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KEYNOTE**Lessons from modeling infectious diseases in Brazil: policy applications, climate dynamics, and disease control strategies**

Daniel A.M. Villela - Fundação Oswaldo Cruz, Brasil / University of Münster, Germany

Over the past decade, Brazil has faced numerous health emergencies, including COVID-19 and recurring outbreaks of diseases such as dengue, Zika, and malaria. In this talk, I will describe how modeling experience has supported Brazilian policies on vaccination, vector-borne disease interventions, and understanding disease dynamics in relation to climate factors. These experiences offer applicable lessons for health surveillance across countries, alongside challenges that remain open and will be discussed in the talk.

Modelling for outbreak response: predictions, evaluation, and utility

Sebastian Funk - London School of Hygiene and Tropical Medicine, UK

Mathematical modelling is now a routine part of public health responses to infectious disease outbreaks. Drawing on experience with real-time reproduction number estimation, collaborative forecasting efforts, and ongoing work on reusable modelling tools, I will look at what these projects have been able to deliver, and where they have fallen short. I will discuss what we have learned about the predictive ability of our models, what systematic evaluation can and cannot tell us, and whether we can tell if the work has been useful for public health. Finally, I will consider how these lessons might shape reusable tools for future outbreak response.

Challenges for the future of infectious disease modelling for global health

Mark Jit - New York University, USA

Innovation in infectious disease modelling has long been closely linked to developments in global health, from malaria and HIV to the COVID-19 pandemic. Ongoing geopolitical, socioeconomic, technological and epidemiological shifts are bringing new challenges that the modelling community must address. In this talk, I will highlight key challenges and outline priority areas that warrant sustained attention. I will draw on some of the findings from the Lancet Commission on Strengthening the Use of Epidemiological Modelling of Emerging and Pandemic Infectious Diseases.

CONTRIBUTED TALKS I - Modelling of interventions & decision-making**Effectiveness and cost-utility of pneumococcal vaccination strategies in adults ≥ 60 years old in Germany**

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Introduction: *Streptococcus pneumoniae* is a leading bacterial pathogen responsible for substantial global morbidity and mortality. In 2023, the German standing vaccination committee (STIKO) recommended the use of a 20-valent pneumococcal conjugate vaccine (PCV20) in adults ≥ 60 years old for the prevention of pneumococcal diseases (PD). Partly based on modeling data. Recently, PCV21 was approved for older adults. The serotype coverage of PCV21 distinctly differs from that of PCV20 as well as the PCV vaccines currently used in infants (PCV13, PCV15).

This study evaluates the performance and cost-utility of PCV20 vs PCV21 for the prevention of PD in older adults in Germany.

Methods: A dynamic transmission model of pneumococcal carriage with eight competing groups of pneumococcal serotypes was developed to predict the epidemiological impact of pneumococcal childhood vaccination (indirect herd effects and serotype replacement) on the incidence and the serotype mix in PD among older adults. Two different infant vaccination scenarios were considered: (1) continuation of PCV13 vaccination, (2) switch from PCV13 to PCV15 vaccination. The analysis focused on the lifelong effectiveness and cost-utility of vaccinating older adults with PCV20 or PCV21 over a ten-year period (vaccine uptake 30%). In the base case analysis, we assumed that PCV20 and PCV21 were equally effective against vaccine serotypes. The study took a societal perspective. Discount rates were 3% for costs and QALYs. **Results:** Preliminary results indicate that in scenario 1 (PCV13 infant vaccination), switching from PCV20 to PCV21 vaccination of adults ≥ 60 years old at current vaccine coverage rates would prevent around 8,400 hospitalizations and 1,000 deaths caused by PD. In scenario 2 (switch to PCV15 infant vaccination), a switch from PCV20 to PCV21 in older adults would prevent about 8,900 hospitalizations and 1,100 deaths caused by PD. From a health economic perspective, PCV21 would dominate PCV20 vaccination of adults ≥ 60 years.

Conclusions: From an epidemiological and economic perspective, vaccination of older adults with PCV21 could possibly prevent more PD cases and be less costly than PCV20 based on previous modeling results. Updating and modifying the previous model is ongoing. **Funding:** Robert Koch Institute.

What influences the success of infectious disease modelling evidence in informing public health decision-making? Developing evaluation criteria to guide knowledge translation

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Infectious disease modeling can inform decision-making, but its effectiveness in this regard remains underexplored. Despite its growing use, there is no formal evaluation of how modeling influences decisions. This study aims to identify the factors critical to successful modeling-for-

decision-making, which can guide future evaluations. We conducted semi-structured interviews with modelers, public health decision-makers, and intermediaries. Using a critical realist approach to thematic analysis, we explored perceptions of success and the factors facilitating modeling-to-decision-making across different contexts, such as international versus national settings. Between 05/25 and 09/25, we interviewed 35 key informants, including 16 modelers, 12 individuals with experience in both modeling and brokering knowledge, 1 pure knowledge broker, and 6 executive decision-makers who had been involved in both knowledge use and brokering. Of the participants, 20 were based in high-income countries, and 15 in low- or middle-income countries, working in national (n=23), international (n=6), or both contexts (n=6). Participants' perceptions of successful use of modeling evidence in decision-making varied – from directly guiding decisions to being one of several factors considered. Risks to success included misinformation due to model misspecifications or communication failures. Model quality, policy relevance and adequate communication were key to successful modeling-to-policy pathways. Facilitators included iterative, bi-directional engagement between modelers and decision-makers, interdisciplinary collaboration, and transparent and adequate uncertainty communication, often facilitated by skilled knowledge brokers. Structural enablers such as formalized policy advising structures, in-house modelers or knowledge brokers, and connections to external experts for rapid scale-up in emergencies were also identified. In international contexts, the involvement of local modelers improved the relevance of models, enhanced communication, and reduced the risk of misinformation. We highlight that modeling can misinform decisionmakers and identify factors influencing success. These provide a foundation for evaluating and improving modelling-to-decision-making in different contexts. The identified structural enablers can inform action towards more effective modeling-decision-making infrastructures.

A Multi-Criteria Benefit-Harm Analysis of Public Health Interventions using the GEMS Framework

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National-scale infectious disease modeling requires frameworks capable of representing both high-fidelity population structures and complex, adaptive policy responses. We present the architecture of the German Epidemic Microsimulation System (GEMS), a high-performance agent-based model utilizing a synthetic population of 83 million agents. The model's design links individuals to hierarchical social settings, including households, schools, and workplaces, to capture structured contact patterns and facilitate targeted interventions. Central to Interventions in GEMS is the Trigger-Strategy-Measure (TriSM) framework, which provides a standardized logic for modeling intervention scenarios. By representing policies as modular sequences of measures (e.g., isolation, testing, or setting-specific closures) initiated by individual or population-level triggers, TriSM enables the simulation of cascading and recursive strategies that reflect real-world public health protocols. The capabilities of GEMS are demonstrated through a multi-criteria benefit-harm and cost-effectiveness analysis of NPIs using SARS-CoV-2 as an example pathogen. The system quantifies epidemiological benefits across several dimensions, including avoided hospitalizations,

life-years gained, mortality reduction, and Quality-Adjusted Life Expectancy (QALE). These outcomes are systematically weighed against intervention-induced harms, specifically lost school days and total person-days spent in isolation. This technical integration allows for the identification of strategy configurations that optimize the balance between effective disease control and societal disruption. Finally, we outline the transition to "Next Generation Modeling" within the ADAPTI-M project. Incorporating longitudinal processes (aging, births, mortality) enables multi-year modeling. Furthermore, we are integrating Reinforcement Learning (RL) to automate the optimization of NPI strategies. By combining explicit demographic models with pathogen evolutionary dynamics, the system is evolving from a scenario-based projection tool into an adaptive framework for autonomous evaluation of NPIs for epidemic control of respiratory infections.

An Approach to Automated Optimization of Non-Pharmaceutical Interventions

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Non-pharmaceutical interventions (NPIs) are commonly used tools for managing infectious disease transmission when pharmaceutical options are unavailable. Yet, identifying effective interventions that minimize societal disruption remains challenging due to the large number of possible strategies. Agent-based simulation frameworks, such as the German Epidemic Micro-Simulation System (GEMS), have emerged as popular tools for projecting the potential impact of candidate NPI strategies. While these systems are most often used to simulate the impact of predefined intervention strategies, we argue that their role can be extended to the autonomous optimization of effective strategies. However, automatically optimizing NPIs using GEMS and similar frameworks is challenging as interventions can target individuals based on multiple attributes (such as age or infection status), affect hierarchical group structures (such as schools, workplaces, and families), and be combined arbitrarily. Due to this multi-level structure and the possibility of combining interventions, the search space grows exponentially with the number of intervention options provided by the model. We aim to support decision-makers by optimizing NPIs for infectious disease simulations using Grammar-Guided Genetic Programming (GGGP), which uses formal grammars to generate and optimize programs inspired by natural selection, i.e., by iteratively selecting, recombining, and mutating candidate programs according to a fitness function. First, we introduce a domain-specific language for expressing NPIs in agent-based simulations that structures the intervention search space through a context-free grammar. The language is model-agnostic, defining how NPI elements can be combined, while model-specific vocabulary is added separately. To make optimization more efficient, we reduce the search space by excluding semantically invalid intervention patterns through the attachment of constraints, which we refer to as "bans". This prevents the generation of interventions that are syntactically correct but semantically meaningless in the context of the model. We then apply grammar-guided genetic programming to automatically generate and optimize interventions using this constrained language within the GEMS framework. We argue that our approach can support decision makers by formalizing the development of efficient NPI strategies and by enabling the system to propose intervention strategies directly.

Optimizing non-pharmaceutical interventions under constraints on epidemic dynamics**Betz Maximilian¹, Litz Julian¹, Hannemann-Tamas Ralf¹, Dahmen Manuel², Martin Kühn³**¹ Forschungszentrum Jülich FZJ, Germany² Institute of Multimedia and Interactive Systems, University of Lübeck (UzL), Germany³ German Aerospace Center (DLR), University of Bonn, Germany

Non-pharmaceutical interventions (NPIs) are essential for controlling infectious disease outbreaks, especially in the early phases of epidemics or when pharmaceutical options are limited. To support decision-making, epidemiological models can quantify the expected outcome for NPIs of different strictness. In this talk, we demonstrate the effect of different intervention strategies using an ordinary-differential-equation-based metapopulation model. Initializing the model with case and population data from the SARS-CoV-2 outbreak in autumn 2020, we compare static intervention policies with dynamic, incidence-driven NPIs. To do so, we formulate a dynamic optimization problem and identify the optimized NPI strictness using optimal control. The objective is to balance competing goals, namely minimizing infection burden and mortality while limiting contact reductions. Combining optimal control with dynamic NPIs responding to local incidence levels allows locally acting measures to be described with only a few global parameters, which keeps the optimization problem computationally feasible. Our study reveals that dynamic NPIs can achieve a similar reduction in transmission as static NPIs with a higher number of realized contacts. Optimal control performs even better and removes the need for hand-tuned parameters, demonstrating the applicability of this approach for public health decision-making.

Optimal control of a pandemic: A multi-objective framework to navigate pandemic interventions**Schulte Marvin¹, Leithäuser Neele¹, Süß Philipp¹, Mohring Jan¹**¹ Fraunhofer Institute for Industrial Mathematics ITWM, Germany

During the Covid-19 pandemic, decision-makers faced difficult choices about which interventions to deploy and how to allocate budgets for contact-reduction, testing, and vaccination strategies. These strategies aim to reduce the number of (severe) infections and thus the burden on the healthcare system by reducing contacts, enabling earlier self-isolation of infectious individuals and immunizing against infections. However, all interventions come with costs - monetary costs for vaccines, tests, and infrastructure, as well as social costs, especially for non-pharmaceutical interventions. Quantifying and comparing these costs is challenging, and a single optimal strategy does not exist in general. Instead, multiple trade-offs arise: improving one objective (e.g., reducing testing costs) may worsen another (e.g., ICU occupancy). Strategies that fulfill such a trade-off are called Pareto, while strategies dominated by others (those can be improved in every objective) can be discarded. To assist decision-makers, we develop a multi-objective optimization (MCO) framework that minimizes healthcare burden and intervention costs without aggregating distinct objectives. The framework is coupled to an epidemiological model that integrates the three intervention mechanisms. It computes Pareto-optimal trade-offs until a good approximation of the infinite set of optimal strategies is reached. An interactive visualization framework then enables navigating between these trade-offs and filtering solutions according to bounds on objectives (e.g., a cap on peak ICU patients) set by the decision-maker. In this talk, we present the MCO framework and results from a case study representing the onset of a novel pandemic. Epidemiological parameters are aligned with the SARS-CoV-2 wild-type, and interventions are assumed to become available in stages: first non-pharmaceutical interventions, followed by rapid diagnostics and vaccines. We employ stylized cost functions for each intervention type and minimize both peak ICU

occupancy and intervention costs. We illustrate how the optimal trade-offs unfold in this setting and how they shift when bounds on peak ICU demand are imposed. We highlight the central role of vaccination in any realistic strategy and discuss how selecting a lifting date for restrictions can influence contact reduction and health outcomes, noting that higher contact reduction can, paradoxically, lead to worse health outcomes in certain scenarios.

CONTRIBUTED TALKS II - Data acquisition & parameter estimation**grEPI: A global repository of epidemiological parameters**

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Reliable epidemiological parameter estimates are essential for infectious disease modeling, yet there is currently no centralized repository and no consistent standard for reporting these estimates. As a result, parameter estimates are dispersed across a large and growing body of literature, making their identification, interpretation, and synthesis highly resource intensive. This effort diverts time and expertise away from model development and decision support, particularly during the early stages of public health emergencies. To address these challenges, Collaboratory, an initiative of the WHO Hub for Pandemic and Epidemic Intelligence, is leading the development of the Global Repository of Epidemiological Parameters (grEPI). grEPI is a centralized, standardized repository intended to provide the modeling community with rapid access to reliable epidemiological parameter estimates. It is underpinned by a reporting framework developed through extensive consultations and workshops with a global community of practice spanning modeling, epidemiology, and public health. This framework provides guidance for reporting a broad range of commonly used infectious disease modeling parameters, as well as associated uncertainty and relevant contextual metadata. grEPI will also include mechanisms for community review of parameter estimates and rigorous versioning to ensure that estimates remain transparent, traceable, and interpretable over time. The initial release will incorporate parameter estimates generated by the Pathogen Epidemiology Review Group at Imperial College London in a systematic review of over 45,000 journal articles. It will also ingest outputs from an AI-assisted parameter extraction tool developed by the Public Health Agency of Canada. In the future, authors will be able to submit new parameter estimates directly to grEPI as part of their paper submission process, ensuring the repository remains up to date with the latest evidence. Estimates will be accessible via a web interface, programmatic API, and dedicated R package. Together, the repository and its underlying reporting standards will reduce duplication of effort, accelerate model development, and support timely, evidence-informed responses to infectious disease threats.

A comparison of observation models for transmission models of emerging diseases: Application to SARS-CoV-2

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Parameter estimation is often necessary to inform transmission models of infectious diseases. This estimation requires choosing an observation model that links the model outputs to the observed data. Although this choice may be consequential, it has received little attention in the modeling literature. Here, we aimed to evaluate and compare eight observation models, including common distributions such as the Poisson, binomial, negative binomial, and normal (equivalent to least-squares estimation). Specifically, we applied Bayesian inference methods to fit a simple SIR-like model to daily case reports during the first wave of COVID-19 in Belgium, Finland, Germany, 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 inflexible variance structures. Additionally, the binomial and Poisson models produced different point estimates and overly narrow confidence intervals for the basic reproduction number. The other five models - all with a free dispersion parameter scaling the variance to the mean - performed much better, with the negative binomial model ranking first in three countries. We conclude that careful selection of observation models is critical to develop transmission models that properly incorporate all sources of uncertainty.

Who got SARS-CoV-2 infected over time? Insights from a cross-national collaboration between Munich and Luxembourg

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Introduction: As the SARS-CoV-2 pandemic began in Europe, many studies investigated its spread through the population. However, analysis approaches differed, preventing conclusions from being drawn at a European level. To address these gaps, we conducted an intra-European analysis with cohorts from Germany (KoCo19) and Luxembourg (ORCLU).

Methods: Dried blood spot (DBS) samples were collected in both cohorts at three time points between November 2021 and March 2024. All samples from Munich and Luxembourg were tested for anti-Nucleocapsid antibodies at the Munich study site. Further, at each round, questionnaires were used to collect demographic and behavioral information. To obtain results that are representative for the Munich and Luxembourg population, the cumulative seroprevalence was estimated by weighting anti-Nucleocapsid results according to the sampling design of each cohort and then calibrating them for non-response. Results were then adjusted for the test sensitivity and

specificity. Further, by comparing the seroprevalence with the official count, an underreporting factor (URF) was calculated to quantify how well the infections were identified in both places. Further, a risk factor analysis for each cohort and a combined meta-analysis were carried out to quantify the risk of infection using fully adjusted logistic regression models.

Results: The seroprevalence was 23.8% vs. 16.7% at baseline, 68.1% vs. 62.6% at FU1, and 100% at FU2 in ORCLU and KoCo19, respectively, thereby showing a strong increase in seroprevalence in both cohorts between November 2021 and March 2024. The URF was 2.1 for ORCLU and 3.5 for KoCo19 at FU2. Further, an increased age and living alone was shown to decrease the risk of infection at multiple time points (age: 0.98, CI: 0.97-0.99 and living alone: 0.81, CI: 0.69-0.94 in the meta-analysis at FU1).

Discussion: This intra-European analysis enables a comparison of seroprevalence and risk factors associated with infection in Luxembourg and Munich, thereby shedding light on the different public health responses and their effect on the cumulative seroprevalence, and highlighting the importance of intra-European analyses.

Beyond Conventional Surveillance: Biological Validation of Variant and Vaccine Effects on Transmissibility via Contact-Informed Bayesian Modeling

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During acute pandemic phases, routine surveillance rarely links infection outcomes with contact behaviour and immunity, so real-time insight into drivers of transmissibility is limited. Using SARS-CoV-2 in Germany, we estimate time-varying indicators that separate (i) viral fitness (evolution/variant replacement) from (ii) immune fitness (natural infection, primary vaccination, boosters). We derive a daily contact index (Ct) from GPS mobile-phone co-location data and use an adapted Bayesian media-mix model to relate Ct to the effective reproduction number (Rt). This produces biologically interpretable transmissibility components from anonymised contact and infection data, validated against external biological evidence. Variants dynamics from epidemiological evidence Epidemiological benchmarking is feasible because common field outputs (Rt, secondary attack rate, growth rate) are mathematically linked. Across 13 selected epidemiological studies, mean fitness increases relative to wild-type were +16.8% (Alpha), +38.0% (Delta), and +82.9% (Omicron), compared with our model estimates of +29%, +63%, and +108%, respectively. Variants dynamics from virological/immunological evidence Virological and immunological studies report measurements in units not readily convertible to transmissibility (e.g., Ct values at detection, RNA copies/mL or genome equivalents, time to viral clearance; immunoassay, fluorescence intensity and neutralization titres such as ID50). Consequently, they primarily support the direction of fitness evolution rather than qualitatively comparable effect sizes. Across 12 viral-load studies and 6 antibody-titer studies (52 variant comparisons of pairs among wild-type, Alpha, Delta, Omicron), 40 comparisons matched the direction implied by our model, while 12 were opposite. Vaccine induced immunity Validation of vaccine-induced immunity is particularly challenging at population scale. In the single study we identified that reports comparable antibody dynamics across immunity classes, natural immunity to primary vaccination corresponded to a 78% IgG increase and primary to booster vaccination to an 11% increase,

compared with our model estimates of +75% and +8%, respectively. The framework is transferable to LMIC settings: it requires individual mobile phone data (available currently almost everywhere on Earth), while R_t can be derived from sentinel testing or wastewater surveillance, enabling near real-time biological situational awareness.

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

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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 policy-making in Germany.

