

Computational Methods for Quantifying Uncertainty in Biological Modeling

Robert M. Kirby

School of Computing and Scientific Computing and Imaging Institute, University of Utah, 50 S. Central Campus Dr., Salt Lake City, UT 84112 USA e-mail: kirby@cs.utah.edu

Abstract

Numerical simulations entail modeling and approximation assumptions that impact outcomes. Choices concerning items like geometric models and parameters made as part of the numerical simulation process may significantly influence the accuracy of the results, and hence evaluating the sensitivity of simulation results to variations in these choices is essential. Although the field of sensitivity analysis is well developed, systematic application of such methods to complex biological models is limited due to the associated high computational costs and the substantial technical implementation challenges.

In this talk, we present three case studies in which the use of the generalized Polynomial Chaos (gPC) technique offers a computationally feasible alternative to traditional Monte Carlo approaches for assessing the impact of model and parameter variability. In the first study, we examine the impact of torso conductivity parameter values on the forward problem of electrocardiography (ECG). In the second study, we examine the impact of heart position on the forward ECG problem. In the third study, we propose a framework that combines component shape parameterizations with the stochastic approximation methods to study the effect of drug depot shape variability on the outcome of drug diffusion simulations in a porcine model. In all three cases, we demonstrate that once the underlying stochastic process is characterized, quantification of the introduced variability is quite straightforward and provides an important step in the validation and verification process.