

Arcane

ADAPTIVE HEALTHCARE NETWORKS

WORKSHOP · 19–21 OCTOBER 2026

Programme & Book of Abstracts

VENUE

Cnam · Amphithéâtre Abbé Grégoire

292 rue Saint-Martin, 75003 Paris

ONLINE

arcane-project.eu

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ARCANE 2026

Welcome

Welcome to ARCANE 2026 – *Adaptive Healthcare Networks*.

Over three days we bring together researchers working at the crossroads of network science, mathematical epidemiology and infection prevention to discuss how the movement of patients within and between healthcare facilities shapes the spread of antimicrobial-resistant organisms – and how this knowledge can make surveillance and control more effective.

The programme combines six invited talks with fifteen contributed presentations in eight thematic sessions: from the seeding of resistant strains and pathogen-specific dynamics, through data limitations and dynamic risk prediction, to the legal, ethical and societal dimensions of antimicrobial resistance and the trajectories that patients take through the healthcare system. The workshop closes with a round table on perspectives for the field.

We kept the format deliberately compact so that there is plenty of room for questions, discussions over coffee and the workshop dinner. We hope you will leave with new ideas and new collaborators.

Marie-Rachel Garal, Tjibbe Donker & Pascal Crépey
on behalf of the Organising Committee

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Committees & practical information

Organising committee

Shrichand Bhuria	EHESP, Rennes, France
Pascal Crépey	EHESP, Rennes, France
Tjibbe Donker	Medical Center – University of Freiburg, Germany
Marie-Rachel Garal	Medical Center – University of Freiburg, Germany

Scientific committee

Vittoria Colizza	Inserm, Sorbonne Université, Paris, France
Pascal Crépey	EHESP, Rennes, France
Tjibbe Donker	Medical Center – University of Freiburg, Germany
André Karch	University of Münster, Germany
Laura Temime	Cnam, Paris, France

Venue

Conservatoire national des arts et métiers (Cnam), Amphithéâtre Abbé Grégoire
292 rue Saint-Martin, 75003 Paris
Métro: Arts et Métiers (lines 3, 11) · Réaumur–Sébastopol (lines 3, 4)

Talks

Invited talks are 40 minutes, contributed talks 20 minutes including questions. Codes such as D2 refer to the abstracts in this booklet; presenting authors are underlined. Invited talks have no printed abstract – their pages are left free for your notes.

Social programme

Tuesday, 19:00–21:30	Workshop dinner · Salle des Textiles

Stay in touch

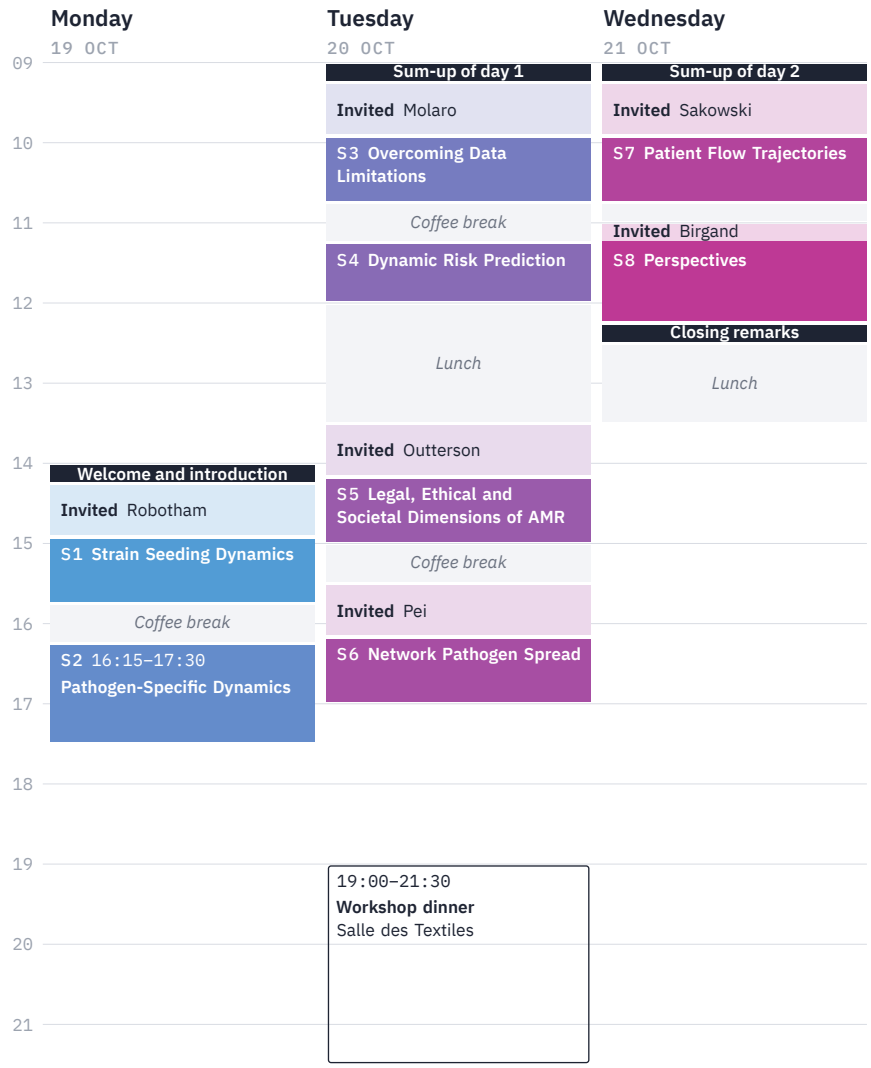
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Bluesky	@arcane-project.bsky.social
Mastodon	@arcane_project@mastodon.social
LinkedIn	linkedin.com/company/arcane-project
Workshop	arcane.sciencesconf.org

