



**South-West German Infectious Disease  
Modelling Workshop**

Welcome to the second **SWIM** Workshop.

- 📍 Interdisciplinary Center for Scientific Computing (IWR), Heidelberg University.  
Im Neuenheimer Feld 205, 69120 Heidelberg.
- 🕒 Tuesday 9 December 2025, 10:00 - 17:00. 🌐 <http://swim-workshop.de/>

**Programme**

**10:00 – 10:30 Registration & coffee.** Common Room, 5th Floor.

**10:30 – 10:40 Welcome by the organizers.** Conference Room 5.104, 5th Floor.

**10:40 – 11:40 Session 1: Real-time modelling.** Conference Room 5.104, 5th Floor.

Sebastian Funk (London School of Hygiene and Tropical Medicine): *Modelling of emerging threats and epidemics.*

Friederike Becker (Karlsruhe Institute of Technology): *The influence of ensemble size and composition on the performance of combined real-time COVID-19 forecasts.*

Chair: Luise Nottmeyer (Heidelberg University).

**11:50 – 12:30 Session 2.1: Forecasting.** Conference Room 5.104, 5th Floor.

Michael Opata (Heidelberg University): *Predicting highly pathogenic avian influenza outbreaks in Europe.*

Enrique Guerrero (TWT GmbH Science & Innovation, Stuttgart): *Supporting hospital decision makers by forecasting the impacts of infectious disease spread in hospital workflows.*

Chair: Barbora Němcová (Karlsruhe Institute of Technology).

**11:50 – 12:30 Session 2.2: Estimating disease prevalence.** Room: 4.414, 4th Floor.

Lucas Böttcher (Frankfurt School of Finance & Management): *Prevalence estimation for infectious disease surveillance.*

Nina Schmid (University of Bonn): *Universal differential equations for wastewater-based epidemiology.*

Chair: Adrian Lison (ETH Zurich).

**12:30 – 13:40 Lunch.** Common Room, 5th floor.

**13:40 – 14:20 Session 3.1: Multivariate modelling.** Conference Room 5.104, 5th Floor.

Sophie Reichert (FAU Erlangen): *Endemic-epidemic models: recent extensions and case studies for pertussis and norovirus in Bavaria.*

Ariane Hanebeck (Karlsruhe Institute of Technology): *Dependence modelling across major causes of death via time-varying copula state space models.*

Chair: Charles Hatfield (Heidelberg University).

**13:40 – 14:20 Session 3.2: Contacts and behaviour.** Room 4.414, 4th Floor.

Billy Quilty (Charité, Berlin): *Automating Ebola contact network extraction from outbreak narratives using large language models.*

Andreas Reitenbach (Karlsruhe Institute of Technology): *From influence to incidence: comparing aligners and contrarians.*

Chair: Burcu Gürbüz (University of Mainz).

**14:20 – 15:20 Group picture, poster session and coffee break.** Foyer and Common Room, 5th Floor.

**15:20 – 16:45 Session 4: Vaccination and immunity.** Conference Room 5.104, 5th Floor.

David Hodgson (Charité, Berlin): *Correlates of protection through multidimensional immune modelling across respiratory viruses.*

Felix Günther (Robert Koch Institute, Berlin): *Effectiveness and efficiency of immunisation strategies to prevent RSV among infants and older adults in Germany: a modelling study.*

Juliette Paireau (Institut Pasteur, Paris): *Assessing the effect of nirsevimab on hospitalisations due to RSV in France: combining epidemiological and modelling approaches for public health decision-making.*

Chair: Johannes Bracher (Karlsruhe Institute of Technology).

