

# Editorial: Improving pandemic and epidemic responses - novel methods and lessons learned from previous infectious disease outbreaks

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## ARTICLE INFO

### Keywords:

Infectious disease modelling  
Pandemic science  
Epidemics  
Network models


## ABSTRACT

Recent outbreaks, including the coronavirus disease 2019 (COVID-19) pandemic, have highlighted the importance of mathematical and statistical modelling in understanding the drivers of transmission and how to tailor responses. Improving future responses requires lessons from these previous outbreaks to be learned and the remaining challenges overcome. This requires developing appropriate mathematical, statistical and computational frameworks that accurately capture the studied mechanisms, leading to a better understanding of how different data can affect these formulations or the simulated interventions. Furthermore, improving model validation and quantifying uncertainty in the model parameter estimates and projections when applied responsively across settings and diseases is also required. Via a collection of 22 papers, this special issue brings together both theoretical advances and applied modelling innovations aimed at improving epidemic and pandemic preparedness and response. It includes articles that develop novel statistical inference approaches, as well as sophisticated and data-informed mathematical models, enhanced simulation techniques, exploration of heterogeneities in disease transmission both across ages and settings and the use of modelling techniques to evaluate intervention strategies across different diseases and settings to improve public health outcomes.

## 1. Introduction

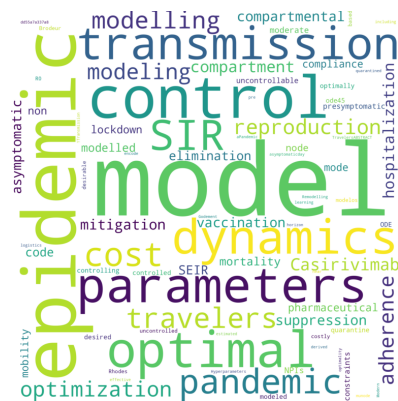
The infectious disease outbreaks of modern times have highlighted the importance of mathematical and statistical modelling in understanding the drivers of transmission and how to optimally control the spread through pharmaceutical and non-pharmaceutical interventions. Mathematical modelling played a crucial role in producing informed advice for public health policy makers on the control of the COVID-19 pandemic (Thompson, 2020), with mathematicians and statisticians at the forefront providing real-time and responsive modelling projections and scenario analyses.

There is now also an increased public awareness of the risk posed by infectious diseases and a need to learn lessons from previous epidemics and pandemics to improve future outbreak responses. This special issue concerns the topic of novel approaches to infectious disease modelling, including methods for informing models with infectious disease data, drawing on lessons learned from epidemics in recent history. Articles covering both theoretical aspects of infectious disease modelling and applied examples are included, showcasing how novel modelling methodologies can be useful when responding to and tackling outbreaks, as well as their integration with existing mathematical approaches. The 22 articles in the issue span analysis of model structure and demographic heterogeneities, uncertainty quantification, economic cost-effectiveness, data assimilation and public health strategies.

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**Figure 1:** Wordcloud generated from the papers in the special issue.

This editorial summarises the key themes covered in this special issue, collating the different aspects of modelling knowledge and tools that promote open and transparent pandemic science research. Although each of the articles within the collection makes a significant individual contribution to pandemic scientific modelling, there are themes that link them. In Section 2, we summarise the main contributions of each of the 22 papers under four overarching themes that represent one possible partition. Finally, Section 3 highlights future directions we see as priorities for the infectious disease research community in preparing for future outbreaks.

