1064-60-171 **David F. Anderson*** (anderson@math.wisc.edu), Mathematics Department, University of Wisconsin, 480 Lincoln Drive, Madison, WI 53706. *Numerical methods for stochastic models of biochemical reaction networks.*

This talk will focus on stochastically modeled biochemical reaction networks, and will have a special emphasis on a pathwise representation for such models usually termed the "random time change representation." Such a representation is incredibly useful in that it allows us to (i) see the natural algorithms that can be used to simulate the processes and (ii) perform error analyses that can, in a rigorous manner, tell us what the algorithms are doing.

While exact simulation methods exist for discrete-stochastic models of biochemical reaction networks, they are oftentimes too inefficient for use because the number of computations scales linearly with the number of reaction events; thus, approximate algorithms have been developed. However, stochastically modeled reaction networks often have "natural scales" and it is crucial that these be accounted for when developing and analyzing numerical approximation methods. I will show that conducting such a non-standard error analysis leads to fundamentally different conclusions than previous analyses. (Received September 07, 2010)