Structural analysis of kinetic systems with interval-type uncertainty using optimization methods

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Abstract

The chemical reaction network (CRN) models obeying the mass action law give an important subclass of nonnegative polynamial dynamical systems. One can use this dynamical system class to model the dynamical behaviour several important natural systems such as biochemical reaction networks or the spreading of diseases. The well-known Lotka Volterra model of population dynamics also belongs to CRN's. Even certain transportation models (queuing networks) can be represented as CRNs.

There exist linear programming and mixed integer linear programming based algorithms for the computation of structurally different dynamically equivalent realizations of a given CRN model. However for the computation of the structurally importan dynamically equivalent realizations it is necessary to know the exact parameter values of a given CRN model, but generally we have uncertain parameters in the model due to noisy measurements or modelling errors. One can only build up an uncertain model using measurement data, which can be represented as an interval model based on confidence intervals from a parameter estimation procedure. This means that we have for all parameters an interval. Based on the interval model we have a so-called uncertain CRN model.

This report generalizes some earlier computation methods and results for the uncertain case. The result of the thesis that we can compute all possible structurally different dynamically equivalent realization of an uncertain kinetic polynomial system. The presented algorithms make use of linear programming, therefore, the time complexity of the new algorithms is polynomial. Based on the new algorithms I examine the properties of uncertain CRN models depending on the degree of uncertainty. I also study the realation among uncertain models of different extent of uncertainity. The results are useful in the network reconstruction of kinetic polynomial systems, namely one can build up a possible set of network structure based on an estimated interval model. From the set of possible reaction networks with the usage of additional constraints, it might be possible to extract the original network structure. I also present real biological examples that highlight the fact that it could be quite hard to identify the original network structure bacause of the huge amount of possible network structures.

The thesis gives a general overview of the representation and structure computation of uncertain CRN models. After the overview of related results from the literature, presents a new algorithm able to computing dynamically equivalent realization containing maximal number of reactions. A new algorithm which returns all possible structurally different realizations of an uncertain CRN model is also presented. After the presentation of the algorithms, shows the results on literature examples and studies the uncertain CRN's with different extent of uncertainities.