

# Agenda – October 31<sup>st</sup> 2025



Time	Session
09:00 – 09:30	Registration
09:30 – 09:40	Opening Remarks
09:40 – 10:30	<b>Keynote Presentation</b>  <b>James Hay:</b> A quantitative world: should we stop binarizing our epidemiological data?
10:30 – 11:10	<b>Scientific Session</b>  <b>Alexis Martin:</b> Coupling models together! The love story of two mathematical models for malaria  <b>Anabelle Wong:</b> Assessing the effect of social contact structure on the impact of pneumococcal conjugate vaccines
11:10 – 11:40	Coffee Break and Posters
11:40 – 12:20	<b>Scientific Session</b>  <b>Matthieu Domenech de Cellès:</b> Immune boosting and the perils of interpreting pertussis seroprevalence studies  <b>Louis Colliot:</b> How virus genomics can help to understand the past (and present) of HIV epidemics in France?
12:20 – 13:00	<b>Speed Talks</b>  <b>Baptiste Elie:</b> Impact of viral blips and low level viremia on HIV-specific antibody responses  <b>Cana Kussmaul:</b> Modeling the effect of weather on infectious diseases: why causal structure matters  <b>Daniella Figueroa-Downing:</b> How well does this vaccine work? Navigating efficacy, effectiveness, and modelled impact  <b>Dennis Partl:</b> Compartmental Model on the Introduction of Zoliflodacin in South Africa  <b>Adrian Lison:</b> Real-time estimation of pathogen transmission dynamics from wastewater
13:00 – 14:00	Lunch (served at ground floor)

Time	Session
14:00 – 14:50	<b>Keynote Presentation</b>  <b>Eva Bons:</b> Forecasting and Scenario Modelling of Respiratory Infections in Europe: Leveraging the Ensemble Approach
14:50 – 15:30	<b>Scientific Session</b>  <b>Martin Wohlfender:</b> Machine learning-based short-term forecasting of COVID-19 hospital admissions using routine hospital patient data  <b>Branwen Owen:</b> Cost-effectiveness of typhoid conjugate vaccine across sub-Saharan Africa: Random forest analysis reveals primacy of cost over epidemiological drivers
15:30 – 15:50	Break
15:50 – 16:50	<b>Speed Talks</b>  <b>Diane Duroux:</b> Early antifungal resistance identification using MALDI TOF mass spectrometry and machine learning  <b>Luzia Nora Felber:</b> Simulating Mosquito Flight Paths with a Random Walk Model  <b>Javier Perez-Saez:</b> Evolving infectious disease dynamics shape school-based intervention effectiveness  <b>Elizabeth Lee:</b> Improving the timeliness of cholera outbreak response with case-based early warning signals  <b>Sarah Kramer:</b> Purely statistical methods of inferring causality fail to accurately characterize pathogen-pathogen interactions  <b>Pietro Gemo:</b> Are time series regressions reliable for estimating the effects of weather on infectious diseases?  <b>Nicolas Banholzer:</b> The relative contribution of close-proximity contacts, shared classroom exposure and indoor air quality to respiratory virus transmission in schools
16:50 – 17:00	Final Words
17:00	Apéro and Networking

## Posters:

**Johannes Bracher:** Unjustified Poisson assumptions lead to overconfident estimates of the effective reproductive number

**Anika John:** Characterizing influenza A virus lineages and clinically relevant mutations through high-coverage wastewater sequencing

**Martina Reichmuth:** Grippenet: Working together to track the spread of respiratory infections in Switzerland

**Auguste Rimaite:** Wastewater-based genomic surveillance of respiratory syncytial virus enables tracking of lineages and identifying mutations at antigenic sites

**Berit Siedentop:** Using machine learning to create a new diagnostic algorithm for infective endocarditis

**Timothy Vaughan:** Bayesian phylodynamic inference of heterogeneous epidemic trajectories using genomic data