

PANDEMIC INTELLIGENCE CONFERENCE

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ABSTRACT BOOK

Table of Contents

Keynote talks **3**
Non-traditional data for pandemic preparedness: first and last mile challenges 3
Bridging Epidemic Analytics and Public Health Practice 5
What is pandemic preparedness worth? 6
Communicating During a Pandemic Crisis 7
Building a stronger modelling ecosystem for infectious disease preparedness 8
TBD 9
Invited talks **10**
Session 1 11
Session 2 12
Session 3 13
Session 4 14
Session 5 16
Session 6 18
Contributed talks **19**
Session 1 20
Session 2 22
Session 3 24
Session 4 28
Session 5 31
Session 6 33
Session 7 36
Session 8 39
Session 9 41
Session 10 43
Acknowledgements **45**

Keynote talks

Non-traditional data for pandemic preparedness: first and last mile challenges

Speaker: Daniela Paolotti

Organisation: ISI Foundation

Abstract:

The COVID-19 pandemic brought nontraditional data sources, including mobility traces, wastewater surveillance, online contact surveys and participatory surveillance, into the mainstream of epidemic modelling. It also showed that the most critical bottlenecks lie not in the models but at the two ends of the data-to-policy pipeline. In this talk we present the findings of a survey of 29 European epidemic modelling teams and an expert workshop with about 50 participants from academia, industry and public health, recently published in the Journal of Medical Internet Research. In the first mile, the data exist and are needed: 90% of respondents used at least one nontraditional source, yet only 10% could use all the data they required, and about two thirds of datasets had access problems. Access to these data is still ad hoc rather than streamlined. In the last mile, it is still unclear how data and models can best inform decisions. Insights often fall into a data-to-action chasm, and data that go unused give their holders little reason to keep sharing them. We argue that decision-makers and communicators, including journalists, should take part in data collaborations from the outset. We conclude with three recommendations for future public health emergencies: institutionalizing readiness, building data preparedness, and fostering a trusted, collaborative ecosystem grounded in data solidarity.

Bridging Epidemic Analytics and Public Health Practice

Speaker: Fuminari Miura

Organisation: RIVM, National Institute for Public Health and the Environment

Abstract:

Effective pandemic intelligence requires more than the collection and interpretation of epidemiological data. It also depends on our ability to translate emerging evidence into timely, actionable insights that support public health decision-making. Mathematical modelling and analytical tools play an important role in bridging this gap, particularly when information is incomplete, uncertainty is substantial, and decisions must be made rapidly.

In this talk, I will share experiences from developing and applying epidemic modelling tools in both international research collaborations and national public health practice. Drawing on the ESCAPE project, I will discuss efforts to strengthen epidemic forecasting and analytical capacity through the development of flexible, accessible tools that can support preparedness and response across different settings. I will also highlight examples from the Dutch National Institute for Public Health and the Environment (RIVM), where mathematical models and analytical frameworks are used to inform infectious disease surveillance, risk assessment, and public health interventions.

What is pandemic preparedness worth?

Speaker: Katharina Hauck

Organisation: Imperial College London, Abdul Latif Jameel Institute for Disease and Emergency Analytics

Abstract:

Pandemics impose costs far beyond illness and mortality, disrupting economies, education and societies. Economic analysis can help countries make better choices about how much to invest in preparedness, which interventions to deploy, and when to act.

Drawing on research on the wider societal costs of pandemics, the value of vaccine R&D and manufacturing, vaccine stockpiling, and outbreak response, I will argue that pandemic preparedness should be viewed as an investment rather than simply a health expenditure. Investments made before an outbreak can buy speed and flexibility, reducing both health losses and the need for costly emergency responses.

I will also consider why conventional approaches to cost-effectiveness may be insufficient for novel pathogens. With exponential transmission, profound uncertainty and the possibility of catastrophic escalation, the relevant counterfactual is often an outbreak that did not occur precisely because action was taken. Economics can help decision-makers navigate these uncertainties and identify preparedness and response strategies that deliver the greatest value to society.

Communicating During a Pandemic Crisis

Speaker: Bas van den Putte

Organisation: University of Amsterdam

Abstract:

Bas van den Putte provides an overview of research on public communication during the COVID-19 pandemic. Drawing on literature reviews and his own research, he examines how communication affected citizens' adherence to behavioural recommendations as well as their mental well-being.

He will discuss which communication elements were more effective and which were less effective. He will also consider communication aimed at underserved groups, including people with low literacy levels or low trust in government.

Finally, he will address the role of misinformation. He will examine how journalists and information intermediaries, such as community leaders, respond to it.

Building a stronger modelling ecosystem for infectious disease preparedness

Speaker: Eva Bons

Organisation: ECDC

Abstract:

Capacity for modelling infectious disease dynamics varies substantially across Europe, as do the surveillance systems that inform modelling outputs. European-level modelling projects provide opportunities to combine expertise and data to address shared questions, while building connections among modellers and with other public health experts. The European modelling hubs, for example, bring together modellers from across Europe (and the world) to answer key questions in public health. Shared expertise makes for more reliable outputs to inform public health policy, while enabling development of new techniques and methods. Having these communities, collaborations and methods in place before they are urgently needed is an important part of preparedness for future public health threats.

Mobilizing global networks and strengthening systems for decision-ready analytics

Speaker: Dina Raus Saulo

Organisation: WHO Hub for Pandemic and Epidemic Intelligence

Abstract:

When the next pandemic or epidemic emerges, how quickly and effectively we detect and respond to it will depend on relationships, systems, and ways of working built long before the crisis begins.
The WHO Hub for pandemic and epidemic intelligence has set out a new ambitious 2030 strategy to detect and understand a new health threat within 24 hours. Through the lense of the current Bundibugyo outbreak this presentation will demonstrate key initiatives and how global expert networks, collaboration and innovation can contribute towards a rapid public health intelligence response that informs policy and decision making.
By investing in connection, collaboration and agreed ways of working, the global public health intelligence community can move from fragmented efforts to a coordinated network that delivers timely, relevant and actionable insights for decision makers.

Invited talks

Session 1

Preparedness as decision readiness: from decisions to information and data needs

Speakers: Barbara Tornimbene, Wim Van Bortel, Institute of Tropical Medicine

Co-authors: Soledad Colombe, Pierre Hubin

Abstract:
COVID-19 showed that large volumes of data do not automatically lead to timely public health action. Within the Belgian Pandemic Intelligence Network (BE-PIN), we started from the decisions authorities must take during an epidemic and worked back to the information and data needed to support them. Using a respiratory pandemic scenario, we matched 36 operational decisions across surveillance, clinical care, and prevention and control to 215 candidate information needs. A national survey and two stakeholder consultations with participants from 14 institutions prioritised 77 needs, which we organised into a layered collaborative surveillance framework. The framework has 57 core needs, covering situational awareness, system and response readiness, and decision translation and societal context, plus 20 cross-cutting enabling needs on governance, communication and financing. The layers align closely with WHO's all-hazards collaborative surveillance model. A dependency analysis identified eight foundational needs, and 40 of the 57 core needs rely partly or entirely on non-traditional data. To bring back the timing of decisions, we built an evidence-generation matrix based on the WHO PRET framework. It links each epidemic phase, operational stage and response target to information needs, suggested analytical approaches and 144 data needs, and can be navigated through an online tool. The matrix is a starting point rather than a prescription, to be tested in simulation exercises.

Data availability for pandemic intelligence

Speaker: Pierre Hubin, Sciensano

Co-authors: Soledad Colombe, Barbara Tornimbene, Wim Van Bortel

Abstract:
Effective pandemic intelligence depends on timely access to the relevant data. As part of the BE-PIN collaborative surveillance work package, we inventoried datasets relevant for pandemic intelligence. This inventory was built on a retrospective analysis of the data used during the COVID-19 pandemic, as well as on existing routine data collections and registers. In parallel, the work package identified data needs critical to decision making, the inventoried datasets were then mapped to these needs. As a result several types of data gaps were underlined. We notably emphasize the need for an improved data sharing framework in pandemic situation.

Session 2

Evaluation of the modelling and analysis during the COVID-19 pandemic

Speaker: Marie-Cécile Dupas, UHasselt, ULB

Co-authors: Niel Hens, Simon Dellicour

Abstract:
The COVID-19 pandemic required timely quantitative evidence for epidemic monitoring and public health decision-making. Here, we conduct a scoping review of quantitative COVID-19 studies relevant to the Belgian epidemic context. The literature showed strengths in genomic surveillance, social contact analysis, and forecasting, but gaps remained: limited sub-national analyses, weak integration of individual-level datasets, delayed estimation of variant-specific transmission parameters, insufficient characterisation of superspreading, and limited evaluation of digital contact tracing. These findings highlight the need for improved data governance, faster access to linked datasets, and integrated epidemic intelligence systems to support epidemic intelligence systems and evidence-based decision-making during public-health crises.