Methods: This ongoing multi-centre study consists of two waves of cross-sectional data collection: the first conducted outside of the influenza season (wave 1), and the second during the influenza season (wave 2). Elderly care homes were recruited on a voluntary basis across Germany. In each of the participating care homes, long-term residents and staff record all physical or conversational contacts over the 24 hours preceding the interview. Wave 1 serves as the baseline. In wave 2, participants with a recent (lab-/antigen-/clinically-) confirmed influenza or ARI episode (cases) will recall 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) will report contacts only for the preceding 24 hours. Based on both waves, we will estimate changes in contact patterns from baseline. Multilevel regression analyses with post-hoc weighting and random effects for care homes will be used to estimate these changes and adjust for demographic and health-related factors.

Results: Preliminary descriptive analyses of baseline data from wave 1 and a subset of participating elderly care homes indicate higher contact rates in the elderly care homes than previously reported for the general German population. The unadjusted contact rates were higher among staff than residents, with between-care-home heterogeneity. Data collection for wave 2 is ongoing, and robust results will be presented.

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

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Drivers of erratic RSV seasonality in Japan

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Respiratory syncytial virus (RSV) typically circulates with predictable seasonal patterns in temperate climates such as Germany. However, in Japan, RSV seasonality has shifted significantly a few times during the last decade, and after the SARS-CoV-2 pandemic identifying a single RSV season still poses a challenge. This unpredictable seasonality complicates evaluating the optimal timing for administration of RSV prophylaxis. This study aims to identify the mechanisms underlying this seasonality in Japan. We fitted a deterministic transmission dynamic model to the weekly reported Japanese RSV notification incidence from 2013 to 2025. Our model allowed for multiple factors potentially contributing to shifts in seasonality. These include, reduced transmission rates during the pandemic and increased post-pandemic susceptibility owing to reduced transmission during the pandemic, as well as potentially weak seasonal forcing, changes in transmission rates due to behavioral change and changes in birth rates. We fitted our model in a Bayesian framework using Hamiltonian Monte Carlo. Initial results suggest that RSV transmission in Japan may be less seasonally pronounced than the disease incidence suggests. The estimated RSV transmission rate was 1.6-fold (95% CrI: 1.4, 2.0) higher in week 49 compared to week 18. We estimate that the transmission rate decreased by 60% (95% CrI: 49%, 70%) at the start of the pandemic, disrupting the regular patterns of RSV transmission. The resulting accumulation of a large pool of RSV-susceptible individuals may have disrupted the epidemic cycle in 2021. Assuming that the contact rates have again stabilised in March 2023 but increased by year, we estimate that in 2025 the contact was 1.8-fold (95% CrI: 1.6, 1.9) higher than the pre-pandemic level. Further model exploration is needed to assess the robustness of the findings and the roles of other potential contributors, such as changes in childcare attendance, viral interference, and climate change.

CONTRIBUTED TALKS III - Transmission pathways & behaviour**How social dynamics impact adherence to mask wearing and infection spread**

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Human behaviour critically shapes infectious disease transmission, yet many local-scale models neglect behavioural dynamics. We address this gap by investigating, through simulating studies, how sharing a social identity combined with observing the adherence or non-adherence of others to mask-wearing affect people's own adherence to mask wearing and subsequently pathogen exposure. We look at crowd settings typical for sports events. We use Vadere, an agent based pedestrian simulation software, that integrates aerosol transmission. In this model, infectious agents move about a location. If infectious, they also breath out aerosol clouds containing COVID-19 pathogen that susceptible agents breathe in. We simulate a ticket-checkpoint scenario with 100 susceptible agents. First, a 'role-model group' (20 agents) passes, of which either everybody or nobody wears a mask. Next, an 'imitating group' of 80 agents, including one infectious agent, enters. They identify to a certain degree with the role-model group, measured through a parameter called shared social identity (SSI). Based on SSI and observed adherence of the other group, we sample each agent's mask-wearing probability from UK Government survey data collected by the second author. The simulations show that when the role-model group wears masks, adherence in the imitating group remains high regardless of SSI, resulting in only one agent, on average, being highly exposed to pathogen. However, when the role-model group is non-compliant, SSI becomes decisive. Agents with low SSI tend to ignore the non-compliant role-model group and continue to adhere, keeping the number of highly exposed agents to a low 4 on average. In contrast, agents with high SSI align with the non-adherence of the role models, significantly increasing the number of highly exposed agents to about 12. These findings indicate that shared social identity amplifies the effect of observing others' non-adherence and thus underline the importance of considering social dynamics when designing interventions to reduce exposure at crowded events.

Variations in non-household contact behaviour based on prior disease status during the COVID-19 pandemic: Results from the German National Cohort (NAKO)

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Background: Infectious diseases are often particularly dangerous for individuals with prior health conditions. Non-pharmaceutical interventions (NPIs) can be used to decrease transmission by forcing a reduction in social contacts. Given that individuals with prior conditions were more susceptible to severe outcomes during the COVID-19 pandemic, we investigated whether their contact behaviour in response to NPIs differed from that of healthy individuals in Germany.

Methods: We used data from the German National Cohort (NAKO). Only participants with complete data on age, sex, prior conditions, and non-household contacts were included. Prior condition was considered as the number of disease types (e.g. eye diseases, skin diseases; possible range: 0-12) an individual had. Contacts were collected at times with NPIs; participants were also asked to report on their normal contact behaviour when NPIs are not in place. Contact ratios (CRs)

by prior condition were calculated using negative binomial fixed effects regression models that were adjusted for age and sex. CRs were calculated for times without NPIs, times with NPIs, and times with compared to without NPIs (i.e. reduction in contacts due to NPIs).

Results: Our analysis included 94 552 participants. Individuals had an average of 2 prior disease types (range: 0-11) and 11.9 non-household contacts at times without NPIs and 3.9 with NPIs. At times with NPIs, individuals with more prior diseases had fewer contacts compared to healthy individuals (CR 0.94 (95%CI 0.90-0.98) for 4+ prior disease types); this trend was also seen at times without NPIs (CR 0.93 (95% CI 0.90-0.95) for 4+ prior disease types compared to 0 prior disease types). The overall reduction in contacts at times with vs without NPIs was similar regardless of the number of prior diseases (CR 0.32 (95%CI 0.31-0.33) for 4+ prior disease types; CR 0.34 (95%CI 0.33-0.35) for 0 prior disease types). However, reduction in close (<1.5m) contacts at times with compared to without NPIs was slightly greater for individuals with 4+ prior disease groups (CR 0.24 (95%CI 0.23-0.25)) than for 0 disease groups (CR 0.28 (95%CI 0.27-0.28)).

Conclusions: Overall, contact behaviour differs dependent on an individual's prior disease status, but the relative reduction in contacts during times with compared to without restrictions is relatively similar. Some infectious disease models may benefit from considering prior health conditions when parameterising contact behaviour.

Assessing population-wide COVID-19 transmission across venues using a venue-based individual-based model with airborne and droplet transmission

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The transmission of COVID-19 occurs through both contact-based and airborne pathways, yet most individual-based models (IBMs) are limited to a single transmission pathway, most commonly contact-based transmission. The STRIDE IBM (Willem et al., 2021) was originally designed to simulate person-to-person contact transmission using demographic data and age-specific contact patterns, with leisure interactions represented in aggregated community pools. While effective for modelling social contacts, this structure limits the representation of environmental heterogeneity relevant for airborne transmission, which is important for capturing venue-driven superspreading and for evaluating intervention strategies. We extend STRIDE by introducing a venue-based community structure that explicitly represents locations, such as shops and restaurants. Individuals are assigned to specific venues based on empirical time-use data, enabling heterogeneity in venue attendance and contact behaviour at the population scale. Explicit representation of distinct venue types is essential for simulating population-wide intervention scenarios, which are beyond the scope of single-venue or microscale models. Each venue is characterised by environmental parameters (i.a. ventilation, occupancy, and exposure duration) enabling the explicit modelling of airborne transmission. In addition, droplet transmission (representing contact-based spread) is further refined by incorporating contact duration and proximity. The model was tested on a computer-generated population of 600,000 individuals designed to statistically mirror the actual population of Belgium. Using the venue-based extension of STRIDE, we simulated a baseline scenario against the conditions of Belgium's first lockdown, where only essential retail remained open. In addition, we explored a counterfactual scenario assessing the potential impact of maintaining societal activity in all venue types, but with enhanced ventilation. Where data were

unavailable, assumptions were guided as much as possible by existing literature. This integrated framework enables population-level analysis of how behaviour, environment, and transmission pathways jointly shape COVID-19 dynamics and superspreading. Moreover, our approach supports the evaluation of tailored interventions and provides a realistic basis for assessing interventions across the entire population and their venues.

From Contact Trajectories to Age-specific contact matrices: An Observational Diary Study in Germany with Comparison to POLYMOD

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Background: Contact surveys often summarize daily totals and overlook within-day variation in when and where contacts occur. We used time-ordered contact diaries to characterize daily contact trajectories and to derive age-specific contact matrices for comparison with an established benchmark.

Methods. We conducted an observational contact-diary study in which participants completed a 24-hour time-use contact diary spanning 05:00 on the previous day to 05:00 on the survey day. Participants recorded up to 12 activities in chronological order and reported the number of contacts during each activity episode. Participants also provided detailed information for up to the first 20 close contacts, including characteristics (e.g., age and sex) and the activity episode/setting in which each contact occurred. Using the contact-trajectory data, we estimated contact rates by setting, age group, and weekday/weekend, and derived contact matrices. We compared matrices with POLYMOD Germany (2008) using row- and column-normalized matrices.

Results: A total of 770 participants provided valid contact-trajectory information (mean age 53.7 years; 66.5% female), reporting a mean of 7.7 activities and 10.17 close contacts per day (including repeated contacts with the same person). Across trajectories, “at home” or “sleep” dominated early and late activity orders. Weekdays showed a mid-sequence shift towards work/study and travel-related settings, while weekends showed less work/study and relatively more discretionary settings (outdoors, errands, and other). On weekdays, participants aged 20–39 reported slightly

more activities than those aged ≥ 60 (8.09 vs 7.67). On weekends, participants aged ≥ 60 reported more activities than those aged 20–39 and 40–59 (7.35 vs 7.21 and 6.92, respectively). By age group and setting, participants aged 40–59 reported the highest close-contact rate in work/study episodes on weekends (10.75), while the lowest close-contact rate was observed during sleeping episodes on weekdays among participants aged 20–39 (0.73). Compared with POLYMOD, DigiHero exhibited slightly lower overall contact rates, while the broad age-mixing structure was similar after normalization.

Conclusions: Time-ordered contact diaries provide a trajectory-based view of daily contacts and enable construction of contact matrices that are broadly consistent with established benchmarks, while revealing setting-, age-group-, and day-type differences in contact timing and intensity.

Comparing registry-based and cohort-reported mass gathering events in Germany: GEMA registrations versus DigiHero self-reports

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Background: Quantifying mass gathering events (MGEs) is important for characterizing population exposure patterns and parameterizing infectious disease transmission models. However, different data sources vary in coverage and may be subject to distinct biases. We compared MGEs captured in a national music-licensing registration system (GEMA) with participant-reported MGEs from a national cohort study (DigiHero).

Methods: We analyzed GEMA registrations for events requiring music licensing in Germany in 2024. Events were summarized by month, venue setting (outdoor vs non-outdoor), federal state and attendance-size categories. We compared these distributions with DigiHero, a national cohort study in which participants reported MGE participation in 2024. Participants provided details on up to their four most recent MGEs, including month of attendance, setting (indoors/outdoors/mixed), estimated event size, and travel distance to the venue.

Results: In GEMA data, 190,043 events were recorded in 2024. GEMA registrations showed pronounced seasonality and were dominated by smaller events. The majority of registered events involved 10,000 participants). Outdoor events represented a minority peaking between May and September. In DigiHero, 4,209 participants reported 10,921 events between January to May 2025. Reported MGEs in DigiHero were larger on average (approximately half 1,000 and a non-trivial share >10,000) and exhibited a higher proportion of outdoor events compared to GEMA. Travel and patterns differed by region; participants residing in Thuringia and Saxony-Anhalt were more likely to report long-distance travel (>100 km) to attend MGEs. Both sources indicated elevated event activity in December, consistent with holiday-season gatherings.

Conclusions: GEMA and DigiHero provide complementary perspectives on MGEs: GEMA offers broad enumeration of music-related events, while DigiHero captures participant-experienced exposures across event types but is influenced by recall and “last four events” truncation. Integrating registry-based and cohort-based data may improve estimates of MGE exposure distributions for infectious disease risk assessment and modeling.

Integrating Behavioral Survey Data into Epidemic Models: A Data-Driven Modeling Framework

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Human behavior plays a crucial role in how infectious diseases spread. People change their actions in response to risk - adjusting mobility, adopting protective behaviors, and reacting to policies or rising case numbers. Yet, most epidemic models still treat behavior indirectly, assuming fixed transmission rates or inferring behavioral effects from case trends alone [1,2]. In this work, we develop a modeling framework that directly integrates measured behavioral change into epidemic dynamics and allows comparison across alternative behavioral compartmental formulations. We use repeated survey data from the COSMO project in Germany to quantify temporal variation in risk perception and protective behavior, and link these behavioral responses to policy interventions using indicators from the Oxford COVID-19 Government Response Tracker. Behavioral change is incorporated via explicit transitions between behavioral states and through behavior-dependent modulation of social contacts and transmission intensity. Population mixing is represented using age-structured contact matrices from POLYMOD, rescaled by time-varying mobility data from Google. We compare different behavioral compartmental structures within this unified framework to assess how alternative representations of behavioral adaptation influence epidemic outcomes. All model variants are calibrated to weekly COVID-19 mortality data across 16 German states using Approximate Bayesian Computation with Sequential Monte Carlo [3]. Our results highlight the importance of jointly modeling behavioral responses and policy interventions using real-world data, and demonstrate that integrating survey-based behavioral measurements leads to more realistic and policy-relevant epidemic models.

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CONTRIBUTED TALKS IV - Methodological research & transmission dynamics**Understanding the Potential Drivers of Differential RSV Risk by Birth Month**

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Respiratory syncytial virus (RSV) is an important cause of respiratory illness in young children, and infects almost all children by the age of two. Younger infants are at highest risk for severe outcomes, and hospitalization rates typically peak in children aged 1-2 months. In addition to age, evidence suggests that RSV risk varies by birth month: infants born 2-3 months prior to peak RSV incidence typically have the highest risk of hospitalization due to RSV during their first year of life. Although this pattern is consistently observed across locations, the mechanisms that drive it remain poorly characterized. Here, we conducted a simulation study to explore several potential drivers of differential RSV risk by birth month. First, we fit an age-structured MSEIRS model of RSV transmission to positivity data from four countries. We then ran simulations where one of five potential mechanisms was incorporated into the model: 1) seasonal variation in maternal protection of newborns, 2) differential susceptibility to RSV by age, 3) differential severity (and therefore reporting) of RSV infection by age, 4) differential susceptibility by birth month, and 5) differential severity by birth month. Interactions between these mechanisms were also tested. We find that, of the tested mechanisms, only differential severity by age yields patterns in risk by birth month consistent with observations (mean Pearson correlation coefficient between modeled and observed risk = 0.89). All other mechanisms yielded negative correlation coefficients for all or most countries. For models considering both differential severity by age and one additional mechanism, correlation coefficients between the modeled and observed risk by birth month did not differ significantly from those obtained when only differential severity by age was modeled. Finally, differential severity by age was also the only mechanism that correctly reproduced the observed peak in hospitalizations in children aged 1 to 2 months. Our results suggest that observed patterns in RSV risk by birth month are driven primarily by higher RSV severity in younger infants. Critically, this does not imply that the other tested mechanisms play no role in the epidemiology of RSV, simply that they are not responsible for variations in risk by birth month specifically. More rigorous model fitting to multiple data types, including hospitalization and seroprevalence data, will be useful in confirming our findings.

Comparing agent-based and equation-based models with respect to their inherent assumptions

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Two popular approaches for modeling epidemiological dynamics are agent-based models (ABMs) and equation-based models (EBMs), each offering distinct advantages and limitations. Mostly, EBMs are built from ordinary-differential-equation (ODE)-based models with exponentially distributed sojourn times. Well established extensions using the Linear Chain Trick (LCT) also allow Erlang-distributed sojourn times and further generalizations through integro-differential-equation (IDE)-based models permit arbitrarily distributed sojourn times. ABMs likewise allow arbitrary

sojourn time distributions. Furthermore, ABMs enable detailed individual-level simulations, explicitly modeling transmission events and distinguishing between different locations. In contrast, EBMs typically assume homogeneous mixing within (sub-)populations and model transmission on an aggregated level. While ABMs offer greater realism, they are computationally more demanding, thus limiting their applicability. The objective of this study was to more systematically investigate how differing modeling assumptions affect simulation outcomes. To ensure comparability, we simulated synthetic trajectories with an ABM, creating a very general baseline, which was then used to initialize ODE-, LCT-, and IDE-based models as well as the ABM ensemble simulations. As a consistency check, we first considered exponentially distributed sojourn times for all models and a single location per type in the ABM. After harmonizing transmission rates of the ABM and the ODE-based model, all approaches produced similar results. We then studied the impact of different sojourn time distributions using lognormal distributions for both the ABM and the IDE-based model, following literature on COVID-19. The Erlang and exponential distributions in the LCT- and ODE-based models were chosen to approximate these distributions. Despite identical sojourn time assumptions, the IDE-based model deviated from the ABM, likely due to differences in the transmission process. Overall, IDE- and LCT-based models showed similar dynamics, with the IDE-based model more closely approximating the ABM in specific compartments, while the ODE-based model deviated more strongly. Finally, we examined the effect of incorporating multiple locations per type in the ABM. In both exponential and lognormal settings, substantially fewer infections occurred due to reduced interactions between individuals, a mechanism that could not be captured by the EBMs.

Hybrid frameworks for accurate and efficient simulation of epidemiological processes in highly stochastic regimes

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Mathematical epidemiological models are essential for studying transmission dynamics of infectious diseases and supporting public health decision-making. These models range from deterministic mean-field approaches, to metapopulation models and detailed individual-based models. Selecting the appropriate modeling framework is a non-trivial task and depends on research objective, data availability, and computational constraints. Especially in highly stochastic regimes, the computational cost can become prohibitive as numerous simulations are required to reliably approximate the full probability distribution. While mean-field methods reduce this demand, they fail to capture the stochasticity inherent in such systems. Hybrid modeling approaches aim to balance this trade-off between accuracy and computational efficiency. In this work, we present two hybrid frameworks that combine stochastic individual-based models with deterministic equations-based methods. The first framework implements a per-simulation switch based on a single sample trajectory. The second combines stochastic simulation with the Method of Moments (MoM) utilizing moment equations to describe the dynamics of the mean and higher order central moments of a stochastic process. While the MoM-based model allows for the switching condition to be evaluated against the probability distribution rather than a single realization, it requires moment closure methods to resolve higher-order dependences. We apply both approaches to a spatially-resolved stochastic Susceptible-Infected-Recovered (SIR) model and

analyze their performance and computational effort under varying conditions. Furthermore, we compare different switching criteria for transitioning between the stochastic and deterministic components of the hybrid model. Overall, our results demonstrate that these hybrid modeling frameworks significantly outperform the purely deterministic approach while substantially reducing computational costs compared to the fully stochastic model.

A semi-continuous flow-based formulation to avoid quadratic system growth in Lagrangian metapopulation models

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If not adequately addressed, human mobility can become a key driver of infectious disease spread. Lagrangian metapopulation models, which explicitly track commuting subpopulations and their infection status, offer a valuable mesoscopic approach for capturing these dynamics while preserving the spatial affiliation of commuters. However, the standard approach of introducing separate state vectors for each commuter group leads to a near-quadratic growth in the size of the Ordinary Differential Equation (ODE) system with respect to the number of spatial patches. This methodological scaling substantially increases the computational demands, particularly when more finely resolving mesoscopic models in highly connected mobility networks. In this work, we present a semi-continuous flow-based reformulation that resolves this dimensionality issue and thus substantially reduces computational demands. Instead of integrating commuter states directly as coupled ODEs, our method integrates only the patch totals (residents plus commuters) and reconstructs commuter-specific dynamics by proportionally rescaling the integrated total flows at discrete synchronization points. Numerical benchmarks using an age-stratified SEIR model demonstrate that our approach reduces the computational complexity from near-quadratic to near-linear. For highly connected networks with 1024 patches, we observe speedups of over four orders of magnitude (>20,000x faster) compared to the standard Lagrangian formulation. The method ensures that explicit Lagrangian tracking remains computationally feasible even for large-scale epidemiological scenarios while additionally providing integrated transition counts (e.g., daily infections or hospitalizations) as direct outputs without additional post-processing.