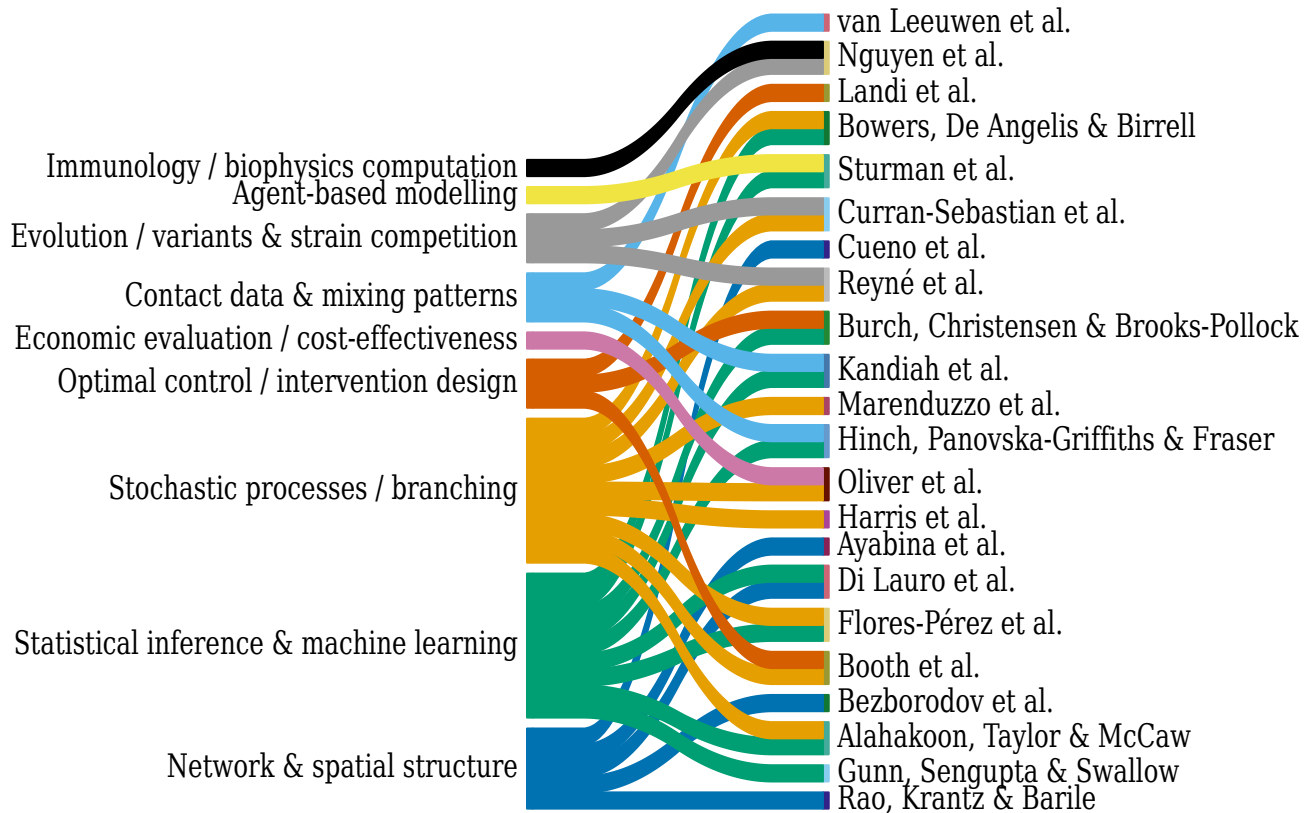


Figure 2: Sankey plot showing the relationship between papers by shared modelling/data method.

## 2. Key Themes and Contributions

Figure 1 illustrates a wordcloud generated from the papers in the special issue, while Figure 2 aims to show one non-unique thematic separation of the articles in the special issue.

### Improved Epidemic Transmission and Network Structures

One regularly occurring theme within the special issue is how the structure of models and their constituent components determine heterogeneous transmission structures and how they alter epidemic outcomes and control measures.

Srinivasa Rao, Krantz and Barile (2026) extend classical SIR models by embedding community-level geographical networks into higher-dimensional dynamical systems. The framework improves epidemic control during rapid spread by capturing spatial coupling missed by standard deterministic and stochastic models.

Bezborodov, Krueger, Pokalyuk, Szymański and Velleret (2025) develop and analyze epidemic models to compare two regional lockdown strategies based on infection thresholds that are either proportional to city size or uniform across cities, using mobility and infection data. They find that size-proportional thresholds can be more effective in reducing

the number of secondary infections in settings with highly heterogeneous city size distributions.

