ABSTRACT:

I will focus on computational methods for continuous time Markov chains, which includes the large class of stochastically modeled biochemical reaction networks (and other population processes). I will show how different computational methods can be understood and analyzed by using different representations for the processes. In particular, I will discuss a new multi-level Monte Carlo method that produces an unbiased estimator for the approximation of expectations, though with only a fraction of the computational cost of the traditional exact algorithms (such as Gillespie's algorithm) combined with crude Monte Carlo. Time permitting, I will also discuss some related work on estimating parameter sensitivities.

TITLE:

Computational Methods for Stochastic Models of Bio-chemical Systems (and other population processes)

SPEAKER:

Professor David Anderson
Department of Mathematics
UW-Madison

TIME & PLACE:

Wednesday, December 7, 2011
Room 140 Bardeen
4pm

Cookies & Coffee @ 3:30p in Rm 1210 MSC