

South-West German Infectious Disease Modelling Workshop

Welcome to the third **SWIM** Workshop.

Institute of Statistics, Karlsruhe Institute of Technology,
Blücherstraße 17, 76185 Karlsruhe.

Wednesday 9 December 2026, 10:00 - 17:00. `https://swim-workshop.de/`

Preliminary Programme as of 9 November 2026

10:00 – 10:30 Coffee & welcome. Atrium.

10:30 – 11:20 Keynote. Atrium

Anne Cori (Imperial College London): *TBA.*

Chair: Theo Schäfer (Karlsruhe Institute of Technology).

11:30 – 12:30 Session 1.1: Computational methods and agent-based models. Room: 320, 3rd Floor

Aleksandr Bryzgalov (IMEBI, Universitätsmedizin Halle): *Modelling presenteeism in agent-based epidemic models: implications for transmission and workforce availability.*

Martin Kühn (German Aerospace Center): *MEmilio: A high performance Modular EpideMIcs simuLatIOn software – from modeling infections to post-acute infection syndromes.*

Mohd Kashif Ansari (University of Koblenz): *When do neural networks become useful for solving ODE systems? An SIR case study.*

Chair: Burcu Gürbüz (University of Mainz).

11:30 – 12:30 Session 1.2: Cohort studies. Room: 124, 1st Floor.

Mathilde Grimée (Robert Koch Institute): *Contact patterns of people in elderly care homes in Germany, 2025-2026: Changes in residents and staff due to influenza or acute respiratory infection episodes (preliminary results).*

Miracle Amadi (LUT University, Lappeenranta): *Sustaining herd immunity against measles: Insights from a serological cohort study in an outbreak-free population.*

David Hodgson (Charité - Universitätsmedizin Berlin): *Disentangling correlates of protection from exposure history in a Group A Streptococcus household cohort.*

Chair: Franziska Frederking (Max Planck Institute for Infection Biology, Berlin).

12:30 – 13:30 Lunch. Ground Floor, on the right as you come through the door.

13:30 – 14:30 Session 2.1: AI and Deep Learning. Room 320, 3rd Floor.

Seth Flaxman (RPTU Kaiserslautern-Landau): *Learning to learn with deep learning for global health.*

Sten de Schrijver (Robert Koch Institute): *When does graph structure matter? Spatial resolution and influenza forecasting with graph neural networks.*

Kilian Volmer (University of Bonn): *Creation and evaluation of an agentic workflow to predict Ebola outbreak statistics.*

Chair: Lucas Böttcher (Frankfurt School of Finance & Management).

13:30 – 14:30 Session 2.2: Vaccines and immunity. Room 124, 1st Floor.

Kaige Dong (Charité - Universitätsmedizin Berlin): *Changes in serotype-specific pneumococcal carriage, multiple serotype carriage, and pneumococcal density following PCV10 introduction in Viet Nam: a secondary analysis of a cluster-randomised trial.*

Burcu Gürbüz (University of Mainz): *Dynamics and control of an SIRS model with waning immunity and revaccination.*

Yulia Evsyukova (ZEW Mannheim): *Capacity contracts for vaccines and incentives for pathogen disclosure in the planned PABS system.*

Chair: Natalie Böhm (Karlsruhe Institute of Technology).

14:40 – 15:20 Session 3.1: Stochasticity and observation models. Room 320, 1st Floor.

Matthieu Domenech de Cellès (Max Planck Institute for Infection Biology, Berlin): *The impact of observation models on epidemic inference for emerging infectious diseases: SARS-CoV-2 as a case study.*

Theo Schäfer (Karlsruhe Institute of Technology): *Making sense of the negative binomial renewal equation.*

Chair: Barbora Němcová (Karlsruhe Institute of Technology).

14:40 – 15:20 Session 3.2: Climate and weather. Room 124, 1st Floor.

Cana Kussmaul (Max Planck Institute for Infection Biology, Berlin): *U-shaped effects of humidity and the impact of misspecified weather-transmission relationships in epidemic models.*

Peter Fransson (Heidelberg University): *An explainable covariate compartmental model for predicting the spatio-temporal patterns of dengue in Sri Lanka.*

Chair: Adrian Denz (SwissTPH, Basel).

15:20 – 16:10 Group picture, poster session and coffee break. Atrium.

16:10 – 17:00 Keynote. Atrium.

