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Bayesian Experimental Design for Stochastic Biological Models with Computational Demanding Likelihoods

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Here I present a methodology for designing experiments for efficiently estimating the parameters of models with computationally intractable likelihoods. The approach combines a commonly used methodology for robust experimental design, based on Markov chain Monte Carlo sampling, with approximate Bayesian computation (ABC) to ensure that no likelihood evaluations are required. The utility function considered for precise parameter estimation is based upon the concentration of the ABC posterior distribution, which we form efficiently via ABC rejection based on precomputed model simulations. The motivation for this methodological development stems from experimental design problems in epidemiology, biology and medicine where the model is governed by a stochastic process. For example we consider optimal experimental designs for continuous time models described by Markov processes, non-Markovian processes and stochastic differential equations.

Keywords:

approximate Bayesian computation; Bayesian experimental design; Markov chain Monte Carlo; Markov process; non-Markovian process; stochastic differential equation.