An Ensemble Learning Method for Generic Track Annotation in Live Cell Imaging

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Abstract

Automated tracking of cells can reduce bias and increase throughput from single cell experiments. We develop a method of inferring time of apoptosis using common cell trajectory data, while also determining lineage to understand the impact of cell and circadian cycle on heterogeneous cellular response to stress. We use single time-point features as input into a classifier to predict biological fate classification on a per-frame basis. We show that useful statistics of this classifier are stationary and can be used as input into a Hidden Markov Model for time series correction and subsequent time of event prediction for single cells. We show results on several biological datasets and describe the use of the method across cell types. This method makes use of limited features from live cell tracking time series to be able to efficiently annotate existing datasets without reprocessing whole movies or applying convolutional classification approaches except in narrow temporal and spatial windows to validate or correct time of death predictions for cells. We discuss a minimal feature set to enable the use of this method across a variety of experimental designs (different nuclear markers and cell types) and imaging setups. We provide a software package to facilitate external use.

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