Abstract

Application of fuzzy temporal logic to biological systems modelling

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Modelling has become an indispensable tool in the design of novel and the analysis of existing biological systems. Due to demands for modelling from both, synthetic and systems biology perspective, various quantitative deterministic and stochastic approaches are available or being developed. However, in order to establish a quantitative model of a biological system, detailed knowledge of the systems components and their interactions is required.

Although kinetic parameter values are generally obtained from either literature, electronic databases or experimental measurements, and mathematical models are acquired from literature and suitable automatic programming tools, data is sometimes unavailable or contradictory. In this case, different methods for parameter and model estimation are used, often by fitting a model to experimental data by minimizing the mismatch between predictions and data. Another useful approach to cope with uncertain data are fuzzy logic methods.

Fuzzy models are built upon linguistic description. The concept of a linguistic variable provides a means of approximate characterization of phenomena which are too complex or too ill-defined to be applicable to describing in conventional quantitative terms. For each variable, its term-set, the collection of linguistic (fuzzy) values, and a compatibility function are defined. Additionally, a set of fuzzy terms in the form of 'IF-THEN' rules is constructed, defining the relations between linguistic variables.

Here we establish a dictionary of fuzzy terms and rules and apply its use to construct a fuzzy model of the MAP-kinase signalling pathway. The defined set of terms and rules we propose simplifies the establishment of such models and therefore enables their intuitive construction even in cases when our knowledge of the biological system is not exact.

Keywords: computational biology, fuzzy logic, fuzzy time, uncertainty modelling