Spreading Dynamics on the World Air Transportation Network During COVID-19

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Air travel plays a key role in the initial spread of infectious diseases and the emergence and dissemination of new variants. The disease spreading dynamics in the World Air Transportation Network (WAN) has therefore been studied extensively and at the start of COVID-19 triggered a true “paper hurricane” of publications. Most of the works tested established modeling approaches and aimed to forecast case importations and their timing. What remains scarce are thorough examinations of the structural changes of the network and their impact on spreading dynamics, especially beyond the initial shock and across the network as a whole. In our work we address this gap: While total travel volume dropped by more than 85%, the reduction was highly

heterogeneous. Very short and especially very long connections were suppressed disproportionately, and many links disappeared entirely. This has a big impact of the shortest path trees spanning from potential outbreak sites and the effective distances between locations. We demonstrate that these structural changes had profound implications for disease spreading potential: While many link reductions had minimal impact on spreading dynamics, overall, the pandemic-induced slowdown was significantly stronger than what would be expected from travel volume reductions alone, as evidenced by comparing simulations on the real data against null models based on rescaled 2019 networks. Interestingly, the deviations from this null model were less pronounced in early 2020 but became stronger after the first 2 months. Consequently, the impact on spreading dynamics was also more persistent than the rebound of absolute traffic suggests. These insights reveal that pandemic models must account for network restructuring, not just traffic reduction, to accurately predict disease dynamics and inform intervention strategies.

How to evaluate the robustness of causal findings in observational studies: Application of E-values and bounding factors

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Background: Observational studies are often susceptible to unmeasured confounding. Traditional sensitivity techniques frequently require strong and untestable assumptions, making a sensitivity analysis challenging in causal analysis. Frameworks such as GRADE (Grading of Recommendations, Assessment, Development and Evaluation) and the TARGET (Transparent Reporting of Observational Studies Emulating a Target Trial) encourage robustness and transparency in causal inference. GRADE recommends assessing the impact of residual confounding, whereas TARGET encourages routine reporting of sensitivity techniques.

Objectives: This article provides an overview of E-values and the bounding factor, a relatively new metric to assess robustness to unmeasured confounding. It discusses their practical application, advantages, limitations, and best practices for interpretation in epidemiologic research.

Sources: Relevant peer-reviewed literature, methodological and applied papers, and tools for E-value calculation were reviewed until October 2025.

Content: E-values quantify the minimum strength an unmeasured confounder would need to have with both the exposure and the outcome to explain away an observed effect, conditional on the measured covariates. E-values require no additional assumptions, easy to compute and enhance transparency when routinely reported. Limitations include the absence of a universal cut-off for interpretation, inability to account for other biases, and potential for selective reporting. E-values should be reported within the context of the study and the measured confounders. Researchers are encouraged to identify plausible unmeasured confounders to guide future investigations. Bounding factors quantify how much an observed effect estimate would be altered if an unmeasured confounder of a specific strength was associated with both the treatment and outcome. This approach enables the investigators to evaluate realistic bias scenarios and assess their potential impact on the observed effect estimate.

Implications: E-values and bounding factors should be considered as complementary approaches to other sensitivity techniques. Routine application of such techniques can help researchers to explore the plausibility of unmeasured confounders in causal studies.

Keywords: E-value, Bounding factors, Unmeasured confounders, Causal inference.

CONTRIBUTED TALKS V – Other & Environmental & climate impact on infectious diseases**Global collaboration under uncertainty: WHO Collaboratory**

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Introduction: The World Health Organisation Hub for Pandemic and Epidemic Intelligence Collaboratory initiative is a digital environment that convenes global experts through structured Communities of Practice (CoPs). These CoPs seek to advance collaborative analytics for epidemic and pandemic preparedness by providing a trusted, open space for modellers, public health professionals, and policymakers to co-design solutions for health emergencies.

Context and aim: Health emergencies are characterised by high uncertainty, fragmented evidence, and competing priorities. The aim of Collaboratory is to foster more confident, transparent, and evidence-informed decision making at both national and global levels.

Method: Through the establishment of thematic CoPs, Collaboratory mobilises geographically dispersed expertise via webinars, workshops, and in-person meetings. In this presentation, we would walk participants through the life cycle of a CoP, including how it can connect across sectors, foster knowledge creation, and develop digital tools.

Findings: Pilot initiatives have demonstrated that co-created analytic resources improve comparability of data, lower entry barriers to analysis, and strengthen decision makers ability to weigh policy trade-offs against incomplete information. Open analytic discussions have further enhanced transparency, allowing diverse perspectives to be tested and refined in real time. Innovative contribution to policy, practice and/or research Collaboratory exemplifies an innovative approach to what can be considered a distributed yet coordinated response to health emergencies. By connecting global expertise, Collaboratory aims to build enduring analytic capability via the establishment of timely and relevant CoPs.

Uncovering temperature sensitivity of West Nile virus transmission

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Temperature strongly influences mosquito-borne pathogen transmission, with major implications for disease risk under climate change. Accurate predictions of transmission require understanding how mosquito and pathogen traits respond to temperature. We introduce a new framework that integrates experimental data across mosquito species and traits to estimate temperature-dependent transmission dynamics, focusing on West Nile virus (WNV). By synthesizing data from 15 mosquito species and eight key traits, and applying Bayesian hierarchical models, we quantified species- and experiment-level variation in temperature responses. Our results show that WNV transmission peaks around 24°C across Culex species, with minor species-specific differences, while differences in modeling assumptions can shift temperature optima by up to 3°C. Trait variability, especially in biting rate, lifespan, and egg viability, strongly shapes uncertainty in transmission estimates, highlighting priorities for future experiments. This approach improves

mechanistic understanding of temperature-sensitive transmission and provides a foundation for anticipating changes in WNV risk under climate change.

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Climate variability is associated with chikungunya outbreaks across the Indian Ocean Region

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In the Indian Ocean Region (IOR), chikungunya virus (CHIKV) outbreaks have surged, driven by climate factors influencing vector ecology and transmission. We analyzed GeoSentinel traveller surveillance data from 2010 to 2024 alongside multiple climate indices representing dominant modes of regional variability, including the Mascarene Subtropical High (MSH), Indian Summer Monsoon, and El Niño Southern Oscillation. Here we identified region-specific associations: in South-Central Asia, chikungunya activity correlated strongly with intensified MSH area during El Niño; in sub-Saharan Africa, links were weaker and influenced by monsoon onset and cross-equatorial flow; in Southeast Asia, outbreaks followed moderate-to-large eastward MSH expansions with lagged effects. These findings suggest that large-scale climate variability modulates chikungunya transmission dynamics across the IOR. Incorporating such climate indicators into early warning systems may enhance outbreak forecasting and guide targeted public health interventions to mitigate chikungunya spread.

Predictiveness and drivers of highly pathogenic avian influenza outbreaks in Europe

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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 spill over.

Network-induced control of sustained oscillations in SIRS epidemics

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Sustained oscillations in SIRS epidemic models are well understood in well-mixed populations when infectious and immune periods deviate from exponential waiting times. In contrast, the role of contact network structure in generating or suppressing such oscillations has received little attention. Existing work on small-world networks reports oscillations but does not relate them to effective transition-time distributions. This work investigates how network topology shapes oscillatory SIRS dynamics by simulating a stochastic SIRS process on self-similar modular hierarchical (SSMH) networks. These networks interpolate between random-like graphs and strongly modular, hierarchical structures while preserving system size and mean degree. A single structural parameter controls edge placement across hierarchical levels, reshaping effective distances between communities. Simulation results show that random-like networks support robust, coherent oscillations in global prevalence, whereas increasing hierarchical modularity desynchronizes outbreaks across communities and gradually destroys the global limit cycle, leading to damped or irregular fluctuations. These findings support an interpretation of epidemic oscillations as a synchronization phenomenon of individual SIRS cycles, where network topology promotes or inhibits global coherence by reshaping the time-to-infection distribution through changes in effective distances.

Impact of NPIs on SARS-Cov-2 infection numbers and transmission dynamics

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Background: The COVID-19 pandemic prompted governments worldwide to implement non-pharmaceutical interventions (NPIs) to mitigate transmission and prevent healthcare system collapse, particularly during periods when pharmaceutical measures were unavailable or insufficient. While the effectiveness of NPIs has been widely studied, less attention has been given to understanding the drivers behind their implementation and whether government responses were primarily reactive or proactive.

Methods: We conducted a global, observational time-series analysis using data from the Oxford COVID-19 Government Response Tracker (OxCGRT) to examine the relationship between NPI stringency and epidemiological indicators, including COVID-19 case incidence, mortality, hospitalizations, and reproduction number trends. The Stringency Index was used to quantify the intensity of government interventions. Lagged analyses were applied to assess whether changes in epidemiological burden preceded policy responses (reactive behavior) and whether increased stringency was followed by reductions in disease burden (policy impact). Analyses were conducted across multiple pandemic phases and stratified by region where data permitted.

Results: During the early phase of the pandemic, increases in NPI stringency were largely reactive, occurring after sustained rises in cases, deaths, or hospitalizations. Policy escalation typically followed epidemiological deterioration with short temporal delays. In later pandemic phases, some governments adopted more proactive approaches, implementing precautionary NPIs in anticipation of emerging waves or variants. However, this shift was inconsistent across countries and diminished over time as political, economic, and social pressures increasingly influenced decision-making. Higher NPI stringency was generally associated with subsequent reductions in transmission indicators, particularly when implemented early and consistently.

Conclusions: Government responses to COVID-19 were predominantly reactive during the initial stages of the pandemic, with limited but uneven movement toward proactive policymaking over time. While NPIs were effective in reducing transmission and healthcare burden, their implementation was shaped by a complex interplay of epidemiological signals and socio-political constraints. These findings underscore the importance of adaptive, data-driven public health strategies and institutional preparedness to enable timely and effective responses to future pandemic threats.

CONTRIBUTED TALKS VI - Modelling of interventions & decision-making**Pandemicsim – A General Simulation and Estimation Tool for Epidemic Outbreaks**

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The COVID-19 pandemic highlighted the importance of flexible and reliable computational tools for simulating infectious disease dynamics under varying intervention strategies. To support the practical application of comprehensive epidemic models, we introduce an R package that implements a general compartmental modeling framework for infectious diseases. The package is built upon a unified mathematical model that extends the classical Kermack-McKendrick (SIR) structure to accommodate diverse transmission mechanisms, population structures, and control measures within a single, adaptable framework. The R package provides a modular and extensible environment for defining, simulating, and analyzing epidemic scenarios across a wide range of pathogens. Users can specify different modes of transmission – including airborne, vector-borne, and direct contact – as well as multiple intervention strategies such as vaccination, quarantine, and social distancing. By encapsulating the underlying mathematical properties within a pre-established general model, the package eliminates the need to redevelop and reanalyze disease-specific models for each new application. The package includes tools for numerical simulation, parameter estimation using outbreak data, and comparative analysis of intervention scenarios. The framework adapts to pathogen-specific transmission characteristics while preserving a consistent model structure. Simulation results calibrated to real-world data illustrate the package's ability to reproduce observed epidemic dynamics and assess the impact of alternative control strategies. Integrated in a shiny application, the package provides an easy-to-understand user interface. If provided with outbreak data, such as incidence tables, the package estimates missing parameter values automatically and provides key values, such as the basic reproduction rate R_0 . Different intervention measures can be included and compared to analyze the individual impact of different containment strategies. Overall, this R package provides a practical tool for researchers and practitioners, bridging mathematical theory and applied epidemic modeling to support data-driven decision-making in the management of emerging infectious diseases.

Estimating Severe COVID-19 Cases Averted and Vaccine Effectiveness in Brazil

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Brazil started the COVID-19 mass vaccination in January 2021 with CoronaVac and ChAdOx1, followed by BNT162b2 and Ad26.COVS vaccines. By the end of 2021, more than 317 million vaccine doses were administered in the adult population. In the first part, a mathematical model will be presented in a study to analyze the impact of vaccination, social distancing, and isolation measures on SARS-CoV-2 transmission, using surveillance data from Rio de Janeiro as a case study. Results indicate that combining vaccination with transmission suppression policies significantly reduced hospitalizations and deaths, with vaccination alone preventing over 230,000 hospitalizations and 43,000 deaths. The study highlights the need to maintain health surveillance and structured vaccination planning until widespread coverage is achieved. The second part will present a study aimed at estimating the effectiveness of the primary series of COVID-19 vaccination and booster shots in protecting against severe cases and deaths in Brazil during the first year of vaccination. A registry-based cohort study analyzing over 158 million vaccination and severe case records from Brazil used a mixed-effects Poisson model to estimate vaccine effectiveness, adjusting for multiple factors. Results showed that vaccine effectiveness against severe cases and deaths remained above 25% and 50%, respectively, after 19 weeks, with boosters providing enhanced protection, especially heterologous boosters. Despite waning effectiveness, the study confirms continued protection during the Omicron wave, though vaccine comparisons should consider potential biases related to age, timing, and behavioral factors.

Hybrid Modelling for Comparison of Vaccination Programs against Endemic Diseases

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Whether a vaccination program is funded by the health care system is an important and complex decision. The costs of purchasing and administering vaccines must be put in contrast with the population's higher immune competence, the corresponding improved public health, and the related savings from a payer's perspective due to the reduced burden of the disease. While the decision on whether one vaccination program should be funded by the system is already complex and multifaceted, it becomes particularly challenging when a decision for individual programs must be made at the expense of others, for example, due to financial constraints. Questions such as "Should the budget of €X million be used to promote the vaccination program against disease A or disease B?" have massive impact but often must be answered with little basis for decision making. In this paper, we present EpiVacc, the first epidemiological modelling framework for the comparative assessment of vaccination programs. The model consists of a continuous-time immunity model and a linear outcomes model supported by a SIRVS-type epidemiological compartmental model. The prior translates the vaccination program into individual immunity curves. Furthermore, the outcomes model uses matrix operations to translate them into various model results, such as symptomatic cases, hospitalisations, or sick leave costs. Hereby it applies additional discounting factors from the compartmental model to account for potential sterilising effects of the vaccine. The framework stands out by solving the major challenges associated with the research question with elegance and simplicity: interventions are evaluated for one year in the

steady state which avoids any questions related to the initial vaccine rollout phase, thus enabling a fair evaluation period, and reduces the amount of data required. In addition, the immunity model offers the necessary flexibility for depicting even complex vaccination programs. Finally, the special integration of the compartment model makes the framework independent of disease and transmission mode, which is a basic prerequisite for unbiased comparison. While the model is greatly simplified in many aspects and therefore limited in its application, it can be seen as a good compromise between validity and usability. In a study conducted for the Austrian Ministry of Health in 2025, it successfully helped us to examine and compare 15 different vaccination programs against 12 different pathogens.

Optimal seasonal timing of infant immunization to prevent RSV hospitalizations in Japan, a modelling study

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The seasonal circulation of respiratory syncytial virus (RSV) in countries such as Japan, together with the transient nature of passive immunity conferred to infants via maternal vaccination or monoclonal antibody administration, may warrant a differential strategy for those born during the RSV inter-seasonal period. Maximal effectiveness may be achieved by deferring the immunisation of this cohort from birth to their first RSV season as catch-up cohort using monoclonal antibody. However, the magnitude of the potential benefit of such a seasonal and catch-up programme to confer the strongest protection during their first RSV season is currently unclear, making it difficult to weigh the additional benefit of the seasonal and catch-up programmes against the potential logistical challenges that come with the programmes. To estimate the additional impact of defining seasonal timing of RSV immunisation programmes in reducing RSV infant hospitalisations in Japan, we developed a static cohort model parameterised by Japanese data on weekly and municipality-specific RSV incidence during 2018 to 2025 and on the risk of being hospitalized among RSV cases. We used Bayesian inference to estimate the efficacy and its waning for maternal vaccine (RSVpreF) and long-acting monoclonal antibody (nirsevimab) from clinical trial data. We estimate that year-round administration with RSVpreF or with nirsevimab could reduce RSV hospitalisations by 46% (95% uncertainty range (UR): 31%, 65%) or 58% (95%UR: 39%, 79%), respectively. In comparison, seasonal programmes with catch-up administration of nirsevimab for infants born outside the season could achieve 1.1 (95%UR: 0.83, 1.6) times or 0.98 (95%UR: 0.85, 1.2) times more impact measured as reduction in RSV infant hospitalisations. If seasonality matches immunization timing perfectly, using 2024 as an example, the impact was 1.2 (95%UR: 0.95, 1.6) or 1.1 (95%UR: 0.97, 1.2) times higher than for year-round administration. In sensitivity analyses where protection from nirsevimab remained substantial after 6 months, the year-round programme was often more effective than the seasonal and catch-up programme. Both RSVpreF and nirsevimab have the potential to substantially reduce RSV infant hospitalisations in Japan. The benefit of seasonal RSV infant immunisation programmes depends on predictability of RSV seasonality and potential logistical challenges.

Evaluating Hypothetical Interventions Effects on Hospital-Acquired Infection Outcomes with Stacked Probability Visualization: R Shiny Apps based on a Multistate Modelling Approach

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Hospital-acquired infections (HAIs) contribute to increased morbidity, prolonged hospital stays, and higher healthcare costs. Robust analytical frameworks are essential to assess how hypothetical interventions can alter outcomes in dynamic clinical settings.

The objective of this work was to develop tools to evaluate the effects of potential interventions on mortality and length of hospital stay. A six-state extended illness-death multistate model was built with a time-constant transition hazard assumption. The multistate model maps patient trajectories involving healthcare-associated infections as an intermediate event, and mortality and discharge as absorbing events in order to describe the time-dependent dynamics within hospitals. Using two settings, we simulated the implementation of hypothetical treatments by modifying hazard rates: Setting 1 (improved treatment intervention only) and Setting 2 (combined enhanced treatment and infection prevention). These were used to create the interactive and user-friendly R Shiny Apps HAISim (HAIs Interventions Simulator) and StaViC (Stacked probAbility Visualization & Comparison). The Shiny Apps use inputs from literature or user data, such as transition-specific hazard rates and intervention-related parameters. HAISim models the effects of hypothetically improved treatment and infection prevention on outcomes such as the number of lives saved and the number of patient days decreased by simulating a hypothetical scenario based on actual clinical data. StaViC makes it possible to compare potential interventions and their impacts before and after implementation by visualizing the stacked probabilities of patients across various health conditions. These tools bridge methodological rigor and practical implementation, offering hospitals a flexible framework to prioritize cost-effective IPC strategies.

Keywords: Hospital Acquired Infection, Intervention evaluation, Shiny App, Multistate modelling.

Modeling of antimicrobial-resistant bacterial colonization through a nationwide patient-based network in French healthcare settings

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Patient movement within and between hospitals creates an invisible, complex healthcare network that enables the spread of antimicrobial-resistant bacteria (ARB) and contributes to the burden of healthcare-associated infections (HAIs). Yet most national-scale studies infer spread from aggregated hospital-to-hospital patient sharing, leaving patient-to-patient contact pathways - and the pathogen-agnostic structural risk of colonization - poorly characterized. Here, we reconstruct these contact pathways using France's 2023 national hospital discharge database (PMSI-MCO) to build a high-resolution patient-based network (PBN) of 4,086,926 inpatients across 1,278 hospitals, with ≈96 million weighted edges representing overlapping overnight stays in the same hospital wards. We simulate ARB transmission across 365 daily PBN layers using a stochastic susceptible-infected (SI) model, initiating 2,000 runs on randomly selected start dates to avoid outbreak-timing bias. This yielded an estimated colonization probability for each patient, which we aggregated to

wards, hospitals, and residential codes. Patient-level colonization risk maps, plotted at the residential-code level, revealed spatial clusters of elevated risk in both urban and rural areas and showed how hospital-acquired colonization can extend into communities through discharged patients. We also observed strong heterogeneity in risk between wards and hospitals, revealing concrete hotspots for enhanced monitoring and intervention. To characterize the main drivers of this variation, we used generalized additive models (GAMs) to estimate key patient- and hospital-level predictors of colonization risk. This framework provides, to our knowledge, the first nationwide, temporally resolved reconstruction of real-world patient contacts to model ARB colonization risk and to support structurally targeted surveillance and early prevention when Pathogen-specific data are limited.

