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Microscopy images comprise one of the most common data outputs from biological experiments and often depict rich topological information. While deep learning models have exhibited remarkable success at analyzing these and other image data sets in recent years, advances have largely focused on designing models that automate human judgments. Accessible and effective exploratory analyses that produce new hypotheses from small data sets remain challenging.

In this talk, I will present an image analysis pipeline that combines a new set of topological data analysis (TDA) features with machine learning. The features are based on two TDA methods: persistent local homology and persistence landscapes. I will then discuss results from applying the pipeline, TDAExplore, for image classification and image segmentation of multiple microscopy data sets. The segmentation model was applied to fluorescence microscopy images of the actin cytoskeleton and is "weakly supervised". It learns to identify image regions whose topological features most strongly characterize classes of images using only image labels. A software implementation of TDAExplore is publicly available, consumes modest computational resources, and is effective on data sets containing as few as 20-30 high resolution images. (Received September 21, 2021)