Session 3

Towards a multi-criteria framework for pandemic management

Speaker: Philippe Beutels, Antwerp University

Co-authors:

Abstract:
COVID-19 was managed against objectives that were seldom stated, with metrics chosen by default, and with evidence that reached decision makers through expert groups created during the crisis. Developing a framework for pandemic management requires knowing how success should be measured, and in what form evidence should reach decision makers.

Our research shows that success is multidimensional and depends on the stage of the pandemic. No single metric suffices. Countries that do well on excess mortality and economic growth may do badly on self-reported wellbeing.

Excess mortality was singled out as a key metric during the COVID-19 pandemic, but how deaths are counted matters. Weighting excess deaths by the quality-adjusted life expectancy lost (DRQALYs) moves the burden towards adults aged 50–74. Belgium, with about 23,300 excess deaths and 181,400 DRQALYs lost over 2020–22, sits in the lower half of 36 European and other high-income jurisdictions. Its deaths were concentrated at very old ages. High vaccination coverage was more strongly associated with lower losses than the stringency of restrictions; the outliers suggest that the type of vaccine used also mattered.

QALYs are a core measure of health loss used routinely in health policy, but they are not a welfare measure or a sufficient decision rule. Cost per QALY gained suits decisions confined to the health sector. It does not suit situations of widespread behavioural change, or measures such as lockdowns and school closures, whose costs fall on the wider economy, education and public finances.

For economic assessments, Belgium did not lack data but the capacity to link and release them fast.Therefore, support instruments should be legislated before the next crisis. The next crisis, however, may very well start with less fiscal room.

The proposed framework rests on layered decision support: the same scenarios assessed in parallel for health, wellbeing, the economy and the social fabric. These are brought together in an explicit synthesis that leaves the weighting to decision makers. Pre-built, validated integrated models add value where feedbacks matter. The framework has four evidence layers and three cross-cutting mechanisms: behaviour, trust and equity. Priorities change by stage. The shift to cost-per-QALY evaluation comes once a technological fix like a vaccine or the natural evolution of the pathogen allows restrictions to be lifted and risk perceptions no longer perturb the economy as a whole. International cooperation is a cross-cutting domain, assessed by how commitments hold under scarcity.

Session 4

Exploring Belgian citizens' perspectives and expectations regarding public communication during health crises

Speaker: Annelies Mondelaers

Co-authors: Marlies Saelaert, Caroline Van Swieten, Erika Vlieghe

Abstract:
This study aimed to explore Belgian citizens' perspectives and expectations regarding public communication during health crises. A concept mapping exercise was conducted of the scientific and grey literature, using the PubMed and Web of Science databases alongside relevant reports and project documentation. Key themes and evidence gaps were identified and used to inform the next phase of the study.

Next, a qualitative study was conducted using focus group discussions with Belgian citizens to explore the principles, values, and communication approaches that should guide public communication during health crises. The themes identified during the concept mapping exercise formed the basis of the semi-structured interview guide. By actively involving citizens as key stakeholders, the study aimed to co-create recommendations for more effective, trustworthy, and citizen-centred communication strategies for future health crises. This presentation will highlight the main findings and propose recommendations for future public health communication during health crises.

Capacity building and training needs

Speaker: Caroline Van Swieten, I3h institute

Co-authors: Mathias Dewatripont, Hilde Stevens

Abstract:
This work identifies training needs and proposes capacity-building modules to strengthen pandemic communication and preparedness among young people in Belgium. Addressing a gap identified in the project's training mapping analysis, it recommends integrating structured, age-appropriate and interdisciplinary learning into education, beginning in primary school. Drawing on the COVID-19 experience, the report emphasises the importance of recognising young people as active partners in preparedness efforts. Training should combine basic knowledge of infectious diseases and public-health measures with critical thinking, communication, digital and psychosocial skills, enabling learners to assess information, understand scientific uncertainty and contribute to collective protection. Six modules are proposed: health and scientific literacy; science communication and uncertainty; misinformation and social media; mental health; practical preparedness; and a One Health approach. Together, these modules aim to connect the scientific, social and ethical dimensions of pandemic preparedness while supporting young people's informed and meaningful participation.

The role of knowledge brokering in the production of scientific advice

Speakers: Ingrid van Marion, David Domingo, ULB

Abstract:
The first stage for the production of evidence-informed policymaking during the management of a health crisis is the transformation of scientific knowledge and data into concrete scientific advice. This presentation summarizes the challenges identified by a diversity of stakeholders involved in the management of the COVID-19 pandemic (public servants, cabinet advisors, scientists in and outside of advisory boards, communication professionals and journalists) during semi-structured interviews, complemented with the analysis of over a hundred advisory reports. The presentation explores how knowledge brokering activities can help overcome three key challenges of science communication during health crises: dealing with information overload, communicating uncertainty, and integrating knowledge from a diversity of disciplines.

Session 5

UNITY: A Framework for Integrated Scientific Advice for Pandemics in the Netherlands

Speaker: Charlotte Waltz, Erasmus University Rotterdam / Pandemic & Disaster Preparedness Center

Co-authors: Tomris Cesuroglu, Jeannette de Boer, Bart Blokland, Femke Overbosch, Emily Scott, Alois Kessener, the UNITY Consortium

Abstract:
Pandemics generate policy challenges that extend beyond biomedical concerns, requiring governments to consider health, social, economic, ethical, and behavioural dimensions simultaneously. During COVID-19, scientific advice in the Netherlands was provided separately by domain-specific advisory bodies. As a result, integrating knowledge across disciplines proved challenging, leading to advice that was fragmented, difficult to compare, and insufficiently attentive to cross-domain effects. Since 2022, research efforts have therefore explored how integrated scientific advice for pandemics can be organised, enabling policymakers to consider both the consequences of infectious disease outbreaks and the impacts of response measures across biomedical, social, behavioural, economic, and ethical domains. The UNITY framework was developed as a practical approach to organising and coordinating such integrated advisory processes. Recognising that different policy questions require different combinations of expertise and varying levels of integration, the framework is built around an iterative and adaptive process that supports context-sensitive advisory pathways. By providing structured guidance for transdisciplinary collaboration, UNITY aims to strengthen the quality, coherence, and usability of scientific advice for pandemic decision-making.

Connecting scientific advice to policy during COVID-19: a seven-country comparative study

Speakers: Tomris Cesuroglu, PDPC - Pandemic and Disaster Preparedness Center

Co-authors: Charlotte Waltz, Inger Abma and Anja Schreijer

Abstract:
COVID-19 exposed a design challenge for pandemic preparedness: how can scientific advice remain responsive to policy needs while preserving clear scientific roles? We compared the organisation and evolution of scientific advisory arrangements in Belgium, France, Germany, Ireland, the Netherlands, Switzerland and the United Kingdom. The study drew on policy documents, scientific literature and 30 semi-structured interviews with advisory committee members, policymakers and researchers. Iterative comparative analysis examined mandates, disciplinary participation, adaptation and science–policy interaction.

The arrangements varied in how they mobilised expertise and connected advice to decision-makers. Across cases, formal committee structures explained only part of this interaction. Chairs, chief medical or scientific advisers and other intermediaries helped translate policy questions and scientific input, while informal exchanges complemented formal reporting routes. Countries also adapted their arrangements

during the pandemic by changing mandates, activating subgroups or creating new bodies. The comparison does not rank national performance. It highlights design questions for future preparedness: which functions belong where, how expertise should interact, and who should synthesise separate inputs into advice. Making these responsibilities and policy interfaces explicit may help future systems combine continuity with adaptation.

The UNITY Tool: Developing a Multidisciplinary Evidence Integration Tool for Pandemic Policy Advice

Speaker: Emily Scott, PDPC

Co-authors: Charlotte Waltz, Alois Kessener, Femke Overbosch, Tomris Cesuroglu, Anja Schreijer, Michel Dückers, Inger Abma and further UNITY consortium members

Abstract:
Pandemic response requires decision-makers to consider evidence from multiple disciplines, including epidemiology, healthcare, economics, and behavioural and social sciences, under severe time constraints and high levels of uncertainty. Yet few tools support a structured assessment of the health, societal, and economic impacts of public health and social measure (PHSM) options under crisis conditions. To address this challenge, within the UNITY project, we developed a prototype tool that depicts these impacts in a single, high-level overview to support balanced decision-making.