**16:45 Closing.** Conference Room 5.104.

## Posters

1. Hammad Aamer (Heidelberg University): *Prototyping an internet-of-things-based bioacoustic system to support research and surveillance of avian-associated infectious disease.*
2. Omid Airom (Heidelberg University): *Leptospirosis in Europe: A fine-scale assessment of environmental and socio-economic risk drivers.*
3. Yogesh Bali (University of Mainz): *Integrating behavioral survey data into epidemic models: a methodological framework.*
4. Natalie Böhm (KIT): *A comparison of outbreak detection methods under reporting delays.*
5. Aness Chelfat (Heidelberg University): *tba.*
6. Peter Fransson (Heidelberg University): *Vector-borne disease modelling in Germany: preparing for contemporary and future risk.*
7. Thomas Götz (University of Koblenz): *SIR model for households.*
8. Raisa Kociurzynski (Medical Center - University of Freiburg): *Detection of SARS-CoV-2 variants of concern in Swiss wastewater without prior lineage classification.*
9. Yichao Liu (Heidelberg University): *A comparison of deep neural network compression for citizen-driven tick and mosquito surveillance.*
10. Nil Hassan Mahamat (Heidelberg University): *Nature-Based Solutions and Health-Database.*
11. Barbora Němcová (Karlsruhe Institute of Technology): *Unjustified Poisson assumptions lead to overconfident estimates of the effective reproductive number.*
12. Luise Nottmeyer (Heidelberg University): *Modelling environmental antimicrobial resistance drivers.*
13. Marvin Schulte (Fraunhofer ITWM, Kaiserslautern): *The influence of the mutation process on the long-term behavior of infectious diseases.*
14. Theo Schäfer (Karlsruhe Institute of Technology): *Making sense of the negative binomial renewal equation.*
15. Manuel Stapper (London School of Hygiene and Tropical Medicine): *Mind the baseline: The hidden impact of reference model selection on forecast assessment.*
16. Kilian Volmer (University of Bonn): *Modelling a potential spread of foot-and-mouth disease on the German animal trading network.*

## Practical information

- Internet access via eduroam is available throughout the building.
- Lunch and coffee breaks are free of charge for registered participants and take place in the Common Room.
- 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:** Barbora Němcová (KIT), Joacim Rocklöv (IWR), Johannes Bracher (KIT), and Luise Nottmeyer (IWR).

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

# Abstracts

## Session 1: Real-time modelling.

### **Modelling of emerging threats and epidemics.**

*Sebastian Funk (London School of Hygiene and Tropical Medicine)*

Mathematical models are essential tools for combining observed data with theoretical assumptions to generate actionable insights during disease outbreaks—but how do we know which models to trust, and how well can we actually predict epidemic trajectories? This talk explores the role of modelling in outbreak response before turning to the specific challenges of forecasting infectious disease dynamics. Drawing on systematic evaluations from Ebola and COVID-19, I examine what limits our ability to predict: unpredictable changes in human behaviour, pathogen evolution, or the models themselves? I discuss how proper scoring rules allow us to compare forecasts and what we've learned about the reliability of predictions at different time horizons. Beyond forecast accuracy, I present recent work on developing frameworks to assess the broader utility of modelling for decision-making and on understanding how modelling actually informs policy in practice. Finally, I consider how we can better prepare for future epidemics by investing in reusable modelling tools and collaborative efforts to systematically evaluate model performance.

### **The influence of ensemble size and composition on the performance of combined real-time COVID-19 forecasts.**

*Friederike Becker (Karlsruhe Institute of Technology)*

During infectious disease outbreaks, short-term forecasts can play an important role for both decision makers and the general public. While previous research has shown that combining individual forecasts into an ensemble improves accuracy and consistency, practical guidance for organisers of multi-model prediction platforms on how to construct an ensemble has been scarce. In particular, it is not entirely clear how ensemble performance relates to the size of the underlying model base, a relevant question when relying on voluntary contributions from modelling teams that face competing priorities. Furthermore, the exact composition of an ensemble forecast may influence its performance. Ensembles can either include all models equally or, alternatively, discriminate based on past performance or other characteristics. Using data from the European COVID-19 Forecast Hub we investigated these questions, with the aim of offering practical guidance to organisers of multi-model prediction platforms during infectious disease outbreaks. We found that including more models both improved and stabilized aggregate ensemble performance, while selecting for better component models did not yield any particular advantage. Diversity among models, whether measured numerically or qualitatively, did not have a clear impact on ensemble performance. These results suggest that for those soliciting contributions to collaborative ensembles there are more obvious gains to be made from increasing participation to moderate levels than from optimising component models.

## Session 2.1: Forecasting.

### **Predicting highly pathogenic avian influenza outbreaks in Europe.**

*Michael Opata (Heidelberg University)*

Avian Influenza (AI) outbreaks are on an increasing trajectory. This disease carries a substantial economic burden, resulting in considerable losses to farmers with profound impacts on economies. As the outbreaks continue in birds and other unusual host species, further virus evolution and spillover to humans' risk is anticipated to grow and potentially involve into new pandemics. Despite this, the underlying drivers of the outbreaks remain elusive. We develop machine learning models capable of predicting HPAI events in Europe dynamically uncovering the critical determinants of their onset. Temperature, water index, vegetation index, and poultry density play pivotal roles, with their importance coming into play at different times of the year. Temperature, water index, and vegetation index are important in the ecology of pathogen transmission as well as environmental ecological processes while water index determines how birds aggregate at different locations depending on the season of the year. Combining these drivers, the outbreak pattern is predicted with an accuracy of 94% for model two (M2). A true out of sample with the same model yielded 88% accuracy highlighting its predicting capability. These insights lay a robust foundation for elucidating the intricate landscape of AI outbreaks, offering valuable insights for proactive preventive interventions to mitigate spillover.