CONTRIBUTED TALKS VII - Technical implementation of models & applications**The world air transportation network, import risk of diseases and pandemic preparedness**

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Disease propagation between countries strongly depends on their effective distance, a measure derived from the world air transportation network. It reduces the complex spreading patterns of a pandemic to a wave-like propagation from the outbreak country, establishing a linear relationship to the arrival time of the unmitigated spread of a disease. However, in the early stages of an outbreak, what concerns decision-makers in countries is understanding the relative risk of active cases arriving in their country, essentially, the likelihood that an active case boarding an airplane at the outbreak location will reach them. We (i) introduce the "import risk" model, which defines import probabilities using the effective-distance framework [1] and (ii) show its application to estimate the pandemic potential of emerging variants of COVID-19 [2]. The model [1] assumes that airline passengers are distributed along the shortest path tree that starts at the outbreak's origin. In combination with a random walk, we account for all possible paths, thus inferring predominant connecting flights. Our model outperforms other mobility models, such as the radiation and gravity model with varying distance types, and it improves further if additional geographic information is included. The import risk model's precision increases for countries with stronger connections within the WAN. In the second part we show that, in the early stages of an emerging variant, integrating data from national genomic surveillance and global human mobility with large-scale epidemic modeling allows to quantify its pandemic potential [2]. We validate our framework on worldwide spreading variants and gain insights about the pandemic potential of sub- and lineages. We combine the different sources of information in a simple estimate of the pandemic delay and show that only in combination, the pandemic potentials of the lineages are correctly assessed relative to each other.

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Evaluating performance potentials for metapopulation models of infectious diseases

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Metapopulation models are well suited approaches for spatially heterogeneous infectious disease spread. In contrast to agent-based models their complexity only scales quadratically with the

number of considered regions or subpopulations, meaning that many alternative outcomes of a considered metapopulation system can be computed relatively fast. As a measure of practicability and efficiency in a pandemic setting, the “time-to-solution” of a model run is a valid first metric. However, this leaves potential improvements entirely unexplored. As for any CPU or GPU, a computational peak performance and maximum memory bandwidth can be given, calculating theoretical floating-point operations is a first step towards performance engineering of the application. With established tools like LIKWID, realized performance in floating point operations (FLOP) and memory bandwidth can be measured. Considering whether an application is then compute- or memory-bound generates knowledge on the potential peak performance of the model run. In this talk, we will present a thorough computation of FLOP in a scalable metapopulation model and therefore present an approach to better understand computational limitations, chances for considered hardware architecture, and, eventually, optimal estimates for obtaining modeling results.

Impact of transmission chain information loss on agent-based epidemic model predictions

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During emerging epidemics, surveillance systems detect aggregate case counts but lack detailed transmission chain information, forcing modelers to make initialization assumptions. This work quantifies how missing transmission chain data affects agent-based model predictions and demonstrates limitations of conventional uniform initialization approaches. Our methodology couples two agent-based models in a three-stage framework. Vadere generates detailed superspreading scenarios with complete transmission tracking, capturing precise who-infected-whom relationships as synthetic ground truth. MEmilio-ABM conducts epidemic simulations at district scale, where agents move between discrete locations such as households, workplaces, and schools. We investigate two outbreak scenarios: a restaurant event with 89 agents from multiple households, and a workplace event with 26 agents from different workplaces. Each scenario begins with one infectious agent. To isolate effects of missing transmission information, we compare two initialization approaches. Here, Transmission-informed initialization preserves exact contact network information and clustering patterns. Uniform initialization distributes infections randomly across participants, simulating typical surveillance limitations where contact tracing identifies outbreak participants but cannot reconstruct complete transmission networks. Both approaches initialize identical 10-day MEmilio-ABM simulations in a synthetic 1000-person German district. Vadere results reveal infections are highly clustered within households for the restaurant scenario and within workplaces for the workplace scenario. Uniform initialization consistently overestimates epidemic spread, producing 41.3% and 46.0% higher cumulative infections by day 10 for workplace and restaurant scenarios respectively. Uniform initialization reaches 100 infections 1.0 days earlier in the restaurant scenario.

Inferring Mobility Reductions from COVID-19 Disease Spread along the Urban-Rural Gradient

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The COVID-19 pandemic reshaped human mobility through NPIs and voluntary behavioral changes, limiting contacts and mitigating disease spread. Viewing mobility behavior as a measurable, immediately available indicator of population response, existing research has focused on national/metropolitan levels, leaving rural areas unexplored. Simultaneously, our understanding of which environmental, social, and demographic factors facilitated mobility reductions remains incomplete. To improve our understanding of the interrelation of mobility behavior and disease spread, we follow a 3-step approach: 1st, we introduce a Bayesian hierarchical model to quantify heterogeneity in mobility responses across Germany's 400 districts using mobile phone data from 03/20 to 03/21. We decompose mobility into a disease-responsive and three disease-independent factors (temperature, school vacations, holidays). The disease-responsive factor combines national and local incidence through a weighted finite-memory signal and allows for pandemic fatigue, yielding district-specific reaction strengths. 2nd, we build a linear model to attribute cross-district variation in mobility decrease to population density and demographic and socioeconomic covariates. 3rd, we present a structural equation model linking cross-district variation in peak incidence to the same covariates and average mobility decrease. The hierarchical model successfully disentangles the four factors, inferring the two major decreases during spring 2020 (1st wave) and winter 2020/2021 (2nd wave). Mobility is dominated by the disease-responsive component. During the 1st wave, the disease factor reached a median multiplicative impact of 0.77 (IQR: [0.73, 0.80]) in mid-April 2020. Despite higher incidences in winter 2020/2021, it only reached 0.83 (IQR: [0.81, 0.86]), suggesting pandemic fatigue fully compensated for higher incidences. Temperature and holiday factors provide secondary reinforcing effects. Analysis reveals significant differences along the urban-rural gradient, with large cities reducing mobility most strongly. Employment variables explain variance during the 1st wave, while political variables gain significance during the 2nd wave. However, reduced mobility only partially translates to lower peak incidence, indicating other factors remain influential. Overall, our results advance knowledge of factors driving mobility reductions and highlight mobility's potential as an operational proxy for population response.

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

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Endemic-epidemic models are a well-established statistical approach for analysing and predicting the spread of infectious diseases based on count time series, implemented in the R package "surveillance". 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). 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. Furthermore, we assess gains in forecast performance by applying extended models to norovirus counts from the same region and period. For certain models, an additional stratification by age group is applied. After aggregating forecasts over age groups for comparability, the weighted interval score (WIS) shows no improvement in forecast accuracy compared to simpler models, with geometric lag models performing best.

FluModell: A Discrete SEIRS Model Applied to the Simulation of Seasonal Influenza: A Study Case Applied to the German Health System

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FluModell is a periodic discrete SEIRS model designed to explore the epidemiology of seasonal influenza. The model integrates age structure, vaccination status, multiple viral variants, contact patterns, severity strata, and time-varying non-pharmaceutical interventions (NPIs). Seasonal variation in transmissibility is represented by a deterministic annual forcing term, while short-term deviations are captured through an ARIMA component fitted to residual fluctuations in transmission indicators, improving parameter estimation and short-horizon forecasts without duplicating the explicitly defined annual seasonal term. The practical use of FluModell is illustrated through a study case focused on the German health system, aiming to support public health planning and hospital resource management.

CONTRIBUTED TALKS VIII - Methodological research & transmission dynamics**Calibrating Epidemiological models using only Stylized Facts**

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Often, when developing models, there is little or no data available for validating or calibrating simulation models. One possible approach to assess model behavior in such cases is to use so-called stylized facts [3]. Stylized facts express shared empirical regularities within a domain. For example, Death growth rates declined rapidly from high levels during the initial 30 days of the epidemic worldwide [1]. We use the domain-specific language, SF-DSL [5, 2], for the formalization and evaluation of stylized facts. SF-DSL has been used to validate simulation models [5]. Therefore, SF-DSL offers a variety of statistical, logical, and descriptive operators that allow many different stylized facts to be expressed. These operators can be used to make statements about simulation outputs in the form of time series that describe the characteristic behavior of the modeled system. For example, the requirement could be set that the number of infected people will eventually fall for 100 consecutive days. Recently, we enhanced SF-DSL, enabling its use for calibration [2]. Therefore, we equipped each operator with a distance-based robustness calculation that indicates whether an SF is fulfilled and, with what certainty [2]. This quantitative evaluation of models enables the application of established parameter estimation algorithms. Based on this robustness calculation, we calibrate an epidemiological simulation model created with the German Epidemic Microsimulation System (GEMS) framework [4] in a case study. We use stylized facts about COVID-19 from multiple independent literature sources. For calibration, we used PSO to determine suitable parameter values that generate simulation outputs which adhere to the stylized facts. In addition, we calculated posterior distributions for parameter values based on ABC-SMC.

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On the effects of contact recurrence on disease transmission

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Introduction: Human-to-human transmission of infectious diseases typically requires contact between two individuals. In order to model disease spread, the contact behaviour that gives rise to these contacts must be represented in infectious disease models. One aspect of this behaviour relevant to the spread of disease is the recurrence of contacts, i.e., how often a contact between two individuals is repeated. By limiting the number of contact partners, and thus the number of possible transmissions, contact recurrence impacts disease dynamics. Information on contact recurrence is available from egocentric contact surveys such as COVIMOD but rarely used in modelling studies. Despite its potential impact and available data, contact recurrence is often omitted from models and rarely studied explicitly.

Our study aims to address this issue by examining the impact of contact recurrence at different frequencies on disease transmission.

Methods: We use a multi-layered network model to simulate the spread of infectious disease. Each network realises a specific contact recurrence frequency. We model the two limits of recurrence, i.e. static contacts and non-recurrent contacts, as a static network and a randomly mixing population, respectively. To study the potential effects of recurrence, we vary the contact recurrence frequency while maintaining the daily average degree. Additionally, we use COVIMOD data to parameterise contact frequencies and the proportion of contact partners at each frequency, comparing the effects of static, recurrent and random contacts.

Results: Our preliminary results show a substantial effect of contact recurrence on disease transmission. While a population that mixes randomly, i.e. without recurrent contacts yields the highest attack rate, including recurrent contacts while maintaining the average degree decreases the attack rate. The preliminary results indicate that these effects also arise for contact frequencies smaller than the inverse infectious period, i.e., for contacts that on average do not reoccur during the infectious period. Using COVIMOD data to parameterise recurrent contacts also yields substantially different disease dynamics compared to those observed for random or static contacts.

Conclusion: Our preliminary results demonstrate the effect of contact recurrence on infectious disease dynamics. It highlights the importance of incorporating recurrent contacts into infectious disease models as they shape the arising disease dynamics.

The Impact of Contact and Infectivity Structure on Infection Spread

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Classical models that describe the spread of infection in a population usually simplify important details, such as non-uniform contact rates, due to model structure or data uncertainty. In this work, we aim to incorporate several key aspects into the modeling that are based on real-world observations: (1) daily contact rates [1,2]; (2) time-dependent infectivity following infection [3]; (3) distributions of infectious and latent periods; and (4) reductions in the number of contacts associated with severe or critical disease courses. We study both the individual and combined impacts of these factors on infection spread. We use a specially developed agent-based model within the GEMS (German Epidemic Micro-Simulation System) framework [4] to simulate the spread of wild-type COVID-19 in the German population. In the baseline scenario, we assume constant weekday contact rates, a uniformly distributed infectivity profile, contact numbers independent of disease severity, and fixed infectious and latent periods. In the alternative scenarios, we adjust these factors individually and in combination to reproduce observed data while maintaining the same mean values as in the baseline case. As a result, the alternative scenarios exhibit an increase in cumulative infections, with the magnitude depending on the specific combination of factors applied.

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Assessing Hospital Staffing Resilience During Epidemics Through Agent-Based Simulation

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Introduction. Hospital operation under COVID-19 pandemic conditions represents a severe stress test that can be effectively addressed using modeling tools. However, modeling a hospital in isolation, without its surrounding population, fails to capture key drivers of personnel availability. Factors such as household quarantine measures, childcare obligations, and sick leave depend strongly on the epidemiological situation in the surrounding region and evolve dynamically over the course of a pandemic.

This work addresses the need for an integrated modeling approach that jointly considers hospital operations and regional epidemic dynamics.

Methods. We use an agent-based model developed within the GEMS (German Epidemic Microsimulation System) framework. The simulated population includes the city of Halle (Saale) and the surrounding Saalekreis region, comprising approximately 440,000 individuals. The University Hospital Halle (UKH) is explicitly represented with 614 physicians, 1,245 nurses, and 89 other medical staff members assigned to 27 departments. Medical staff contacts are modeled at multiple organizational levels (office, department, and hospital-wide), alongside household, workplace, and leisure contacts for the general population. Household quarantine policies and vaccination scenarios are incorporated to capture their impact on workforce availability.

Results. We simulate pandemic scenarios across a wide range of basic reproduction numbers ($R_0 = 1.0-5.0$), with household quarantine applied to all household members of infected individuals at high incidence levels. Personnel availability is quantified as the daily fraction of available medical staff relative to the total workforce. In addition, the model enables a systematic assessment of how vaccination of medical staff modifies availability patterns over the course of the epidemic.

Conclusions. The proposed modeling approach provides a detailed and flexible framework for assessing hospital personnel availability under epidemic stress while explicitly accounting for interactions with the surrounding population. The resulting daily availability trajectories can support hospital workforce planning not only during pandemics but also during seasonal infection waves. Moreover, the framework enables the evaluation of mitigation strategies, such as vaccination, aimed at reducing periods of critical staff shortages. The approach is transferable to other hospitals and regions and can serve as a decision-support tool for healthcare preparedness planning.

Scaling up incomplete secondary data about hospital stays to inform models of nosocomial infections

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Background and Aim: Nosocomial transmissions are a major contribution to the spread of multi-drug resistant bacteria in the human population. Models that aim to represent their spread must therefore take into account hospital-associated transmission routes - not only within a hospital but also on the network of hospitals defined by patient transfers between them. Quantitative insights

into this network, required to properly parameterise such a model, can only be gained via data about individual hospital stays in a wide geographical region. In Germany, secondary data from health insurance providers usually prove to be the easiest-to-access source of such data. However, data from any given health insurance provider cover only a small fraction of all hospital stays, and cannot be linked with data from any other provider. This means that such data need to be scaled up to provide a representative picture of the complete patient transfer network between hospitals. The aim of this research is to compare methods to scale up these data and investigate how the methods affect results of transmission models based on the scaled-up data.

Methods: We consider two ways of scaling up incomplete hospital stay data. The first is randomly replicating patient records. The second involves building up records from scratch. Broadly, the simulated patients are assigned demographic characteristics, based on which they are then assigned hospital stints - defined as a period of consecutive days spent in one or more hospitals and diagnoses. They are assigned an initial hospital, an admission date, and a final discharge date for each stint. All assignments are done based on distributions from the incomplete dataset. Finally, hospital transfers (and their dates) within a stint are generated as a Markov process, with transfer probabilities once again informed by the incomplete dataset. We compare these two methods of scaling up data in terms of differences in the patient transfer networks obtained from the scaled-up datasets, as well as differences in the results of infectious disease models based on them.

Results and discussion: Replicating patient records leads to more connected patient transfer networks, and thus faster disease transmission in models, than simulating patient records. Work is still needed to establish which method creates datasets that are closer to empirical data, and we plan to test both methods on a sample of data about hospital stays in France, for which a complete dataset is available.

Assessing the Birth Month Impact of Monoclonal Antibodies on Infant RSV Hospitalizations

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Respiratory syncytial virus (RSV) is a leading cause of hospitalization among infants, with age-specific and seasonal patterns. An infant's birth month relative to the RSV season has been identified as an important determinant of hospitalization risk, with infants born shortly before peak seasonal activity often experiencing the highest burden. Recent epidemiological observations further suggest shifts in RSV seasonality, with earlier seasonal onset compared to pre-pandemic years. Extended half-life monoclonal antibodies have recently been introduced to protect newborns against severe RSV disease in Germany, but their potential effectiveness may depend on the timing of birth relative to seasonal transmission dynamics. To investigate these interactions, we adapt the German Epidemic Microsimulation System (GEMS), an agent-based modelling framework, to simulate RSV transmission among infants. The model incorporates birth month specific cohorts, age and contact setting dependent susceptibility, waning immunity, and seasonal transmission dynamics. Using this framework, we simulate weekly RSV hospitalizations under varying monoclonal antibody coverage scenarios to explore how birth month and seasonal timing influence intervention impact. This study aims to quantify birth month specific RSV hospitalization

risk, assess the prospective impact of monoclonal antibody interventions, and examine how shifts in RSV seasonality may affect immunization strategies. By integrating epidemic dynamics with birth month specific modelling, our findings are intended to inform decisions on the timing and coverage of RSV monoclonal antibody programmes.

CONTRIBUTED TALKS IX - Modelling of interventions & decision-making**Modeling RSV Immunity and Intervention Scenarios Using a Deterministic Framework Informed by RespiCompass Data**

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Introduction: Respiratory Syncytial Virus (RSV) continues to impose a substantial seasonal disease burden, particularly among infants and older adults. The increasing availability of prevention strategies, including maternal vaccination and monoclonal antibodies (mAb) for infants, calls for modeling approaches that explicitly represent immunity dynamics. The European RespiCompass initiative supports epidemic preparedness by providing synthetic surveillance data and scenario-based projections for multiple respiratory pathogens. We applied a transmission model with explicit RSV immunity structure, informed by RespiCompass-derived data, to enable mechanistic scenario-based analysis of RSV epidemic dynamics.

Methods: We developed a deterministic SEIRS (Susceptible-Exposed-Infected-Recovered-Susceptible) transmission model incorporating multiple levels of RSV immunity to represent partial and waning protection following infection or immunization. The model was parameterized using notification data derived from synthetic outputs generated by the RespiCompass framework. A scenario-based approach was applied to evaluate five intervention scenarios, including baseline assumptions and alternative representations of population immunity shaped by maternal vaccination and infant-targeted monoclonal antibody strategies.

Results: The model captured pronounced differences in RSV epidemic dynamics across intervention scenarios. Scenarios incorporating maternal vaccination and monoclonal antibody-induced protection resulted in reduced peak incidence and shifts in epidemic timing compared to baseline assumptions. Explicit representation of immunity levels revealed age-specific effects, with the strongest impact observed in infant age groups, while indirect effects on older populations were mediated through changes in overall transmission intensity.

Discussion: These findings highlight the importance of explicitly representing immunity structure when assessing RSV intervention strategies. By integrating maternal vaccination and monoclonal antibody-based protection within a single transmission modeling framework, this work provides a mechanistic perspective on how targeted infant interventions may influence population-level dynamics. While the deterministic framework does not capture stochastic or spatial heterogeneity, it offers a transparent and computationally efficient tool for comparative scenario analysis to support seasonal RSV preparedness.