Christian Althaus (University of Bern) *Modelling emerging infectious diseases: The past, the present, and the future.*
Chair: Johannes Bracher (Karlsruhe Institute of Technology).

Posters

1. Miracle Amadi (LUT University, Lappeenranta): *Correcting structural bias in dynamical models of infectious disease using a Bayesian state-space framework.*
2. Antonia Bockhorn and Johannes Bracher (Karlsruhe Institute of Technology): Reviewer agreement in infectious disease modelling.
3. José Daniel Conejeros (ISI Foundation, Turin): *A Bayesian space-time analysis of seasonal and spatial patterns of tuberculosis and their determinants in Chile, 2011-2025.*
4. Franziska Frederking (Max Planck Institute for Infection Biology, Berlin): *Quantifying natural immune boosting in pre-vaccine-era pertussis.*
5. Sophie Reichert (FAU Erlangen-Nürnberg): *Fitting endemic-epidemic models using RTMB.*

Practical information

- Internet access via `eduroam` or the `KIT` WiFi is available throughout the building.
- Lunch and coffee breaks are free of charge for registered participants and take place in the Atrium.
- We would like to take a group picture at the beginning of the afternoon break. This picture shall be published on the workshop website after the event. Joining the group photo is of course voluntary.

Organizers: Natalie Böhm (KIT), Johannes Bracher (KIT), Barbora Němcová (KIT), and Theo Schäfer (KIT).
Burcu Gürbüz (University Mainz) serves as a session organizer.

Funding: We are grateful for support from the Helmholtz Information and Data Science School for Health and the German Research Foundation (DFG).

Abstracts

Keynote 1.

TBA.
Anne Cori (Imperial College London

Session 1.1: Computational methods and agent-based models.

Modelling Presenteeism in Agent-Based Epidemic Models: Implications for Transmission and Workforce Availability.
Aleksandr Bryzgalov (IMEBI, Universitätsmedizin Halle)

Symptomatic infections create an important modelling challenge: individuals may stay at home to reduce transmission or continue their usual activities, including working while ill. The implications of this choice may differ between influenza and COVID-19, given differences in the proportion of symptomatic infections and the timing of symptom onset relative to infectiousness. Using an agent-based epidemic model, we examine how alternative assumptions about symptomatic healthcare workers staying at home or continuing to work affect infection transmission and workforce availability. We investigate the trade-off between reduced transmission and increased staff non-availability, considering the heterogeneity of individual contacts and the resulting effects on epidemic dynamics. In particular, we assess how these assumptions influence estimates of the attack rate and reproduction number, and how the relationship between these measures changes under different assumptions about symptom-related work restrictions. This analysis highlights the importance of explicitly representing symptom-related work restrictions and evaluating their consequences for epidemic dynamics and healthcare workforce availability.

MEmilio: A high performance Modular EpideMIcs simuLatIOn software – from modeling infections to post-acute infection syndromes.
Martin Kühn (German Aerospace Center)

Epidemic and pandemic preparedness with rapid outbreak response rely on timely, trustworthy evidence. Mathematical models are crucial for supporting timely and reliable evidence generation for public health decision-making with approaches from compartmental and metapopulation models to detailed agent-based simulations. Yet, the accompanying software ecosystem remains fragmented across model types, spatial resolutions, and computational targets, making models harder to compare, extend, and deploy at scale. Here we present MEmilio, a modular, high-performance framework for epidemic simulation that harmonizes the specification and execution of diverse dynamic epidemiological models within a unified architecture. MEmilio couples an efficient C++ simulation core with coherent model descriptions and a user-friendly Python interface, enabling workflows that run on laptops as well as high-performance computing systems. Standardized representations of space, demography, and mobility support straightforward adaptations in resolution and population size, facilitating systematic inter-model comparisons and ensemble studies. The framework integrates readily with established tools for uncertainty quantification and parameter inference, supporting a broad range of applications from scenario exploration to calibration. Finally, strict software-engineering practices, including extensive unit and continuous integration testing, promote robustness and minimize the risk of errors as the framework evolves. By unifying implementations across modeling paradigms, MEmilio aims to lower barriers to reuse and generalize models, enable principled comparisons of implicit assumptions, and accelerate the development of novel approaches that strengthen modeling-based outbreak preparedness. Moreover, we will show how recent advancements in agent-based modeling of post-acute infection syndromes (PAIS) can be coupled with MEmilio to study the long-term effects of epidemic or endemic developments.

