

A WEB-BASED APPLICATION FOR EVALUATING PARAMETER IDENTIFIABILITY OF BIOCHEMICAL MODELS IN POLYNOMIAL FORM

Dynamical models of physical phenomena are an established framework in the quantitative modelling and prediction of many systems. They are particularly relevant in the emergent area of systems biology, where the simulation of metabolic networks is often accomplished through state-space models taking the form of coupled nonlinear first-order differential equations. A fundamental issue in model identification is whether the structure of the model and the available experimental data allow for the determination of a unique value for each of the model parameters.

There are two complementary approaches to the problem of model identification: Data-based identifiability relies on statistical and/or heuristic methods, taking into account the quality of actual data; the other major aspect is *structural* identifiability, which concerns itself with the algebraic structure of the model and whose goal is to establish the formal existence of unique values to the set of parameters of a dynamical model, assuming availability of error-free and infinite-resolution data. Analysis of structural identifiability is then an essential precursor to a complete assessment of identifiability, and to parameter estimation itself. Typically, it is also a technically demanding procedure.

We present an online application that provides structural identifiability evaluations of arbitrary polynomial-differential models in a completely automated manner. The requirements on the part of the user are simply a web browser and minimal knowledge regarding his intended experimental setup. Although this application is built upon state-of-the-art methods of computer algebra, no familiarity with this field is assumed and absolutely no use of programming languages is required.