Wi-Fi & contact

Wi-Fi: eduroam
Emergency contact: Marie-Rachel Garal, +49 151 28789369

PROGRAMME

At a glance



DAY 1 · 19 OCTOBER 2026

Monday

14:00–14:15 **Welcome and introduction**

Pascal Crépey & Tjibbe Donker

14:15–14:55 **From network model to national surveillance: operationalising hospital network analysis in England**

Julie Robotham INVITED p. 11

SESSION 1 Strain Seeding Dynamics

Chair: Tjibbe Donker

14:55–15:15 **Seeding Antimicrobial-Resistant Bacteria in the French Hospital Network: How the Characteristics of the Index Hospital Shape Colonization Dynamics**

Rany Octaria A1 p. 12

15:15–15:35 **Seeding Antimicrobial-Resistant Bacteria in the French Hospitalized Patient Network: How Index-Patient Characteristics Shape Colonization Dynamics**

Shrichand Bhuria A2 p. 13

15:45–16:15 *Coffee break*

SESSION 2 Pathogen-Specific Dynamics

Chair: Laura Temime

16:15–16:35 **Modelling of *E. coli* resistance to 3rd generation Cephalosporins in Italy across community and hospital settings**

Tommaso Bertola A3 p. 14

16:35–16:55 **Effectiveness of interventions to reduce MRSA carriage in a pediatric hospital**

Alfredo De Bellis A4 p. 15

16:55–17:15 **Patient transfers and heterogeneous hospital clearing capacity shape regional vulnerability of the French healthcare system to *C. difficile* infections**

Marco Mancastroppa A5 p. 16

DAY 2 · 20 OCTOBER 2026

Tuesday

09:00–09:15 **Sum-up of day 1**

09:15–09:55 **From Disease-Specific to Whole-Healthcare-System Simulations: Challenges in Integrated Modelling**

Margherita Molaro INVITED p. 17

SESSION 3 Overcoming Data Limitations

Chair: Pascal Crépey

09:55–10:15 **Limitations in patient-transfer data introduce contrasting biases in estimates of nosocomial infection persistence across healthcare systems**

Marco Mancastroppa D2 p. 18

10:15–10:35 **Scaling up incomplete hospital admissions data for the construction of healthcare transfer networks**

Madhav Chaturvedi D1 p. 19

10:45–11:15 *Coffee break*

SESSION 4 Dynamic Risk Prediction

Chair: André Karch

11:15–11:35 **Data-Driven Infection Risk Forecasting in Hospital Contact Networks: Integrating Mechanistic Compartmental Models with Graph Neural Networks**

Yamil Vindas M1 p. 20

11:35–11:55 **Dynamic graph machine learning for early detection of antimicrobial resistant infections from acute care data**

Oskar Fraser-Krauss M2 p. 21

12:00–13:30 *Lunch*

13:30–14:10 **Antibiotics as infrastructure for civilization**
Kevin Outterson · remote INVITED p. 22

