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Variance reduction approaches to efficient simulation of biochemical reaction network models

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The complexity of biochemical reaction networks means that we often rely on stochastic simulation to investigate their potential behaviours, generating multiple sample paths from the model and using them to estimate summary statistics of interest. However, for realistic models, existing Monte Carlo methods are often prohibitive when it comes to exploring the range of possible model behaviours, conducting parameter sensitivity analysis, or parameter inference and model selection.

One approach that has the potential to mitigate these issues is that of variance reduction. Instead of attempting to reduce the computational cost of generating individual sample paths, we instead aim to reduce the variability in the summary statistics we are interested in. Computational savings can then be made because fewer sample paths are required to generate estimates to within a specified error. In this talk I will describe variance reduction approaches biochemical reaction network models. I will first show how point estimates can be generated simply and efficiently, and then outline how extensions to the basic method allow variance reduction approaches to be applied to a range of problems and summary statistics.

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