The UNITY tool was developed through an iterative design process drawing on existing frameworks and decision-support tools, including the WHO-INTEGRATE and Dutch Societal Impact Team (MIT) frameworks, complemented by evidence from grey literature, expert consultation and testing during three pandemic simulation exercises.

The resulting prototype provides a framework for integrating evidence across domains, by guiding users in identifying relevant evidence, considering uncertainty, and visualising trade-offs between policy objectives and potential consequences of PHSM options.

The UNITY tool represents a novel approach to supporting integrated scientific advice for pandemic preparedness and response. By facilitating structured interdisciplinary discussion and providing a transparent overview of potential impacts across multiple domains, the tool aims to support more balanced and comprehensive assessments of PHSM options, ultimately strengthening evidence-informed decision-making during future pandemics.

Session 6

Strengthening the Belgian advisory system for pandemic preparedness

Speaker: Eveline Cleynen, Miriam Saso, Sciensano

Abstract:
COVID-19 demonstrated that good scientific evidence alone is insufficient to support decision-making. How evidence reaches policymakers, who provides advice and how the advisory system is governed are equally important. Within BE-PIN, literature and document reviews, stakeholder interviews and focus groups examined how Belgium organised scientific advice during the COVID-19 pandemic.

The presentation will highlight key features of the Belgian advisory system, including its ability to mobilise substantial expertise and adapt rapidly to emerging needs during COVID-19. It will also examine the challenges associated with successive advisory bodies, including overlapping responsibilities, complex coordination and reliance on a limited number of experts and informal relationships. Beyond the advisory bodies themselves, the findings underline the importance of supporting capacities, such as timely data access, modelling, evidence synthesis and multidisciplinary expertise.

Contributed talks

Session 1

It doesn't matter which virus you had. Or does it? What participatory surveillance can show about co-circulating respiratory viruses

Speakers: Nadine Barth, Hasselt University

Co-authors: Gesa Carstens, Eva Kozanli, Wanda Han, Lisa Hermans, Daniela Paolotti, Steven Abrams, Geert Molenberghs, Niel Hens, Christel Faes, Dirk Eggink, Albert Jan van Hoek, Andrea Torneri

Abstract:
For most people with a cold, knowing which virus caused it changes little. For public health, it can matter a lot. Every winter, several respiratory viruses circulate together and might influence each other's spread. Knowing how they relate could help decide when and where to look for a pathogen, and anticipate how an intervention against one virus might affect the others. We explored this using data from Infectieradar in the Netherlands, a participatory surveillance platform where participants report symptoms weekly and a subset of those with symptoms is tested for several respiratory viruses. At the population level, we looked at how the circulation of seven viruses relates over different time scales and found several virus pairs showing consistent associations. Anticipating the effect of interventions, however, requires knowing whether viruses truly interact. At individual level, co-infections occurred less often than expected by chance for every virus pair, suggesting that something shapes which infections occur together. Ongoing work examines how the risk of one infection changes after another. Together, these results show that participatory surveillance data can inform surveillance and preparedness beyond counting cases.

From systematic review to expert-informed questionnaire: on conducting diary-based social contact surveys to inform transmission models of close-contact infections

Speaker: Neilshan Loedy, UHasselt

Co-authors: Giulia Lumia, Laura Di Domenico, Joeri Verbiest, Janik Suer, Steven Abrams, Lander Willem, Philippe Beutels, Niel Hens

Abstract:
Diary-based social contact surveys are widely used to parametrize transmission models of close-contact infections. However, substantial variation in study design, contact definitions, and questionnaire content limits comparability across studies. These challenges became particularly evident during the COVID-19 pandemic, when there was an urgent need for rapid and repeated data collection, often without harmonised instruments. We aimed to develop an expert-informed questionnaire and update recommendations for future diary-based social contact studies, building on the previous systematic review by Hoang et al. (2019). To this end, we conducted a systematic review of diary-based social contact surveys published between 31 January 2018 and 25 September 2025. We extracted survey items from available questionnaires identified through the review, and we classified the questions as core, secondary, or optional, based on the results of a structured online expert assessment involving 26 respondents. In total, we found 129 study entries across 62 countries, with most study entries conducted during the COVID-19 pandemic (59.7% in 2021–2022). Retrospective reporting (86.0%) and non-probability sampling (77.5%) predominated and became increasingly common during the pandemic,

while non-paper-based data collection rose sharply from 2021 onwards. Across 36 retrievable questionnaires conducted in the general population, 54 survey items were derived, of which 22 were classified as core, forming the proposed expert-informed questionnaire. We also updated recommendations on sampling, survey method, contact definitions, and essential contact information, and expanded recommendations on data governance. Together, these provide practical guidance for harmonised diary-based social contact data collection and support preparedness for future public health emergencies.

Does Your Data Identify Your Model? A Primer on Identifiability Analysis for Infectious Disease Modelling

Speaker: Roel Bagaforo, UHasselt

Co-authors: Ilaria Misuri, Pieter Libin, Steven Abrams, Niel Hens

Abstract:
Infectious disease models are only as reliable as the data used to fit them, but that data is only useful if it can actually determine the model's parameters. Identifiability analysis evaluates this through two lenses: whether parameters could, in principle, be recovered uniquely from perfect data (structural identifiability), and whether they can be recovered from the data we actually have (practical identifiability). Ignoring non-identifiability increases uncertainty and can lead to conflicting epidemiological interpretations, yet formal identifiability checks are rarely integrated into the current modelling workflow. In this work, we review and contextualise identifiability analysis for infectious disease models, illustrated through a case study related to the early phase of the Belgian COVID-19 pandemic described by means of a discrete-time stochastic compartmental model (Abrams et al., 2021). Furthermore, using a simulation study, we assess which data streams inform which parameters, and which mitigation strategies help when they do not. We found that parameters describing unobserved model processes were poorly identified, and that more data does not always imply more information, as both quantity and quality matter. Building on these findings, we present a primer for integrating identifiability analysis structurally into modelling workflows. We hope that, with this primer, identifiability analysis will become a standard practice to help modellers balance which data to collect, with which resolution, and how complex a model can be responsibly.

Session 2

Whose data are prepared for pandemic research? A global scoping review and web atlas

Speakers: Nicola Low, University of Bern

Co-authors: Diana Buitrago-Garcia, Meret Pfister, Luisa Murcia Soriano, Beatrice Minder, Leonie Heron, Poorya Amini, Eva Maria Hodel

Abstract:
Researchers and decision makers need epidemiological data quickly when a new pandemic pathogen emerges. 'Pandemic preparedness cohort studies', established before an outbreak, should speed up early pandemic research data for emerging infectious disease threats. We conducted a global scoping review to create an atlas of potential pandemic preparedness cohort studies. We searched electronic databases and websites from Jan 2020 to May 2025. We included cohort studies with prospective enrolment of at least 500 participants that aimed to describe the epidemiological characteristics of an emerging pandemic pathogen. We identified 5713 reports and included 743 potentially eligible cohort studies. Of these, 148 have ethical approval to continue data collection; 55 are designed to collect data about infectious diseases, 14 about the consequences of infectious diseases and 79 are designed for non-communicable disease research but have published on infectious diseases, mainly during the COVID-19 pandemic. Our interactive atlas https://globalatlas.shinyapps.io/cohorts_pandemics/ shows cohorts according to geographic location, pathogen, types of data collected, study populations, and inclusion of animals. The atlas has been used to identify cohort studies for ongoing inter-pandemic research. Future updates would ensure that the atlas is an essential resource for the next pandemic.

A standardized data framework for pandemic preparedness in Belgium

Speaker: Wouter Smeets, UHasselt

Co-authors: Hanne Van Dijck, Lode Godderis, Geert Molenberghs, and Johan Verbeeck

Abstract:
Since Fall 2020, and throughout the COVID-19 pandemic, Belgium has linked employment and COVID-19 infection data to produce biweekly reports, enabling real-time monitoring of workplace infection patterns and informing non-pharmaceutical interventions (NPIs). In retrospect, the monitoring process revealed key weaknesses, such as limited access to vaccination data, slow legal approvals, delays caused by complex linkages, and dependency on ad hoc arrangements that are not guaranteed to hold in future crises. Therefore, a retrospective evaluation of biweekly surveillance reports was conducted to develop a standardized multicriteria framework. This framework integrates optimal data flows, prespecified data formats, user-friendly R scripts, and legislative considerations to support faster analyses. It shows that Belgium's broad surveillance architecture, covering hospital admissions, mortality, vaccination uptake, and infections, is a major asset. Sector-level analyses revealed clear patterns, such as lower incidence in highly vaccinated sectors and the impact of school reopening on education-related sectors. Periodic try-outs of the framework are recommended to ensure long-term readiness.

