Department of Mathematics

Chair of Mathematical Modeling of Biological Systems

Technische Universität München

Master's Thesis in Bioinformatics

Single-cell analysis of cancer drug response using computer vision and learning algorithms on time-lapse microtrench data

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Wirkungsanalyse von Krebsmedikamenten in Einzeller Auflösung durch die Anwendung von Computer-Vision- und Machine-Learning-Algorithmen auf Microtrench-Videoaufnahme

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Abstract

Quantitative measurement of cancer drug response is esential to objectively gauge the efficacy of cancer drugs. So far, there has been no method to track and quantitatively measure single-cell response of of cancer drug treatment. A novel pipeline is presented in this thesis. First, a high-throughput method to track cells and quantitatively analyze single-cell response to drugs. We investigate the response of model cancer cell lineagues, MOLM and Jurkat, to known anti-cancer drugs Vincristine and Doxorubicine. Second, a machine learning-based was developed which was able to predict cancer cells' time-to-death upon the introduction of the medications, based on the differential cellular morphology of the cells alone. While these two-fold methods enabled accurate and high-throughput analysis of cancer treatment *in vitro*, our pipeline could also be adapted in varios contexts involving single-cell analysis.

Chapter 1

Intro

Lorem ipsum

Chapter 2

Background