When Do Neural Networks Become Useful for Solving ODE Systems? An SIR Case Study.
Mohd Kashif Ansari (University Koblenz)

Neural networks offer an alternative to classical ODE solvers, but their value depends on the problem and computational workload. Using the susceptible–infected–recovered (SIR) model, we compare RK45 with a data-assisted physics-informed

neural network. For the fixed-parameter forward problem, RK45 achieves greater accuracy at substantially lower total cost, showing that this simple benchmark does not justify neural training. Preliminary experiments also show no systematic improvement in solution accuracy with increasing network size. For inverse estimation, neural reconstruction of a time-varying transmission rate captures the main infection waves and produces errors more concentrated near zero than piecewise-constant and Gauss–Newton-based reconstructions. However, peak discrepancies remain, and accurate infection fits do not establish accurate parameter recovery. Future work will investigate criteria for choosing between classical and neural solvers, potentially based on quantities such as stiffness and dimensionality. Once regimes of neural advantage are established, we will investigate appropriate network architectures.

Session 1.2: Cohort studies.

Sustaining herd immunity against measles: Insights from a serological cohort study in an outbreak-free population.
Miracle Amadi (LUT University)

Purpose: Measles antibody levels decline after MMR vaccination, raising concerns about individual protection and maintenance of herd immunity. In Finland, MMR vaccinations started in 1982, and only sporadic measles cases have been observed since the late 1980s. This suggests that a high proportion of individuals are unlikely to transmit measles. We examine the sustainability of herd immunity by inferring the antibody threshold sufficient to interrupt measles transmission.

Methods: We utilized measles antibody data collected after the second MMR vaccine dose from 157 individuals in a Finnish MMR-vaccinated cohort at 8 sampling rounds during 1987–2012 (ages 6–31 years), with antibody concentrations measured using the haemagglutination inhibition assay and/or enzyme immunoassay depending on the round. Antibody decline after vaccination was estimated and extrapolated beyond the study age range to predict the proportion exceeding candidate antibody thresholds in the 2022 Finnish population. Threshold sufficiency was evaluated by comparing this proportion with the critical proportion required to sustain the absence of measles epidemics.

Results: The mean follow-up time was over 20 years, with 68% of all potential samples available. After age 13, antibody levels declined slowly or very slowly, with first and second half-lives of 10 and 20, or 22 and 67 years, respectively. No unique threshold was identified. However, the continued absence of measles epidemics suggests a very slow decline and/or a low (< 120 mIU/ml) antibody threshold to interrupt transmission.

Conclusions: Vaccine-induced protection against measles transmission appears long-lasting. For herd immunity, declining vaccine uptake poses a greater risk than waning immunity.

Contact patterns of people in elderly care homes in Germany, 2025-2026: Changes in residents and staff due to influenza or acute respiratory infection episodes (Preliminary results).
Mathilde Grimée (Robert Koch Institut)

Aims: This study aims to measure transmission-relevant contact patterns within elderly care homes in Germany, and how these patterns change with influenza or acute respiratory infection (ARI) episodes. Among others, the results will be used to generate evidence for infectious disease modelling of antiviral influenza post-exposure prophylaxis to inform immunization policymaking in Germany.

Methods: This multi-centre study consisted of two waves of data collection in 12 elderly care homes: the first conducted outside of the influenza season (wave 1), and the second during the influenza season (week 40, 2025-week 20, 2026; wave 2). Elderly care homes were recruited on a voluntary basis across Germany. In each care home, informed consent was obtained from individual residents and staff. Afterwards, all physical or conversational contacts in the last 24 hours were obtained in interviewer-led surveys. Wave 1 serves as the baseline. In wave 2, participants with a recent (lab-/antigen-/clinically-) confirmed influenza or ARI episode (cases) recalled contacts during the worst day of the episode and during the 24 hours preceding the interview, while participants without a recent influenza or ARI episode (controls) reported contacts only for the preceding 24 hours. Based on both waves, we estimated changes in contact patterns from baseline. Multilevel regression analyses will be used to estimate these changes and adjust for demographic and health-related factors.

Results: Preliminary results of data from waves 1 and 2 indicated higher contact rates in this setting than previously reported for the general German population. The unadjusted contact rates were higher among staff than residents, and higher outside of an ARI episode than on the worst day of the episode, with notable heterogeneity.

