

Annual meeting of the Coordinated Action « Modelling infectious diseases »

12-14 November 2025

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| Wednesday 12 NOV – ‘Early Career Researcher Day’ |
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13:00: Gates opening - Welcome coffee and tea
Hall principal de l’amphithéâtre Duclaux

14:00-15:00 Round table about French research centres’ and universities’ permanent recruitment

Speakers:

- Quentin Leclerc (Tenured Assistant Professor, CNAM and Mesurs, <https://qleclerc.github.io/index.html>)
- Quentin Clairon (Permanent researcher, Inria, Bordeaux Population Health Research Center, <https://scholar.google.com/citations?user=io8ZaeIAAAAJ>)
- David Smith (Permanent researcher, INSERM and Institut Pasteur)
- Hélène Cecilia (Permanent researcher, INRAE, UMR 1300 BIOEPAR <https://bioepar.angers-nantes.hub.inrae.fr/l-unite/annuaire2/membres-c/cecilia-helene2>)
- Jérémie Guedj (Research Director, Inserm, UMR IAME, <https://www.viral-dynamics.com/>)
- Pierre-Yves Boëlle (University Professor - Hospital Practitioner, Team leader "Surveillance and Modelling of Communicable Diseases" at iPLesp, Director of ED393)

15:00-15:15 Coffee break
Hall principal de l’amphithéâtre Duclaux

15:15-16:15 Seminar "Uses and misuses of AI in Scientific Writing",
Speaker: David Del Álamo (Fellowsherpa)

David del Álamo received his Ph.D. in developmental biology at the Severo Ochoa Center for Molecular Biology in Madrid and postdoctoral training at the Mount Sinai Hospital in New York and the Pasteur Institute in Paris. David was scientific editor for The EMBO Journal and EMBO reports, managing editor of Review Commons, and the head of the EMBO Fellowship Programme. David obtained a Master of Business Administration (MBA) degree in 2017. He collaborates as an editorial consultant for The Journal of Cell Biology and Life Science Alliance.

16:30-17:30 Speed networking and community building activities

19:00

Social dinner

Location: Restaurant L'Authentique 167 rue de Vaugirard, 75015 Paris

Thursday 13 NOV

9:30-10:00

Presentation of the activities of the Coordinated Action

SESSION 1 (*Chairs: Camille Pelat & Thomas Bénéteau*)

10:00-10:35

David Smith

INSERM and Institut Pasteur

Modelling to inform investment cases for vaccines targeting emerging infectious diseases

10:35-11:00

Bastien Reyné

CNRS

Leaky or polarised immunity: Non-Markovian modelling highlights the impact of immune memory assumptions

11:00-11:25

Aurélie Maurin

INSERM, Institut Pasteur, and CNAM

Evaluation of pneumococcal vaccination policies using mathematical modelling of serotype-specific carriage dynamics

11:25-11:55

COFFEE BREAK

SESSION 2 (*Chairs: Amandine Véber & Lucille Calmon*)

11:55-12:20

Francesco Parino

INSERM and Sorbonne Université

Defining regimes to control and contain the spatial dissemination of emerging infectious diseases

12:20-12:45

Aurélien Velleret

Université d'Evry-Val d'Essonne

Inter-city infections and the role of size heterogeneity in containment strategies

12:45-14:15

LUNCH BREAK

SESSION 3 (*Chairs: Raphaëlle Metras & Constanze Ciavarella*)

14:15-14:40

Lina Cristancho-Fajardo

Institut Pasteur

Accounting for heterogeneity in mosquito exposure is necessary to forecast chikungunya outbreaks in Reunion Island

- 14:40-15:05** Fernando Saldana
INRAE
Multiscale Modeling of Vector-Borne Diseases: The Role of Dose-Dependent Transmission
- 15:05-15:30** Jonathan Bastard
INSERM, ANSES, and Sorbonne Université
Mapping the bird reservoir potential for West Nile virus in Europe and its relationship with disease occurrence in humans

15:30-16:00 COFFEE BREAK

SESSION 4 (Chairs: *Lulla Opatowski & Intila Yalikun*)

- 16:00-16:25** Pourya Toranj Simin
INSERM and Sorbonne Université
Impact of the human contact network on the selective advantage of emerging viral variants
- 16:25-16:50** Boxuan Wang
INSERM and Sorbonne Université
An analytical method to calculate epidemic threshold within spatial structure
- 16:50-17:15** Natalie Olson
Université de Montpellier
Simulating Zoonotic Spillover in the Context of Extractive Industrial Land Use Change
- 17:15-17:40** George Shirreff
Université Claude Bernard Lyon 1
Respiratory hospitalisations with Human Metapneumovirus (MPV) – how many cases are unidentified?

