

Speaker:

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Title:

Machine learning methods for high-content microscopic data analysis

Abstract:

In this talk I will give an overview of the computational steps in the analysis of a single cell-based high-content screen. First, we present a novel microscopic image correction method designed to eliminate vignetting and uneven background effects which, left uncorrected, corrupt intensity-based measurements. In contrast traditional methods which require reference calibration images, our method learns the vignetting function from the images themselves. We show that our method outperforms reference-based methods as well as the state-of-the-art image-based methods popularly used for high-content screens. I will also touch on the image analysis and feature extraction methods. First, I discuss the Advanced Cell Classifier (ACC) (www.cellclassifier.org), a 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. In addition, we developed the Suggest a Learner (SALT) toolbox, which selects the optimal machine learning algorithm and parameters for a particular classification problem. For cases where discrete cell-based decisions are not suitable, we propose a method to use regression to analyze continuous phenotypes. Using the ACC program, it is possible to identify discrete and continuous cell types parallel. Finally, our new developments will be proposed to track bacteria (or any spot-like objects) in 3D using only 2D image sequences in high-throughput manner.