Effectiveness and Efficiency of pre-season administration of long-acting monoclonal antibodies for infants born to RSV vaccinated mothers, a modelling study

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The respiratory syncytial virus (RSV) is responsible for most severe respiratory tract infections in

young children. Antibodies against RSV can be transferred from mother to child during pregnancy. However, the protection they offer wanes swiftly, leaving the children susceptible to infection about six months after birth. Two immunisation options are currently available: a maternal vaccine (MV) and a monoclonal antibody (mAB, nirvesimab) that can be given to infants at birth. The current immunisation strategy in Germany prioritises mAB, with a seasonal administration. Yet some women might choose to receive the MV instead. However, children born to vaccinated mothers at the end of the RSV season or shortly after will be left without much protection in their first RSV season later in the year. Administering the mAB to these children right before the start of the new RSV season could help reduce the risk for RSV disease. To estimate the impact of administering mAB to children born to vaccinated mothers in Germany, we built an age and birth season-structured compartmental catalytic model including maternally derived immunity. We used the `odin2` package in R to specify the model and fit it to RSV seroprevalence in the first year of life using Markov Chain Monte-Carlo (MCMC). We used estimates of age-dependent case: hospitalisation rates to estimate age and season specific disease burden and posterior estimates of efficacy of RSV immunisation to evaluate the added benefit of pre-season mAB for children born to vaccinated mothers. We estimate that 44% (95% CI: 39-50) and 47% (42-51) of summer- and autumn-born infants respectively get infected with RSV in their first year of life. If unimmunised, their RSV associated hospitalisation incidence is highest at 14.8 (14.1- 6.9) and 24.4 (19.0-25.4) per 1,000 infants. Spring-born infants are of lowest risk as born after the main RSV season. In winter-born children, MV reduces the risk for hospitalisation due to RSV from 9.6 (9.1-10.8) per 1,000 to 5.3 (3.5-6.5). Administration of nirsevimab at 11 months, right before their first RSV season, further reduces this risk by 0.4 (0.1-0.7) per 1,000. In comparison, reduction in hospitalisation incidence from pre-season mAB administration in addition to MV in spring-, summer-, and autumn-born children was 0.6 (0.2-1.1), 2.7 (1.4-4.1), and 3.3 (1.8-5.1) per 1,000. Pre-season administration of nirsevimab to infants born to vaccinated mothers offers modest additional protection.

Identifying the optimal age for pneumococcal vaccination in older adults in Germany

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Background: Older adults are at increased risk of severe pneumococcal infection associated with substantial morbidity and mortality. Recently, the German Standing Committee recommended the usage of a 20-valent pneumococcal conjugate vaccine (PCV20) in 60+ years old to prevent pneumococcal diseases in elderly. This study aims to identify the optimal age for PCV20 vaccination in older adults in Germany under infant vaccination PCV15.

Methods: An SIS dynamic transmission model of pneumococcal carriage was developed to estimate the effects of vaccination in older adults considering indirect herd effects and replacement diseases induced by infant vaccination. The model incorporated eight competing groups of serotypes. The analysis evaluated four vaccination ages (60, 65, 70, 75 years old) based on effectiveness (e.g. saved hospitalizations). Outcomes were cumulated over a 10-year vaccination period plus a 40-year follow-up to capture long-term vaccine effects. Due to lack of data on waning of vaccine effectiveness, a range of durations of protection were tested (7.5-20 years).

Results: For duration of protection 7.5-year, vaccination at age 70 years prevented most hospitalizations (9,116) followed by age 65 years (8,166), age 75 years (7,663), and age 60 years

(6,313). Vaccination at age 75 years prevented most fatal cases (1,240) followed by age 70 years (1,238), age 65 years (1,005) and age 60 years (711). Vaccination at age 70 years saved most life years (LYs) (10,945) followed by age 65 years (10,763), age 60 years (9,125) and age 75 years (8,660). On the other hand, the optimal age is consistent across the durations of protection ≥ 10 years but 20-years duration of protection prevented most hospitalizations (31,241) at age 65 years followed by (28,763) at age 70 years, (23,187) at 60 years, and (19,985) at age 75 years. Furthermore, vaccination at age 70 years prevented most fatal cases (4,595) followed by age 65 years (4,480), age 75 years (3,661) and age 60 years (3,005). Vaccination at age 65 years saved most LYs (30,294) followed by age 70 years (26,703), age 60 years (24,758) and age 75 years (18,309).

Conclusion: Given the current model parametrization, the results suggested that the optimal age for adult PCV20 vaccination depends on the durations of protection. The shorter duration 7.5-year favoured a vaccination age shifted 5 years later to maximize prevention across all outcomes, whereas the longer durations of protection gave the higher results.

Spatial spread and optimal control of West Nile virus in Germany

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The recent emergence and rapid spread of West Nile virus (WNV) in Germany between the years 2018 and 2025 highlight the need for modelling approaches that explicitly capture species movement patterns, environmental heterogeneity, and the ecological drivers of transmission. In this work, we develop a spatially explicit partial differential equation (PDE) model describing WNV spread among mosquitoes, resident birds, migratory birds, equids, and humans across Germany. Seasonal migratory bird flyways are incorporated through the advection process, while mosquito and resident bird movements are governed by diffusion, enabling a realistic representation of heterogeneous large-scale spreading patterns, including long-distance jumps and the seeding of new hotspots observed in the surveillance data. Building on this spatial framework, we formulate and solve an optimal control problem representing key intervention strategies, including mosquito population control, equid vaccination, and human protective behaviour, with the objective of balancing epidemiological burden against intervention costs. The resulting optimal control system provides quantitative guidance on when and for how long mosquito control measures should be implemented to achieve maximal impact. The results are translated into an interactive Shiny application, providing an accessible decision-support tool for exploring intervention strategies across scenarios, without the need to do the background computations.

Recurrent malaria infections, development of immunity and implications for vaccine efficacy trials

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In high-endemic areas, recurrent malaria infections are common, and each experienced infection contributes to the development of (partial) immunity. In recent years, different malaria vaccines have been developed and tested in clinical trials. The studies were conducted at study sites with different levels of malaria endemicity. However, the development of immunity is dependent on endemicity. In particular, unvaccinated study participants develop immunity faster in highly

endemic areas than in low-endemicity areas. This may affect the results of vaccine trials. Here, we simulate malaria trials conducted in low- and high-endemicity areas to demonstrate the impact of acquired natural immunity on estimated vaccine efficacy (VE). The occurrence of recurrent malaria infections in individuals was simulated using Markov Chains. Infections in cohorts of 500 vaccinated and 500 unvaccinated participants were modelled assuming a VE of 36%. Susceptibility to malaria infection was assumed to drop from the first to the sixth recurrent infection from 1 to 0.9, 0.7, 0.5, 0.3, 0.2, and 0.1, respectively. One thousand cohorts were simulated using malaria incidence rates of 0.2, 0.5, 1.0, 1.5, and 2.0 infections per person-year, representing study areas with varying infection risks. Hazard ratios (HRs) were estimated using Cox regression for correlated events (i.e., the Anderson-Gill model, AG; often used in VE studies) and Cox regression stratified by the number of recurrent infections (i.e., the Prentice, Williams, and Peterson model, PWP). The median VE (1-HR) and 95% confidence interval (CI) from the simulations are reported. The simulated VE calculated with the AG model decreased constantly with increasing IRs. The simulated VE estimated using the AG model decreased with increasing IRs from 36% (95% CI: 22–47) at an IR of 0.2 to 26% (95% CI: 22–29) at an IR of 2.0. However, the VEs estimated using the PWP model remained constant at 36% over different transmission intensities. In our simulation study, higher malaria endemicity is associated with lower VE for recurrent infections, an effect also seen in malaria vaccine trials. This effect can be controlled using appropriate regression methods. However, they are not commonly applied in the analysis of recurrent events. While our model is based on simplified assumptions, the results underline the importance of natural immunity in clinical trials and the need to apply appropriate statistical methods.

A conditional prediction framework for vertical HIV transmission with missing key biomarker

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Background: Vertical HIV transmission (VHT) has declined globally; still, an estimated 120,000 children acquired HIV in 2024, predominantly in sub-Saharan Africa. Maternal viral load (mVL) is the strongest predictor of VHT, yet it is frequently unavailable at delivery due to limited laboratory infrastructure.

We aim to develop a prediction model to support identification of infants at high-risk for VHT, including when mVL is unavailable.

Methods: We developed a two-model prediction framework for VHT, accounting for missing mVL, using data from the LIFE and LIFE2Scale studies conducted in Mozambique and Tanzania (N=10,468 mother–infant pairs), with infants followed for at least 12 weeks after birth; 178 infants acquired HIV. To evaluate model performance under high-missingness conditions, we randomly excluded mVL values until the total missingness (natural and induced) reached 40%. The dataset was split into training (80%) and testing (20%) sets based on transmission status and mVL availability. We fit two weighted elastic-net logistic regression models: one using mVL when present (60% of the training set) and one excluding mVL (trained on the full training set). Class imbalance was handled with inverse-prevalence weights. This pipeline was repeated over 20 runs with different random

seeds to simulate varying data splits and missingness patterns. We report the mean and standard deviation across repetitions.

Results: Across repeated runs, the mean test-set achieved 82.4% (SD 7.1%) sensitivity and 73.0% (SD 5.0%) specificity. Among infants with mVL excluded at delivery, sensitivity declined to 71.1% with increased variability (SD 14.4%) and specificity to 70.6% (SD 10.5%). Besides mVL at delivery, which was the strongest predictor when present, the model additionally incorporated infant and maternal characteristics.

Conclusion: A conditional modeling strategy that explicitly accounts for unavailable mVL improves risk stratification for VHT and remains informative when the primary biomarker is missing, a common constraint in resource-limited settings. Despite this advantage, high performance variability highlights the challenge of modeling low-transmission events. Further refinement is therefore needed to enhance the model's robustness and utility for identifying high-risk infants when mVL at delivery is unavailable for clinical decisions.

MINI-SYMPOSIUM I**Population Health Decision-Making: Integrating Evidence, Values, and Real-World Constraints**

Population-level decisions for infectious disease control increasingly require navigating complex trade-offs under finite resources. Policy decision-makers evaluating interventions, such as immunization programmes or non-pharmaceutical, must balance clinical and epidemiological evidence, benefit-harm considerations, cost-effectiveness and budget impact, equity implications, and the priorities of patients, the public, and the health system. This mini symposium brings together international experts to explore how local decision frameworks and institutional contexts shape population level infectious disease policy. Speakers will highlight how health technology assessment (HTA), including mathematical modeling, is integrated into or sometimes constrained within real-world decision processes. The Canadian case will illustrate how the National Advisory Committee on Immunization (NACI) applies a values informed framework to complex vaccine recommendations under its expanded mandate. Austria's recent investment in immunization programs highlights how rapid modeling supported prioritization decisions across more than twenty vaccines. Brazil illustrates how maternal RSV modeling drives HTA decisions, underscores major disease-burden reductions, and supports price talks. OptimAgent in Germany exposes the difficulties of optimal epidemic control under heterogeneity, including use-case design and multi-criteria decision support with GEMS. Finally, perspectives from industry modelers will help illuminate how evidence generation can better address the needs of diverse partners.

Integrating Economic Evidence into Immunization Policy: Experience from Canada's National Advisory Committee on Immunization

Sander Beate - Health Systems and Policy Research Collaborative Centre, University Health Network (UHN); Institute of Health Policy, Management and Evaluation (IHPE), University of Toronto, Canada

Population-level immunization decisions require integrating diverse evidence with societal values and implementation realities. In Canada, the 2019 expansion of the National Advisory Committee on Immunization's (NACI) mandate to formally incorporate economic evidence into vaccine recommendations created new opportunities and challenges for evidence-informed policy-making. This presentation examines how NACI applies a values-informed framework that integrates epidemiologic, clinical, economic, ethical, and equity considerations in real-world vaccine deliberations. Drawing on the development and application of Canadian national guidelines for economic evaluation of vaccines, the presentation illustrates how modeling and health technology assessment are adapted to capture population-level program impacts and distributional consequences. Using recent immunization examples, including respiratory syncytial virus prevention strategies, it highlights how evidence is synthesized within deliberative processes balancing benefit-harm trade-offs, budget constraints, public trust, and implementation feasibility. The Canadian experience demonstrates progress alongside persistent methodological and operational challenges, particularly in incorporating equity and societal impacts. By situating technical evidence within institutional decision processes, this case study illustrates how HTA can support complex population health decisions while remaining responsive to evolving policy priorities.

From Models to Decisions: Embedding Simulation into Transparent Vaccination Prioritisation in Austria

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Health policy decisions on the prioritisation of vaccination programmes require transparent, traceable and fair comparative frameworks. Against this background, the Austrian Federal Target-Based Governance Commission decided in June 2024 to develop a prioritisation list for vaccinations in Austria, considering medical and clinical, health economic and macroeconomic aspects. All vaccinations generally recommended in Austria that are not part of the existing childhood vaccination programme were to be assessed. The project presented here addressed this task by embedding a simulation-based solution as an integral component of an institutionalised decision-making process. The work was closely aligned with existing governance structures organized by the Ministry of Health: for each vaccination, a structured PICO question (Population, Intervention, Comparator, Outcome) was developed within the Nationales Impfgremium of Austria (NIG). To ensure scientific guidance and quality assurance, a dedicated Sounding Board was established within the NIG, bringing together experts from epidemiology, immunology, clinical care pathways, methodological design, dynamic modelling, health economics and ethics. A central objective of the project was the development of a sustainable digital infrastructure that can be used beyond a single decision context. The simulation framework EpiVacc was designed at TU Wien as a basis for a digital twin of the system under consideration, enabling reuse, updating and extension across different policy questions. This approach avoids the repeated development of isolated and non-comparable analytical tools for individual prioritisation decisions and instead establishes a consistent decision basis that supports learning over time. Emphasis was placed on transparency and legitimacy. The involvement of vaccine manufacturers was organised in a structured and open manner, including the opportunity to provide relevant data and publications. At the same time, key analyses - most notably systematic literature reviews on vaccine effectiveness and duration of immunisation - were conducted independently at Medical University of Vienna. Model assumptions, data sources and limitations were explicitly documented and discussed within the expert advisory framework. The contribution demonstrates that simulation-based decision support unfolds its full potential when it is designed not as a black-box output, but as a transparent and quality-assured process.

Multidimensional Challenges in Brazil’s Vaccine Adoption Decision-Making Process: The Case of the Maternal Respiratory Syncytial Virus Vaccine

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The implementation and integration of a vaccine into a National Immunization Program (NIP) requires strategic decision-making and a steadfast, long-term commitment. In 2005, the General Coordination of the NIP, in an innovative manner, requested the first economic evaluation studies for the incorporation of new vaccines. At that time, health economic evaluation was a relatively new field of research in Brazil, both from an academic perspective and in terms of its use in decision-making in the management of the Ministry of Health.

Between 2006 and 2025, the NIP incorporated eleven new vaccines into the routine vaccination schedules: rotavirus, 10-valent pneumococcal conjugate vaccine (PCV10), meningococcal C

conjugate vaccine (MenCc), inactivated polio vaccine (IPV), varicella, and hepatitis A, in the childhood vaccination schedule; HPV, meningococcal ACWY conjugate, and dengue for adolescents; and the adult diphtheria, tetanus, and acellular pertussis (DTaP) vaccine and respiratory syncytial virus (RSV) vaccine for pregnant women. In addition to these, the COVID-19 vaccine, used in a vaccination campaign for the entire population from 2021 to 2023, became part of the schedule for children and adults aged 60 and over starting in 2024. This expansion of the vaccination schedule represents progress, but it also poses significant challenges in terms of sustainability, prioritization, and evaluation of health, economic, and social outcomes.

It is important to identify how challenges in the decision-making processes of adopting new vaccines into NIPs have been met, particularly in middle-income countries, considering economic conditions, new health priorities and a permanent limited budget. This presentation examines how Brazilian NIP applies besides efficiency, ethical, and equity considerations in vaccine deliberations. Using the recent example of the respiratory syncytial virus (RSV) vaccine (1), this case illustrates how evidence is generated through close collaboration with the National Immunization Program and assessed through deliberative processes at Conitec – the National HTA body - balancing cost-effectiveness, budget impact, access barriers, and social and political pressures.

In middle-income settings such as Brazil, vaccine adoption decisions should be grounded in HTA, structured deliberative processes, and stakeholder alignment. The RSV case shows that these processes are context-specific, shaped by political prioritization, technical considerations, and the strength of public health institutions. While Brazil has advanced in HTA institutionalization and decision-making capacity, methodological and operational challenges remain, particularly in systematically incorporating equity and broader societal impacts - an essential step to enhance the responsiveness of HTA to the needs of the Brazilian Unified Health System and to support more inclusive and sustainable health policy decisions.

Reference: Aguiar Monteiro Borges S, Ohanesian Polli E, Nonato AC, Cerchiari N, Verguet S, Christovam Sartori AM, Coelho de Soárez P. Maternal RSV vaccination to protect infants in Brazil: a model-based cost-effectiveness analysis for incorporation into the National Immunisation Program. *Lancet Reg Health Am.* 2025 Dec 22;53:101356. doi: 10.1016/j.lana.2025.101356.

Population Health Decisions with OptimAgent-GEMS: Multi-Criteria NPI Assessment under Heterogeneity

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Background: Population health decisions during epidemics must balance epidemiological evidence, benefit-harm considerations, cost effectiveness, and equity, while accounting for heterogeneity. Within OptimAgent, the German Epidemic Microsimulation System (GEMS), an agent-based platform built on a synthetic German population to support population health decision-making was developed.

Goal: To implement a GEMS-based use case that demonstrates a decision-support framework evaluating non-pharmaceutical interventions (NPIs) under multiple criteria and heterogeneity, enabling transparent trade-off analysis for decision making.

Methods: In a hypothetical pandemic, we specified nine NPIs spanning contact restrictions, remote work, school closures, testing, and lockdowns with varying intensity and duration. Scenarios combined epidemiologic and policy assumptions, and outcomes included health (infections, deaths, life-years, quality-adjusted life years (QALYs)), health system (hospital occupancy), societal harms (confinement days, lost school/work days), and economic outcomes (treatment costs; health care perspective). Heterogeneity analyses stratified outcomes by age; equity impacts for age groups were summarized using the Theil index T .

Results: Strategies were compared by epidemic trajectories, cumulative mortality, and hospital occupancy. Benefit-harm trade-offs yielded a non-dominated efficiency frontier that shifted with the selected societal harm. Targeted contact restrictions for households with older adults and lockdowns consistently appeared on the frontier; however, lockdowns had unfavourable incremental harm per health benefit. Cost-effectiveness analysis indicated, for example, that school closures incurred high costs with limited health gains. Age-specific analyses showed strategy re-prioritization across age groups when focusing on health outcomes alone. Equity analysis found differences in the Theil index T , for example, lockdowns produced the highest between-group inequality in life-years lost, but not in QALYs. Framework implementation also revealed data gaps (e.g., comorbidity distributions) needed to further populate GEMS.

Conclusion: Using GEMS, we show that multi-criteria, values-informed analysis improves decision-making under heterogeneity, surfacing trade-offs and equity. We will expand heterogeneity, evaluate combined NPIs, and enhance equity and economic evaluations. This work was conducted through collaboration across OptimAgent subprojects, with key support from the GEMS development group and subproject 6.

MINI-SYMPOSIUM II**Modeling Animal Health: Learnings and Challenges for future epidemic threats**

In autumn 2025, highly pathogenic avian influenza dominated news headlines, spreading rapidly among migratory birds and causing substantial losses on poultry farms. The recently observed outbreaks of African swine fever, Foot-and-mouth, Bluetongue and Lumpy Skin Disease in Europe as well as the increasing threat for animals and humans through emerging pathogens like H5N1 highlight the importance to not forget about veterinary diseases in infectious disease modeling. The challenges of veterinary epidemiology are often similar to those of human epidemiology, but differ in detail. In practice, interventions to emerging disease spread are often radical, such as culling all animals on a farm. Vaccinations are recommended for some diseases, but for other diseases they must not be used preventively due to associated trade restrictions. While for some livestock, trading and movement data are recorded precisely, data on wild animal movement is poorly characterized. In this mini-symposium, we will discuss learnings from the long history of veterinary epidemiology, current challenges, data streams, and suitable modeling approaches. By bringing together researchers of various fields, we aim to foster exchange on methods and future directions for controlling infectious diseases in animal population and, eventually, to also avoid potential infections in humans.

