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A mathematical modeling framework to simulate and analyze cell type transitions

Daniella Schittler

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The quantitative understanding of changes in cell types, referred to as cell type transitions, is fundamental to advance fields such as stem cell research, immunology, and cancer therapies.

This thesis provides a mathematical modeling framework to simulate and analyze cell type transitions. The novel methodological approaches and models presented here address diverse levels which are essential in this context: Gene regulatory network models represent the cell type-determining gene expression dynamics. Here, a novel construction method for gene regulatory network models is introduced, which allows to transfer results from generic low-dimensional to realistic high-dimensional gene regulatory network models.For populations of cells, a generalized model class is proposed that accounts for multiple cell types, division numbers, and the full label distribution. Analysis and solution methods are presented for this new model class, which cover common cell population experiments and allow to exploit the full information from data.

The modeling and analysis methods presented here connect formerly isolated approaches, and thereby contribute to a holistic framework for the quantitative understanding of cell type transitions.

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