István Z. Kiss • Joel C. Miller • Péter L. Simon

Mathematics of Epidemics on Networks

From Exact to Approximate Models

Springer

Preface

Over the past decade, the use of networks has led to a new modelling paradigm combining several branches of science, including physics, mathematics, biology and social sciences. The spread of infectious diseases between nodes in a network has been a central topic of this growing field. The fundamental questions are easily stated, but answering them draws on observations and techniques of many fields.

There is a long successful history of mathematical modelling informing policies to mitigate the impact of infectious disease. Typically, models divide the population into compartments based on infection status and use simple assumptions about mixing and movements between these compartments. Over time, these models have grown more sophisticated to more accurately incorporate the contact structure of the population and to take advantage of increased computational resources. For example, sexually transmitted diseases have been investigated using high-dimensional compartmental models separating individuals by contact rates, socio-economic status and many other factors. However, when we make the additional observation that partnerships may be long-lasting, a new paradigm is needed, leading naturally to a network representation of the population structure.

Progress in model development has been extremely fast and has attracted interest from a diverse set of researchers. The fundamental objective is to combine the underlying population contact structure and the properties of the infectious agent to yield an understanding of the resulting spectrum of epidemic behaviours. To do this, researchers translate observed population and disease properties into a well-defined model. In many cases, the model sits at the interface of graph/network theory, stochastic processes and probability theory, dynamical systems, and statistical physics. The diversity of researcher backgrounds and the variety of applications considered have led to the development of many different modelling approaches. As the field matures, there is a need to increase understanding of how these different models fit together, how they relate to the underlying assumptions and how to develop an appropriate mathematical framework to unify different approaches.

This book sets out to make a contribution to modelling epidemics on networks by synthesising a large pool of models, ranging from exact and stochastic to approximate differential equation models, so that we may:

1. recognise underlying model assumptions and the resulting model complexity;
2. provide a mathematical framework with which we can describe observed phenomena and predict future scenarios;
3. permit direct comparison of the main models and provide their hierarchy; and
4. identify research gaps and opportunities for further rigorous mathematical exploration.

Chapter 1 introduces the reader to the fundamentals of disease transmission models and the underlying networks. Chapter 2 takes a rigorous probabilistic view and frames disease transmission on a network as a continuous-time Markov chain. In contrast, Chapter 3 builds a hierarchy of models starting at the node level which depend on the node–neighbour pairs, which in turn depend on triples formed by considering the next-nearest neighbours. Chapter 4 focuses on mean-field and pairwise models and their analysis on homogeneous networks. Chapter 5 extends approaches of Chapter 4 to heterogeneous networks and introduces effective degree models. In Chapter 6, the focus is primarily on SIR epidemics, and percolation theory methods are used to derive the low-dimensional edge-based compartmental model. Chapter 7 brings the different SIR models together, showing that under reasonable assumptions, the high-dimensional models of earlier chapters reduce to the low-dimensional model of Chapter 6. Chapter 8 extends the earlier models to account for the simultaneous spread of the disease and change in the network, considering several scenarios for how networks vary in time. Chapter 9 generalises the pairwise and edge-based compartmental models to non-Markovian epidemics, leading to integro-differential and delay differential equations. Chapter 10 starts from a Markov chain to derive the Fokker–Planck equation for the distribution of the number of infected individuals as a function of time and uses the resulting partial differential equation (PDE) to investigate epidemic processes. Finally, Chapter 11 shows that our models can perform surprisingly well even in networks, including empirically observed networks, for which the assumptions they are based on do not appear to be satisfied. The Appendix gives efficient simulation algorithms and discusses issues encountered in simulating epidemics on networks.

With more space, we would have liked to make a stronger emphasis on probabilistic models. Moreover, we would have examined epidemic control measures such as vaccination and contact tracing, as well as household models. Many other topics, for example, multilayer networks (networks with multiple types of connections), are left out, although many of the techniques we discuss apply to them. An additional topic, deserving of a book on its own, would be the use of real-world data to parametrise network models.

