

Accurate simulations of models of epidemics  
(with interventions)

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Abstract

International experts in computational biology have developed models of epidemics and most of these involve systems of ordinary differential equations (ODEs) and some data data fitting.

In this talk, we will consider models based on an underlying classical SEIR epidemic model and show that dramatic improvements in the accuracy and reliability of simulations of these models can be obtained by employing carefully chosen numerical methods to approximate the ODEs and using inverse data fitting to match the observed data (of the simulation) to the model parameters.

In particular the ODE method must automatically detect and handle discontinuities that are often associated with the true solutions of these simulations. In addition the component-wise relative error of the approximate solution must be directly estimated and controlled.

We show, using an example of modelling a COVID-19 outbreak and employing an order 6 CRK ODE method (developed locally), that our approach is able to efficiently determine an accurate simulation of a real epidemic over different accuracy requests (without making strong assumptions regarding the problem or data).