Di Lauro, Probert, Pickles, Cori, Hinch, Ferretti, Panovska-Griffiths, Abeler-Dörner, Dunbar, Bock, Donnell, Ayles, Fidler, Hayes and Fraser (2025) use a calibrated individual-based model to examine HIV transmission networks in high-burden African communities. The authors show that a large connected component dominated by young, highly sexually active individuals accounts for most transmission, implying targeted interventions can be highly effective.

In the paper Marenduzzo, Brown, Miller and Ackland (2025), the authors revisit classic SIRS compartmental models to understand oscillatory behaviours seen in some epidemics, showing that when stochastic effects or spatial structure are included the system can exhibit intrinsic boom-and-bust oscillations in infection levels even without external drivers like seasonal forcing. They argue these oscillations arise from waning immunity and the cyclic loss of herd immunity, offering a simple explanation for non-seasonal epidemic waves such as those observed during the COVID-19 pandemic.

Flores-P rez, Gonz lez-Olvera, Ch vez-Pe a, Gallardo-Hern andez and Torres (2025) develop a time-delay enhanced SIR model to analyze six distinct COVID-19 waves

in Mexico by explicitly incorporating incubation and recovery delays into the classical SIR framework. The authors show that including time delays substantially improves the model's ability to reproduce observed epidemic dynamics and that the Particle Swarm Optimization and Genetic Algorithms used provide robust parameter estimates across waves.

### Statistical and Computational Modelling

Other contributions within the special issue develop stochastic models and statistical and machine-learning approaches to better calibrate and capture real-world dynamics and prediction challenges.

Alahakoon, Taylor and McCaw (2025) use a Bayesian hierarchical statistical model to estimate parameters across six rural counties in the US simultaneously, allowing county-specific parameters to be estimated, improving robustness and pooling information across locations. Counterfactual analyses are performed by sampling from the posterior distributions to simulate alternative scenarios of earlier lifting of non-pharmaceutical interventions.

Bowers, De Angelis and Birrell (2025) introduce a stochastic modelling framework designed to estimate the probability that an emerging infectious disease will lead to sustained transmission based on very early case detections and limited data. By incorporating randomness in transmission and incorporating long waiting times between secondary cases, the approach helps quantify how many initial cases are needed before an outbreak is likely to take off, offering practical guidance for early epidemic response.

Gunn, Sengupta and Swallow (2026) also focus on fast stochastic modelling, demonstrating how Gaussian process models can be used to flexibly represent and project infectious disease trajectories without relying on rigid mechanistic assumptions. Using GPU acceleration and sparse computation to make inference feasible on large datasets, the authors show improved predictive efficiency and uncertainty quantification for epidemic trends.

Curran-Sebastian, Dyson, Hill, Hall, Pellis and House (2025) develop a multi-type branching process framework to derive analytical expressions for the probability of epidemic extinction and the distribution of peak timing when multiple pathogen types or variants co-circulate. Applying this to COVID-19 variants of concern, the authors show how differences in transmissibility and competitive interactions alter both the likelihood of fade-out and the expected timing of epidemic peaks.

### Incorporating Heterogeneity, Demographics, and Disease-specific Trait modelling

This set of papers highlights how individual and demographic differences impact outbreak progression and control strategy effectiveness.

In Harris, Gallmeier, Dushoff, Beckett and Weitz (2025), the authors explore how heterogeneity in individual susceptibility and transmissibility, and the covariation between them, influences the course of an epidemic. They show that

positive correlation (where highly susceptible individuals are also more transmissible) can substantially accelerate spread and increase outbreak size, while negative correlation dampens transmission, highlighting the need to account for correlated individual differences in epidemic predictions and control strategies.

Reyné, Djidjou-Demasse, Sofonea and Alizon (2025) study how the success of an emerging mutant pathogen strain depends not only on its biological advantages but also on the timing of its introduction relative to the population's evolving immunity. Using a two-strain model with waning and cross-immunity, the authors show that identical mutants can either fail or invade successfully depending on the host immunisation landscape at emergence.

