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. The data is the following:

- 28 3D high resolution microscopy images of mutant cells.
- 42 3D high resolution microscopy images of control cells.

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. Our methodology estimates relative persistent homology, a novel application approach. This is accomplished by adding an artificial boundary to each patch sample as in Figure 2.

Methodology

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, see Figure 3.

Principal Component Analysis

Figure 4: Image: Plot of the first two PCA components and variance by components.

Figure 5: Ordering of a range of images based on the average principal component values of their patches.