Control and prevention of animal diseases

Gethmann Jörn - Friedrich-Loeffler-Institut, Germany

Animal diseases severely affect animal welfare, the production of animal-derived foods, and the wider socio-economy. Therefore, disease prevention and control have been central in Germany for centuries. A basic control strategy typically involves: (1) identifying affected farms, (2) isolating affected farms or regions, and (3) stopping animal movements. Measures may include culling livestock on affected and contact farms, destroying potentially contaminated products, or installing fences to control the movement of susceptible wildlife. During the 2024 Foot-and-mouth disease outbreak, 36 premises with 1700 animals were within the containment zone, and the animal trade in Berlin and Brandenburg was prohibited (trade volume ~2 million animals/year). To prevent spread and to establish disease-free regions, vaccination and pathogen testing are used, either voluntarily or compulsorily. To increase acceptance of control measures and to encourage timely reporting, Germany established animal disease compensation funds. These funds compensate losses caused by notifiable animal diseases or zoonoses and by related control measures. Unlike human public health settings, livestock are kept on farms, forming clustered host populations. In Germany, every farm must be registered and animal movements are recorded by species. For cattle, movements are tracked for each individual animal, providing high-resolution data over time. Sheep, goats, and pigs are tracked at batch level, limiting individual tracing, especially when batches are mixed and reassembled at livestock markets. Nevertheless, during an outbreak the system enables rapid identification of farms that received animals from affected holdings. While movement data are crucial for understanding spread, other routes - such as contacts via people or vehicles - are much harder to reconstruct and usually require detailed field epidemiological investigations. For several diseases, wildlife hosts can also be infected and contribute to transmission, or even serve as the main reservoir. In these scenarios, wildlife surveillance and management are critical alongside on-farm control. Options depend on the situation and disease ecology and may include vaccination programmes (e.g. classical swine fever)

and strategic fencing to limit the movement of infected animals (e.g. African swine fever). We will present details on different control strategies that are commonly used for several diseases and explain the differences to public health disease control.

The HPAI Modelling Challenge - a global initiative to improve animal health epidemic preparedness and response

Hayes Brandon - University Toulouse, ENVT, INRAE, IHAP, Toulouse, France

Highly pathogenic avian influenza continues to pose a major challenge to animal health authorities, due to both its epidemiological complexity as well as the limited availability of validated modelling frameworks that are ready to be deployed during outbreaks. While a wide range of mathematical and statistical methods exist to analyse epidemic dynamics or reproduce outbreak trajectories, the models employing these methods can differ substantially in their underlying transmission and control assumptions. Such structural differences can result in mixed or conflicting policy guidance, further complicating the decision process. To strengthen modelling preparedness and to support evidence-based decision-making, we have organised the HPAI Modelling Challenge (“the Challenge”) - an international collaborative modelling exercise designed to broaden the range of HPAI models while fostering transparency and cross-team exchange. The Challenge is built around a single synthetic fully-reproducible epidemic scenario, generated in-silico, that imitates the spread of HPAI in a heterogenous poultry population with explicit surveillance and control mechanisms. Epidemic scenarios, contextual datasets (i.e. population, farm activity, and animal movements), and policy-oriented questions are provided to participating teams in stages. Around 40 modelling teams, distributed across five continents, registered to the initiative and were asked to predict the spatio-temporal development of the epidemic and provide model-based recommendations on different management approaches. As teams are unconstrained in the approaches they can take, a diverse array of model frameworks is able to be applied onto and evaluated in the context of a shared scenario. Here we introduce the motivations, design, organization, and utility of the Challenge, map the different modelling approaches deployed and discuss how these exercises can improve communication between modelling teams and decision-makers, contributing to improved global preparedness for emerging health threats.

Modeling the spread of Foot-and-mouth disease on the German cattle trading network

Volmer Kilian - University of Bonn, Germany

In January 2025, the first outbreak of the Foot-and-mouth Disease (FMD) for more than 30 years has been detected in Germany. Several FMD simulation models already exist but they have certain disadvantages, e.g. the code not being freely accessible or long runtimes that make quick responses needed for decision-making difficult. For spatial spreading across herds, one of the main transmission pathways is trade with infected animals. The animal trade network in Germany is very well documented, consisting of about 1.5 million edges in pig trade and 1.8 million in cattle trade per year. Working with large-scale datasets requires efficient and scalable simulation software. One such software package is the open-source "Modular EpideMIcs Simulation Software" MEmilio that we adapt to simulate a potential outbreak of FMD on animal trading networks. In particular, we use the German cattle trading network based on individual animals, together with sheep and pig trading networks based on batches, and combine these datasets in a metapopulation based approach where spatial units are given by farms. Together with high performance computing

infrastructure, this approach allows the exploration of various intervention strategies in a short time to inform veterinary health authorities.

Similar tools for different battles

Thulke Hans-Hermann - Helmholtz Centre for Environmental Research – UFZ, Germany

Infectious disease outbreaks pose growing challenges for policy makers across human, animal, and plant health, requiring decision-support tools that can account for spatial spread, heterogeneity, and uncertainty. This presentation discusses how explicitly formulated modelling approaches can support outbreak management decisions across the One Health remit, with a focus on their practical value for planning, prioritisation, and evaluation of control strategies. In ecological and agricultural disease contexts, management-oriented modelling has become an essential instrument for exploring alternative interventions, anticipating unintended consequences, and comparing policy options before implementation. The presentation draws on applied examples from plant, livestock, and wildlife health to illustrate how modelling can inform decisions despite limited data, imperfect surveillance, and competing socio-economic objectives. Key differences between these systems and human-focused ABMs are highlighted, including constraints on direct intervention, reduced observability, and the need to represent management actions and compliance rather than individual behaviour alone. Three case studies illustrate how modelling has been used to address concrete policy questions. The first examines landscape-level control of the bacterium *Xylella fastidiosa* in Italian olive stands, where rule-based spatial modelling supported the evaluation of containment and tree removal strategies under high uncertainty and strong social resistance. The second case addresses bovine viral diarrhoea (BVD) in cattle, assessing the risks and potential benefits of shifting from highly precise but costly monitoring systems to cheaper, less informative surveillance approaches, thereby informing trade-offs between epidemiological certainty and economic feasibility. The third example uses an individual-based spatial model to forecast the potential extent and duration of Foot-and-mouth disease (FMD) outbreaks in wild boar populations, supporting preparedness planning by identifying plausible outbreak scenarios and limits of control under highest uncertainty. The presentation concludes with key lessons for policy-oriented modelling, emphasizing transparency, explicit treatment of uncertainty, and close interaction with domain experts and decision-makers to ensure credible, usable, and relevant models for outbreak management.

MINI-SYMPOSIUM III**10 Years of Infectious Disease Modelling for Vaccine Recommendations in Germany: Past, Present, Future**

In 2026 it's been 10 years since the Standing Committee on Vaccination (STIKO, the National Immunization Technical Advisory Group in Germany) first published its guidance on modelling methods for predicting epidemiological and health economic effects of vaccinations in 2016. It followed 5 years after the publication of the updated methodology and standard operating procedure (SOP) for the epidemiological-medical risk-benefit analysis of the STIKO in 2011. In light of the experience with the methods in Germany as well as those of other NITAGs abroad, both for routine immunization and during the COVID-19 pandemic, this mini-symposium will shed light on the translation of mathematical modelling into applied epidemiology as part of evidence-based immunization policy making. The first talk will outline the historic processes of how the methods for the development of immunization recommendations by STIKO have been established. The second talk will present in detail the current methods by STIKO in their latest versions, and it will provide an outlook on how future plans to further develop the methods may look like. The third talk will reflect on how modelling has been helpful for STIKO in supporting them to make recommendations, and what stakeholders like STIKO members seek to learn from applied epidemiological modelling. The fourth talk will provide context on the methods of other NITAGs in different countries and from an international perspective.

Process of developing evidence-based methods for vaccination recommendations in Germany: a historic view

Wichmann Ole - Robert Koch Institute, Germany

The National Immunization Technical Advisory Group of Germany (STIKO) was founded in 1972. Since 2001, the tasks of STIKO have been codified in law, and STIKO started using a standard set of questions to be addressed when developing recommendations and decided to publish alongside its recommendation also the scientific rationale. In 2007, STIKO recommendations became the basis for the vaccination directive of the Federal Joint Committee (G-BA), which defines the reimbursement of vaccines by statutory health insurances. Partly in response to the national and international rise of evidence-based medicine, the methods were further refined, which culminated in the Standard Operating Procedure (SOP) for the systematic development of vaccination recommendations in 2011. The epidemiological-medical risk-benefit analysis of STIKO has been central to its evidence-based immunization policy making. Fundamental for this analysis are results from systematic reviews on vaccine effectiveness and safety. Since STIKO considers risk and benefits not only at individual level but also from a public health perspective, population-level effects are equally relevant. Hence, mathematical modelling has become an integral aspect of the evidence synthesis for estimating the population-level effects and projections into the future. Health-economic evaluations can also provide additional insights and nuance. In 2016, a guidance was published on modelling methods for predicting epidemiological and health economic effects of vaccinations and how results from such models can be considered by STIKO. With the 2018-update of the SOP, STIKO adopted the use of an evidence-to-decision (EtD) framework, which contains among others questions on the size of the anticipated effects and resource use. This talk will outline the historic process of how and why the methods for the development of evidence-based immunization recommendations by STIKO have been established in Germany. It will

illustrate that the establishment, implementation and further refinement of these methods and procedures have been a process of more than two decades. The talk will also focus on the methods development for the modelling guidance, which was a project over three years funded by the Federal Ministry of Health and involving multiple stakeholders and academics, both nationally and internationally. Looking back at the historic origins, this first talk will hence set the scene for what the methods currently entail (Talk 2).

Methods of the STIKO to inform evidence-based immunization policy making: status quo and future plans

Schlaberg Johanna - Robert Koch Institute, Germany / STIKO-Secretariat

The second talk will present the current methods of STIKO in their latest versions. Central to the work of STIKO is the general SOP published in 2011 and last revised in 2018. For the epidemiological-medical risk-benefit analysis, assessments of patient-relevant endpoints, vaccine effectiveness and safety follow the principles of evidence-based medicine (EbM). Systematic literature reviews are conducted following the PRISMA guidelines and guided by a PICO-question on the Population, Intervention, Comparator and Outcome. To evaluate the quality of evidence, the approach of the “Grading of Recommendations Assessment, Development and Evaluation” (GRADE) Working Group is applied. Results from the evidence synthesis are summarized in evidence-to-decision tables. STIKO is involved in all parts from the start to the end of the process, and supported by a secretariat at RKI. The final recommendation by STIKO is published alongside a detailed scientific rationale. Within the general process of STIKO, the results of epidemiological-mathematical models can be used to project the future epidemiological impact of a (new) vaccination recommendation or immunization strategy in (a sub-group of) the population. This may include positive effects like indirect herd protection, or negative effects like serotype replacement. If STIKO is in favor of a vaccination after the medical-epidemiological risk-benefit assessment, the most efficient vaccination strategy may be identified based on the results from an additional health-economic evaluation. The details of these methods have been outlined in a separate document published in 2016 and last revised in 2024. This talk will hence illustrate how the different epidemiological methods interface with each other, and how the modelling is an integral part in the toolbox of public health for vaccination policy making. The talk may finish with an outlook on how future plans to further develop the methods may look like. This will also lead to the next talk on current experiences of applying the methods.

Experience and reflections on how modelling of applied epidemiology is supporting evidence-based decision

Lange Berit - Helmholtz Centre for Infection Research HZI; Hannover Medical School MHH, Germany

The third talk will reflect on how modelling has been a useful addition within the deliberations of STIKO in supporting evidence-based immunization recommendations, and what stakeholders like STIKO members seek to learn from applied epidemiological modelling that is difficult to obtain from other tools in the epidemiological toolbox. The talk will touch upon recent experience of mathematical modelling to support STIKO, including for example the recommendations around introducing RSV interventions in 2024 and 2025; around the change in the vaccine product used against pneumococcal vaccination with recommendations by STIKO in 2016, 2021 and 2023 as well

as a statement in 2025; and around the shift in meningococcal vaccination in infants and teenagers in 2025 following the re-evaluation of a vaccination recommendation. As part of the evidence synthesis that underlies the STIKO methodology, the modelling has been able to provide valuable insights from different perspectives to complement the existing evidence. Modelling has also pinpointed gaps in data and scientific knowledge, and the potential impact that these uncertainties may have for decision making. Selected examples will be used to illustrate the meaningful impact that science translation can have in different applied epidemiological projects. An outlook will be given towards new ways of collaboration and modeling to support vaccine development and vaccine effectiveness monitoring as part of the German Centre for Infection Research (DZIF), clinical and public health networks and European initiatives.

Modelling for NITAG support internationally, opportunities for the future

Flasche Stefan - London School of Hygiene and Tropical Medicine, UK; Charité Berlin University of Medicine, Germany

The fourth talk will take a broader, international view and provide context on the methods of other NITAGs in different countries and from an international perspective. For example, in the UK the NITAG published guidance as to how they should determine if a vaccination programme is cost-effective, taking into account uncertainty, in 2013. These methods have been applied ever since, and they differ in key parts from the STIKO methods (for example, the chosen perspective). Supra-national organizations like the World Health Organization have also supported or engaging in evidence synthesis methods and applications. Examples will be given surrounding the work of the WHO Immunization and vaccines related implementation research advisory committee (IVIR-AC), and the WHO Strategic Advisory Group of Experts (SAGE) on Immunisation. Methods development continues for epidemiological modelling too, not least because of the wealth of modelling that occurred during the COVID-19 pandemic. This included the development of guidelines for model reporting and vaccine model interpretation.

POSTERSESSION**Methodological research & transmission dynamics.
Data acquisition & parameter estimation****Normative Sleep Trajectories from Wearables to Quantify Acute and Long COVID Deviations**

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Normative modelling offers a statistical framework to map biological measures onto behaviourally and clinically relevant variables (e.g., age, sex, diagnosis) and to quantify individual-level deviations relative to a reference population. This approach has proven valuable in neuroimaging and psychiatry because it accommodates heterogeneous data and supports personalised inference beyond group averages. Here, we propose to build normative reference models for wearable-derived sleep features in the Datenspende cohort, focusing on commonly used features such as sleep duration, timing, and regularity. Using these models as a healthy baseline, we will quantify the magnitude and time course of deviations in individuals with acute COVID-19 and Long COVID. This enables a longitudinal characterisation of sleep disruption that captures both temporal dynamics and inter-individual heterogeneity. From a modelling perspective, representing individual sleep trajectories as deviations from a normative reference enables a quantitative, time-resolved description of post-infectious dynamics, rather than relying on static group-level comparisons. This framework naturally accommodates heterogeneous longitudinal data and allows us to study recovery patterns, persistence, and variability across individuals following SARS-CoV-2 infection. Because deviation scores are defined relative to a shared population-level model, they are transferable across cohorts with comparable data structures, facilitating reproducible comparisons and model reuse. We will evaluate whether these deviation-based representations improve the detectability and characterisation of Long COVID-related alterations in sleep compared with standard feature-based approaches, thereby contributing to methodological research and data-driven modelling of post-viral disease dynamics.

The SARS-CoV-2 pandemic in German federal states: A long-term compartmental analysis using non-linear mixed-effects modeling

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Background and Methods: In Germany, COVID-19 showed substantial regional heterogeneity, driven by changing population immunity and successive SARS-CoV-2 variants. We developed a compartmental transmission model and fit the model to national/state time series of infections, hospitalizations, intensive care unit (ICU) utilization, mechanical ventilation, and fatalities from January 2020 to February 2023 using non-linear mixed-effects (NLME) modeling. Time-varying covariates captured vaccination and booster coverage, variant-specific transmissibility and severity, testing dynamics, and demographics of infections, while changepoints accounted for shifts due to non-pharmaceutical interventions and waning vaccine protection. Variant replacement was modeled using logistic growth functions.

Results: Compared with the ancestral virus, Alpha and Delta variants exhibited higher clinical severity (relative hospitalization rates: Alpha=1.00; Delta=1.19; relative ICU admission rates: Alpha=1.50; Delta=1.59), with relative fatality rates declining modestly over time (0.86 for both

variants). In contrast, Omicron lineages exhibited substantially reduced severity (relative hospitalization rates: BA.1=0.48, BA.2=0.38, BA.4/5=0.47; relative ICU admission rates=0.21–0.75; relative fatality rates <0.20 compared with wild type). Vaccination lowered the risk of severe disease throughout the study period (relative hospitalization risk=0.13 for wild-type, Alpha, and Delta infections), although protection against infection and hospitalization waned during the Delta-dominated phase (relative hospitalization risk increased to 0.33 among vaccinated individuals) and was partially diminished for Omicron infections (relative hospitalization risk=0.53). Model-based simulations indicated that vaccination and variant-specific changes in intrinsic severity jointly drove the observed decoupling of infection incidence from healthcare burden in later pandemic waves.

Conclusion: NLME-based transmission modelling enabled joint estimation of national vaccination and variant-specific effects and state-level random effects, capturing regional differences in transmission and clinical severity. Thereby, the analysis disentangled how viral evolution and population immunity fundamentally altered the epidemiology of COVID-19 in Germany, emphasizing the critical role of vaccination in mitigating severe disease and the importance of accounting for variant-specific dynamics in long-term epidemic modeling.

Respiratory pathogen dynamics in the LoewenKIDS birth cohort: baseline patterns and pandemic disruption

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Background: The COVID-19 pandemic created an unprecedented natural experiment: what happens to the respiratory pathogen ecosystem when non-pharmaceutical interventions suppress transmission? We used a unique longitudinal pediatric cohort spanning the years 2015–2024 to characterize baseline seasonal patterns, age effects, and co-detection of bacterial and viral pathogens in children, and assessed their disruption and recovery across pandemic phases.

Methods: We analysed 5,285 nasal swabs from 441 children of the LoewenKIDS birth cohort collected during asymptomatic phases (asymptomatic samples, AS) and ARI episodes (symptomatic samples, SS) across pre-pandemic (2015–2019), pandemic (2020–2021), and post-pandemic (2022–2024) periods. Multiplex PCR (Seegene) detected 17 respiratory viruses and 7 bacterial pathogens. Hierarchical clustering was used to group viral pathogens by seasonal patterns, and generalized estimating equations to examine age, seasonal, and pandemic phase effects.

Results: Pre-pandemic, *S. pneumoniae* (SP) and *H. influenzae* (HI) were the predominant bacteria, detected in SS and AS (SP: 60.2% and 45.4%; HI: 52.5% and 34.4%). Other bacterial pathogens were rare. Unlike bacteria, viral detection showed clear sample-type-specific patterns. Human rhinovirus was with 62.2% detection in SS and 18.4% in AS the most common pathogen overall. AdV and HBoV were detected at comparable prevalences in both sample types (SS/AS: 8.7%/6.2% and 8.8%/7.8%), while RSV and MPV were only found during ARI with a prevalence of 7.7% and 5.1%, respectively. Hierarchical clustering identified distinct seasonal patterns for viral pathogens. Age was positively associated with bacterial detection in both sample types. Co-detection of up to four pathogens was common pre-pandemic. During the pandemic, pathogen detection declined substantially in both AS and SS and seasonal patterns were disrupted. Co-detection rates

decreased, especially in AS. Post-pandemic recovery was pathogen-specific with heterogeneous re-establishment of seasonal patterns.

Conclusion: Pre-pandemic respiratory pathogen dynamics in children are structured by age, seasonality, and clinical presentation in pathogen-specific ways. Pandemic interventions differentially disrupted symptomatic versus asymptomatic pathogen circulation, with heterogeneous post-pandemic recovery patterns across pathogens. These comprehensive data are essential for interpreting future surveillance signals and informing pandemic preparedness strategies.

A wearable-derived framework for early detection of infectious disease activity

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Timely situational awareness during infectious disease outbreaks remains a central challenge for public health, particularly when traditional surveillance systems are affected by reporting delays, changes in testing practices, or limited clinical coverage. Wearable devices provide continuous, objective physiological measurements at population scale and offer a complementary data source for earlier detection of abnormal health trends. We present a wearable-based syndromic surveillance framework that identifies population-level deviations in fever-related physiology using unlabeled data from consumer wearable devices. The approach combines individual-level deviations in resting heart rate and physical activity relative to personalized baselines and aggregates these signals across space and time to produce a daily detection rate suitable for ongoing monitoring. The system was developed and deployed in real time during the COVID-19 pandemic in Germany, where it operated as a real-time surveillance signal monitored in parallel with established public health indicators. We evaluate the framework using both retrospective and real-time analyses to assess temporal alignment, lead-lag relationships, and early warning characteristics relative to independent epidemiological data, including reported incidence, symptom onset, and indicators of healthcare burden. Real-time analyses explicitly account for reporting delays and data revisions to reflect operational surveillance conditions. Early deployment during the pandemic demonstrated consistent alignment with epidemic dynamics during major epidemic waves. Although developed in the context of COVID-19, the framework is intentionally pathogen-agnostic and applicable to infectious diseases for which fever is a core symptom. This work illustrates how wearable-derived signals can complement existing surveillance infrastructures and support scalable early warning approaches for public health decision-making.

