

Image processing pipeline for segmenting and tracking MCF10A epithelial cells

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This thesis describes a novel implementation of an image and data processing chain that segments, tracks, and extracts features of epithelial cells imaged in timelapse microscopy experiments. It is written in Python, employs a combination of traditional machine- and deep-learning techniques, and introduces a novel cell declumping strategy. Our benchmarks demonstrate that the pipeline is faster, requires less user interaction than previous implementations, and significantly reduces the amount of manual work required from users. The new pipeline is an all-in-one analysis solution that will form a core of the novel real-time feedback-control microscopy platform currently under development in the Pertz lab.

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