Federated data analysis in healthcare using one-time shared summary statistics

Speaker: Liz Limpoco, UHasselt

Co-authors: Christel Faes, Niel Hens

Abstract:
Data privacy has increasingly become a daunting challenge because it limits data availability, which is essential in deriving insights from healthcare data. Access to personal health data often involves considerable time, effort, and paperwork, which can impede research progress and collaboration especially during a health emergency such as a pandemic. Existing approaches that do not use individual-level data for model estimation are either prone to ecological bias, cannot handle heterogeneity, or require iterative communication. In this paper, we propose an approach to analyze personal health data based on summary statistics shared only once. Our strategy involves generating pseudo-data whose summary statistics match those of the actual but unavailable data. These pseudo-data are then used for model estimation instead of the actual data. The statistical inference we achieve is identical (up to the third decimal place) to those derived from actual data and has a similar bias, coverage, and prediction performance. Communication and resource efficiency distinguish our approach from existing methods.

Session 3

BARN-CM: A Bayesian Framework for Propagating Contact-Matrix Uncertainty into NPI Portfolio Decisions

Speakers: Robyn Irawan, Parahyangan Catholic University

Co-authors: Benny Yong, Farah Kristiani

Abstract:
Public health agencies designing age-targeted non-pharmaceutical interventions (NPIs) typically select a single synthetic contact matrix and proceed, discarding the uncertainty that choice carries. For Indonesia, two credible synthetic matrices, Prem et al. (2017) and the conmat package (Tierney et al., 2026), differ by 43% in dominant eigenvalue, yet neither has been validated against local contact data. We present BARN-CM, a four-layer Bayesian decision-analytic framework that embeds both matrices in a one-parameter mixture, updates the mixture weight against national COVID-19 surveillance data through a Bayesian age-structured SEIR model, and propagates the resulting posterior into a Pareto-classified non-pharmaceutical intervention portfolio recommendation. Applied to Indonesia's first epidemic wave, the posterior mixture weight remains close to uniform (mean 0.48, 95% credible interval [0.02, 0.97]), showing that national aggregate case counts cannot discriminate between the two matrices. A two-sweep Sobol sensitivity analysis shows that, once the reproduction number is calibrated, contact-matrix choice explains 9.1% of final epidemic-size variance, enough to shift portfolios near the elimination threshold between tiers. The framework separates nine portfolios into mitigation and elimination tiers and identifies the minimum-cost strategy within each, giving decision-makers a structured, uncertainty-aware basis for NPI design that is transferable to any country with competing synthetic contact matrices.

Combining mechanistic modeling of disease spread with nowcasting of delayed case counts: a simulation-based perspective

Speaker: Ilaria Misuri, Hasselt University

Co-authors: Steven Abrams, Pieter Libin

Abstract:
Nowcasting is the prediction of past, present, or near-future phenomena and serves as a fundamental tool for real-time epidemiological surveillance. However, surveillance data, such as case or hospitalization counts, are often delayed by biological timelines and administrative lags. Relying on uncorrected data to infer epidemiological parameters can lead to biased estimates, therefore, correcting for delays is crucial to accurately nowcast current counts and ensurevalid inference.

The statistical literature has studied nowcasting in detail, coupling a delay process model with an observational model describing underlying disease spread.

However, these approaches are typically fully statistical, whereas disease transmission inherently follows mechanistic steps driven by individual contacts. Furthermore, statistical models often lack directly

interpretable epidemiological parameters that are fundamental to guide public health policy. In this work, we incorporate mechanistic dynamics into the nowcasting paradigm by jointly estimating parameters for the disease process and the reporting delays. We propose a Bayesian hierarchical joint inferential approach tailored to estimating model parameters from new case incidence. Our simulation-based perspective generates data from a mechanistic model while adjusting delay hazards for covariates like weekday effects. Finally, we evaluate the use of an emulator instead of the true mechanistic model to lower computational complexity.

Predicting contact rates in response to control measures: A validated protocol for generating contact matrices relevant to transmission modelling of respiratory diseases

Speaker: Willem Frederiks, National Institute for Public Health and the Environment

Co-authors: Ka Yin Leung, Jantien Backer, Marijn de Bruin, Jos de Haan, Jacco Wallinga, Don Klinkenberg

Abstract:
Transmission models predict the course of epidemics and inform policy makers. For respiratory diseases, many models incorporate rates of contacts within and between age groups, summarized in contact matrices. Control measures may change contact rates. To forecast transmission, contact matrices should reflect this impact before measures are introduced. We present a protocol to predict future contact matrices using data on time-use, contacts, and demographics, collected before an epidemic.

For each set of control measures, we identified activities on which less time will be spent. The protocol assumes that reductions in time lead to proportional reductions in numbers of contacts made during these activities. School and work time were stratified by educational level and profession based on demographics. We validated the protocol by applying it to COVID-19 measures, comparing predicted to observed matrices.

Predicted matrices agreed with observed matrices. By age, predicted contact rates matched observed rates, especially for contacts involving adults. For child-child contacts, predicted rates were lower than observed rates, with observed school contacts likely overreported. Predicted workplace contact rates matched office occupancy data.

The protocol uses pre-epidemic data, providing consistent and transparent contact matrices for transmission models. It is suited for future epidemics when data are periodically collected.

Assessing the role of travelers in cross-community connectivity of malaria parasites using Exponential Random Graph Models (ERGMs)

Speaker: Mahdi Safarpour, Antwerp University

Co-authors: Andrea Torneri, Jean-Pierre Van geertruyden, Steven Abrams, Christopher Delgado-Ratto

Abstract:
Introduction: Human mobility can introduce malaria parasites into new communities, but travel history alone cannot determine whether traveler-associated infections remain distinct or become integrated into local parasite transmission networks. We used exponential random graph models (ERGMs) to assess whether traveler-associated Plasmodium vivax infections contribute to genetic connectivity between communities in the Peruvian Amazon.

Methods: Genetic data from 56 infections (16 travelers and 40 non-travelers) across three were used for network analysis. Genetic networks were constructed across relatedness thresholds ranging from 5% to 80%. The role of travelers in cross-community connectivity and structural bridging was evaluated using 10,000 within-community permutations. The ERGMs were used to assess whether travel history and community of residence were associated with the probability that infections were genetically connected.

Results: Travelers did not disproportionately connect communities, and no evidence of structural bridging was detected (all adjusted p≥0.39). Fully adjusted ERGMs showed negative coefficients for traveler-associated infections across all relatedness thresholds (β=−0.50 to −0.12), indicating a lower propensity to form genetic links, with significant p-value at 5–40% relatedness, but not at 60–80%. In contrast, pairs of infections from the same community were much more likely to be genetically connected (β=1.47–2.10; OR=4.37–8.14; all p<0.001).

Conclusion: Traveler-associated infections were integrated within the broader parasite genetic network but did not appear to bridge communities disproportionately. Genetic connectivity was driven more strongly by shared community membership than by travel history.

Decomposing Key Drivers of ILI Incidence Dynamics across Europe

Speaker: Pauline Bakker, National Institute for Public Health and the Environment

Co-authors: Jacco Wallinga, Fuminari Miura

Abstract:
Previous studies have identified several drivers of influenza-like illness (ILI) incidence dynamics in temperate regions, yet it remains unclear whether these associations are reproducible across countries or shaped by local context. This study quantifies the relative contributions of climate and behavioral factors to ILI incidence dynamics across multiple European countries, using weekly incidence data from 2014 to 2025 reported to ERVISS, the surveillance database maintained by ECDC. We compute the weekly effective reproduction number () from incidence data and model them as a function of explanatory variables within a regression framework. These variables include absolute humidity, holiday periods, and the Normalcy Index. The framework separates persistent associations from season-specific baseline components and reporting-related variation, and enables comparison between pre- and post-pandemic periods. We find that absolute humidity shows consistent negative associations with weekly across countries, whereas behavioral factors exhibit greater heterogeneity. This framework provides a way to distinguish between generalizable and context-dependent drivers by comparing

cross-regional dynamics, informing interpretation of epidemic trends during both normal and disrupted periods, such as the COVID-19 pandemic.

This work was presented at ECMTB 2026.