Ayabina, Sevil, Kleczkowski and Gomes (2025) discuss how metapopulation epidemic models which assume homogeneous mixing within patches systematically underestimate the basic reproduction number and the effort required for disease control when individual heterogeneity is present. By incorporating within-patch variation in susceptibility or connectivity and proposing an inverse framework to infer these distributions from stratified data, the authors use COVID-19 in Scotland as a case study to demonstrate how accounting for individual heterogeneity fundamentally exaggerate both the strength of disease transmission and the expected impact of interventions.

Similarly, Hinch, Panovska-Griffiths and Fraser (2025) use an age-structured transmission model fitted to epidemiological data from England to quantify how differences in contact patterns and susceptibility across age groups shaped the COVID-19 epidemic trajectory over the Alpha and Delta waves. They find that age structure influenced both the timing and number of cases and deaths, with younger age groups driving transmission while older groups bore a disproportionate burden of severe outcomes.

van Leeuwen, Sandmann, Eggo and White (2026) also study heterogeneities in age-specific mixing, analysing how seasonal and age-specific patterns of social contacts and daily activities influence infectious disease transmission dynamics and the resulting age distribution of cases. They find that variations in time use (the time spent on different activities and in different settings) across seasons can substantially shift both contact rates and who gets infected most, suggesting that accounting for temporal changes in mixing is crucial for accurate epidemic forecasting and intervention planning.

Nguyen, Nguyen, Dang, Tran-Thi, Tran, Le, Tuong, Tran, Hoai Huynh and Thai (2026) use molecular docking and dynamics simulations to evaluate how mutations in the SARS-CoV-2 receptor-binding domain (RBD) affect binding affinity with neutralizing antibodies. The authors find that specific RBD substitutions in variants of concern leads to a marked reduction in antibody binding strength, indicating potential for immune escape and decreased vaccine effectiveness.

## Evaluating Public-Health Interventions

The next set of articles focus on evaluating and optimising interventions, from non-pharmaceutical measures to novel biomedical countermeasures.

Kandiah, van Leeuwen, Birrell and De Angelis (2025) retrospectively analyse empirical contact survey data and COVID-19 case dynamics to quantify how reductions in social contacts during the first UK lockdown influenced SARS-CoV-2 transmission. Their work finds that the dramatic decline in contact rates was associated with a substantial decrease in the effective reproduction number, underscoring the role of physical distancing in controlling early epidemic spread.

In Burch, Christensen and Brooks-Pollock (2025), the authors use mathematical modelling to demonstrate that the choice of outcome metric — such as minimizing infections, hospitalizations, or deaths — can substantially alter optimal COVID-19 vaccine dose allocation strategies across age and risk groups. The paper shows that strategies optimised for one outcome may perform poorly for another, highlighting that policy priorities critically shape vaccination recommendations.

The paper by Booth, Hadjichrysanthou, Rice, Frallicciardi, Magyarics, de Wolf, Goudsmit, Beukenhorst and Anderson (2025) uses transmission modelling to assess how antiviral intranasal sprays that reduce viral shedding or susceptibility might impact superspreading events. The authors show that widespread use of such sprays could substantially lower the frequency and size of superspreading clusters, particularly when combined with other interventions, and could therefore be a useful tool in outbreak control.

Landi, Pisaneschi, Laurino and Manfredi (2025) develop an optimal control model that balances the health costs of infection with the societal costs of social distancing, explicitly incorporating ongoing importation of infective travellers into the epidemic dynamics. The authors show that, under persistent external infection pressure, prolonged moderate distancing strategies can outperform short-intense lockdowns, highlighting the need to account for traveller influx and economic factors in pandemic preparedness planning.

## Improved Model and Calibration Reliability

Finally, additional papers in this special issue reflect an increasing emphasis on robust decision-support tools that account for uncertainty and model performance.

In Antony Oliver, Graham, Manolopoulou, Medley, Pellis, Pouwels, Thorpe and Hollingsworth (2025), the authors propose a novel framework for quantifying uncertainty in cost-effectiveness analyses of infectious disease interventions by combining stochastic transmission models with probabilistic cost and health outcome data, enabling more robust decision support under epidemiological variability. Using surveillance data from lymphatic filariasis, the authors demonstrate how incorporating model and parameter uncertainty alters estimates of intervention value, highlighting

the importance of fully accounting for stochasticity in both disease dynamics and economic outcomes.

