

Abstract:

In recent years statisticians have been provided with a range of breakthrough Monte Carlo methods to perform exact (Bayesian) inference for stochastic models. However in some cases it is challenging to apply exact methodologies with large datasets and increasingly complex models. In the last 15 years "likelihood-free" methodologies and most notably Approximate Bayesian Computation (ABC) have been of help in attacking problems previously unrealistic to contemplate (starting with genetics studies and now expanding in many other areas), where the evaluation of the likelihood function is substituted with simulations from the model of interest. After a brief introduction to the basics of ABC we will focus on our methodologies for stochastic differential equation models and some preliminary results on protein folding modelling.