### **Supporting hospital decision makers by forecasting the impacts of infectious disease spread in hospital workflows.**

*Enrique Guerrero (TWT GmbH Science & Innovation, Stuttgart)*

The COVID-19 pandemic caused massive disruptions within healthcare systems around the globe: the usual challenges were increased by supply-chain bottlenecks, additional admission of infectious patients and shortfalls in personnel due to illness. Infectious disease spread within hospitals can occur despite countermeasures, thus exacerbating the situation. To assist decision makers in hospitals, the software tool Delphis has been developed. Therein, they can simulate the effects of external disturbances and of measures within the hospital for the next few weeks and make therewith better-informed decisions. In this talk, we demonstrate the new capacities of Delphis to include the effects of hospital-internal disease spread in the hospital's workflows. The simulation uses stochastic models to include patient arrivals, patient-patient or patient-personnel disease transmission, disease severity and patient journey. On the other hand, hospital responses such as relocating patients into isolated rooms after the disease is detected, and others, are included via rule-based models. The interface is based on, and compatible with, the German Epidemic Microsimulation System (GEMS).

## Session 2.2: Estimating disease prevalence.

### **Prevalence estimation for infectious disease surveillance.**

*Lucas Böttcher (Frankfurt School of Finance & Management)*

Gathering observational data for infectious-disease surveillance often involves uncertainties arising from both type I (false positive) and type II (false negative) errors. In this talk, I will present a statistical model to improve infectious-disease surveillance by aggregating results from repeated and combined tests. This approach is especially valuable in situations requiring rapid and cost-effective testing methods, as seen during the SARS-CoV-2 pandemic. Our model enables the development of testing protocols with an arbitrary number of tests, which can be customized to meet requirements for type I and type II errors. This allows us to adjust sensitivity and specificity according to application-specific needs. Additionally, we derive generalized Rogan–Gladen estimates of disease prevalence that account for an arbitrary number of tests with potentially different type I and type II errors. I will also briefly discuss a few clinical applications where combined testing is useful beyond infectious-disease surveillance.

### **Universal differential equations for wastewater-based epidemiology.**

*Nina Schmid (University of Bonn)*

Wastewater-based epidemiology provides a low-cost, scalable view of community infection dynamics, but converting these signals into actionable epidemiological quantities remains difficult. Mechanistic models offer interpretability. Yet, standard assumptions like a constant transmission rate limit realism over long simulation horizons and heterogeneous settings. We present a susceptible–exposed–infectious–recovered (SEIR) universal differential equation (UDE) that links wastewater viral loads to case counts, and embeds neural networks to represent time-varying parameters. Utilizing ensembles it quantifies uncertainty and identifiability. Applied to COVID-19 data from Bonn (Germany), it produces plausible out-of-sample projections of case counts over an up to 50-week reconstruction horizon; and across five cities in Rhineland-Palatinate, it learns city-specific mappings to prevalence that generalise within each locale. Compared to SEIR models with fixed transmission, the UDE captures non-stationary drivers (policy, behaviour, seasonality) without sacrificing epidemiological structure, while propagating observation and model uncertainty into the projections. More broadly, this framework provides a flexible basis for integrative infectious-disease modelling, in which additional data modalities (e.g., mobility, clinical testing, meteorological covariates) can inform the learned components to improve interpretability and calibration.

## Session 3.1: Multivariate modelling.

### **Endemic-epidemic models: recent extensions and case studies for pertussis and norovirus in Bavaria.**

*Sophie Reichert (FAU Erlangen)*

Endemic-epidemic models are a well-established statistical approach for analysing and predicting the spread of infectious diseases based on count time series. Several methodological extensions have expanded their capabilities over time, with recent ones including the handling of zero inflation and incorporating higher-order autoregressive lags or social contact data. In this work, we examine the impact of these extensions on the effects of covariates, in particular vaccination coverage, by an application to pertussis counts in Bavaria (2014-2019). Furthermore, we assess gains in forecast performance by applying extended models to age stratified norovirus counts from the same region and period. We found that including vaccination coverage in the epidemic model component only, alongside geometric lags, using a parsimonious two-component structure, provided the best fit while improving interpretability. The forecast performance is under evaluation.