Sturman, Swallow, Kerr, Stuart and Panovska-Griffiths (2025) improve the calibration efficiency and predictive performance of complex agent-based models, using the HPVsim model of human papillomavirus transmission as a case study. The authors find that targeted pruning of the data and the model simulations during the calibration process can reduce computational cost and overfitting while maintaining or even enhancing calibration accuracy. The authors thus suggest that pruning is a promising strategy for streamlining calibration of high-dimensional infectious disease simulations.

Cueno, Shintaku, Hayasaki, Migita and Imai (2025) construct network models of the human hematopoietic system to investigate how SARS-CoV-2 spike protein interactions at different infection points could affect blood cell development. The authors show that while isolated infection points have little effect, an integrated infection network primarily disrupts erythropoiesis and thrombopoiesis, suggesting potential mechanisms for COVID-19-related blood abnormalities from the improved model.

## 3. Future directions

Broadly grouped into these four categories, the articles collectively illustrate how modern epidemic modelling is converging with data science, statistical inference, and network science to tackle complex outbreak challenges. As co-editors, we set out to produce a special issue that would advance the knowledge across pandemic sciences. With these 22 papers, the authors have advanced knowledge in developing tools to predict outbreak trajectories under uncertainty, improved understanding of the role of demographic and behavioral heterogeneity, showcased theoretical and computational tools for real-time outbreak analysis, integrated high-resolution data sources into mechanistic models and constructed methods for optimizing different public health interventions.

With increasing resolution and availability of more complex and sophisticated data, mathematical modellers and statisticians will need to further account for realistic heterogeneities in the population demographics and disease-specific traits in their analyses. These heterogeneities are exhibited across different networks and demographic structures, with this special issue showing challenges remain in building sophisticated models that can be efficiently calibrated with clearly quantified uncertainty. Future work must build across traditional discipline boundaries to ensure effective evaluation of different strategies and optimise future outbreak control (Thompson, Bansal, Clapham, Dyson, Gutierrez, Hadley, Hart, Heesterbeek, Hollingsworth, House, Howerton, Isham, Lessler, Leung, Li, McBryde, McCaw, Mollison, Pan-Ngum, Parag, Pellis, Scarabel, Swallow, Thumbi, Tran-Kiem, Viboud and Plank, 2026).

In summary, this collection of 22 papers brings together both theoretical advances and applied modelling innovations aimed at improving epidemic and pandemic preparedness and response. Within its wide scope of articles are papers that develop novel statistical inference approaches and more sophisticated and data-informed mathematical models, enhance simulation techniques, explore heterogeneities in disease transmission both across ages and settings, and use modelling techniques to evaluate intervention strategies across different diseases and settings to improve public health outcomes. Through these, we aimed to not only showcase cutting edge approaches for pandemic science modelling but also methods and techniques that will remain relevant for possible future pandemics.

