

**University of California, Irvine  
Statistics Seminar**

***Stochastic Compartmental Models of Infectious Disease without  
Tiresome Simulation or Gross Approximation***

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(Bldg. #314 on campus map)**

Stochastic compartmental models are important tools for understanding the course of infectious diseases epidemics in populations and in prospective evaluation of intervention policies. However, calculating the likelihood for discretely observed data from even simple models – such as the ubiquitous susceptible-infectious-removed (SIR) model – has been considered computationally intractable, since its formulation almost a century ago. Recently researchers have proposed methods to circumvent this limitation through data augmentation or approximation, but these approaches often suffer from high computational cost or loss of accuracy. We develop the mathematical foundation and an efficient algorithm to compute the likelihood for discretely observed data from a broad class of stochastic compartmental models. The computational complexity scales polynomially with the changes in population sizes between observations. We achieve this through a novel re-parameterization of the stochastic compartmental model into a multivariate coupled birth process and identify a convenient recursion to express the Laplace transform of the finite-time transition probabilities. We also give expressions for the derivatives of the transition probabilities using the same technique, making possible inference via Hamiltonian Monte Carlo (HMC). We use the 17th century plague in Eyam, a classic example of the SIR model, to compare our recursion method to sequential Monte Carlo, analyze using HMC, and assess the model assumptions. We also apply our direct likelihood evaluation to perform Bayesian inference for the 2014-2015 Ebola outbreak in Guinea under a hierarchical and time-inhomogeneous extension of the SIR model. The results suggest that the epidemic infectious rates have decreased since October 2014 in the Southeast region of Guinea, while rates remain the same in other regions, facilitating understanding of the outbreak and the effectiveness of Ebola control interventions.