronal cells in Drosophila. Previously, electron microscopy images were annotated manually in search of neuronal tracts. A skeleton of neuron can be represented as a directed graph with the beginning in the cell body. Today, machine learning algorithms (like flood-filling neural networks) vastly improve the tracing of neurons, but they leave tracers with a number of false positives and negatives. One artefact of the method (related also to the imperfect EM data collection process) is lack of continuity between certain neuronal branches.

Currently, as a remedy, a simplistic assumption is made to interpolate missing part of the neuron as a straight line. Generative graph models could help to render more biologically plausible replacement of the missing part of the neuron, which on the other hand could facilitate the process of visual inspection of annotations and neuron matching.