Discussion: This is the first study of its kind conducted in elderly care homes in Germany that provides evidence on contact rates since the coronavirus disease 2019 (COVID-19) pandemic in an understudied epidemiological setting. The results will inform outbreak modelling in German care homes and help to investigate the added value of using antiviral influenza post-exposure prophylaxis.

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Acknowledgements: Data collection was supported by Lilly Aepfelbach, Anna Kuhn, Hannah Lauer, Vanessa Lisser, and Mahboobe Shaffafi (all RKI).

Disentangling correlates of protection from exposure history in a Group A Streptococcus household cohort.
David Hodgson (Charité - Universitätsmedizin Berlin)

Background: Group A Streptococcus (GAS) has no licensed vaccine, partly because no correlate of protection has been established. In endemic settings, antibody titres, cumulative exposure and age are tightly coupled, so protection and age are hard to separate.

Methods: We built a Bayesian daily-hazard model for a Gambian household cohort (323 participants, 44 households, 132 GAS events). Serology was repeated against five antigens in serum (IgG) and oral fluid (IgA). The hazard combines a baseline rate, a household-exposure rate ratio and a titre-dependent susceptibility term. We fitted models with and without age, and compared them by leave-one-out cross-validation (ΔELPD).

Results: Accounting for age improved prediction (ΔELPD +19.1, SE 6.7; AUC 0.63 to 0.72). Without age, mucosal IgA looked like the leading correlate: SpyCEP and SpyAD IgA gave the largest gains (ΔELPD +4.7 and +4.0). Once age was included, all five IgA markers lost predictive value and four of five serum IgG markers gained. SpyAD and SpyCEP IgG became the leading correlates (+3.0 and +2.7). The more strongly a marker tracked age, the more its signal fell (Spearman $\rho = -0.88$). Mucosal IgA rose steadily from infancy into adulthood. Serum IgG reached its plateau by 5–11 years.

Conclusions: Mucosal immunity is so closely tied to age that its apparent protective effect is largely confounded by age. Future GAS correlate studies should treat age as a confounder, and should be cautious about transporting correlates to age groups outside those studied. Serum IgG remained the stronger correlate after adjustment.

Session 2.1: AI and Deep Learning.

Learning to learn with deep learning for global health.
Seth Flaxman (RPTU Kaiserslautern-Landau)

Gaussian Processes (GPs) provide a flexible and statistically principled foundation for modeling spatiotemporal phenomena, but their $O(N^3)$ scaling makes them intractable for large datasets. I will present two forthcoming AISTATS papers from Machine Learning & Global Health network researchers that tackle this problem in very different ways:

DeepRV: Accelerating spatiotemporal inference with pre-trained neural priors: `https://arxiv.org/abs/2503.21473`

Scalable Spatiotemporal Inference with Biased Scan Attention Transformer Neural Processes: `https://arxiv.org/abs/2506.09163`

When Does Graph Structure Matter? Spatial Resolution and Influenza Forecasting with Graph Neural Networks.
Sten de Schrijver (Robert Koch Institut)

Background: Graph Neural Networks (GNNs) are increasingly used for spatio-temporal epidemic forecasting [1]. Whether their performance gains arise from spatial structure remains poorly understood. This study examines when graph structures improve GNN forecasts in an epidemiological context, and how this depends on spatial resolution.

Methods: We forecasted weekly influenza incidence in Germany 1-9 weeks ahead at three different spatial resolutions: 16 federal states, 38 NUTS 2 regions and 400 districts. Models were evaluated on four held-out influenza seasons. Two GNN architectures (Graph Convolutional Network and Graph Attention Network) were trained on three types of graph structures: a geographic contiguity graph, random graphs and an identity graph. The latter removes all spatial information and thus connects each region only to itself. We used Lin's concordance correlation coefficient (CCC) to evaluate model

predictions, and Moran's I to assess spatial autocorrelation.

Results: At district level, the contiguity graph improved forecasts over the identity and random graphs from 4 weeks ahead onward, and the improvement increased with horizon. At nine weeks ahead, the contiguity graph improved CCC scores on average by 10% and outperformed the identity graph in 75% of the districts for the primary season. This was driven by the increase in variance ratio from 0.63 to 0.79, and a reduction in the mean bias of 16%. At coarser resolutions, the choice of graph structure mattered less, and at the coarsest resolution, identity graph performed the best. The benefit offered by the contiguity graph coincided with strong, seasonally regular and low-noise spatial autocorrelation (noise ratio in Moran's I was 0.18 at district-level, 0.23 at NUTS 2 and 0.49 at state-level). Both GNN architectures showed similar patterns across resolutions.