This book contains a number of rigorous mathematical arguments and proofs. However, a guiding principle throughout is to appeal to and be useful for audiences in fields outside of mathematics. Some quantitative sophistication will be

necessary; in particular, previous exposure to linear algebra, calculus, differential equations, dynamical systems and basics of probability and stochastic processes would be useful. We do not assume knowledge of graph theory.

Advanced undergraduate and graduate students can use the book as a foundation for learning the main modelling and analysis techniques. There are many exercises designed to develop a deeper understanding of the topic. Models and results of immediate applicability are signposted through the use of grey boxes.

We use this format to highlight readily implementable models or to summarise model outcomes, such as steady states, final epidemic size, basic reproductive ratio R_0, probability of an epidemic, etc.

Doctoral students, researchers and experts in this area can use the book not only as a reference guide or synthesis of the major modelling frameworks and model analysis tools but also to (i) confirm the validity and optimal range of applicability of models, (ii) understand how mathematical tools have been and are used in network modelling and (iii) identify further synergies between mainstream mathematical methods and problems arising in network modelling.

To enhance the flow of the presentation, citations to previous research are concentrated either at the beginning or end of chapters. This allows us to (a) build up models from the ground up by unifying different approaches leading to synthesised models and (b) cite further new developments that we could not cover.

Pseudocode for efficient epidemic simulation algorithms is given in the Appendix, and ready-to-run source code is available at the following website:

https://springer-math.github.io/Mathematics-of-Epidemics-on-Networks/

These include stochastic simulation of SIS and SIR on networks and numerical solutions of many differential equation models we present in the book. An extensive Python package using NetworkX [130] is provided, and many of these are also available in Matlab. We hope to add additional languages. These will help readers to complete many of the simulation-based exercises proposed in the book and may assist other researchers with their own projects. Other resources are available; for example, a useful package in C++ is EpiFire [143]. Solutions to exercises will be made available for instructors who use the book. Inevitably, small errors creep into any book. Please contact us directly for solutions or to report errors.

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Final thoughts: We would like to end with a memorable summary of our book about epidemics on networks. We hope this epidemic sonnet works:

When partnerships endure so long that to
Disease they are like frozen ties that bind,
Mass action fails us till new paradigms
Emerge; and networks then are useful tools.

Equation counts are exponential till
Reduced — through automorphic symmetries
Or caref'ly cutting out some vertices.
But yet complexity is too high still.

And so our mod'ler must approximate
And close equations — but not too simply.
For she must doubly count a high degree.
Or, she may watch diseases percolate.

With these techniques our mod'ler has new keys
To learn how partnerships affect disease.

Brighton, UK — István Z. Kiss
Bellevue, WA, USA — Joel C. Miller
Budapest, Hungary — Péter L. Simon
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About the Authors

Dr I.Z. Kiss is a Reader in the Department of Mathematics at the University of Sussex with his research at the interface of network science, stochastic processes and dynamical systems. His work focuses on the modelling and analysis of stochastic epidemic processes on static and dynamic networks. His current interests include the identification of rigorous links between approximate models and their rigorous mathematical counterparts and the formulation of new models for more complex spreading processes or structured networks.

Dr J.C. Miller is a Senior Research Scientist at the Institute for Disease Modeling in Seattle. He is also a Senior Lecturer at Monash University in Melbourne with a joint appointment in Mathematics and Biology. His research interests include dynamics of infectious diseases, stochastic processes on networks and fluid flow in porous media. The majority of his work is at the intersection of infectious disease dynamics and stochastic processes on networks.

Prof P.L. Simon is a Professor at the Institute of Mathematics, Eötvös Loránd University, Budapest. He is a member of the Numerical Analysis and Large Networks research group and the Head of Department of Applied Analysis and Computational Mathematics. His research interests include dynamical systems, partial differential equations and their applications in chemistry and biology. In particular, his work focuses on the modelling and analysis of network processes using differential equations.

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