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Statistical inference for reaction constants in stochastic biochemical networks

The problem of estimating values of reaction constants in biochemical networks if fundamental for any network reconstruction from the trajectory data. The talk will outline some recent developments in statistical inferential procedures for reaction constants in stochastic biochemical network models. We will especially focus on some newly proposed dynamical programming methods, which are similar to the Viterbi-type imputation algorithms for hidden Markov chain and are especially suitable when observed trajectories contain missing data for some species. It will be shown how the use of dynamic programming principles allows for efficient inference via either the Gibbs sampler or the EM algorithm and g the so-called uniformization representation of a Markov jump process. The applicability of the inferential procedures will be illustrated with data from the longitudinal mamalian genetic studies as well as the US CDC data from the onset of the 2009 H1N1 flu pandemic in the US