Conclusion: Geographical resolution may determine whether GNNs can exploit spatial information. At sufficient spatial resolution (districts), a contiguity graph improved influenza forecasts by bringing the mean and scale of the predictions closer to the observed incidence. We recommend that GNN forecasting studies report the spatial autocorrelation of their data and include graph-controls such as the identity graph as a spatial-ablation baseline.

Creation and evaluation of an agentic workflow to predict Ebola outbreak statistics.
Kilian Volmer (University of Bonn)

Forecasting an ongoing outbreak of an infectious disease classically relies on mechanistic models that are fitted to surveillance data. Contextual information included in situation reports, social media or local news reports are difficult to incorporate systematically. Human forecasters can use such information and have achieved competitive quality in some outbreak settings. This motivates the question whether large language models (LLMs) are capable of generating accurate forecasts by integrating all these available data modalities and what we might learn form their reasoning.

We present a reproducible workflow for the automatic summary of situation reports and forecasting of the ongoing Bundibugyo virus outbreak in the Democratic Republic of Congo, using commercial LLMs. We assess forecast performance across different workflow and agentic configurations, including comparison against baseline models. Furthermore, we investigate driving factors of good forecasts, such as specific sources, computational methods, and agentic settings.

Session 2.2: Vaccines and immunology.

Changes in serotype-specific pneumococcal carriage, multiple serotype carriage, and pneumococcal density following PCV10 introduction in Viet Nam: a secondary analysis of a cluster-randomised trial.
Kaige Dong (Charité - Universitätsmedizin Berlin)

Background: Pneumococcal vaccination of infants leads to ecological replacement of vaccine-targeted serotypes by non-vaccine serotypes, but it remains unclear how dominant and minority serotypes contribute to serotype replacement. We assessed post-PCV10 serotype replacement among young children in Nha Trang, Viet Nam, and the robustness of replacement estimates to alternative analytical approaches.

Methods: We analysed seven pneumococcal carriage surveys from October 2016 to July 2022 among children aged 4-24 months in a PCV10 scheduling trial. Microarray serotyping identified dominant and minority serotypes. Bayesian models estimated serotype-specific carriage prevalence and adjusted prevalence ratios (aPRs) post-vaccination based on serotype-specific density. We also compared four allocation approaches for dominant and minority serotypes within multiple serotype carriage. Primary comparisons were between October 2016 and October 2019.

Findings: Between October 2016 and July 2022, 18899 children aged 4-24 months were enrolled across seven surveys. Overall carriage was 29.2% in 2016 and 28.9% in 2019. By 2019, PCV10 serotype carriage declined from 12.7% to 1.8%, whereas non-PCV10 serotype carriage increased from 16.5% to 27.1% (aPR: 1.69 [1.52-1.89]). Multiple serotype carriage prevalence was 4.3% in 2016. Among children with multiple serotype carriage, non-PCV10-only carriage increased from 34.1% to 82.5%. Serotypes 15B/C, 15A, and 23A together increased from 4.0% to 57.9% of non-PCV10 serotype carriage. If carried, non-PCV10 serotype density was 56% higher in 2019 than in 2016.

Interpretation: PCV10 introduction was accompanied by selective expansion of non-PCV10 serotypes 15B/C, 15A, and 23A, restructuring of multiple serotype carriage, and increased density of non-PCV10 serotype carriage.

Dynamics and Control of an SIRS Model with Waning Immunity and Revaccination.
Burcu Gürbüz (University Mainz)

We investigate an SIRS epidemic model incorporating waning vaccine efficacy and periodic revaccination. In order to account for changes in protection over time, the vaccinated population is structured by time since vaccination. This leads to a coupled ODE–PDE formulation and a high-dimensional ODE approximation. We analyse the disease-free and endemic equilibria, derive the basic reproduction number, and investigate the nonlinear dynamics of the model using numerical continuation and bifurcation analysis. Our results reveal backward bifurcation and bistability, showing that a reproduction number below one does not necessarily guarantee disease elimination. We further examine state-dependent contact restrictions and the resulting periodic epidemic dynamics, highlighting how vaccination and intervention parameters influence long-term infection levels. The study illustrates the value of combining mathematical analysis and numerical continuation to understand complex epidemic dynamics and evaluate intervention strategies.

