Background

Networks of filaments assembled from the protein actin contribute significantly to cells’ ability to move and change shape. Actin also makes crucial contributions to a variety of cellular processes, from wound healing to precise wiring of the neuronal circuitry. Actin networks typically exhibit distinct local geometric structure, see Figure 1. The networks contain regions of straight and tightly packed fibers, for instance, as well as loops of varying sizes.

Figure 1: High resolution live-cell microscopy images of cells’ actin filaments. The cells are of two distinct types. The cell on the left is a mutant and the cell on the right is a control type. Source: Eric Vitriol

Topological Data Analysis

Topological data analysis (TDA) leverages ideas from mathematics to quantify the geometry of data. Persistent homology is one of the most popular TDA methods. Intuitively, homology in degree $n$ counts the number of $n$-dimensional holes a space has. Persistent homology captures information about the size and scale of the holes.

Figure 3: Filtered simplicial complex built on points sampled from patches as in Figure 2 and its corresponding persistence diagram and landscape.

Pipeline

Our methodology detects localized features using image segmentation, relative persistent homology, and persistence landscapes. Persistence landscapes are transformations of persistent homology shape summaries to feature vectors.

Unsupervised segmentation

Figure 5: Using t-SNE clustering, we can also segment the cells in an unsupervised way.

Classification accuracy

- CK666 vs CK689 - 88%
- Control KD vs PFN1 KD - 100%
- Control KD vs Cofinilin KD - 91%
- Control KD vs TB4 KD - 84%
- AP4 vs FP4 - 79%