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An Efficient Method for Linear PDE with Stochastic Input

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Summary

Linear PDE are often appropriate as mathematical models for space-time biological phenomena. Among these are 1) Rall's equivalent cylinder model for cable neurons (see [1,2] and references therein), and 2) morphogen gradients with low receptor occupancy (see [3.4] and references therein). For some of these problems including cable neurons under synaptic current injection, we are interested in the system's response to stochastic excitations. The present paper offers a practical and efficient method for determining the statistical properties of the model response. For linear problems, the solution of an initial-boundary value problem in PDE is in principle given by the relevant Green's function representation. Statistical properties such as mean, correlations and higher order moment functions can be determined from the corresponding measures of the input by appropriate ensemble averaging appropriate combinations of the Green's function representation, e.g., [1,2]. In practice, analytical expression of the needed Green's function is not available for most problems. To compute the needed Green's function numerically and then evaluate the multi-dimensional integrals involved in the desired statistical (requiring at least a four fold integration or more to get the second or higher moments for a spatially one dimensional problem) require unattractively excessive or infeasible amount of computing. An equally serious problem is the huge storage requirement for a function of at least four variables, a requirement that may be impractical for the needed level of accuracy. While Monte Carlo simulations offer a try and true method for these problems, it is desirable to be able to determine the statistical properties of interest by reducing the stochastic problem to solving conventional initial boundary value problems in PDE for which there is a large body of knowledge on their numerical solutions. This paper develops such a method; applies it to several problems in the biological sciences to illustrates its usefulness, and shows how the method lends itself to take advantage of some recent advances in efficient algorithms which minimize storage requirements by orders of magnitude [5].

References

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