Capacity Contracts for Vaccines and Incentives for Pathogen Disclosure in the planned PABS system.
Yulia Evsyukova (ZEW Mannheim)

We study the timing of strategic pathogen information sharing. We develop a dynamic model in which countries balance the benefits of early disclosure against the strategic advantages of delay. The analysis explores how these incentives shape the timing of information sharing and global response, and examines their implications for the efficiency of pandemic preparedness and international benefit-sharing arrangements

Session 3.1: Stochasticity and observation models.

The impact of observation models on epidemic inference for emerging infectious diseases: SARS-CoV-2 as a case study.
Matthieu Domenech de Cellès (Max Planck Institute for Infection Biology)

Parameter estimation is often necessary to inform transmission models of infectious diseases. This estimation requires choosing an observation model, defined here as the probability distribution linking model outputs to observed data. Although potentially consequential, this choice has received little attention in the literature. Here, we compared eight observation models, including common distributions such as the Poisson, binomial, negative binomial, and normal. Using Bayesian inference, we fit an SIR-like model to daily case reports during the first wave of COVID-19 in Belgium, Finland, Germany, Sweden, Switzerland, and the UK. We found considerable differences in the log-likelihoods of the observation models, spanning three orders of magnitude between the best and the worst. Compared with the best models, the binomial, Poisson, and normal models received no support due to their rigid variance structures. Additionally, the binomial and Poisson models produced overly narrow prediction and confidence intervals, especially for key parameters such as the basic reproduction number. The other five models—each with a free dispersion parameter scaling the variance to the mean—performed much better, with the negative binomial model ranking among the top models in all countries. We conclude that flexible observation models are essential for transmission models to accurately capture all sources of uncertainty.

Making sense of the negative binomial renewal equation.
Theo Schäfer (Karlsruhe Institute of Technology)

The renewal equation is a widely used tool for real-time estimation of the effective reproduction number. The negative binomial renewal equation, as an extension to the Poisson renewal equation to accommodate overdispersion, has received increasing attention in recent years. We delve into the mechanistic underpinnings of two variations of this model, identifying five distinct interpretations of the additional overdispersion parameter. These are based on the notions of temporal variation in transmissibility, individual variation in transmissibility, clustered infection events, incomplete observation of infections, and generation times which are shorter than the observation interval. Some of these mechanisms turn out to also change how the effective reproductive number has to be computed from the model parameters. As in reality different mechanisms are likely to be at play simultaneously, we moreover combine pairs of sources of overdispersion. This, however, results in

identifiability issues, which can only be resolved if additional data are available to determine certain model parameters. We illustrate our findings in a case study on the Ebola epidemic 2014-2015 in Freetown, Sierra Leone.

Session 3.2: Effect of climate on infectious diseases.

U-shaped effects of humidity and the impact of misspecified weather-transmission relationships in epidemic models.
Cana Kussmaul (Max Planck Institute for Infection Biology)

Understanding the relationship between weather conditions and infectious disease transmission has important public health implications; nevertheless, the functional form of this relationship often remains poorly understood. Humidity has previously been suggested to have a U-shaped effect on the transmission of respiratory pathogens, with optimal transmission occurring at both low and high levels. Here, to assess the impact of this functional form and of its potential misspecification, we first simulate transmission rates based on the U-shaped relationship and then test whether an exponential function accurately estimates these rates across a range of climates. We further use a transmission model to simulate incidence data for a range of hypothetical pathogens, comparing outbreak dynamics under the U-shaped forcing function to those under the best-fit exponential approximation. In our simulations, the model fit for the exponential function is climate-dependent, performing best in very dry and very humid environments. In locations where specific humidity values centre around the vertex of the U-shaped function, the exponential model underestimates the amplitude and frequency of incidence peaks. These findings demonstrate the potential consequences of assuming an incorrect functional form for weather-infectious disease relationships and highlight the need for more careful consideration of this functional form in modelling practice.

