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Life beyond the pixels: deep learning methods in cancer and virus research

In this talk I will give an overview of the computational steps in the analysis of a single cell-based large-scale microscopy experiments. First, I will present a novel microscopic image correction method designed to eliminate illumination and uneven background effects which, left uncorrected, corrupt intensity-based measurements. New single-cell image segmentation methods will be presented using differential geometry, energy minimization and deep learning methods (www.nucleAIzer.org).

I will discuss the Advanced Cell Classifier (ACC) (www.cellclassifier.org), a machine learning software tool capable of identifying cellular phenotypes based on features extracted from the image. It provides an interface for a user to efficiently train machine learning methods to predict various phenotypes. For cases where discrete cell-based decisions are not suitable, we propose a method to use multi-parametric regression to analyze continuous biological phenomena. To improve the learning speed and accuracy, we propose an active learning scheme that selects the most informative cell samples.

Our recently developed single-cell isolation methods, based on laser-microcapturing and patch clamping, utilize the selection and extraction of specific cell(s) using the above machine learning models.