## APPROXIMATING OPTIMAL SMC PROPOSAL DISTRIBUTIONS IN INDIVIDUAL-BASED EPIDEMIC MODELS

Lorenzo Rimella\*, Christopher Jewell and Paul Fearnhead

Lancaster University

Abstract: Many epidemic models are naturally defined as individual-based models, in which we track the state of each individual within a susceptible population. However, inference for individual-based models is challenging because of the highdimensional state-space of such models, which increases exponentially with the population size. Here, we consider sequential Monte Carlo algorithms for inference for individual-based epidemic models, where we make direct observations of the state of a sample of individuals. Standard implementations, such as the bootstrap filter and auxiliary particle filter, are inefficient, owing to a mismatch between the proposal distribution of the state and future observations. We develop new efficient proposal distributions that consider future observations, leveraging the following properties: (i) we can analytically calculate the optimal proposal distribution for a single individual, given future observations and the future infection rate of that individual; and (ii) the dynamics of individuals are independent if we condition on their infection rates. Thus, we construct estimates of the future infection rate for each individual, and then use an independent proposal for the state of each individual, given this estimate. Empirical results show orders of magnitude improvement in efficiency of the sequential Monte Carlo sampler for both SIS and SEIR models.

*Key words and phrases:* Individual-based model, proposal distribution sequential Monte Carlo.

## 1. Introduction

Dynamical disease transmission models are increasingly being used to inform disease control policy related to both human and livestock outbreaks, for example, the SARS and H1N1 pandemic influenza in humans (Zhou, Ma and Brauer (2004)), avian influenza in poultry (Van der Goot et al. (2005)), and foot-andmouth disease in cloven-hoofed livestock (Zhou, Ma and Brauer (2004); Jewell et al. (2009)). Most recently, such models have been central in informing nationallevel decisions on social distancing and vaccination strategies for the SARS-CoV-2 pandemic (Brooks-Pollock et al. (2021); Funk et al. (2020)). In addition to managing outbreaks, such models are useful for studying the dynamics of endemic diseases, with the ability to explain random fluctuations around an otherwise

<sup>\*</sup>Corresponding author