Modelling the yeast cell cycle – as the model becomes parametrized

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Saccharomyces cerevisiae is a famous model organism in systems biology to study the mitotic cell cycle in eukaryotic cells. Cyclins, CDKs (cyclin-dependent kinases) and CKIs (CDK inhibitors) are typical proteins involved in cell cycle control. We measured the absolute number of mRNA molecules of unsynchronized single cells for *SIC1*, *CLN2* and *CLB5* by smRNA-FISH (single molecule RNA-fluorescence *in situ* hybridization). This measurement yields mRNA distributions per cell cycle phase. We quantified the relative number of protein molecules of a synchronized cell population for Sic1, Cln2 and Clb5 by Western blots. The number of proteins is given as time course over the cell cycle. These both methods are not directly comparable. However, the measured molecules are key players in the regulation of the G1 to S phase transition, called START. At this control point the decision for the entrance in a new cell cycle is made. In the present work we combine both data types to parameterize a small model describing the transition by using a maximum likelihood approach. The optimization process is highly sensitive to initial conditions and its performance depends on the optimization algorithm. This is why we scan a large amount of different initial conditions to identify local and global optima. The parameter distributions in the global optima allow us to assess the goodness of the fitted value.