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Special Section on Inference for Infectious Disease Dynamics

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Introduction to the Special Section on Inference for Infectious Disease Dynamics

Theodore Kypraios and Vladimir N. Minin

Approximate Bayesian Computation and Simulation-Based Inference for Complex Stochastic Epidemic Models

Trevelyan J. McKinley, Ian Vernon, Ioannis Andrianakis, Nicky McCreesh, Jeremy E. Oakley, Rebecca N. Nsubuga, Michael Goldstein and Richard G. White

Abstract. Approximate Bayesian Computation (ABC) and other simulation-based inference methods are becoming increasingly used for inference in complex systems, due to their relative ease-of-implementation. We briefly review some of the more popular variants of ABC and their application in epidemiology, before using a real-world model of HIV transmission to illustrate some of challenges when applying ABC methods to high-dimensional, computationally intensive models. We then discuss an alternative approach—history matching—that aims to address some of these issues, and conclude with a comparison between these different methodologies.

Key words and phrases: Approximate Bayesian Computation, history matching, emulation, Bayesian inference, infectious disease models.

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Comparison and Assessment of Epidemic Models

Gavin J. Gibson, George Streftaris and David Thong

Abstract. Model criticism is a growing focus of research in stochastic epidemic modelling, following the successful addressing of model fitting and parameter estimation via powerful computationally intensive statistical methods in recent decades. In this paper, we consider a variety of stochastic representations of epidemic outbreaks, with emphasis on individual-based continuous-time models, and review the range of model comparison and assessment approaches currently applied. We highlight some of the factors that can serve to impede checking and criticism of epidemic models such as lack of replication, partial observation of processes, lack of prior knowledge on parameters in competing models, the nonnested nature of models to be compared, and computational challenges. Based on a wide selection of approaches as reported in the literature, we argue that assessment and comparison of stochastic epidemic models is complex and often, by necessity, idiosyncratic to specific applications. We particularly advocate following the advice of Box [*J. Amer. Statist. Assoc.* **71** (1976) 791–799] to be selective regarding the model inadequacies for which one tests and, moreover, to be open to the blending of classical and Bayesian ideas in epidemic model criticism, rather than adhering to a single philosophy.

Key words and phrases: Epidemic models, model comparison, model criticism, Bayesian methods, classical methods.

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Evidence Synthesis for Stochastic Epidemic Models

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Abstract. In recent years, the role of epidemic models in informing public health policies has progressively grown. Models have become increasingly realistic and more complex, requiring the use of multiple data sources to estimate all quantities of interest. This review summarises the different types of stochastic epidemic models that use evidence synthesis and highlights current challenges.

Key words and phrases: Evidence synthesis, state-space models, epidemic modelling, mechanistic modelling.

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Bayesian Nonparametrics for Stochastic Epidemic Models

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Abstract. The vast majority of models for the spread of communicable diseases are parametric in nature and involve underlying assumptions about how the disease spreads through a population. In this article, we consider the use of Bayesian nonparametric approaches to analysing data from disease outbreaks. Specifically we focus on methods for estimating the infection process in simple models under the assumption that this process has an explicit time-dependence.

Key words and phrases: Bayesian nonparametrics, epidemic model, Gaussian process.

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Modeling and Inference for Infectious Disease Dynamics: A Likelihood-Based Approach

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Abstract. Likelihood-based statistical inference has been considered in most scientific fields involving stochastic modeling. This includes infectious disease dynamics, where scientific understanding can help capture biological processes in so-called mechanistic models and their likelihood functions. However, when the likelihood of such mechanistic models lacks a closed-form expression, computational burdens are substantial. In this context, algorithmic advances have facilitated likelihood maximization, promoting the study of novel data-motivated mechanistic models over the last decade. Reviewing these models is the focus of this paper. In particular, we highlight statistical aspects of these models like overdispersion, which is key in the interface between nonlinear infectious disease modeling and data analysis. We also point out potential directions for further model exploration.

Key words and phrases: Maximum likelihood, iterated filtering, particle filter, compartment model, Lévy-driven stochastic differential equation, continuous-time Markov chain, environmental stochasticity.