Session 4

Population ageing as a dominant structural driver of West Nile virus burden in Europe: a Bayesian spatiotemporal analysis

Speakers: Daniele Da Re, ULB

Co-authors: Camille Morlighem, Diana Erazo, Simon Dellicour

Abstract:
West Nile virus (WNV) risk in Europe is shaped by the convergence of a growing viral hazard, climate-driven changes in vector activity, and increasing population vulnerability. While spring temperature anomalies are known to modulate interannual transmission intensity, the independent contribution of demographic ageing to disease burden remains poorly quantified.
We developed a Bayesian negative binomial incidence model for WNV neuroinvasive disease in Europe (2006–2021), using age-stratified TESSy surveillance data with Eurostat population denominators and ERA5 spring temperature anomalies. The model included spatially structured random effects at country level to account for geographic heterogeneity in surveillance intensity and reporting practices.
Age was a dominant and robust predictor: adults aged ≥70 years had approximately ten times the incidence of those under 40 years, stable across all model specifications. Using counterfactual analysis, we show that population ageing contributed between 12% and 25% of observed WNV burden in individual years — a fraction growing steadily over the study period as European populations aged. Spring temperature variability explained interannual fluctuations but showed no directional trend, and its annual attributable fraction had posterior credible intervals spanning zero in all years.
These findings suggest that demographic ageing is a primary vulnerability driver of rising WNV burden in Europe, with implications for targeted public health preparedness in ageing populations.

MEmilio: A high performance Modular EpideMIcs simuLatIOn software – from modeling infections to post-acute infection syndromes

Speaker: Sascha Korf, University of Bonn

Co-authors: Julia Bicker, Carlotta Gerstein, David Kerkmann, Rene Schmieding, Anna Wendler, Henrik Zunker, ..., Michael Meyer-Hermann, Jan Hasenauer, Martin J. Kühn

Abstract:
Epidemic and pandemic preparedness with rapid outbreak response rely on timely, trustworthy evidence. Mathematical models are crucial for supporting timely and reliable evidence generation for public health decision-making with approaches from compartmental and metapopulation models to detailed agent-based simulations. Yet, the accompanying software ecosystem remains fragmented across model types, spatial resolutions, and computational targets, making models harder to compare, extend, and deploy at scale. Here we present MEmilio, a modular, high-performance framework for epidemic simulation that harmonizes the specification and execution of diverse dynamic epidemiological models within a unified architecture. MEmilio couples an efficient C++ simulation core with coherent model descriptions and a user-friendly Python interface, enabling workflows that run on laptops as well as high-performance computing systems. Standardized representations of space, demography, and mobility

support straightforward adaptations in resolution and population size, facilitating systematic inter-model comparisons and ensemble studies. The framework integrates readily with established tools for uncertainty quantification and parameter inference, supporting a broad range of applications from scenario exploration to calibration. Finally, strict software-engineering practices, including extensive unit and continuous integration testing, promote robustness and minimize the risk of errors as the framework evolves. By unifying implementations across modeling paradigms, MEmilio aims to lower barriers to reuse and generalize models, enable principled comparisons of implicit assumptions, and accelerate the development of novel approaches that strengthen modeling-based outbreak preparedness. Moreover, we will show how recent advancements in agent-based modeling of post-acute infection syndromes (PAIS) can be coupled with MEmilio to study the long-term effects of epidemic or endemic developments.

The Impact of COVID-19 Vaccination on Mortality and Stringency Measures in Belgium: A Retrospective Analysis

Speaker: Nicolas Franco, UNamur

Co-authors: Nicolas Herman, Maikel Bosschaert, Toon Braeye, Lander Willem, Steven Abrams, Niel Hens

Abstract:
Many studies have estimated the deaths averted by the initial COVID-19 vaccination campaign. However, they often assume unchanged population behaviour, although the absence of vaccination would likely have increased hospital burden, requiring stricter transmission control measures and behavioural adaptations to prevent healthcare system collapse.

Using an age-structured stochastic compartmental model calibrated to Belgian hospital data and accounting for vaccination status, we simulated retrospective transmission scenarios without vaccination. These scenarios incorporate potential behavioural adaptations and the additional restrictions needed to keep hospital burden manageable.

Our findings highlight the critical role of vaccination in reducing mortality and hospital burden, even after accounting for behavioural adaptations, particularly during Delta variant dominance. Without vaccination, stringent social restrictions would have been essential to protect hospitals, potentially requiring lockdowns to be extended by up to two years.

Sensitivity analyses further show that the timing and intensity of restrictions influence infection rates and the duration of healthcare system pressure. Stricter restrictions are more effective at preventing renewed hospital strain and additional deaths, while milder restrictions allow herd immunity to be reached more quickly. These findings illustrate the trade-offs between controlling hospital burden and accelerating the build-up of population immunity.

EpiDelays: A Software for Estimation of Epidemiological Delays

Speaker: Oswaldo Gressani, Hasselt University

Abstract:
State-of-the-art statistical methods form an important dimension of pandemic preparedness. They permit to analyze epidemic data collected by public health systems to shed light on the disease dynamics of an invading pathogen. Epidemiological delays, the time intervals between two well-defined events related to a pathogen, play a key role to understand disease transmission. Information on delay quantities can be leveraged to mitigate the public health impact caused by epidemic and pandemic-prone pathogenic organisms. We present recent developments in the EpiDelays software, an emerging R toolkit to fit epidemiological delay distributions from coarse data. EpiDelays provides user-friendly routines to analyze singly and doubly interval-censored data under classic parametric models or via a nonparametric model based on uniform mixtures. Model parameters are estimated by using the maximum likelihood principle, while standard error estimates and confidence intervals are computed by leveraging the bootstrap. A fully Bayesian approach based on epidemiologically anchored priors combined with an efficient adaptive Metropolis sampler is currently under development.

Session 5

Evolving psychological distress from first lockdown towards first reopening using a repeated cross-sectional large general population study in Belgium (March–June 2020)

Speakers: Zita Zsabokorszky-Paeleman, Hasselt University

Co-authors: K. Pepermans, K. Van den Broeck, P. Beutels, N. Hens

Abstract:
Objectives/Background: The COVID-19 pandemic placed considerable psychological burden on the Belgian population, with elevated rates of anxiety, depression, and psychological distress documented throughout the crisis. How associations between key factors and psychological distress changed across different phases of the pandemic remains largely unexplored.
Methods: Data from eleven consecutive weekly waves of the Great Corona Study (GCS, 31 March – 13 June 2020) were analysed using three complementary GLM-based approaches: (1) tracking associations between 11 pre-identified variables and psychological distress (GHQ-12, 2/3 cutoff) across waves; (2) a household composition model; and (3) wave-specific variable selection via random forests followed by GLMs.
Results: Age, gender, region, COVID-19-like symptoms, and perceived adaptation to measures in some public places, in-person interaction were consistently associated with distress across all eleven waves. Education lost significance over time, while the significance of occupational factors and lower number of in-person contacts varied considerably. Living alone and single-parent households were most persistently and strongly associated with higher distress. Wave-specific analyses identified loneliness, financial difficulties, and type of housing consistently associated with distress throughout the study period.
Conclusions: Psychological distress and its associated factors evolved dynamically across the Belgian lockdown and deconfinement period, reflecting shifts in the population's risk perception regarding the disease throughout the study period. The results underscore the importance of continuous mental health monitoring and targeted psychosocial interventions during public health crises.

Health Products Manufacturing Modelling for Pandemic Preparedness and Response

Speaker: Nico Vandaele, KU Leuven

Co-authors: Catherine Decouttere

Abstract:
The KU Leuven Access-To-Medicines Research Center is modelling various aspects of pandemic preparedness and response, related to vaccines, therapeutics, diagnostics and general medical products. This presentation focuses on vaccine manufacturing modelling. It is showcased by modelling work performed with CEPI, PATH and Gates Foundation for policy making stakeholders (such as HERA, EU-FAB, ZEPAI, A-CDC, WHO,…) as well as manufacturing stakeholders (such as RJ, CZ, Afrigen, ITD, …).
The methodology is discrete event simulation, combined with stakeholders' engagement and scenario analysis. The scientific contribution lies mainly in the embedding the modelling of Quality Control and

Quality Assurance processes as well as (critical) raw materials. Several vaccine platforms have been modelled so far: mRNA, viral vector, protein based while live-attenuated is underway. It serves both decision making for preparedness (keeping capacity warm) as well as for response (scaling up and down), but also covers tech transfer: for instance to support the WHO mRNA Vaccine Technology Transfer hub or to shift from clinical trial volumes to larger scale volumes.
The results are vaccine manufacturing models and subsequent scenarios, used for decision support and offering typical Key Performance Indicators such as time-to-first-batch, throughput (volumes per time unit), inventory and stockpile levels, utilization levels, bottleneck detection and resolution, among others.

