Despite considerable advances in the topological analysis of metabolic networks, inadequate knowledge of the enzyme kinetic rate laws and their associated parameter values still hampers large-scale kinetic modelling. Furthermore, due to the widespread robustness of dynamic properties to parameter changes, the behaviour of a system is widely constrained by underlying network structures. Also, the integration of gene expression and protein levels into kinetic models is not straightforward and well-researched. Here, we present GRaPe, a platform-independent tool, which allows for streamlining the construction of large-scale kinetic models by generating generic rate equations for all reactions in a model. It also allows for the seamless integration of gene expression and protein levels into a reaction and generates equations for both transcription and translation which most current software tools lack. GRaPe provides methods for estimating parameters from experimental time series.

We modelled the yeast glycolysis pathway using GRaPe; our generic model had 15 enzyme species and 116 kinetic parameters. All parameters were estimated from data produced by a precise model. Our results show a near-perfect agreement with the training data and justifies that the behaviour of the system can be accurately described using generic kinetic equations. Our model also accurately describes dynamic experiments with a changed glucose influx, even though such data were not used for parameter estimation, showing that the generic model has predictive value.