May 19th, 3:30 PM - 4:00 PM

Methods for Parameter Estimation of a Stochastic SEIR Model

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This project aims to extend the framework of stochastic analysis epidemic models that are derived from a set of ordinary differential equations (ODEs) and are based on the underlying biological and spatial spread of disease. By implementing Bayesian Inference, this project proposes novel parameterizations of infectious disease models in the susceptible, exposed, infectious, removed (SEIR) class, and explores various methods to estimate these parameters. This allows for the rigorous assessment of these methods as models are extended to a spatial framework. Markov chain Monte Carlo (MCMC) is typically used as a method to estimate parameters, however this process is computationally demanding for models with high dimensional parameter spaces due to difficulties in obtaining converged chains. Additionally, these processes have limited ability to be parallelized. Approximate Bayesian Computation (ABC) is an alternative choice for estimating population distributions and the model parameters. ABC uses a batch of proposed parameters to generate simulated data that can be assess as "close to" or "far from" the real data under some norm. Rigorous statistical justification then allows for approximate parameter posterior distributions to be obtained. This process is parallelizable as subsequent parameter proposals do not depend on previous proposals. One of the challenges of ABC is that the convergence of the approximate posterior distributions to the true posterior distributions depends on the choice of norms used in the accept/reject procedure. It is often difficult to pinpoint the sufficient statistics needed to promote appropriate convergence. Sequential Monte Carlo ABC (SMC) aims to marry the two methods above by generating smaller sequential batches of ABC parameter estimates that can be used to inform the next batch of ABC so that convergence is quicker and aimed at the range of parameter values that have been successful in generating epidemics that closely resemble the data. Historically, these methods are limited from extension to spatial models, as many SEIR models consider infectious counts, rather than proportions of people relative to the total population. Thus, there are considerable modeling challenges that must be assessed in conjunction with these computational difficulties to develop viable spatial models. The final stage of this project aims to develop ABC methods that can propose parameters and generate populations using proportions. This will allows us to extend the framework to stochastically analyze systems of PDEs, which is novel is the spatial epidemic literature. Developing new and effective means by which stochasticity can be integrated into a spatial model and evaluating the efficacy of such methods will have a lasting impact on our current understanding of epidemics.