The dynamics of pandemic vaccine supply chain through a systems lens: a case study of Belgium

Speaker: Junior Ocira, KU Leuven

Co-authors: Leonor Guariguata, Catherine Decouttere, Nico Vandaele

Abstract:
Most vaccine supply chain (VSC) models do not fully integrate vaccine manufacturing, allocation, distribution, administration, and disease epidemiology. Having integrated VSC model can help decision makers to understand how vaccine supply chain decisions and disruptions may influence disease dynamics, and vice versa, when managing country-wide vaccination programs. In this study, we aim to conceptualise the integration of vaccine supply chain and disease epidemiology using a systems approach based on Belgium's experience in managing a successful pandemic vaccination campaign. We collected data through multiple channels: interview of 22 key stakeholders with experience in pandemic vaccine supply chain, review of technical reports, guidelines and literature. These datasets were used to map: the flow of vaccines from manufacturers to vaccination centres, the process of prioritising, inviting, and vaccinating the population. We use casual loop diagram (CLD) and stock and flow diagram (SFD) to show: the complexities of pandemic VSC, the existing delays, the feedback loops within, and between the VSC subsystems, and how changes in disease epidemiology impact different subsystems of pandemic VSC. The CLD and SFD are currently a work in progress and will be further validated by key stakeholders, and translated into a simulation model using system dynamics approach.

Session 6

Characterizing the population patterns of COVID-19 transmission in Belgium, Netherlands and the United Kingdom

Speakers: Constantino Caetano, Instituto Nacional de Saúde Doutor Ricardo Jorge

Co-authors: Irma Varela-Lasheras, Andreia Leite, Leonardo Angeli, Pietro Colleti, Fuminari Miura, Ana Paula Rodrigues, Niel Hens, Sónia Namorado

Abstract:
Non-pharmaceutical interventions like school closures and lockdowns limited COVID-19 transmission but carried substantial social and economic costs, motivating more targeted interventions that account for how demographic groups and social settings drive spread. We analyse COVID-19 transmission dynamics in Belgium, the Netherlands, and the United Kingdom from late 2020 through 2021, using an elasticity analysis to quantify the contribution of age groups and social settings (e.g. home, work, school) to the reproduction number (Rt), and performed a cluster analysis to identify recurring temporal and cross-country patterns.

School, workplace, and younger age-group contributions increased during epidemic growth (Rt>1) vs. control periods (Rt<1) across all three countries. Cluster analysis identified three recurring regimes: suppression, reopening/school-driven, and summer. The suppression regime featured low Rt and higher contributions from older groups and the home setting. The reopening/school-driven regime featured an Rt around 1 with high variability, lower stringency, and increased contribution from schools, children, and younger adults, coinciding with school reopening and recurring after the summer holidays. The summer regime featured high transmission, low stringency, and high contribution from younger adults. These findings provide group- and setting-specific insights that could inform public health measures and offer a transferable approach for future epidemics.

Structuring school-closure decisions: a phase-based knowledge agenda for pandemic preparedness

Speaker: Tomris Cesuroglu, Pandemic and Disaster Preparedness Center (PDPC)

Co-authors: Lois van Eck, Anja Schreijer

Abstract:
School-closure decisions require policymakers to weigh infection control against educational, psychosocial and economic consequences under uncertainty. Lessons from COVID-19 cannot simply be transferred to future pandemics with different pathogens, risk groups and societal contexts. Within PRESENT, we developed a phase-based knowledge agenda to structure evidence needs for future school-closure decisions.

A scenario-based visioning exercise brought together stakeholders from education, public health, mental health, youth representation and policymaking (n=11), alongside researchers (n=9). Participants identified knowledge needs using a fictional avian influenza scenario. Contributions were synthesised,

thematically analysed and refined through subsequent stakeholder discussions and emerging project findings.

The resulting framework connects four phases: inter-pandemic preparedness, before closure, during closure and after reopening. Across these phases, it links decision points to epidemiological, educational, psychosocial and economic evidence needs, mitigation measures, actor responsibilities and evaluation. Feedback loops connect monitoring during closures with adjustments to measures, recovery support and longer-term research. Adolescents' perspectives and differentiated vulnerabilities cut across the framework.

The agenda provides a structured approach to organising evidence generation and use across sectors and phases. It makes trade-offs, timing and responsibilities explicit, offering a basis for more transparent and adaptive school-closure decision-making.

Household viewpoint on telework characteristics during the COVID-19 pandemic

Speaker: Hanne Van Dijck, Hasselt University

Co-authors: Philippe Beutels

Abstract:
Background: During the COVID-19 pandemic, telework was one of the first measures taken wherever possible to reduce virus transmission while keeping the economy open. However, not all workers were able to work from home, and others could not work at all.

Methods: Data were drawn from the Great Corona Study (GCS), a large-scale non-probabilistic observational survey conducted cross-sectionally under a citizen science framework in Belgium. Data from the first nine waves were used (March 17th 2020 – May 12th 2020), covering the beginning of the pandemic. Respondents were restricted to those with an age between 18 and 70, and indicating having a job as their primary occupation. For each wave, logistic regression was used to identify the characteristics of those who did not work the week preceding the wave. Among those who did work, quasi-Poisson regression with the number of days worked as an offset was used to describe the teleworking rate. Covariates included age, sex, educational level, occupational position and sector, family situation, type of housing and degree of urbanization.

Results: The number of respondents within each wave varied from 80 000 to 550 000. The ability to work and telework evolved by wave, but generally women had a higher odds of not working than men, as were those with lower versus higher educational levels. The results for occupational position revealed that labourers, self-employed workers and schoolteachers had a higher odds of not working than employees. Workers in repair of motor vehicles and household goods, wholesale, retail, and socio-cultural and personal services had higher odds than those working in financial institutions. Households with children under 12 consistently had higher odds of not working than those cohabiting only with other adults across all waves. There are three striking characteristics for teleworkers. The higher the education level, the higher the teleworking rate, and labourers, health workers, and emergency services had a lower teleworking rate than employees. Lastly, families with a young child had a higher teleworking rate than people cohabiting with adults while single-person households had a lower teleworking rate.

Conclusion: Educational level, family situation, occupational sector and position are important characteristics in describing the working and teleworking habits within the first phase of the COVID-19 pandemic.

Building Shared Understanding of Pandemic Response: A Co-Created System Dynamics Interactive Learning Model from the LEAPS Project

Speaker: Sanjeet Kumar Jaiswar, KU Leuven

Co-authors: Nico Vandaele, Catherine Decouttere

Abstract:
The Learning and Adaptive European Pandemic Preparedness System (LEAPS) is an EU Horizon project coordinated by KU Leuven, with partners across Belgium, Denmark, France, Switzerland, and Greece. LEAPS brings together innovations in pathogen detection, surveillance, modelling, and threat assessment to support evidence-informed pandemic preparedness and response.

This work presents a system dynamics model-based interactive learning tool developed in Work Package 6 (WP6), co-created with stakeholders through workshops and validation across four European countries. The model is designed to help decision-makers build a shared understanding of epidemic response by experiencing feedback loops, delays, and unintended long-term consequences. The model structures are informed by how scientific advice, policy decisions, and public responses unfolded during COVID-19 while supporting learning for future unknown threats such as “Pathogen X”.

The tool integrates epidemiological, behavioral, and governance factors, connecting scientific, policy, and public response processes. Its epidemiological component builds on concepts from the SIMID compartmental models, with country and age-stratified contact patterns from SOCRATES. Scientific and governance components capture how early-warning signals, surveillance-data availability, interpretation, and risk assessment, including delays in these processes, shape response timing and coordination, alongside social dimensions such as public trust and compliance.

By interacting with the deterministic system dynamics simulation model, stakeholders can explore how decisions and responses unfold over time, how feedback loops and delays shape outcomes, and how actions taken to control an epidemic can create wider social consequences. This supports learning and preparedness by helping decision-makers recognize system behavior and anticipate potential trade-offs before facing future threats.

Session 7

Spatio-Temporal Endemic–Epidemic Modelling for Outbreak Preparedness: Insights from COVID-19 in South Africa

Speakers: Rashider Aloni, Hasselt University

Co-authors: Tarylee Reddy, Ziv Shkedy, Niel Hens

Abstract:
The COVID-19 pandemic highlighted the need for surveillance methods that explain changing transmission patterns and provide timely forecasts. In South Africa, epidemic waves differed across provinces in timing and magnitude. We examined whether a spatio-temporal endemic–epidemic model could distinguish background incidence, within-province transmission, and spread between provinces while supporting short-term forecasting.

We analysed daily cases from South Africa's nine provinces between March 2020 and July 2022. The model incorporated variants, vaccination, stringency, seasonality, and reporting effects, with power-law spatial weights and province-specific random effects. The model reproduced the observed multiwave pattern across the study period. Within-province transmission dominated incidence in most provinces.

