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A new method for parameter estimation for differential equations applied to the biochemistry of the Min protein system

The Min system is a well-studied two-protein interaction that plays a central role in setting the location of the division ring during E.coli cell division. Numerous models have been proposed to explain a wide range of fascinating patterns that have been observed in both in vivo and in vitro experiments. However, it is only (relatively) recently that in vitro experiments have provided clear time courses for the protein concentrations throughout typical oscillations. In this talk, I will describe a new parameter estimation method that extends the General Profiling method. Using the method to fit two existing and two novel biochemical models to the Min data, model selection leads us to propose a new model for the Min system. This model is the first Min model to be validated against biochemical time series and we hope that it will provide explanations for some of the as-yet-unexplained experimental observations (in progress). This work formed the PhD thesis of Will Carlquist.