SESSION 5 Legal, Ethical and Societal Dimensions of AMR

Chair: Laura Temime

14:10–14:30 **Estimation of hospital catchment populations from patient flows in France**
George Shirreff D3 p. 23

14:30–14:50 **Regional structuring of healthcare networks, and their shared AMR problems**
Tjibbe Donker D4 p. 24

15:00–15:30 *Coffee break*

15:30–16:10 **Inference and control of antimicrobial-resistant organisms in hospitals**
Sen Pei INVITED p. 25

SESSION 6 Network Pathogen Spread

Chair: Vittoria Colizza

16:10–16:30 **Evidence for patterns of colonization risk in the nationwide hospitalized patient network in France**
Shrichand Bhuria M3 p. 26

16:30–16:50 **Modelling pathogen spread and control across a regional patient-sharing network**
Elise Hodbert M4 p. 27

19:00–21:30 **Workshop dinner**

Salle des Textiles

DAY 3 · 21 OCTOBER 2026

Wednesday

09:00–09:15 **Sum-up of day 2**

09:15–09:55 **Modelling and targeted control of healthcare-associated infections in regional healthcare networks**
Konrad Sakowski INVITED p. 28

SESSION 7 Patient Flow Trajectories

Chair: André Karch

09:55–10:15 **The patient trajectories forming healthcare networks**
Tjibbe Donker M5 p. 29

10:15–10:35 **Patterns of Patient Contact and Transfer Across Clinical Settings in the French Hospital System: Potential Pathways for Pathogen Dissemination**
Pascal Crépey M6 p. 30

10:45–11:00 *Coffee break*

SESSION 8 Perspectives

11:00–11:15 **Summary and perspectives**
Gabriel Birgand · Introduced by Laura Temime INVITED p. 31

11:15–12:15 **Round table discussion**
Gabriel Birgand (chair) with all invited speakers

12:15–12:30 **Closing remarks**
Pascal Crépey

12:30–13:30 *Lunch*

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Abstracts

In programme order. Each abstract carries its programme code and slot; presenting authors are underlined.

INVITED MON 19 OCT · 14:15–14:55

From network model to national surveillance: operationalising hospital network analysis in England

Julie Robotham

UK Health Security Agency / University of Oxford, United Kingdom

No abstract is available for this invited talk – the rest of this page is left for your notes.

MON

Seeding Antimicrobial-Resistant Bacteria in the French Hospital Network: How the Characteristics of the Index Hospital Shape Colonization Dynamics

Rany Octaria[1], Shrichand Bhuria[2], Madhav Chaturvedi[3], Daniel Goseberg[4], Marco Mancastroppa[5], Lucille Calmon[5,6], Vittoria Colizza[5], Tjibbe Donker[4], André Karch[3], Pascal Crépey[2], Laura Temime[1]

[1] Laboratoire Modélisation, épidémiologie et surveillance des risques sanitaires (MESuRS), Conservatoire national des arts et métiers, Paris, France [2] RSMS - U 1309, ARENES - UMR 6051, EHESP, CNRS, Inserm, Université de Rennes, Rennes, France [3] Institute of Epidemiology and Social Medicine, University Münster, Münster, Germany [4] University Hospital Freiburg, Freiburg, Germany [5] Sorbonne Université, INSERM, Sorbonne Public Health Institute, Sorbonne Université Modeling Outbreaks Center (SUMOC), France [6] ISI Foundation, Italy