### **Dependence modelling across major causes of death via time-varying copula state space models.**

*Ariane Hanebeck (Karlsruhe Institute of Technology)*

We propose a time-varying copula state space approach, which quantifies and visualises the joint dynamics across major causes of death, utilising data both before and during the COVID-19 pandemic. Our research investigates how the COVID-19 pandemic has affected mortality experience of five major causes, and more importantly how COVID-19 has changed the dependence structure across these causes. This enables us to gain more insights into the potential impact of COVID-19 on future life expectancy, and conduct scenario-based projections. Based on U.S. weekly mortality data from January 2015 to November 2022, we find that COVID-19 has elevated mortality levels for the majority of causes and altered the dependence structure across these causes, particularly for Alzheimer's and respiratory diseases. In our scenario-based analysis, we observe a noticeably wider prediction interval for total deaths when the number of COVID-19 deaths is assumed to be high, confirming the significant impact of the pandemic on population mortality. This finding could help explain the extreme mortality levels experienced during the pandemic.

## Session 3.2: Contacts and behaviour.

### **Automating Ebola contact network extraction from outbreak narratives using large language models.**

*Billy Quilty (Charité, Berlin)*

*Background:* Contact tracing is fundamental to outbreak control, yet critical contact network data often remain trapped in unstructured narratives within linelists. This labour-intensive manual extraction process means rich contact network data are not typically useable in a timely fashion for epidemiological analysis during rapidly evolving outbreaks. Large language models (LLMs) offer a potential solution, but their reliability for epidemiological data extraction remains unvalidated.

*Methods:* We developed and validated an LLM-based pipeline (GPT-4o) to extract structured contact network data from free text fields in 5,761 Ebola case records from the 10th epidemic in the Democratic Republic of Congo, in collaboration with Epicentre, Médecins Sans Frontières. The system employs two-phase extraction with few-shot learning (15 examples) and was validated against 100 hand-labelled records at row, contact, and field levels.

*Results:* The pipeline processed 5,761 records in 51 minutes. Validation demonstrated strong performance: row-level F1=77% (precision=96.6%, recall=64%), contact-level F1=80.7% (precision=97.3%, recall=68.9%). Only 2 of 106 ground truth contacts were completely missed, and only 2 false positives occurred (both legitimate but unlabelled mentions of unnamed contacts). Moderate recall primarily reflected minor formatting variations (e.g., "le 23/11/18" vs "23/11/18") rather than substantive errors, with 85% of false negatives having correct contact names but differing secondary details. Field-level performance: names F1=97.7%, relationships F1=96.2%, locations F1=97.7%.

*Conclusions:* LLM-based extraction achieves near-perfect contact identification with minor format standardisation challenges, demonstrating readiness for operational deployment. This automation enables rapid transformation of outbreak narratives into analysis-ready contact network data when speed matters most, and is adaptable to other infectious disease contexts where narrative data impede timely analysis.

### **From influence to incidence: comparing aligners and contrarians.**

*Andreas Reitenbach (Karlsruhe Institute of Technology)*

To manage a pandemic, it is critical that citizens voluntarily engage in protective behavior such as masking or vaccinating. However, voluntary behavior is subject to complex dynamics of social influence. While numerous models couple social influence dynamics with disease spreading, assumptions about how individuals influence each other differ markedly. Models of alignment assume individuals imitate others, while others assume contrarian behavior: the tendency to do the opposite of one's peers, potentially free-riding on others' efforts. Here, I present two main findings. First, following a recent call I use Influence-Response functions to compare the two behavior models. While contrarians self-coordinate on moderate levels of protection, aligning behavior can produce recurrent cycles of high incidence followed by strong mitigation. Both paradigms display complex dynamics across the parameter space, highlighting the importance of clearly defining evaluation objectives, such as minimizing attack rates or avoiding ICU overload. Second, when including both behavior types (heterogeneity), model predictions change in drastic and unexpected ways. The same change in population composition can prevent or induce violent disease cycling, depending on parameters. These findings underscore the importance of accounting for behavioral heterogeneity in epidemiological modeling.

## Session 4: Vaccination and immunity.

### **Correlates of protection through multidimensional immune modelling across respiratory viruses.**

*David Hodgson (Charité, Berlin)*

*Introduction:* Next-generation vaccines aim to induce broadly neutralising immune responses, but identifying reliable correlates of protection (CoP) remains a challenge. Most current approaches rely on measuring a single immune marker, which is unlikely to fully characterise the complexity of a highly valent immunological response.

*Context and aim:* We aimed to develop and apply a generalizable framework for estimating CoP across each of RSV, SARS-CoV-2, and influenza using seroepidemiological data. This framework accounts for the joint effects of multiple immune biomarkers, such as titres to several viral proteins, on infection risk. The goal is to move beyond one-dimensional thresholds toward more flexible, accurate, and scalable correlates of protection for a given pathogen.