An explainable covariate compartmental model for predicting the spatio-temporal patterns of dengue in Sri Lanka.
Peter Fransson (Heidelberg University)

A majority of all infectious diseases manifest some climate-sensitivity. However, many of those sensitivities are not well understood as meteorological drivers of infectious diseases co-occur with other drivers exhibiting complex non-linear influences and feedback. This makes it hard to dissect their individual contributions. Here we apply a novel deep learning Explainable AI (XAI) compartment model with covariate drivers

and dynamic feedback to predict and explain the dengue incidence across Sri Lanka. We compare the compartmental Susceptible-Exposed-Infected-Recovered (SEIR) model to a deep learning model without a compartmental structure. We find that the covariate compartmental hybrid model performs better and can describe drivers of the dengue spatiotemporal incidence over time. The strongest drivers in our model in order of importance are precipitation, socio-demographics, and normalized vegetation index. The novel method demonstrated can be used to leverage known infectious disease dynamics while accounting for the influence of other drivers and different population immunity contexts. While allowing for interpretation of the covariate driver influences, the approach bridges the gap between dynamical compartmental and data driven dynamical models.

Keynote 2.

Modeling emerging infectious diseases: The past, the present, and the future.
Christian Althaus (University of Bern

Mathematical modeling has played a crucial role in understanding the transmission and control of infectious diseases for more than two centuries. From the pioneering work of Daniel Bernoulli to the development of compartmental models and the basic reproduction number, early approaches were largely theory-driven. The emergence of new infectious diseases, including Ebola and COVID-19, has accelerated the development of data-driven methods to quantify epidemic dynamics and inform public health responses. More recently, the integration of diverse data sources, including genomic surveillance, wastewater, serological, and social contact data, has opened new opportunities for real-time monitoring and forecasting. In this talk, I will review key milestones in infectious disease modeling and explore how advances in data integration, statistical methods, and computational tools could shape the future of epidemic preparedness and response.

Posters.

Correcting structural bias in dynamical models of infectious disease using a Bayesian state-space framework.
Mircle Amadi (LUT University)

Deterministic dynamical models are widely used in infectious disease modelling, but they often become systematically biased when key drivers such as seasonality and random environmental variation are simplified or omitted. This paper proposes a practical way to account for structural bias while preserving the underlying mechanistic model. We model the observed time series as the sum of (i) a deterministic transmission component given by a reduced Ross malaria model and (ii) a latent stochastic seasonal component that captures unresolved seasonal forcing and other unmodelled variability. The seasonal component is defined as a mean-reverting stochastic differential equation with periodic forcing, which can be interpreted as a seasonally forced Ornstein–Uhlenbeck (OU) process and, at the same time, as a dynamically constrained model-discrepancy term. The combined model forms an additive Bayesian state-space system. A key challenge in additive decompositions is identifiability: many combinations of the deterministic and stochastic components can explain the same observations. We therefore use informative priors to stabilise this decomposition, together with anon-centred parameterisation (a reparameterisation that improves MCMC efficiency by sampling standardised noise terms instead of states directly) of the latent stochastic differential equation (SDE) states that enables efficient joint inference with Hamiltonian Monte Carlo (NUTS) in Stan. We validate the approach in three steps: (1) an OU example that contrasts parameter-only inference with latent state-space inference, (2) synthetic experiments that have a good agreement with the observed signal while highlighting the expected negative posterior dependence between components,and (3) an application to five years of monthly malaria case reports from Delta State, Nigeria. In the real-data analysis, the proposed additive ODE–SDE model produces a close fit with coherent uncertainty quantification and a flexible seasonal reconstruction, while keeping the mechanistic transmission model interpretable. Overall, the framework provides a flexible and transferable method for accounting for structural model discrepancy in misspecified dynamical models using a structured stochastic discrepancy.

Reviewer agreement in infectious disease modelling.
Antonia Bockhorn and Johannes Bracher (Karlsruhe Institute of Technology)

Peer review is an important quality control mechanism in scientific publishing, but previous studies in various fields have found agreement between different reviewers to be modest. We present an analysis of reviewer agreement in infectious disease modelling, based on several different data sources.

A Bayesian space-time analysis of seasonal and spatial patterns of tuberculosis and their determinants in Chile, 2011-2025.
José Daniel Conejeros (ISI Foundation, Turin)