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Estimating Transmission from Genetic and Epidemiological Data: A Metric to Compare Transmission Trees

Michelle Kendall, Diepreye Ayabina, Yuanwei Xu, James Stimson and Caroline Colijn

Abstract. Reconstructing who infected whom is a central challenge in analysing epidemiological data. Recently, advances in sequencing technology have led to increasing interest in Bayesian approaches to inferring who infected whom using genetic data from pathogens. The logic behind such approaches is that isolates that are nearly genetically identical are more likely to have been recently transmitted than those that are very different. A number of methods have been developed to perform this inference. However, testing their convergence, examining posterior sets of transmission trees and comparing methods' performance are challenged by the fact that the object of inference—the transmission tree—is a complicated discrete structure. We introduce a metric on transmission trees to quantify distances between them. The metric can accommodate trees with unsampled individuals, and highlights differences in the source case and in the number of infections per infector. We illustrate its performance on simple simulated scenarios and on posterior transmission trees from a TB outbreak. We find that the metric reveals where the posterior is sensitive to the priors, and where collections of trees are composed of distinct clusters. We use the metric to define median trees summarising these clusters. Quantitative tools to compare transmission trees to each other will be required for assessing MCMC convergence, exploring posterior trees and benchmarking diverse methods as this field continues to mature.

Key words and phrases: Infectious diseases, genomics, epidemiology, Bayesian inference, modelling.

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When Is a Sensitivity Parameter Exactly That?

Paul Gustafson and Lawrence C. McCandless

Abstract. Sensitivity analysis is used widely in statistical work. Yet the notion and properties of *sensitivity parameters* are often left quite vague and intuitive. Working in the Bayesian paradigm, we present a definition of when a sensitivity parameter is “pure,” and we discuss the implications of a parameter meeting or not meeting this definition. We also present a diagnostic with which the extent of violations of purity can be visualized.

Key words and phrases: Bayesian inference, misclassification, missing data, selection bias, sensitivity analysis.

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How the Instability of Ranks Under Long Memory Affects Large-Sample Inference

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Abstract. Under long memory, the limit theorems for normalized sums of random variables typically involve a positive integer called “Hermite rank.” There is a different limit for each Hermite rank. From a statistical point of view, however, we argue that a rank other than one is unstable, whereas, a rank equal to one is stable. We provide empirical evidence supporting this argument. This has important consequences. Assuming a higher-order rank when it is not really there usually results in underestimating the order of the fluctuations of the statistic of interest. We illustrate this through various examples involving the sample variance, the empirical processes and the Whittle estimator.

Key words and phrases: Long-range dependence, Long memory, Hermite rank, power rank, non-Gaussian limit, instability, large-sample inference.

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Richard Price, the First Bayesian

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Abstract. Roughly half of Bayes’s famous essay was written by Richard Price, including the Appendix with all of the numerical examples. A study of this Appendix reveals Price (1) unusually for the time, felt it necessary to allow in his analysis for a hypothesis having been suggested by the same data used in its analysis, (2) was motivated (covertly in 1763, overtly in 1767) to undertake the study to refute David Hume on miracles, and (3) displayed a remarkable sense of collegiality in scientific controversy that should stand as a model for the present day. Price’s analysis of the posterior in one particular example, including locating the posterior median and giving and interpreting credible regions, qualifies him as the first person to apply Bayes’s theory.

Key words and phrases: Thomas Bayes, Richard Price, David Hume, history.

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A Conversation with S. R. S. Varadhan

Ofer Zeitouni

Abstract. Sathamangalam Ranga Iyengar Srinivasa (Raghu) Varadhan was born in Chennai (then Madras). He received his Bachelor's and Master's degree from Presidency College, Madras, and his PhD from the Indian Statistical Institute in Kolkata, in 1963. That same year he came to the Courant Institute, New York University as a postdoc, and remained there as faculty member throughout his career. He has received numerous prizes and recognitions, including the Abel Prize in 2007, the US National Medal of Science in 2010 and honorary degrees from the Chennai Mathematical Institute, Duke University, the Indian Statistical Institute, Kolkata and the University of Paris.

The following conversations took place in his office at the Courant Institute on September 20 and September 28, 2017.

Key words and phrases: S. R. S. Varadhan, large deviations, hydrodynamic limits, homogenization, polaron.

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