Inferring the Contact Network Structure of Infectious Diseases: Applications of Likelihood-Free Inference for Epidemiological Agent-Based Modelling

Keywords: Contact networks, Agent-based models, Epidemiology, Compartmental models, Likelihood-free inference

Extended Abstract

Infectious diseases profoundly shape the health and survival of people, other animals, and plants, influencing ecosystems, food security, economies, and wellbeing. Because infection transmission within populations depends on these factors, accurate descriptions of their underlying contact network structures is critical for understanding pathogen spread in populations. Agent-based models (ABMs) simulate emergent interactions between individuals within complex systems to help inform decision making. While ABMs are invaluable tools for epidemiological planning, it is necessary to validate them using empirical data to bolster confidence that these models yield realistic predictions for decision making. Likelihood-free Bayesian calibration is one such approach for the fitting of complex ABMs to empirical data [1].

Here, we present a compartmental ABM framework to simulate the diffusion dynamics of infectious diseases over time and space, integrating both contact network analysis and Bayesian calibration via deep generative modelling. Our ABM leverages epidemiological outbreak data to estimate the hidden contact network structure underpinning the spread of infectious diseases (Figure 1.), combined with sequential neural posterior estimation for scalable Bayesian calibration [2]. The case study with which we have validated our model is the 2019 outbreak of H3N8 equine influenza within Great Britain [3]. By comparing simulated epidemic trajectories with observed outbreak data, we identify plausible network topologies and mixing patterns consistent with real-world transmission. We further demonstrate a generalisation of Approximate Bayesian Computation random forests [4] to perform a sensitivity analysis of network structure statistics derived from our ABM.

However, applying ABMs integrated with contact network analysis raises ethical considerations beyond any single pathogen. Such models often depend on granular movement, contact, and health data from individuals, organisations, or animals, creating risks around privacy, informed consent, and data ownership. The structure and assumptions embedded in agent behaviour and network topology can also encode biases that skew forecasts or policy recommendations. Ethically responsible use therefore requires transparent model design, clear explanation of limitations, stakeholder engagement in data collection and interpretation, and safeguards to ensure that the benefits of the analysis outweigh the potential risks to those whose data or behaviours are being modelled.

Beyond equine health, this work demonstrates how ABMs incorporating network inference can illuminate hidden structures in host–pathogen systems where direct contact data are scarce. Our study introduces a flexible framework for integrating behavioral, spatial, and epidemiological data via the coupling of ABMs with likelihood-free Bayesian inference and contact network analysis.

References

[1] Jakob Grazzini, Matteo G. Richiardi, and Mike Tsionas. "Bayesian estimation of agent-based models." In: Journal of Economic Dynamics and Control 77 (2017), pp. 26-47.

[2] David Greenberg, Marcel Nonnenmacher, and Jakob Macke. "Automatic posterior transformation for likelihood-free inference." In: Proceedings of Machine Learning Research 97 (2019), pp. 2404-2414.

[3] Fleur Whitlock, John Grewar, and Richard Newton. "An epidemiological overview of the equine influenza epidemic in Great Britain during 2019." In: Equine Veterinary Journal 55 (2023), pp. 153–164.

[4] Louis Raynal, Jean-Michel Marin, Pierre Pudlo, Mathieu Ribatet, Christian P. Robert, and Arnaud Estoup. "ABC random forests for Bayesian parameter inference." In: Bioinformatics 35, no. 10 (2019), pp. 1720-1728.

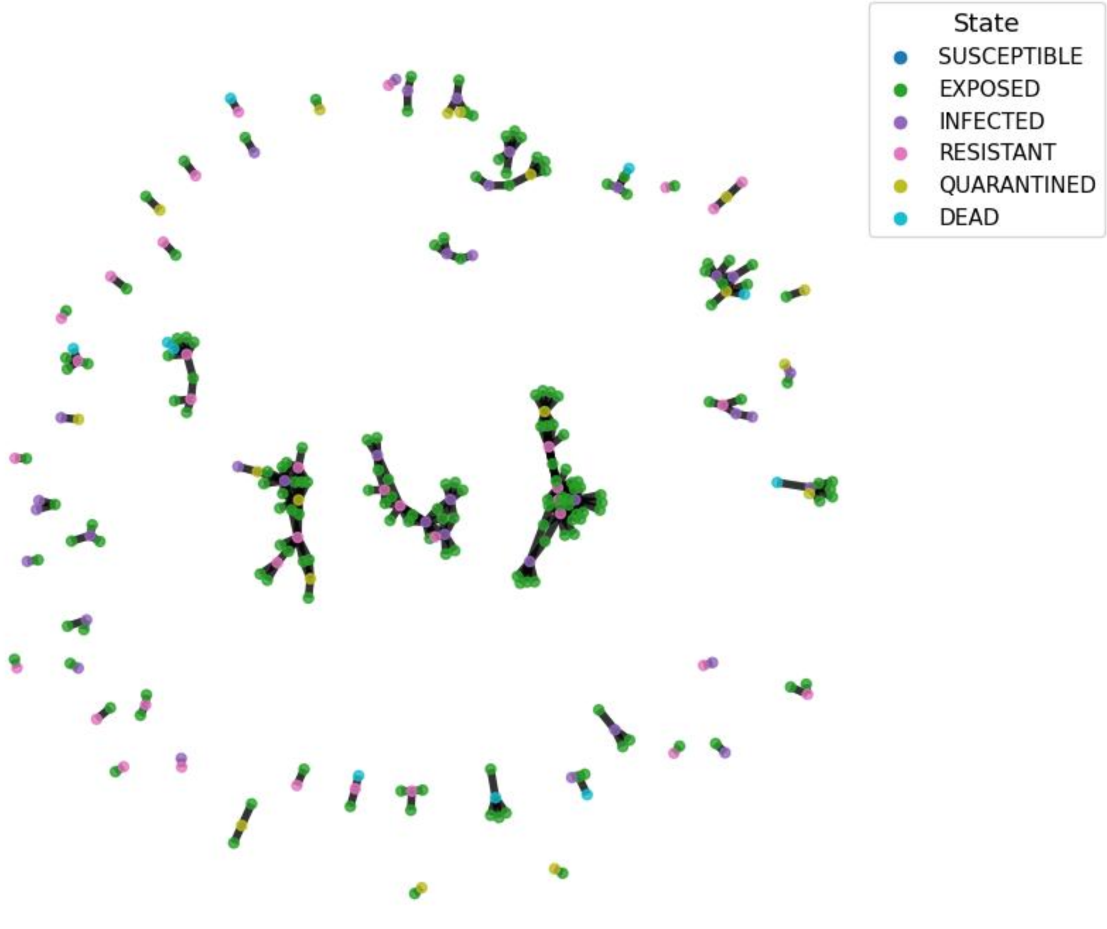

Figure 1. **Simulated contact network structure generated by our agent-based model for two thousand agents.** The epidemiological agent-based model is composed of six compartments, which determine the state of every agent at each timestep: Susceptible; Exposed; Infected; Resistant (i.e., immune); Quarantined; and Dead. Agents are represented as nodes, while transmissions are represented as edges. An infected agent transmits the disease to susceptible agents upon contact, according to defined transmission probabilities.