Background incidence was relatively more prominent in Gauteng, while betweenprovince transmission was stronger in the Western Cape. In a retrospective evaluation, forecast performance was strongest at horizons of one to seven days, with most observations falling within the 95% prediction intervals. By separating components of incidence and generating short-term forecasts, the model shows how routine case data could inform surveillance and outbreak response. The analysis conducted in this study provides a starting point for ongoing AI-LSTM forecasting and non-linear modeling approaches for real-time and short-term prediction of future outbreaks such as Ebola.

Modelling of E. coli resistance to 3rd generation Cephalosporins in Italy across community and hospital settings

Speaker: Tommaso Bertola, University of Padova & Bruno Kessler Foundation

Co-authors: Valentina Marziano, Simone Iacchini, Chiara Sacco, Alfredo de Bellis, Stefano Merler, Roberto Da Cas, Patrizio Pezzotti, Giorgio Guzzetta

Abstract:
Coexistence of drug-susceptible and drug-resistant bacterial strains across neighboring geographies is commonly modeled at country or state level under homogeneous mixing assumptions. We combined data on antimicrobial resistance surveillance, antibiotic consumption in hospitals and community, and hospital admissions, discharges, and transfers to reproduce regional heterogeneity in third-generation cephalosporin (3GC)-resistant Escherichia coli across Italy during 2019–2023.

We developed a metapopulation model representing 19 regions and two autonomous provinces, explicitly incorporating hospitalization and interregional coupling through commuting and hospital

transfers. Transmission followed an ecological model supporting coexistence of susceptible and resistant strains. The model was calibrated to 2019 surveillance data assuming epidemic equilibrium and validated against resistance trends in 2020–2023 using time-varying regional antibiotic consumption. We also evaluated counterfactual scenarios with homogeneous consumption.

More than 90% of new 3GC-resistant carriers arose through community transmission. Hospitals amplified resistance, with antibiotic-mediated selection accounting for one-third of new resistant hospital carriers. If every region adopted the lowest observed 3GC consumption, resistance would fall nationwide from 33% to 14% in hospitals and from 17% to 5% in the community, reducing resistant infections by 60–65%. Regional differences persist because of heterogeneous transmission and interregional coupling. These findings support antimicrobial stewardship in hospitals and communities.

Incorporating spatial heterogeneity in population density and short-range mobility to assess mosquito-borne disease outbreak risk

Speaker: Francesco Menegale, Fondazione Bruno Kessler

Co-authors: Francesco Vairo, Danilo Cereda, Patrizio Pezzotti, Andrea Pugliese, Stefano Merler, Robin N Thompson, Piero Poletti

Abstract:
Metrics commonly used to assess the risk that early cases of an anthroponotic mosquito-borne disease will initiate local outbreaks do not explicitly account for mobility and spatial heterogeneities in human and vector densities, despite their importance for transmission dynamics. We present an operational framework for assessing the risk of substantial local transmission of a mosquito-borne disease following the introduction of a case, incorporating host-vector interactions arising from mobility. We derive appropriate metrics to quantify the expected number of secondary cases generated by one imported case and the probability that this case initiates a major outbreak. We test these metrics using model simulations and apply them to assess the risk of autochthonous transmission of dengue in two illustrative landscapes in Italy. We evaluate the framework under different mobility assumptions, informed by time-use and population data, and estimates of dengue transmission distances. Results show that incorporating mobility substantially affects estimates of the expected number of secondary cases and the probability of a major local outbreak compared to models neglecting mobility. As chikungunya and dengue outbreaks become increasingly frequent in non-endemic countries, this approach provides a comprehensive framework for outbreak risk assessment, which can support public health surveillance and control strategies.

Epidemiological model calibration using wastewater and sentinel hospital surveillance data

Speaker: Esteban Foncoux, University of Namur

Co-authors: Nicolas Franco

Abstract:
Mathematical modelling of infectious diseases often relies on detailed age-stratified nationwide surveillance data for calibration and long-term projections. In Belgium, such data were mostly available for COVID-19 until June 2023. Since then, age-stratified severe acute respiratory infections (SARI) surveillance data have been available but become less reliable when incidence falls below the detection limit of the sentinel network. Wastewater surveillance offers an alternative, although it lacks age-specific information.
This study evaluated the use of SARI and wastewater surveillance data for calibrating epidemiological models. An age-structured compartmental model including vaccination status and waning immunity was calibrated using various strategies for the 2022–2023 period, with nationwide hospital admissions as baseline. To address SARI reporting reliability, wastewater data were normalised using PMMoV, age-group distributions were inferred from SARI data. Both datasets were rescaled to nationwide hospital admissions using SARI catchment population. Ignoring or excluding the reporting issues in SARI data resulted in inaccurate calibration.
Incorporating wastewater data partially constrained the model and applying age-specific proportions from SARI improved the calibration and better captured the age-specific vulnerabilities to COVID-19.
Age-structured SARI data provide a viable alternative for calibrating epidemiological models when appropriate rescaling is available. Wastewater improves calibration during periods of unreliable reporting.

Session 8

Towards disease X preparedness: broad, strain-resolved viral surveillance in wastewater

Speakers: Jelle Matthijnssens, KU Leuven

Co-authors: Elke Wollants, Mustafa Karatas

Abstract:
Pandemic preparedness requires surveillance systems that detect unexpected changes in pathogen circulation before targeted testing is implemented. We evaluated longitudinal hybrid-capture viral metagenomics using the Twist Comprehensive Viral Research Panel on 127 weekly 24-h composite influent samples collected over 31 months from a sentinel wastewater treatment plant in Leuven, Belgium. The panel spans all viral families containing known human-infecting viruses, while hybridization probes retain binding despite sequence divergence, extending detection beyond viruses closely matching represented reference sequences. We recovered 339 viral species and 715 strains, revealing seasonal community turnover and enabling strain-resolved surveillance across multiple pathogens. Rotavirus A dynamics typically preceded clinical surveillance by approximately one week, while genotype distributions closely reflected those observed clinically. Genotyping of norovirus and adenovirus further revealed temporal shifts and replacement of circulating lineages. Wastewater data also identified a marked increase in parvovirus B19 from April 2023, approximately one year before a Belgian national public-health alert. These findings show that broad hybrid-capture metagenomics provides a flexible surveillance approach for establishing viral baselines, tracking evolving viral populations and identifying unexpected circulation signals, thereby strengthening early warning and preparedness for emerging infectious threats, including a future disease X.

PCR-4-ALL: Scalable Ultra-High-Throughput ddPCR Surveillance to Preempt Epidemic Lockdowns

Speaker: Gregor Fritz, KU Leuven

Co-authors: Xavier Casadevall i Solvas, Zhiyuan Ma, on behalf of the PCR-4-ALL Consortium

Abstract:
Controlling emerging pandemic threats demands rapid intervention before vaccines or point-of-care diagnostics can be manufactured. Polymerase chain reaction assays can be operationalized within weeks of pathogen genome sequencing, offering an immediate frontline defense. Epidemiological literature demonstrates that high-frequency population testing reliably suppresses the effective reproduction number, enabling pathogen containment without resorting to blanket lockdowns and their associated collateral societal damage.

However, conventional molecular diagnostics cannot support population-scale screening due to prohibitive costs and reagent bottlenecks. The PCR-4-ALL consortium overcomes these constraints by developing an automated, ultra-high-throughput diagnostic platform based on ddPCR. By combining advanced microfluidics, automation, and assay miniaturization, the platform targets a capacity exceeding

10^5 samples daily per installation while significantly driving down per-test costs to economically feasible levels.

To ensure actionable real-world translation, technical assay engineering is directly coupled with transmission dynamic modelling, macroeconomic cost-benefit evaluations, and evidence-based implementation frameworks for public health authorities. Ultimately, PCR-4-ALL provides decision-makers with a proactive molecular containment blueprint: deploying mass ddPCR surveillance early in an outbreak to break transmission chains, protect essential workforces, and preserve socio-economic stability prior to broad population immunity.

The Role of Global Health Ethics in Climate-Sensitive Infectious Disease Early Warning Systems

Speaker: Phong Hong, Oxford University Clinical Research Unit

Co-authors: Jennifer Van Nuil, Nikiwe Solomon, Jantina De Vries

Abstract:
Infectious disease early warning systems (EWS) have the potential to shift public health response from reactive outbreak control towards proactive planning. This potential rests on ethical decisions as much as mathematical methods: whose data informs a model, whose risk is represented, and whose realities are rendered visible to determine resource provision. Yet few models fully translate into their decision making potentials. A Wellcome-trust commissioned review found that only 37 operational tools among 30,000 publications. We theorize this gap partly reflects treating ethics as a secondary priority rather than a foundational driver of modeling science. Bridging environmental anthropology, global health ethics, and mathematical modeling, we explore the role of ethics in EWS. Through investigating the societal impact of predictive modeling, we surface power asymmetries between developers and implementors, prompt reflection on the worldmaking roles of models, and explore expectations about model's capabilities and limits for decision making. We position ethical judgement (e.g. whose lived realities the model creates) as equally consequential as mathematical reasoning (e.g. how a model is selected). As modeling increasingly informs interventions and policies with social consequences, embedding ethics throughout the EWS-CSID pathway is critical to closing the gap between research development and health practice.