*Method:* We applied a Bayesian model of antibody kinetics to longitudinal serological and PCR data. By accounting for variability in exposure rates, we evaluate nonlinear relationships between multiple immune biomarkers and the probability of protection against disease. We analysed real-world serological data from SARS-CoV-2 and RSV cohorts, and ongoing analyses are extending this to influenza.

*Results:* For SARS-CoV-2 during the Delta wave, we found that serum pseudoneutralization titres (pVNT) provided correlates of protection with better predictive accuracy compared to mucosal IgA (mIgA) titres. However, single biomarker models demonstrate comparable performance to dual biomarker models (including both pVNT and mIgA). For RSV, we found that a dual biomarker model, which included serum IgG and mucosal IgG, had the best predictive capacity over all the single biomarker models considered, suggesting that monitoring the immune responses to two biomarkers could provide improvements in vaccination impact over considering a single biomarker.

*Conclusions:* We demonstrate that modelling underlying multidimensional immune kinetics can improve the estimation of CoP across respiratory viruses, but this depends on the assay and pathogen being considered. As immunological complexity increases with next-generation vaccines, these methods offer a practical path toward data-driven, broadly applicable, and more predictive correlates of protection.

### **Effectiveness and efficiency of immunisation strategies to prevent RSV among infants and older adults in Germany: a modelling study.**

*Felix Günther (Robert Koch Institute, Berlin)*

*Background:* Recently, several novel RSV immunisation products that protect infants and older adults against RSV disease have been licensed in Europe. We estimated the effectiveness and efficiency of introducing these RSV immunisation strategies in Germany.

*Methods:* We used a Bayesian framework to fit a deterministic age-structured dynamic transmission model of RSV to sentinel surveillance and RSV-specific hospitalisation data in Germany from 2015 to 2019. The calibrated model was used to evaluate different RSV intervention strategies over 5 years: long-acting, single-dose monoclonal antibodies (mAbs) in high-risk infants aged 1–5 months; long-acting mAbs in all infants aged 1–5 months; seasonal vaccination of pregnant women and one-time seasonal vaccination of older adults (75+/65+/55+ years). We performed sensitivity analysis on vaccine uptake, seasonal vs. year-round maternal vaccination, and the effect of under-ascertainment for older adults.

*Results:* The model was able to match the various RSV datasets. Replacing the current short-acting mAB for high-risk infants with long-acting mAbs prevented 1.1% of RSV-specific hospitalisations in infants per year at the same uptake. Expanding the long-acting mAB programme to all infants prevented 39.3% of infant hospitalisations per year. Maternal vaccination required a larger number to be immunised to prevent one additional hospitalisation than a long-acting mAB for the same uptake. Vaccination of adults older than 75 years at an uptake of 40% in addition to Nirsevimab in all infants prevented an additional 4.5% of all RSV hospitalisations over 5 years, with substantial uncertainty in the correction for under-ascertainment of the RSV burden.

*Conclusions:* Immunisation has the potential to reduce the RSV disease burden in Germany.

## **Assessing the effect of nirsevimab on hospitalisations due to RSV in France: combining epidemiological and modelling approaches for public health decision-making.**

*Juliette Paireau (Institut Pasteur, Paris)*

Modelling plays a key role in supporting timely and evidence-based public health decision-making. In this talk, I will illustrate how complementary methodological approaches were used to assess the real-world effect of a new monoclonal antibody, nirsevimab, against respiratory syncytial virus (RSV) in France. We first conducted a case-control study based on the test-negative design using data from 20 paediatric intensive care units (PICUs) to estimate the effectiveness of nirsevimab against severe cases of RSV bronchiolitis. Among 288 infants included, nirsevimab effectiveness was estimated at 75.9% (95% CI 48.5–88.7), confirming the high protection observed in clinical trials. In parallel, we developed an age-structured deterministic transmission model to evaluate the population-level impact of the 2023-2024 national nirsevimab immunisation campaign. Assuming 215,000 doses administered, the model estimated a 23% reduction in RSV-associated hospitalisations for bronchiolitis among infants under 24 months (5800 hospitalisations averted; 95%CI 3700–7800), with a 35% reduction among those aged 0–2 months. The estimated effectiveness against RSV-associated hospitalisations for bronchiolitis was 73% (61–84). The consistency of real-world effectiveness across two complementary approaches strengthened the evidence base for decision-makers. These results informed policy planning for subsequent RSV prevention campaigns in France and illustrate the value of integrating modelling and epidemiological data to guide rapid public health responses.

Funded by

**DFG** Deutsche  
Forschungsgemeinschaft  
German Research Foundation