RE:IN Modeling of the Endomesoderm GRN of Purple Sea Urchins and Developing Tools for Efficient GRN Modeling

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Stem cells play a central role in the development of organisms; hence, studying them is of great importance. RE:IN modeling of systems involving them allows us to investigate their behaviors quickly and efficiently. In my research, I constructed a RE:IN model of the GRN of the Purple Sea Urchin, which describes the genetic expression in Purple Sea Urchin stem cells. It consists of a collection of boolean networks, each corresponding to a possible structure of the GRN consistent with experiments. I examined the model's compatibility with observed behavior and explored its robustness. To this end, I developed several methods for modeling with GRNs in RE:IN: methods for handling cases where models don't behave in accordance with observed behavior, tools for fast and efficient RE:IN modeling, and tools for synthesizing complex situations in which models can be tested. My results showed that the model cannot behave according to the entirety of the expected behavior; it is capable of satisfying at most combinations of 3 constraints from the behavior, while the behavior consists of 10 constraints. Moreover, I showed that the model is robust to perturbations in a subset of important genes in the network. These results suggest that there is still work to be done to better capture the intricacies of the GRN in RE:IN and that my model is robust. Furthermore, the tools I developed proved to be useful and are expected to serve future research on GRNs within the framework of RE:IN.

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