

NetLand: A comprehensive tool for simulation and visualization of transcriptional network kinetics

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Transcriptional regulation through a gene regulatory network (GRN) is a major force to change cellular states. During cell differentiation or reprogramming, changes in gene expression profiles are crucial. Thus kinetic models of GRNs have been used to study the determination of cell fates. *In silico* simulation is a common method to analyze the kinetic dynamics of a network, based on a mathematical model generated from the network structure. Through iterative comparisons with experimental results, the model is corrected and adapted, in order to make reliable predictions. For a comprehensive understanding of the modeled GRN, Waddington's epigenetic landscape is a powerful framework to analyze and visualize the global dynamics of the network. Based on the essential idea of Waddington's landscape, changes of cell fates are represented by state transitions overcoming energy barriers between attractors. Thus the quantified epigenetic landscape is the stage on which the play of cell fate decisions is choreographed according to regulatory constraint and stimulations analogous to physical forces.

NetLand is a software tool designed for studying GRN kinetics. It provides comprehensive methods for simulation and visualization of network dynamics. The biological influences in GRN can be converted into the Boolean logics (Boolean or multi-value model) and differential equations (ODE or SDE model). Through *in silico* simulation, the dynamics of the GRN can be visualized in multiple ways, e.g. the state transition graph of a Boolean network, trajectories of continuous models and Waddington's epigenetic landscape. NetLand can be applied to various fields of molecular and cell biology, including stem cell and cancer research.