17:40-19:00 POSTER SESSION

- 19:45** **Conference dinner**
Location: Restaurant Papa Poule 23 rue des Taillandiers, 75011 Paris

Friday 14 NOV

SESSION 5 (Chairs: *Nathanaël Hozé & Anne-Andrée Ruiz*)

- 9:00-9:35** Samuel Alizon
CNRS and Collège de France
Phylodynamics: extracting epidemiological information from microbial sequence data

- 9:35-10:00** Clarisse Schumer
INSERM, Université Paris Cité, and Université Sorbonne Paris Nord
Viral dynamics of the Respiratory Syncytial Virus during experimental human challenge infections: insights for transmission and protection
- 10:00-10:25** Lisa Crépin
INSERM, INRIA, and Université de Bordeaux
Regularized estimation in high-dimensional mechanistic models

10:25-11:00 COFFEE BREAK

SESSION 6 (Chairs: Paolo Bosetti & Paul Petit)

- 11:00-11:25** Juliette Paireau
Institut Pasteur and Santé publique France
An ensemble model for real-time forecasting of seasonal influenza epidemics in France
- 11:25-11:50** Elise Hodbert
Université de Nantes and CNAM
Reconstructing healthcare networks from patient transfer data: a systematic review
- 11:50-12:15** Shrichand Bhuria
INSERM, CNRS, EHESP, and Université de Rennes
Modelling the Spread of Healthcare-Associated Infections through a Nationwide Patient-Based Network in France's Healthcare Settings
- 12:15-12:40** Maria Alexa
INSERM, Institut Pasteur, and Université Paris-Saclay
Modelling the acquisition of extended-spectrum beta-lactamase (ESBL)-producing Escherichia Coli in neonates in Madagascar households.

12:40-14:00 LUNCH BREAK

End at 14:00

POSTERS

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| Aupépin Chloé et al. | Quantifying the impact of bacterial vaccines against antibiotic resistance: the importance of accounting for transmission and selection dynamics |
| Brault Antoine et al. | Reconstructing SARS-CoV-2 antibody dynamics and estimating correlates of protection against infection |
| Calmon Lucille et al. | Vulnerability of the French hospital system to nosocomial infections |
| Camaglia Francesco et al. | Household epidemic modelling with housepi |
| Charniga Kelly & al. | Heterogeneity in activity levels explains changes in transmission advantage of SARS-CoV-2 Alpha variant over time |
| Coustaury Camille et al. | Improving the Sentinelles Network's surveillance of acute respiratory infections in France using spatio-temporal Bayesian modelling |
| D'Ottavi Morgana et al. | Modelling the long-term effects of community-based tuberculosis screening strategies among people who use drugs |
| Duret Loréna et al. | Serological Evidence of Influenza Burden Variability in Connected vs. Isolated Communities in Madagascar |
| Edbrooke Frith et al. | The geography of antibiotic resistance |
| Gonzalez Julia et al. | Animal-human interactions: a nationwide study on direct contacts in the general population |
| Guijarro Matos Ana et al. | Pediatric Emergency Room Activity an Early Indicator of Seasonal Respiratory Hospitalization |
| Kalahasti Suprabhath et al. | Foundation models for time series forecasting and policy evaluation in infectious disease epidemics |

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| Layan Maylis et al. | Evaluating the impacts of the COVID-19 pandemic on antibiotic resistance in hospitals |
| Maniscalco Davide et al. | Balancing preparedness and community response: complementary roles of vaccination and behavioral change in mpox outbreak control |
| Nahmani David et al. | Optimal instant releases for population replacement with Wolbachia in a time-periodic environment |
| Ochida Noé et al. | Quantifying how multiple transmission routes contribute to the spread of HTLV1 in different countries |
| Schneider Camille et al. | Understanding antibiotic resistance transmission within and between humans in <i>Klebsiella pneumonia</i> and <i>Escherichia coli</i> – a theoretical modelling study |
| Seurat Jérémy et al. | Modeling within-host <i>Staphylococcus aureus</i> dynamics in the human nasal microbiota |
| Suhanda Ilona Eveline et al. | Understanding behavioural and environmental factors associated with the risk of human tick bites using seasonal survey data |