Continuous time Markov chains and models of chemical reaction networks

Attempts to model chemical reactions within biological cells have led to renewed interest in stochastic models for these systems. The classical stochastic models for chemical reaction networks were formulated as continuous time Markov chains. These Markov chain models provide a first stochastic modeling approach for intra-cellular systems that is consistent with models based on the law of mass action and is more readily amenable to modifications that capture more realistic features of cellular processes. The basic building blocks of Markov chains are counting processes, and the primary way of specifying a counting process is through its intensity. A variety of methods for precisely determining a model from specified intensities will be discussed, and multiscale methods for model reduction will be described. The methods will be illustrated with the derivation of the Michaelis-Menten model for enzyme reactions and application to more complex systems.

Outline of the course

1. Modeling counting processes by intensities

2. Continuous time Markov chains
   Time-change representation. Martingale problem. Forward equation. Equivalence of the three

3. Transformations of counting processes and Markov chains
   Thinning of counting processes. Girsanov change of measure.

4. Basic limit theorems
   Ergodicity and stationary distributions. Laws of large numbers. Central limit theorems. Large deviations.

5. Reaction networks
   The stochastic law of mass action. Derivation from more detailed models. Models with delays.

6. Special models
   Unary models and their relationship to queueing and branching processes. Models with product form stationary distributions

7. Model reduction by Identifying multiple time-scales

8. Central limit theorems for models with multiple time-scales