

A cell cycle control network of *S. cerevisiae*

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As an essential part of life, cell division is the process that realises the reproduction of a cell. Capturing the complex molecular machinery of the cell division cycle (CDC) in a machine–readable format enables scientists to perform theoretical studies, i.e. investigating how molecular mechanisms combine to determine the global behaviour of the cell. Furthermore, mapping and analysing the available knowledge of the CDC also reveals information gaps. The reconstruction of a network of the size of the CDC using conventional approaches is susceptible to the combinatorial explosion. This inconvenience often forces simplifications in the modeling process. Here, we present a simulatable, large–scale reconstruction of the CDC control network of the yeast *Saccharomyces cerevisiae* annotated in the rxncon format. The rxncon format permits the reconstruction of a mechanistically detailed model while avoiding the combinatorial complexity. Furthermore, the rxncon framework allows export to an executable Boolean model and different graphical visualisations. Our comprehensive model describes the three main transitions during the CDC capturing the state of the art knowledge. We envision to perform a gap filling analysis that can guide empirical interrogation. The model database can be dissected or extended by other scientists.