A mechanistically detailed Boolean network of the cell cycle in *S. cerevisiae*

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Abstract

Formulating signal transduction networks, such as the cell cycle, into computational models facilitates understanding how cellular functions emerge. This requires a modeling formalism which scales with the number of microstates, while covering the states which are empirically described. The reaction-contingency language was developed to overcome these two challenges, enabling the description of mechanistically detailed, yet scalable and executable models of signal transduction networks.

Here, we present a comprehensive, mechanistic, and executable bipartite Boolean network of the cell cycle of the baker's yeast *Saccharomcyes cerevisiae* using the reaction-contingency language [1]. We used this Boolean network to analyze and validate the collective behavior of the integrated data. We determined a biologically relevant attractor in the network which describes the completion of one cycle of cell division. We used this attractor to determine genotype-to-phenotype relationships down to the level of residue mutations, and found that the model accurately predicts 63 out of 85 tested mutants.

This mechanistic and comprehensive model offers a new perspective on cell cycle control, and may pave the way for the development of mammalian whole-cell models. In the future, such models may be adapted to individuals and used as a stepping stone towards personalized medicine.

[1] Ulrike Münzner, Edda Klipp, Marcus Krantz (2018). A comprehensive, mechanistically detailed, and executable model of the Cell Division Cycle in *Saccharomyces cerevisiae*. *bioRxiv*.