Can a single definition serve well for SARS-CoV-2 infections: insights from the SHIP-COVID cohort

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Introduction: Epidemiological studies investigating SARS-CoV-2 infections relied on seroprevalence, RT-PCR or rapid antigen tests, or a combination of these to identify infections with

SARS-CoV-2. Although often interpreted equivalently, these detection methods can affect results because they differ in their sensitivities, specificities and predictive values. Therefore, we identified a need for a comprehensive definition of SARS-CoV-2 infections, especially for epidemiological studies.

Methods: Analyses were conducted using SHIP-COVID data. Participants (n=733) received monthly/four-monthly follow-ups, including a short questionnaire and a dried blood spot test to be carried out at home. The study was conducted between October 2020 and October 2022. We compared the following infection definitions: any self-reported positive test results (D1), seroprevalence assessed via anti-nucleocapsid antibodies > 1.1 (D2), a combination of D1 and D2 (D3), and lastly D3 + a fourfold increase in anti-nucleocapsid antibodies compared to the previous measurement (D4).

Results: The number of detected infections varied between 277 (D2) and 443 (D4). The cumulative incidence ranged from 34.7% (D2) to 53.1% (D4). Reinfection rates were the lowest for D1 (2.3%) and the highest for D4 (7.4%). When stratified by sex, females had higher infection rates than males across all definitions. Until July 2021, D1 identified fewer infections compared to D2. Around the spike of infections in March 2022, D1 identified more infections compared to D2. The share of infections after which symptoms were reported was highest for D1 (73%) and lowest for D4 (56%). The share of reported symptoms that could not be linked to an infection was the highest for D2 (67%) and the lowest for D4 (50%).

Outlook: Varying the criteria for identifying a SARS-CoV-2 infection led to differences in population-level measures. The direction in which the definitions influenced the number of infections varied over time. A single criterion for the infection seems to fall short of consistently identifying individuals who were infected with SARS-CoV-2.

Using a Hidden Markov Model to characterise acute respiratory tract infections in preschool children: a symptom diary-based analysis

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Background: Incidence of acute respiratory tract infections (ARIs) are challenging to estimate as many infections do not require medical treatment and do not lead to specific diagnoses. Several definitions have been proposed to delimit ARI episodes from longitudinal data, often without further differentiation. In this study, we applied a hidden Markov model (HMM) to classify days based on symptom sequences.

Method: Data were obtained from symptom diaries collected in the German LoewenKIDS study (2014-2024). From birth to six years of age, parents reported a panel of infection-related symptoms (respiratory, gastrointestinal, and non-specific) and behavioural changes. Symptoms were dichotomized (presence/absence) and used as response variables in HMMs. Three model structures with varying numbers of states (St) were evaluated (M1: 2-4 states; M2/M3: 3-4 states). Model selection was based on the Bayesian Information Criterion (BIC), and the Viterbi algorithm was used for final state assignment. Episodes were defined according to the reference ARI definition used in the LoewenKIDS study.

Results: 259 children were included in the analyses representing a total of 9,796 ARI-episodes. A four-state model restricted to seven symptoms (M3) was selected, identifying one asymptomatic state (St4) and three symptomatic states, accounting for 80.6% and 19.4% of observed days, respectively. Two respiratory states were identified: a rhinitis-like state (St1; mean duration (MD)

4.5 days, SD 6.3 days) and a respiratory-specific state (St2; MD 7.9 days, SD 7.9 days), occurring in 64.0% and 55.7% of episodes, respectively. A third, non-respiratory state (St3; MD 3.0 days, SD 3.2 days) occurred in 25.4% of episodes. Overall, 5,376 episodes (54.9%) involved a single state, most frequently St1 (45.5%), followed by St2 (30.9%) and St3 (20.8%). Respiratory states (St1/2) characterized episode onset in 80.7% and resolution in 85.3% of multi-state episodes. Seasonally, St1 remained stable, whereas St2 decreased and St3 increased during spring/summer. St3 also occurred at an earlier age than St1/2.

Conclusion: By distinguishing multiple symptomatic states, the model provided insights into the heterogeneity and temporal dynamics of ARI episodes across childhood. The high proportion of single-state episodes raises questions regarding the clinical relevance and potential misclassification of some ARI episodes.

Evaluating contact tracing performance during the SARS-CoV-2 pandemic using retrospective surveillance data from German local health authorities (March 2020 – March 2022)

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Background: During the SARS-CoV-2 pandemic, a reliable system-level indicator for assessing contact tracing capacity and operational performance was lacking. Within the INFRALINK network, we developed a novel indicator of effective contact tracing coverage and evaluated it using surveillance data from eight local public health authorities, comprising 527,776 index cases and 337,694 contacts of the index cases.

We aimed to assess regional heterogeneity in routine contact tracing data quality and to describe contact tracing performance across different epidemic periods.

Methods: We analyzed routinely collected case–contact surveillance data from eight German municipalities from March 2020 to March 2022. Weekly estimates of the effective reproduction number (R_t) were derived from reported case incidence within the same surveillance datasets. Contact tracing coverage was quantified using a Contact Tracing Coverage Index (CTCI), defined as secondary cases per index case (SCI) divided by R_t . To better reflect operational effectiveness and system timeliness, we conducted a sensitivity analysis using a timing-adjusted index (CTCI*), calculated by weighting CTCI with a feasibility function based on the delay from symptom onset date of index case to the start of quarantine among contacts, relative to the generation interval. Results were summarized by county and across six predefined epidemic periods reflecting major pandemic waves and dominant variants.

Results: Across 793 county-weeks, data completeness varied substantially between regions. SCI was available for all weeks, while R_t was available for 88.5% (range 75–98.2%). Timing information required for CTCI* was available for 49.7% of weeks (range 25–79.6%), resulting in CTCI* being defined for 46.3% of weeks. Using CTCI, contact tracing performance varied markedly across regions and epidemic periods, with higher performance in Summer 2020 and pronounced declines during Delta and Omicron periods. Incorporating timeliness reduced estimated effective coverage:

on weeks where both indices were defined, CTCl* yielded more conservative estimates of effective coverage (on average 11% lower than CTCl).

Conclusions: We present a novel indicator that integrates coverage and timeliness into a unified measure of contact tracing performance. This measure enables system-level comparison across regions and epidemic periods and may inform future epidemic preparedness and resource allocation for contact tracing system.

Multi-State modelling for Point Prevalence Surveys of hospital-acquired infections

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Point prevalence surveys (PPS) are widely used to monitor hospital-acquired infections (HAIs) due to their feasibility and low cost, yet their analysis is methodologically challenging. Extended PPS protocols, such as those implemented by the Centers for Disease Control and Prevention (CDC), introduce multiple sources of bias that can severely distort estimates of infection risk and patient trajectories. In particular, the time-dependent nature of HAI acquisition, the presence of competing events, length-sampling inherent to PPS designs, and interval-censored infection times violate key assumptions of standard regression and survival methods. We propose an integrated statistical framework that explicitly addresses these four sources of bias. The time-dependent acquisition of HAIs is handled using a time-to-event formulation within a multi-state model, while discharge alive and death are incorporated as competing transitions. Length-sampling bias induced by PPS designs is corrected through inverse probability weighting based on the inverse length of stay. Under the CDC protocol, interval-censored infection times are accommodated by treating observations as panel data and fitting a parametric multi-state model with constant transition hazards. This method was developed making use of the `msm` package in R. Method performance was evaluated using a high-quality ICU cohort as an unbiased reference and through extensive simulations mimicking standard PPS and CDC-style protocols. Across 100 simulations, inverse probability weighting substantially reduced bias in cumulative hazard functions and covariate-specific hazard ratios. In CDC-style simulations, the proposed panel-data multi-state approach yielded trajectory and hazard estimates consistently closer to the full cohort reference than unweighted analyses. This work provides a unified methodological solution for analyzing extended PPS data while accounting for their complex bias structure. By enabling bias-corrected estimation of infection risks and patient trajectories, the proposed framework strengthens the analytical validity of prevalence-based surveillance and supports more reliable inference for hospital infection control.

Modeling Age-Dependent Vulnerability of the Blood–Brain Barrier to SARS-CoV-2 Spike Protein Using iPSC-Derived Endothelial Cells

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Über 40 % der COVID-19-Patienten zeigen neurologische Symptome. Eine mögliche Ursache ist eine durch das Virus induzierte Schädigung der Blut-Hirn-Schranke (BHS), wobei das Spike-Protein die Funktion der Brain Capillary Endothelial Cells (BCECs) beeinträchtigen könnte. Der

Alterungsprozess erhöht das Risiko einer BHS-Dysfunktion zusätzlich, wobei das Ubiquitin-Proteasom-System (UPS) eine zentrale Rolle für Proteinhomeostase und Immunregulation spielt. Ziel dieser Arbeit ist es, die UPS-Funktion in BCECs im Kontext von Alterung und COVID-19 zu untersuchen. Ein in-vitro-Modell der BHS mit iPSC-abgeleiteten BCECs dreier Altersphänotypen wurde etabliert. Es erfolgte eine Behandlung mit Delta-Spike-Protein in klinisch relevanten Konzentrationen. Die Auswirkungen wurden mittels Barriereintegritätstests, Zellviabilitätsanalysen und RNA-Sequenzierung bewertet. Letztere identifizierte UPS-assoziierte Genexpressions-veränderungen, die durch weitere Analysen validiert wurden. Die Exposition gegenüber dem Spike-Protein beeinträchtigte die Barriereintegrität nicht signifikant, führte jedoch zu einer zellulären Dysfunktion und Energieimbalance. Die RNA-Sequenzierung zeigte eine überschießende Immunantwort, endotheliale Dysfunktion, gestörte UPS-abhängige Abbauprozesse sowie eine beeinträchtigte Zellregeneration. Das Spike-Protein beeinflusst das UPS zweifach: Es aktiviert antivirale Abwehrmechanismen, nutzt es aber zugleich zur eigenen Replikation und zur Immunflucht. Die Ergebnisse belegen, dass das isolierte Spike-Protein erhebliche metabolische Dysregulationen verursacht und zur BHS-Schädigung beiträgt. Dies deutet darauf hin, dass das Spike-Protein neuroinflammatorische Prozesse fördert, die mit neurologischen Symptomen bei akuter COVID-19-Erkrankung sowie Long-COVID in Verbindung stehen.

Improved Prediction of COVID-19 Dynamics in South Korea via Ensemble Learning

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Accurate modeling played a crucial role in understanding and managing the COVID-19 pandemic, particularly for forecasting case counts and mortality to inform public health policies. However, no single modeling approach was sufficient to provide consistently reliable predictions, as each method possesses inherent strengths and limitations. To address this issue, we propose ensemble learning strategies that integrate multiple models to enhance predictive performance and mitigate individual model weaknesses. In this study, we applied stacking, simple averaging, and weighted average ensemble (WAE) methods to combine predictions from seven individual models, including mathematical, statistical, and machine learning approaches, using Korean COVID-19 data. Model performance was evaluated using both training and testing errors, and optimal covariate sets for individual models were selected based on minimal training error. Four evaluation metrics - MSE, RMSE, MAPE, and WMAPE—were employed to assess predictive accuracy. The combination of booster vaccination rates and the prevalence of the Omicron BA.5 variant was most frequently selected as key covariates. No single model consistently outperformed others across all outcomes, including daily confirmed cases, deaths, and ICU admissions. For raw data, GAM showed the best performance for daily cases (WMAPE: 0.244), time series Poisson for deaths (0.172), and both ARIMA and time series Poisson for ICU patients (0.022). For smoothed data, time series Poisson performed best for daily cases (0.065), while ARIMA was optimal for deaths (0.058) and ICU patients (0.013). Ensemble approaches demonstrated superior overall performance. In particular, stacking with SVM achieved the best results for raw data across all outcomes (0.228, 0.11, and 0.02 for cases, deaths, and ICU patients, respectively). For smoothed data, average ensemble and WAE showed the best performance for daily cases (0.058) and ICU patients (0.011), respectively. Additional performance comparisons based on MSE, RMSE, and MAPE further supported these findings. Among the 12 best-performing scenarios, 10 were achieved by ensemble models. Notably, when a single model ranked first, an ensemble model often ranked second, highlighting their robustness. These results demonstrate that ensemble methods effectively compensate for

the limitations of individual models and provide more reliable predictions. Even when individual models exhibit high prediction errors, ensemble strategies - particularly weighted averaging and stacking - can substantially reduce their impact.

Making sense of the negative binomial renewal equation

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Estimation of the reproduction number is often done using renewal equation models. The widely used EpiEstim package by Cori et al popularized the use of a poisson renewal equation model. However, this implicitly assumes equidispersion, which is often not fulfilled in real life dynamics, where factors like superspreading, clusters and underreporting lead to overdispersion. To account for possible overdispersion, the model is often extended to a negative binomial model. This is often done in a pragmatic way, which leads to a lack of interpretability of the overdispersion parameter. We present several distinct mechanisms that lead to a negative binomial model and the resulting interpretation of the overdispersion parameter. If we assume several different factors to be present at a time, this has an impact on the identifiability of the magnitude of the different factors and therefore on the interpretability, where we can only identify a curve the two parameters will fall on rather than the impact of the individual factors.

Modeling the Epidemiology of the Varicella-Zoster Virus Using Partial Differential Equations

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Introduction. Varicella zoster virus (VZV) causes chickenpox in childhood and can later reactivate as herpes zoster (HZ) (shingles) in adulthood. Since the introduction of childhood VZV vaccination, incidence has declined in many countries, including Germany, while in countries without routine vaccination, most children are still infected. Moreover, several studies have reported an increase in HZ cases. Reduced opportunities for natural immune boosting in adults through repeated exposure to infectious children have been discussed as a potential contributing factor. In addition, HZ vaccination has been introduced for older age groups. As HZ predominantly occurs at older ages, an explicit consideration of age and aging processes is crucial for understanding long-term disease dynamics and vaccination effects.

Methods. Most existing models for VZV dynamics are based on compartmental ordinary differential equations (ODEs) with discrete age classes. In this work, we adopt a complementary modeling approach by formulating an age-structured system of partial differential equations (PDEs) that allows age and aging to be represented continuously. The model is an age-dependent SIR-type framework with ten compartments, capturing primary infection, immunity dynamics, and reactivation processes, with dependence on both time and age. This continuous formulation enables vaccination, immunity waning, and reactivation to be represented at specific ages, while remaining closely connected to established compartmental modeling approaches. The model is analyzed mathematically and implemented numerically to explore age-dependent infection and vaccination dynamics.

Results and conclusion. Based on the numerical implementation, the model is used to study vaccination strategies in an age-structured setting. In particular we analyze how childhood VZV vaccination shapes long-term immunity profiles and how age-specific HZ vaccination affects reactivation dynamics at older ages. The results illustrate how continuous age-structured PDE models can be used to analyze long-term epidemic dynamics and to support optimization-based investigations of age-specific HZ vaccination, with the goal of identifying effective vaccination ages. More generally, our work highlights how PDE-based approaches complement classical compartmental models by providing a flexible framework for understanding age-dependent mechanisms in infectious disease epidemiology.

POSTERSESSION
Modelling of interventions & decision-making. Environmental & climate impact on infectious diseases

Exploratory Combined Health-Economic and Epidemiologic Disease Modeling for Pandemic Preparedness in the Case of Nipah Virus Infections

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Background: Pandemic preparedness is essential for efficient responses to emerging infectious diseases. These situations require rapid decision-making with precise resource allocation to not overbear healthcare systems with limited resources. Preparedness efforts often only consider epidemiological models like the SEIR framework simulating how populations move between health states, but do not cover health-economic implications. Integrating SEIR into health economic (HE) disease modelling could provide a helpful tool supporting decision-making bodies.

Objective: Conducting feasibility analyses on the integration of the SEIR approach and its typical disease states into a health economic disease model to investigate the validity of comparing different interventions and their cost-effectiveness. **Methods:** A six state Markov-Monte-Carlo simulation model was developed using data from a structured 2025 literature review on Nipah virus infections. Ribavirin was chosen for comparison against standard care. The model was developed using TreeAge Healthcare Pro 2025 R.1.1. Health economic outcome measures, discounted at 3%, include incremental cost effectiveness ratio (ICER) and net monetary benefit (NMB). The time horizon was set to 120 weeks. Using one-way sensitivity analyses and tornado analyses the model was validated and its robustness against input variability was studied.

Results: The SEIR framework was successfully integrated into a health economic disease model. Quality-adjusted-life-years increased by 2.45 weeks and life expectancy by 2.58 weeks in Ribavirin treatment over the time horizon. Total direct costs increased on average from 1,520.00€ for standard care to 1,598.62€ for Ribavirin treatment. The Net Monetary Benefit on life expectancy resulted to be 2,570,858.53€ in standard care and 2,631,477.96€ in Ribavirin treatment. The Incremental Cost Effectiveness Ratio between the two decision scenarios amounts to only 30.44€ per life year gained. The model robustness against input variability was proven, and highly influential parameters were identified.

Conclusions: The implementation of the SEIR framework in health economic disease modelling proved to be a valid methodological approach for infections with the Nipah virus. A meaningful analysis scenario could be calculated for drug therapy with ribavirin versus standard of care. Due to its flexible structure, the model can be quickly adapted to changing circumstances in the event of a pandemic.

A New Emergence Phenomenon in Influenza Dynamics? Nonlinear Coupling of Two Holiday Contact-Reduction Periods

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Background: Short, policy- or calendar-driven reductions in social contact are typically represented in compartmental models as additive or smoothly varying changes in effective contact rates. Yet near peak transmission, epidemic dynamics may be sensitive to the timing and sequencing of

interventions. Poland provides a natural experiment because winter school holidays are regionally staggered: each voivodeship receives a two-week break allocated to one of three national turns between mid-January and late February, creating systematic inter-regional variation in holiday timing (similar to Germany).

Methods: We implemented a parsimonious SIR model with piecewise time-varying effective contact rates to represent predefined weeks with reduced mixing. We assumed ~30% reduction in potentially infectious contacts during the Christmas/New Year period (school/university closure, partial workplace closure/reduced activity, fewer organized group interactions) and ~20% reduction during winter school holidays (interrupted school-based transmission plus parental leave effects). Reported incidence was linked to modelled infections via a dark-figure adjustment. Surveillance data came from registered cases in a GP sentinel covering ~50% of practices; overall detection was assumed to be ~1/3. Transmissibility was fitted separately by voivodeship to data up to Christmas and evaluated against registered trajectories.

Results: The model reproduced observed influenza dynamics in most regions. However, it systematically overestimated incidence in “short-gap” voivodeships (Mazowieckie, Pomorskie, Świętokrzyskie, Warmińsko-Mazurskie) where the interval between the end of the Christmas non-school period (06 Jan) and the start of winter holidays (17 Jan) was 3 weeks) did not show comparable nonlinearity.

Conclusions: Closely spaced holiday contact reductions may generate threshold-like (critical) behaviour not captured by conventional SIR specifications, especially near peak transmission. We propose follow-up work to distinguish behavioural adaptation - where people change their contact patterns in nontrivial ways during the inter-holiday period - from transmission-mechanistic explanations (e.g., generation-time effects), including *in silico* verification (e.g., in GEMS).