Session 9

Global pandemics, global preparation: Assessing capacity for Ebola in DRC

Speakers: Leonor Guariguata, KU Leuven

Abstract:
All the disease that have triggered a Public Health Emergencies of International Concern in the last twenty years have emerged in countries outside of Europe. The pandemic preparedness and prevention of any country depends on the preparedness of all countries. This study looks at the capacity for response to Ebola Virus Disease (EVD) in the Democratic Republic of Congo applying a system dynamics approach to evaluating diagnostic capacity. A multi-level stakeholder engagement (n=21 interviews and n=30 focus group participants) contributed to the elucidation of system impacts and pathways for outbreak preparedness and response and where diagnostic capacity may play a role. Weaknesses in access to the basic materials needed for outbreak response hampers EVD response in DRC and leads to vulnerabilities that have wide public health impacts, seen today in the ongoing Bundibungyo epidemic. Understanding and addressing access barriers can be integrated into strategies for pandemic preparedness. The newly ratified WHO Pandemic Agreement can provide a platform for developing pandemic preparedness across borders.

Full integration of the SORMAS open-source system in Luxembourg for epidemic and pandemic preparedness

Speaker: Pilar Hernandez, SORMAS Foundation

Co-authors: C Garro, E Janigan, J Böhme, R Bob, OH Nwafor, K Pesula, H Asiimwe, X Collette, Y Pires, C Ernst, D Bejko, T Velez, I Kerrec, E Culetto, D Gashi, G Claquin, R Schober, J Mossong, A Vergison

Abstract:
Background: Luxembourg's epidemiological surveillance system evolved through tools and reporting pathways developed over time, resulting in fragmentation. The COVID-19 pandemic highlighted the need for integrated digital solutions supporting large-scale surveillance and crisis management. In response, the country is implementing SORMAS (Surveillance Outbreak Response Management and Analysis System) as national surveillance and response platform. Following initial deployment for COVID-19, SORMAS is being extended to other notifiable diseases through the PHRESH project, co-funded by EU4Health.
Methods: Adaptation to national needs follows an agile approach combining epidemiological and system requirements analysis with input from Health Directorate and SORMAS Foundation experts. Requirements are documented through GitHub and addressed through iterative development, testing, feedback, and integration. New functionalities are publicly documented, supporting reuse.
Results: SORMAS includes event management and case-based modules for pertussis, tuberculosis, invasive meningococcal and pneumococcal infections, giardiasis, cryptosporidiosis, dengue, malaria, shigella, salmonellosis, and adapted monitoring for measles, influenza, and RSV. Interoperability has been strengthened through electronic doctor notifications, automated laboratory-result processing,

configurable forms, and data exchange with ECDC's EpiPulse Cases. Future developments will cover over 70 notifiable diseases and expand One Health functionalities.
Conclusion: Integrating surveillance and outbreak response in a single platform reduces fragmentation and strengthens Luxembourg's epidemic and pandemic preparedness.

Towards a participatory European social contact observatory

Speaker: Kathleen Nicole Kelley, ISI Foundation / La Sapienza University

Co-authors: Jantien Backer, Pietro Coletti, Nicolò Gozzi, Lisa Hermans, Niel Hens, Neilshan Loedy, Mattia Mazzoli, Andrea Torneri, Albert Jan van Hoek, and Daniela Paolotti

Abstract:
Social contacts shape infectious disease transmission, yet most contact data come from resource-intensive, infrequent surveys lacking longitudinal health information. Digital participatory surveillance offers a lower-resource alternative for continuous data collection. We analyzed over 110,000 contact reports linked with sociodemographic and symptom history data from 18,000 InfluenzaNet participants in Belgium, Italy, and the Netherlands. Comparison with prior studies showed that adult age-stratified matrices reproduced established structural features, including age-assortative mixing. Temporal analyses showed transmission-relevant contact patterns varied, underscoring that contacts are not static. Negative binomial mixed-effects models found reductions in contacts among participants reporting influenza-like illness (ILI) symptoms in Belgium and the Netherlands, when prioritizing the most recent prior symptoms. Considering symptom burden in the prior 30-day window, ILI with fever remained associated with fewer contacts, while milder symptoms were associated with higher contact counts in the Netherlands. Contacts also varied with expected factors like employment, weekends, and holiday periods. These findings demonstrate that participatory surveillance platforms can generate valid, longitudinal contact data integrated with health and behavior information that is difficult to obtain through stand-alone surveys. This infrastructure provides a foundation for a European social contact observatory capable of supplying regularly updated inputs for epidemic modeling and public health preparedness.

Session 10

Developing a Decision Support Tool for Early Pandemic Response

Speakers: Joshua Lambert, London School of Hygiene and Tropical Medicine

Co-authors: Jiaxin Zhou, Jack Ward, John Edmunds

Abstract:
Pandemic preparedness and response requires epidemiological modelling to evaluate effective control strategies. Modelling tools often require domain expertise and programming knowledge to run scenario evaluations. Decision support tooling, specifically web applications, that embed epidemiological models enable public health professionals, analysts and decision-makers to explore, compare and analyse infectious disease outbreak scenarios with prebuilt infrastructure and data visualisations. The proposed decision support tool, developed as part of the ESCAPE pandemics consortium, is an open-source, publicly accessible modelling platform, providing a wide range of pre-packaged analyses to evaluate targeted interventions for outbreak control in the early phase of an epidemic. The tool has been co-developed through a series of stakeholder engagement workshops to maximise the tool's utility to the public health community. Engaged stakeholders include the UK Health Security Agency and World Health Organization. The decision support tool runs the ringbp branching process model with interventions. Both propose and ringbp have been enhanced through stakeholder feedback to provide a flexible framework to model a range of directly transmitted infections and outbreak response strategies. Propose contains a comprehensive user manual and a growing library of case studies on targeted non-pharmaceutical interventions in real-world outbreak response.

Translating health research into evidence-based policymaking in times of crisis

Speaker: Eloïse Dagneau, KU Leuven

Co-authors: Priscilla Van Even, Nico Vandaele

Abstract:
The COVID-19 pandemic showcased the challenges of translating complex scientific evidence into actionable recommendations, as well as the difficulties of communicating these under uncertain and rapidly evolving contexts. Interviews were conducted with healthcare professionals and researchers to investigate the main challenges when providing advice to policymakers. The following thematic analysis sought to identify solutions and strengths to these difficulties. The results express clear challenges with managing a diverse stakeholder landscape influencing the policymaking process, respecting boundaries within different roles and mandates, the complexity of advice leading to misunderstandings and oversimplifications, and, finally, limitations brought on by insufficient data access, infrastructure, and real-time information. The discussion digs into the solutions offered by interviewees and reflects on synergies that can be built – as one aspect is improved, it can provide collateral benefits, expanding its benefits beyond the challenge it aims to tackle. These interviewers show how science communication is a pillar to pandemic preparedness and response.

Policy implications from a modeling study in Flanders, Belgium: impact of changes in measles vaccination schedule under potential waning immunity

Speaker: Laura Di Domenico, Hasselt University

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Abstract:
In 2025, Flanders adapted the time of second dose administration of the measles-mumps-rubella (MMR) vaccine to 2 years of age instead of school-based vaccination around 10 years of age. We aimed to quantify the impact of different vaccination schedules on future measles transmission in Flanders, accounting for potential waning of immunity.

We used an age-structured compartmental transmission model, integrating empirical contact matrices and information on MMR coverage data, and calibrating on serial cross-sectional serological survey data (2002, 2006, 2013).

Recent incidence trends in Flanders are consistent with model results including waning of humoral immunity, although available serial serological data did not allow to infer the waning rate. Under waning assumptions, lowering the age of the second dose increased protection and reduced infections in children in the short term, but led to a shift in susceptibility to older age groups and an increase in cumulative number of infections in the long term. A catch-up vaccination campaign in adults, even with limited uptake, could substantially mitigate the long-term effects of immunity waning.

Given the uncertainty in waning immunity, our findings highlight the need to maintain high vaccination coverage and offer catch-up opportunities to close immunity gaps. Updated serological studies and outbreak analyses are required to better quantify the extent of waning of vaccine-induced immunity.

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