

1014-12-1586

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*Identification: A computational Algebra Approach.*

Laubenbacher and Stigler have developed a method to reverse-engineer (biochemical) networks from experimental time-series data sets. Their method is based on Gröbner basis theory from computational algebra and finite dynamical systems over finite fields. It first finds the set of all dynamic models that fit the data and then a (minimal) dynamic model from this set is selected. However, the chosen model might not be the most compatible with the modeled biological system and a need to limit the search space is evident. In this talk, we present an algorithm that identify all possible static networks that govern a given set of time-series data. Qualitative known properties of the interactions will then be used to chose a static network from the possible ones. The method above is then employed to find a dynamic model based on the chosen static network. (Received September 28, 2005)