

Cover Letter

Dear Editor,

We are writing to ask that you consider our manuscript, “Bayesian epidemic inference via coalescent SIR,” for publication in the journal *Genetics*.

We present a fully Bayesian implementation of epidemic inference under the coalescent which allows key epidemic and population dynamical parameters to be estimated from genetic data. Such inference plays a crucial role in linking the epidemiological study of infectious diseases with molecular genetic data and is relevant to researchers in the fields of genetics, epidemiology, immunology, and other related fields. The results of several analyses performed with these newly implemented *coalescent SIR models* provide valuable insight into their behavior, both intrinsically and in juxtaposition with a recently developed alternative [Kühnert *et al*, 2014, J. R. Soc. Interface]. This work contributes both a new method and a better understanding of existing methods for analyzing molecular genetic data that may be used to aid in prevention, control, and surveillance of epidemic infections.

We implemented two coalescent SIR models (using derivations of coalescent rates described in Volz *et al*, 2009 and Volz, 2012). We extend these models to the full Bayesian treatment on serially-sampled data and also allow for demographic stochasticity in the epidemic trajectories, contrasting this with the deterministic analog.

The original derivations of coalescent rates and semi-analytical likelihoods were also published in *Genetics* by Erik Volz and colleagues (Volz *et al*, 2009; Volz, 2012). This paper significantly builds on the earlier work by implementation of the model in the aforementioned Bayesian framework. We also demonstrate the advantages and pitfalls of both the stochastic and deterministic variants and compare with a recent non-coalescent alternative. We therefore expect this manuscript would be of particular interest to the readership of *Genetics*.

Thank you for considering our manuscript for review, and we look forward to your response.

Best regards,

Alex Poppinga
a.poppinga@auckland.ac.nz

Alexei Drummond
alexei@cs.auckland.ac.nz

Allan Wilson Centre for Molecular Ecology and Evolution
Department of Computer Science,
University of Auckland
Auckland, New Zealand