Modeling Intervention Adherence Behavior in Agent-Based Epidemic Models: An Empirically Grounded Approach using GEMS

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Human behavior is a key driver of infectious disease dynamics. But in epidemic models used for decision support, it is often represented only implicitly or in highly simplified ways. By contrast, agent-based models (ABMs) that do explicitly model behavior tend to prioritize theoretical insight into foundational mechanisms over empirical grounding. This limits their applicability for decision support. This poster addresses the question of whether incorporating an explicit, empirically grounded behavioral model improves the predictive performance of an ABM compared to a model without an explicit representation of behavior. Using the COVID-19 epidemic in Germany as an application case, we present an ABM of coupled infection dynamics and intervention adherence behavior implemented in the German Epidemic Microsimulation System (GEMS). GEMS is a geo-referenced ABM framework that simulates a synthetic replica of the German population. Even complex simulations can be run in comparatively short time. This enables the design of models that both integrate empirically grounded behavioral mechanisms and can theoretically be used for rapid decision support during infectious disease outbreaks. Within this framework, adherence to non-pharmaceutical interventions is modeled via a trigger-based behavioral dynamic. The behavioral module utilizes insights from a representative population survey to parameterize behavioral mechanisms. Each agent's adherence probability evolves as a weighted function of attitudes toward the intervention, perceived epidemiological risk, and subjective social norms. The adherence decision is modeled probabilistically using Bernoulli trials. We present the results of a

qualitative comparison of the epidemic trajectories produced by a model with these dynamic behavioral assumptions compared to those produced by a model with static adherence probabilities. We further present results of a sensitivity analysis assessing the robustness of disease and adherence dynamics to variations in behavioral parameters. Together, these analyses aim to shed light on how explicitly modeling empirically informed behavioral dynamics can alter disease spread patterns and improve the realism of agent-based epidemic models.

Modeling the effect of weather on infectious diseases: why causal structure matters

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Transmission models are widely used for quantifying the effects of weather on infectious disease dynamics and subsequently, for projecting the impacts of climate change. For many pathogens, however, both the magnitude of weather effects and the identification of the climatic drivers of transmission remain unresolved. Weather variables are often highly correlated and causally related to each other, yet the structure of their causal relationships is rarely taken into account. Using influenza as a case study, we investigate the consequences of neglecting this causal structure. We simulated incidence data across diverse climates from a transmission model incorporating various weather variables. We then refitted models with intentionally misspecified weather components to these synthetic data. We show that the causal relationships among weather variables can induce systematic bias in the estimated effects of weather and compromise identifiability of the true causal drivers. Our results illustrate the need to integrate explicit causal frameworks into specifying and interpreting transmission models when assessing weather - infectious disease relationships.

A Multi-Scale Individual-Based Environment for Optimizing Infection Control via Reinforcement Learning

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Managing nosocomial transmission of respiratory diseases requires a complex balance between minimizing infection risks and maintaining operational efficiency. We present HospIBM, a high-fidelity individual-based model developed using the MInD-Healthcare framework. The primary purpose of this model is to evaluate the impact of hospital-level interventions and to serve as a robust environment for reinforcement learning (RL) agents to learn multi-objective policies. The model simulates respiratory disease transmission within a hospital at multiple scales. It explicitly represents the interactions of four distinct entities: Patients, Healthcare Workers (HCWs), Visitors, and Fomites across rooms and wards. To capture the heterogeneity of transmission, the model integrates three distinct pathways: direct droplet transmission during close contact, aerosol transmission via airborne pathogen accumulation in indoor spaces, and fomite transmission through surface contamination. Disease progression follows a SEIIR framework driven by time-dependent viral shedding profiles. The simulation operates on discrete time, tracking the movement, schedules, and health states of individuals, as well as the viral load on surfaces and in the air. By integrating detailed contact networks with environmental variables, HospIBM allows for the granular assessment of infection control strategies, including PPE policies, ventilation

management, testing strategies, cleaning schedules and visitor restrictions. Future work will utilize this framework to train RL agents to optimize multi-objective policies under uncertainty, supporting decision-making and cost-effectiveness analysis in hospital epidemiology.

Evaluation of introducing 20-valent pneumococcal conjugate vaccine (PCV20) in all infants for the prevention of pneumococcal diseases in Germany

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Introduction: Pneumococcal disease is a leading cause of morbidity and mortality worldwide. Despite routine infant vaccination recommendations with pneumococcal conjugated vaccines (PCV), the disease burden remains high.

This study aimed to compare the effectiveness and cost-effectiveness of PCV20 infant vaccination in a 3+1 schedule with PCV13 or PCV15 (2+1 schedule).

Methods: A dynamic age-stratified transmission model projected epidemiologic and economic outcomes over 25 years. The model considered competition in colonization between 8 groups of pneumococcal serotypes to simulate indirect and replacement effects. Carriers of pneumococci could develop invasive pneumococcal disease or non-bacteremic pneumococcal pneumonia. Three scenarios were analysed, differing in assumptions on competition between non-PCV13 serotypes. In each scenario, the vaccine effectiveness (VE) of PCV15 and PCV20 against vaccine-type (VT) carriage was reduced by 0%-40% compared to PCV13, since no effectiveness data existed for the higher-valent vaccines.

Results: Overall population: Across all 3 scenarios, PCV20 achieved the largest reductions in pneumococcal-related hospitalisations. Over the 25-year period, and assuming a reduction in VE against VT carriage of 20-40% compared to PCV13 and PCV15, PCV20 prevented around 102,000–449,000 (vs PCV13) or 23,000–323,000 (vs PCV15) hospitalisations. PCV20 was dominant or cost-effective in all scenarios: assuming a reduction in VE against VT carriage of 40% compared to other strategies, the incremental cost-effectiveness ratio (ICER) remained below €5,000 per quality-adjusted life year (QALY) gained vs PCV13 and below €20,000 vs PCV15. <5 years old only: PCV20 was less effective than the other vaccination strategies, when VE against VT carriage was more than 20% reduced compared to PCV13 and more than 10% reduced compared to PCV15. ICERs for PCV20 exceeded €200,000 per QALY gained in all scenarios. PCV15 vs PCV13: In the overall population as well as in <5 years old, PCV15 typically dominated PCV13 when VE against VT carriage was not reduced by more than 10% and vice versa.

Conclusion: Modelling results suggest that PCV20 infant vaccination in a 3+1 schedule is more effective than PCV13 or PCV15 across a wide range of assumptions in the overall population in Germany. Considering effects in <5 years old only, PCV20 is likely not cost-effective and less effective than PCV13 or PCV15 when its VE against VT carriage is substantially reduced.

Impact of COVID-19 vaccination and socioeconomic deprivation on long-COVID in Germany, 2020-2026

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Introduction: The health and economic burden of long COVID and post-COVID-condition - in absolute terms, and as proportion of the overall burden of COVID-19 - may be substantial and long-lasting. Since 2020, the risk of developing long COVID has varied over time and it is influenced by the immunity status and sociodemographic factors. We aimed to estimate the impact of COVID-19 vaccination on the burden of long COVID by socioeconomic deprivation in Germany, which may help in evaluating and shaping future policies to mitigate the public health and socioeconomic burden of COVID-19.

Methods: We analyzed daily aggregates of COVID-19 incidence and vaccine administration data in Germany since 2020 by socioeconomic deprivation and by district (Landkreis). We built a hybrid statistical-transmission model of the association between COVID-19 vaccination and COVID-19 incidence, which was further adjusted for under-ascertainment of cases and combined with estimates of risk of progression to long COVID. Some model input parameters were informed from international contexts. The resulting model was further used to estimate the counterfactual burden of long COVID in the absence of vaccination and of socioeconomic deprivation across districts.

Results: Preliminary results indicate that the current (January 2026) prevalence of long COVID in Germany is an estimated 20-72 per 1000 individuals, representing a reduction of 62%-66% attributable to vaccination and 17% increase attributable to socioeconomic deprivation (in a comparison against a population where everyone's risk of progression from acute to long COVID is the same as those least deprived), across models. Uncertainties remain in the rate of progression to and duration of long COVID, surrounding under-ascertainment of cases, and in the analytical challenge of estimating the time-varying impact of vaccines in a highly immune-heterogeneous population during the pandemic years.

Discussion: Our district-level statistical-transmission model highlights the substantial and persistent burden of long COVID in Germany, the impact of COVID-19 vaccination and socioeconomic factors on the burden, and opportunities to improve assessment and mitigation of the burden through higher vaccine coverage (especially for high-risk groups) and further research.

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Using person trajectories in order to analyze exposure-based health impacts

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Most infectious disease models focus on the pathogen and its transmission characteristics. Our approach, informed by our group's transport planning and decade-long agent-based modeling experience, centers on individual agents, their movement patterns, and behavior. We present a large-scale agent-based epidemiological model implemented in Julia. Its modular structure allows us to track both communicable and non-communicable diseases, specifically heat-related health problems and influenza, unified through a common dose-response framework. This modularity means disease-specific components can be swapped or extended without redesigning the entire system, facilitating future expansion to other health outcomes or combined scenarios. The model

requires three essential inputs: population data containing demographic information and residential details for each simulated individual; facilities data providing geolocated activity locations and their attributes relevant to disease transmission or exposure; and event files capturing agents' mobility behavior with timestamped activities and locations, which together enable the construction of daily activity plans. For non-communicable diseases like heat-related health problems, the focus is on each agent's activity plan: which activities an agent performs and how they traveled to and from said activity. Tracking each agent's activities allows us to monitor the agents' indoor and outdoor exposure to extreme heat throughout the day. For each time step, we determine whether the agent is indoors (with or without air conditioning), outdoors and stationary, outdoors and walking, in a vehicle, or using public transit. We then assume that agents accumulate heat dose during these activities, which feeds into the dose-response model to calculate heat stroke probabilities and similar health outcomes. Health outcomes are not binary; initial results are probability-based, followed by a disease progression model determining hospital admission and long-term consequences. For influenza, which requires human-to-human transmission, our contact model will exploit the event files to overlay agents' activities to determine when and how long agents meet. Each contact with an infected individual triggers an infection model that also employs a dose-response methodology to compute infection probability based on exposure characteristics.

Assessing the Health System Impact of a Potential H5NX Influenza Pandemic in Ontario, Canada: A Microsimulation Model

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Purpose: H5NX avian influenza viruses pose an increasing pandemic threat due to mammalian adaptation. We estimated the impact of a potential H5NX pandemic on Ontario's health system to inform resource allocation.

Methods: We developed an integrated transmission-discrete event simulation (DES) model of influenza spread and healthcare utilization in Ontario's adult population ($n=16,258,260$), capturing individual clinical trajectories following H5NX infection. A Susceptible–Infected–Recovered model estimated daily infections over one year under three hypothetical scenarios defined by combinations of transmissibility (basic reproductive number) and clinical severity (healthcare use): a high-transmission low-severity scenario based on the 2009 H1N1 pandemic (Scenario 1), a high-transmission moderate-severity scenario (Scenario 2), and a low-transmission high-severity scenario (Scenario 3), assuming no public health interventions. The resulting epidemic curves informed a patient-level DES simulating emergency department visits, ward and intensive care unit admissions, mechanical ventilation, and antiviral use. Patients unable to access required resources were assumed to wait until capacity became available; individuals requiring mechanical ventilation when unavailable were assumed to die. Model parameters were informed by published pandemic data. Analyses were conducted in R 4.4 using the simmer package.

Results: In the base case, we projected 466,859 H5NX infections over one year, leading to 1,885 deaths (case fatality rate [CFR]=0.4%). A total of 10,052 individuals presented to EDs and required antiviral medications. Healthcare resource demand did not exceed Ontario's health system capacity. In scenario 2 (466,859 infections, 10,413 H5NX-attributable deaths [CFR=2.2%]), healthcare resource demand exceeded available capacity, leading to an additional 3,117 deaths due to MV shortages (175 available vs. 1,806 required concurrently per day at the pandemic peak).

Scenario 3 was projected to result in 127,024 infections and 5,873 H5NX-attributable deaths (CFR=4.6%), with an additional 1,870 deaths due to MV unavailability (175 available vs. a peak daily requirement of 759).

Conclusion: An unmitigated H5NX pandemic would overwhelm Ontario's acute care capacity under plausible high-severity or high-transmission epidemiologic scenarios, underscoring the importance of early intervention planning. Our findings provide a foundation for evaluating mitigation strategies.

On the design and development of agent-based models: A review of general concepts and applications to epidemic outbreaks

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Agent based modelling is a well-established framework to describe the behavior of a complex system by its smaller or smallest individual units, generally acting according to simplified rules. Agent-based models (ABMs) allow for integrating stochastic and individual events to study emergent behaviors of the system. ABMs find use in across classical natural sciences such as physics, chemistry, and biology as well as in epidemiology and the public sector for safety or transport research. Due to the recent COVID-19 pandemic, ABMs have seen a surge in the field of epidemiology. In this work, we explore different approaches to formulating ABMs used for epidemic outbreaks, discuss similarities and highlight advantages and disadvantages of particular models. We further look at the realization of these models as computer programs, and discuss design and optimality goals one may want to consider when creating ABMs. Eventually, we will show iteration and optimization cycles for a particular model.

Epidemiological and economic evaluation of a decennial tetanus-diphtheria-acellular pertussis (Tdap) booster vaccination strategy for adult immunization in Germany: a dynamic transmission model

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Background: The German Standing Committee on Vaccination (STIKO) currently recommends a single adult pertussis booster vaccination with the tetanus-diphtheria-acellular pertussis (Tdap) vaccine followed by decennial tetanus-diphtheria (Td) boosters. This modeling study assessed the epidemiological and economic impact of replacing the decennial Td booster with a Tdap booster for all adults in Germany.

Methods: A cost-effectiveness model incorporating a dynamic disease transmission model projected annual incidence of symptomatic and asymptomatic pertussis infections under current (Td) and alternative (Tdap) booster strategies. Health outcomes and societal costs were assessed for both strategies over a 100-year time horizon. According to literature, replacing Td with Tdap was assumed to raise adult pertussis booster coverage from 42.0-46.3% to 68.6-75.6%. Based on published literature, an under-reporting correction factor of 141 was applied to outpatient and

non-medically attended cases. Analyses used a societal perspective with costs and outcomes discounted at 3.0% annually.

Results: Replacing Td with Tdap decennial boosters reduced overall pertussis incidence by 46.5%, from 2,085 to 1,115 cases per 100,000 person-years. Over 100 years, symptomatic cases decreased from 109,863,177 to 58,113,505; hospitalized cases from 74,691 to 39,774; and cases with complications from 10,091 to 5,351. The number of doses needing to be administered to prevent one symptomatic case, hospitalization, and complicated case, were 4, 5,702, and 41,996, respectively. From a societal perspective, the decennial Tdap strategy increased cumulative costs by €1,597,052,752 and quality-adjusted life years (QALYs) by 200,691 over 100 years. The incremental cost-effectiveness ratio was €7,958 per QALY gained. The results were robust and cost-effective across sensitivity and scenario analyses.

Conclusions: Under the model assumptions, substituting the decennial Td boosters with Tdap for adults in Germany is projected to substantially reduce pertussis burden in both outpatient and inpatient settings and to be a cost-effective intervention. Funding: GSK (GSK study identifier: VEO-000471).

Vector-Borne Disease Modelling in Germany: Preparing for Contemporary and Future Risk

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Climate change has led to steadily increasing transmission risk of vector-borne diseases in Europe over recent decades, including West Nile virus (WNV), tick-borne encephalitis virus, and dengue virus (DENV), with projections indicating further spread and rising disease burden. The Vector-Borne Disease Modelling in Germany (VBD-MODE) consortium aims to enhance modeling and prediction of vector-borne disease emergence and outbreak patterns in Germany, and to estimate current and future disease risk and burden across multiple climate- and environment-sensitive pathogens. VBD-MODE will generate predictions for the historical period, the near-, and the long-term future using multi-model ensemble and scenario-based approaches. The results will be used to inform prevention and preparedness needs, and provide recommendations for cost-effective vaccination and surveillance strategies, and thereby strengthen public health and healthcare resilience in Germany. Specifically, VBD-MODE will; (i) Develop and deploy state-of-the-art de-novo models in eco-epidemiology to investigate and validate short-term forecasts of climate-sensitive emerging disease threats, such as West Nile fever, tick-borne diseases, and Aedes-borne diseases, including dengue, over time and space in Germany; (ii) Assess the scenario-based epidemiological threats posed by these diseases under near-current and future climate and land use changes across Germany. (iii) Coupled to these scenarios VBD-MODE will develop intervention models to allow exploring the health and economic impact of different (non-)pharmaceutical interventions and surveillance strategies.

Hand Hygiene as a Dual-Benefit Intervention in Ghana: Modeling COVID-19 and GI Infection Transmission Changes

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Hand hygiene (HH) was strongly promoted in Ghana at the start of the COVID-19 pandemic. It is also a well-established intervention against gastrointestinal (GI) infections, but it usually has a smaller effect on respiratory disease transmission. This study estimates the effect of intensified HH on transmission dynamics of COVID-19 and generalized GI infections in Ghana during the first pandemic phase. We combined routine surveillance with scenario modeling using the German Epidemic Microsimulation System (GEMS) and simplified compartment models (SIR for COVID-19 with detection, SIS for GI). GEMS is a simulation package originally developed for Germany; for this study it was adapted to Ghana by constructing a Ghana population structure based on census-derived demographics and calibrating key parameters to match reported COVID-19 positive cases. Diarrhea hospitalizations were taken from DHIMS2 (monthly, 2015-Sep 2020) to estimate expected seasonal baselines and measure deviations during the intervention period. COVID-19 registered cases (SORMAS) and regional PCR testing data were used for calibration, with uncertainty in under-ascertainment handled through alternative detection/removal rates, implying a “dark figure” from about 3 up to 300 times reported cases. In the Ashanti Region, observed diarrhea cases were 22.3% lower than predicted during April-September 2020; nationwide they were 38.5% lower. Baseline model fits used a 10-day infectious period ($\gamma=0.1$) and estimated transmission/contact rates of $\beta=0.2416$ for COVID-19 and $\beta=0.1315$ for GI infections. Scenario estimates indicate lockdown mainly reduced COVID-19 transmission/contacts (56% for COVID-19 vs 24% for GI), while HH had the opposite pattern, with a modest reduction for COVID-19 (10%) but a substantially larger reduction for GI infections (30%). Overall, the results suggest that intensified HH in Ghana delivered major collateral benefits against GI infections, while its added effect on COVID-19 spread was limited compared with contact reduction during lockdown.

Regional and Seasonal Variability in the Climate-Mediated Associations Between European North Atlantic Circulation Patterns and Mosquito Populations in Germany

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Previous modelling studies of mosquitoes in Europe have primarily focused on local and regional climate drivers, while the influence of large-scale atmospheric circulation patterns (CPs) on mosquito populations remains poorly understood. This study examines how major European - North Atlantic (EUNA) CPs - including the North Atlantic Oscillation (NAO), Arctic Oscillation (AO), East Atlantic (EA), East Atlantic/Western Russia (EAWR), Scandinavian (SCAND), and Summer East Atlantic (SEA) patterns - are associated with variations in mosquito abundance across Germany. Using nationwide mosquito surveillance data (2016-2024), we combined rotated temporal-mode principal component analysis (T-mode PCA) of mean sea level pressure fields with spatiotemporal generalized linear mixed models (GLMMs) to quantify regional- and seasonal-specific relationships among circulation modes, local weather anomalies, and mosquito abundance. Results reveal pronounced regional and seasonal variability in climate-mediated associations between EUNA CPs and mosquito abundance. Circulation-related effects were most consistent and predominantly

positive in the Continental Dry, Northwest Cool, Warmest, and North Coast regions during the main mosquito activity seasons, whereas responses in Alpine and other mountainous regions were weaker or negative due to low temperatures and higher precipitation which constrain mosquito populations regardless of large-scale circulation. Across regions, temperature and humidity anomalies associated with EUNA CPs were associated with increases in mosquito abundance while precipitation and windspeed anomalies exhibited weaker and mostly negative relationships. These findings demonstrate that large-scale atmospheric circulation shapes mosquito population dynamics in central Europe and highlight the value of incorporating teleconnection indices into early-warning and forecasting systems of mosquito-borne diseases in the region.

Keywords: European-North Atlantic teleconnections; ecoclimatic regions; mosquito abundance; climate change; spatiotemporal modelling; mosquito-borne diseases; early-warning systems; Germany.

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