## References

- Alahakoon, P., Taylor, P.G., McCaw, J.M., 2025. Stochastic modelling of early-stage covid-19 epidemic dynamics in rural communities in the united states. *Journal of Theoretical Biology* 615, 112248. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325002140>, doi:<https://doi.org/10.1016/j.jtbi.2025.112248>.
- Antony Oliver, M.C., Graham, M., Manolopoulou, I., Medley, G.F., Pellis, L., Pouwels, K.B., Thorpe, M., Hollingsworth, T.D., 2025. Uncertainty quantification in cost-effectiveness analysis for stochastic-based infectious disease models: Insights from surveillance on lymphatic filariasis. *Journal of Theoretical Biology* 611, 112197. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001638>, doi:<https://doi.org/10.1016/j.jtbi.2025.112197>.
- Ayabina, D., Sevil, H., Kleczkowski, A., Gomes, M.M., 2025. A note on metapopulation models. *Journal of Theoretical Biology* 613, 112213. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001791>, doi:<https://doi.org/10.1016/j.jtbi.2025.112213>.
- Bezborodov, V., Krueger, T., Pokalyuk, C., Szymański, P., Velleret, A., 2025. Inter-city infections and the role of size heterogeneity in containment strategies. *Journal of Theoretical Biology* 615, 112247. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325002139>, doi:<https://doi.org/10.1016/j.jtbi.2025.112247>.
- Booth, G., Hadjichrysanthou, C., Rice, K.L., Frallicciardi, J., Magyari, Z., de Wolf, F., Goudsmit, J., Beukenhorst, A.L., Anderson, R., 2025. Preventing sars-cov-2 superspreading events with antiviral intranasal sprays. *Journal of Theoretical Biology* 615, 112237. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325002036>, doi:<https://doi.org/10.1016/j.jtbi.2025.112237>.
- Bowers, K.H., De Angelis, D., Birrell, P.J., 2025. Modelling with speed: a stochastic predictor of early epidemic detection. *Journal of Theoretical Biology* 607, 112120. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325000864>, doi:<https://doi.org/10.1016/j.jtbi.2025.112120>.
- Burch, E., Christensen, H., Brooks-Pollock, E., 2025. The effect of outcome choice on vaccine dose allocation: a modelling study. *Journal of Theoretical Biology* 610, 112156. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001225>, doi:<https://doi.org/10.1016/j.jtbi.2025.112156>.
- Cueno, M.E., Shintaku, N., Hayasaki, N., Migita, Y., Imai, K., 2025. Network modeling of the different sars-cov-2 spike protein infection points within the human hematopoietic network. *Journal of Theoretical Biology* 609, 112139. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001055>, doi:<https://doi.org/10.1016/j.jtbi.2025.112139>.
- Curran-Sebastian, J., Dyson, L., Hill, E.M., Hall, I., Pellis, L., House, T., 2025. Probability of extinction and peak time for multi-type epidemics with application to covid-19 variants of concern. *Journal of Theoretical Biology* 608, 112135. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001018>, doi:<https://doi.org/10.1016/j.jtbi.2025.112135>.
- Di Lauro, F., Probert, W.J., Pickles, M., Cori, A., Hinch, R., Ferretti, L., Panovska-Griffiths, J., Abeler-Dörner, L., Dunbar, R., Bock, P., Donnell, D.J., Ayles, H., Fidler, S., Hayes, R., Fraser, C., 2025. Large connected components in sexual networks and their role in hiv transmission in sub-saharan africa: A model-based analysis of hptn 071(popart) data. *Journal of Theoretical Biology* 613, 112218. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001845>, doi:<https://doi.org/10.1016/j.jtbi.2025.112218>.
- Flores-Pérez, A., González-Olvera, M.A., Chávez-Peña, G., Gallardo-Hernández, A.G., Torres, L., 2025. Time-delay enhanced sir model for covid-19 waves in Mexico: Parameter estimation using evolutionary algorithms. *Journal of Theoretical Biology* 613, 112229. URL: <https://www.sciencedirect.com/science/article/pii/S002251932500195X>, doi:<https://doi.org/10.1016/j.jtbi.2025.112229>.
- Gunn, E., Sengupta, N., Swallow, B., 2026. Gaussian process modelling of infectious diseases using the greta software package and gpus. *Journal of Theoretical Biology* 616, 112278. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325002449>, doi:<https://doi.org/10.1016/j.jtbi.2025.112278>.
- Harris, J.D., Gallemeier, E., Dushoff, J., Beckett, S.J., Weitz, J.S., 2025. Infections are not alike: The effects of covariation between individual susceptibility and transmissibility on epidemic dynamics. *Journal of Theoretical Biology* 613, 112211. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001778>, doi:<https://doi.org/10.1016/j.jtbi.2025.112211>.
- Hinch, R., Panovska-Griffiths, J., Fraser, C., 2025. Estimating the contribution of age-structure to the covid-19 epidemic in england. *Journal of Theoretical Biology* 611, 112177. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001432>, doi:<https://doi.org/10.1016/j.jtbi.2025.112177>.
- Kandiah, J., van Leeuwen, E., Birrell, P.J., De Angelis, D., 2025. Contact data and sars-cov-2: Retrospective analysis of the estimated impact of the first uk lockdown. *Journal of Theoretical Biology* 610, 112158. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001249>, doi:<https://doi.org/10.1016/j.jtbi.2025.112158>.
- Landi, A., Pisaneschi, G., Laurino, M., Manfredi, P., 2025. Optimal social distancing in pandemic preparedness and lessons from covid-19: Intervention intensity and infective travelers. *Journal of Theoretical Biology* 604, 112072. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325000384>, doi:<https://doi.org/10.1016/j.jtbi.2025.112072>.
- Marenduzzo, D., Brown, A.T., Miller, C.W., Ackland, G.J., 2025. Oscillation in the sirs model. *Journal of Theoretical Biology* 611, 112169. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001353>, doi:<https://doi.org/10.1016/j.jtbi.2025.112169>.
- Nguyen, D.N., Nguyen, Q.T., Dang, T.M., Tran-Thi, P.U., Tran, V.H., Le, M.T., Tuong, L.T., Tran, V.T., Hoai Huynh, P.N., Thai, K.M., 2026. Antibody escape of sars-cov-2 variants of concern on receptor-binding domain: A computational approach. *Journal of Theoretical Biology* 619, 112345. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325003297>, doi:<https://doi.org/10.1016/j.jtbi.2025.112345>.
- Reyné, B., Djidjou-Demasse, R., Sofonea, M.T., Alizon, S., 2025. Mutant emergence timing and population immunisation status impact epidemiological dynamics. *Journal of Theoretical Biology* 608, 112140. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325001067>, doi:<https://doi.org/10.1016/j.jtbi.2025.112140>.
- Srinivasa Rao, A.S., Krantz, S.G., Barile, J.P., 2026. Integrating community level transmission geographical networks into a dynamical system for better epidemic control. *Journal of Theoretical Biology* 618, 112319. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325003030>, doi:<https://doi.org/10.1016/j.jtbi.2025.112319>.
- Sturman, F., Swallow, B., Kerr, C., Stuart, R.M., Panovska-Griffiths, J., 2025. Can pruning improve agent-based models' calibration? an application to hpvsim. *Journal of Theoretical Biology* 611, 112130. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325000967>, doi:<https://doi.org/10.1016/j.jtbi.2025.112130>.
- Thompson, R.N., 2020. Epidemiological models are important tools for guiding covid-19 interventions. *BMC Medicine* 18, 152. URL: <https://www.sciencedirect.com/science/article/pii/S1745275820301152>.