Tuberculosis (TB) notifications in Chile increased from 14.4 to 16.5 cases per 100,000 inhabitants between 2011 and 2025, yet national aggregates conceal where risk concentrates and when it occurs. We conducted an ecological study using a balanced monthly panel of 61,740 observations (343 continental municipalities, 15 years, 12 months) of TB cases notified to the National TB Control and Elimination Programme between 1 January 2011 and 31 December 2025, linked to census, primary-care and satellite-derived climate covariates. We fitted Bayesian hierarchical negative binomial models combining a reparameterised Besag-York-Mollie (BYM2) spatial component, a first-order random-walk annual trend, cyclic monthly seasonality, a municipality-year interaction, 12 standardised covariates, a one-month notification lag and a population offset. Variables and model structures were selected by widely applicable information criterion among 18 nested specifications, estimated with integrated nested Laplace approximations with posterior validation by Markov chain Monte Carlo (four chains of 50,000 iterations).We found that notification risk increased with population density (rate ratio per standard deviation 1.19; 95% credible interval 1.05-1.37), household overcrowding (1.13; 1.05-1.23), foreign-born population shares (1.15; 1.06-1.26) and indigenous population shares (1.14; 1.03-1.25), whereas municipalities with more primary-care facilities notified fewer cases (0.85; 0.75-0.97). Notifications peaked reproducibly in August (1.13; 1.07-1.19) and were lowest in February (0.87; 0.82-0.92), a winter-summer contrast near 30%. The annual trend fell by 11% in 2020 (0.89; 0.84-0.94). The municipality-year interaction was the dominant residual component (standard deviation 0.21 versus 0.42 spatial, 44% structured), indicating increasingly divergent municipal trajectories. TB notification in Chile is spatially concentrated of the north, winter-peaking and heterogeneous between municipalities, supporting geographically targeted active case finding scheduled ahead of the southern-hemisphere winter peak.

Quantifying natural immune boosting in pre-vaccine era pertussis

Franziska Frederking (Max Planch Institute for Infection Biology)

Background & Aims: Despite high vaccination coverage, pertussis has resurged in many countries, exposing gaps in our understanding of its immune dynamics. Natural immune boosting – defined as the enhancement of protective immunity upon re-exposure to the pathogen without leading to transmissible infection – may contribute to the complex non-linear and noisy epidemic patterns observed for pertussis. However, the strength and impact of such boosting are still poorly characterized. This study evaluates estimation strategies for quantifying immune boosting in pertussis transmission models using simulated pre-vaccine-era case data.
Materials & Methods: We developed a compartmental SE_2I_2RS-type model incorporating waning immunity, leaky infection-derived protection, and immune boosting upon re-exposure, embedded within a stochastic observation framework to account for underreporting and surveillance noise. Simulated pre-vaccine-era case data were fitted using a maximum likelihood estimation approach with multiple optimization runs, followed by Markov chain Monte Carlo sampling initialized at the best-fitting parameter sets.
Results: Preliminary analyses reveal that the strength of immune boosting is not straightforwardly identifiable from case data. Specifically, we observe substantial collinearities between boosting strength and the duration of waning immunity, as well as potential interactions with R0 and the degree of leaky protection. Conclusion: Immune boosting quantification is limited by parameter non-identifiability. Approaches leveraging panel data across multiple populations, combined with block maximization strategies, may help mitigate this limitation. These findings highlight a broader methodological challenge in fitting complex immuno-epidemiological models to case data, with implications for pertussis policy modeling.

Fitting Endemic-Epidemic Models Using RTMB.

Sophie Reichert (FAU Erlangen-Nürnberg)

The endemic-epidemic (EE) model is a well-established approach for analysing routine infectious disease surveillance counts. In recent years, various extensions for the original ‘hhh4‘ model in the R package ‘surveillance‘ have been developed, including parameterised contact matrices, higher-order lags and zero-inflation. However, their implementations remain separate prototypes that cannot be combined, and reliance on profile likelihood estimation in certain extensions further complicates their integration. Motivated by this limitation, we implemented several EE models using the R package ‘RTMB‘. Since ‘RTMB‘ supports automatic differentiation, all extensions can be implemented with full maximum likelihood estimation. We compare the models implemented in ‘RTMB‘ with their corresponding (extended) ‘hhh4‘ counterparts by analysing norovirus surveillance data from Berlin. Parameter estimates and log-likelihoods are generally consistent, except for models with random effects. Yet runtimes decrease substantially for extended EE models that previously relied on profile likelihood estimation. For models with parameterised contact matrices, for instance, the runtime decreased from around two minutes to two seconds. Consequently, we are developing ‘eeco‘, a new R package that unifies EE models using ‘RTMB‘ for maximum likelihood inference and allows extensions to be used simultaneously. As an example, we demonstrate a first prototype of ‘eeco‘ using data on norovirus infections in Bavaria, stratified by region and age group. We showcase the modern user interface and the support of multiple stratifications through the multidimensional spatial array format of the R package ‘stars‘, and present a preliminary model incorporating a combination of extensions.

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