- doi.org/10.1186/s12916-020-01628-4, doi:10.1186/s12916-020-01628-4.
- Thompson, R.N., Bansal, S., Clapham, H., Dyson, L., Gutierrez, M.A., Hadley, L., Hart, W.S., Heesterbeek, H., Hollingsworth, T.D., House, T., Howerton, E., Isham, V., Lessler, J., Leung, K., Li, X., McBryde, E., McCaw, J.M., Mollison, D., Pan-Ngum, W., Parag, K., Pellis, L., Scarabel, F., Swallow, B., Thumbi, S.M., Tran-Kiem, C., Viboud, C., Plank, M.J., 2026. Infectious disease outbreak controllability: biological, social and public health factors. *Proceedings of the Royal Society B: Biological Sciences* 293, 20252848. URL: <https://doi.org/10.1098/rspb.2025.2848>, doi:10.1098/rspb.2025.2848, arXiv:<https://royalsocietypublishing.org/rspb/article-pdf/doi/10.1098/rspb.2025.2848/5676237/rspb.2025.2848.pdf>.
- van Leeuwen, E., Sandmann, F.G., Eggo, R.M., White, P.J., 2026. Social mixing and time use throughout the year: Potential changes in disease transmission and age distribution of cases. *Journal of Theoretical Biology* 622, 112349. URL: <https://www.sciencedirect.com/science/article/pii/S0022519325003339>, doi:<https://doi.org/10.1016/j.jtbi.2025.112349>.