Background. Inter-hospital patient transfers drive the spread of antimicrobial-resistant bacteria (ARB) across healthcare systems. Identifying high-risk introduction hospitals requires explicit transfer-network models and appropriate parameterization of within-hospital transmissibility (β). We characterized the French inter-hospital temporal transfer network, calibrated β against incidence benchmarks, and evaluated how introduction site shapes ARB dissemination. **Methods.** We developed a stochastic SIS metapopulation model on the 2024 French inter-hospital transfer network (2,519 facilities: acute care (MCO), rehabilitation (SSR), and mixed-type (MCO-SSR); daily transfer counts). Facility type-specific β were first estimated for validation using regional ESBL-producing *Enterobacterales* (ESBL-E) surveillance data (SPARES), assuming endemicity (5% prevalence on community admission; 2% initial prevalence in all facilities). Next, we explored seeding scenarios for an emerging ARB without community importation, calibrating β via grid search against ECDC benchmarks for two tiers: low (1.3–14.3/1,000 patient-days [pd]; carbapenem-resistant *Enterobacterales*) and moderate (14.3–28.7/1,000 pd; ESBL-E). We simulated 1,200 introductions of five colonized patients over 732 days, comparing seeding at the most central network hub with random introduction by facility type. **Results.** The network showed national connectivity with regional clustering and seasonal declines in transfers in August and December. SPARES-based β estimates ranged from 0.001 in rehabilitation to 0.008/day in private for-profit hospitals, with regional variation, reproducing observed French ESBL-E incidence (mean absolute error 3–16%). For seeding scenarios, calibration yielded β = 0.055/day (95% CI 0.03–0.08; low) and 0.178/day (95% CI 0.085–0.350; moderate). Extinction was highest after random MCO introduction under the low tier (85.3%) and lowest after random SSR under moderate tier (38.0%). Under moderate-tier transmission, hub introduction produced a cumulative incidence of 1.973/1,000 pd (95% CI 1.835–2.112), versus 1.053, 1.003, and 0.895 for random MCO, SSR, and MCO-SSR. **Conclusion.** Introduction site network position determines the scale of ARB dissemination across the French hospital system, supporting network-informed prioritization of surveillance resources.

KEYWORDS transfer networks, antimicrobial resistance, seeding simulations

Seeding Antimicrobial-Resistant Bacteria in the French Hospitalized Patient Network: How Index-Patient Characteristics Shape Colonization Dynamics

Shrichand Bhuria[1], Rany Octaria[2], Marco Mancastroppa[3], Madhav Chaturvedi[4], Daniel Goseberg[5], André Karch[4], Tjibbe Donker[5], Vittoria Colizza[6], Laura Temime[7], Pascal Crépey[1]

[1] RSMS - U 1309, ARENES - UMR 6051, EHESP, CNRS, Inserm, Université de Rennes, Rennes, France [2] Laboratoire Modélisation, Epidémiologie et Surveillance des Risques Sanitaires (MESuRS), France [3] Sorbonne Université Modeling Outbreaks Center (SUMOC), France [4] Institute of Epidemiology and Social Medicine, University Münster, Münster, Germany [5] University Hospital Freiburg, Freiburg, Germany [6] Sorbonne Université, INSERM, Institut Pierre Louis d'Épidémiologie et de Santé Publique, IPLESP, Paris, France [7] Laboratoire Modélisation, Epidémiologie et Surveillance des Risques Sanitaires (MESuRS), Paris, France

Background. Patients colonized with antimicrobial-resistant bacteria (ARB) can introduce resistant organisms into healthcare systems and generate onward transmission through ward-based contacts and subsequent patient movements. However, the consequences of an introduction event depend not only on bacterial transmissibility, but also on the characteristics of the index patient and the context of introduction. Patient-level factors, including the clinical setting at the time of introduction, healthcare exposure, and, indirectly, residential characteristics such as population density and socioeconomic context, may influence whether an introduction remains self-limited or spreads more widely. Understanding how index-patient profiles shape colonization dynamics may help identify high-risk introduction scenarios. **Methods.** Using nationwide French hospital-discharge data from 2023–2024, we reconstruct a temporal patient-based network connecting patients through overnight co-location within the same hospital ward. We simulate ARB colonization using a stochastic susceptible–colonized–susceptible model that allows clearance and recolonization, with transmission probabilities varying across clinical settings according to relative risks calibrated from national surveillance data for carbapenemase-producing *Enterobacterales*. Each simulation starts with a single colonized hospitalized patient and follows colonization dynamics for 90 days. We evaluate how different index-patient introduction scenarios influence subsequent spread and compare them with a reference random seeding strategy based on randomly selected eligible hospitalized patients and introduction dates. **Results.** We quantify heterogeneity in colonization trajectories following single-patient introduction events and identify scenarios associated with greater potential for onward dissemination. We characterize how differences in index-patient profiles and introduction contexts affect transmission patterns within the national patient-based network. **Conclusion.** By integrating a nationwide patient-based network with ARB transmission modelling, we provide a framework to assess how the characteristics of the first colonized patient shape antimicrobial resistance dissemination after introduction. Identifying high-risk introduction scenarios may complement surveillance approaches focused on healthcare facilities and support more targeted strategies to prevent ARB transmission.

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

Tommaso Bertola[1,2,3], Valentina Marziano[3], Simone Iacchini[4], Chiara Sacco[4], Alfredo De Bellis[3], Stefano Merler[3], Roberto Da Cas[4], Patrizio Pezzotti[4], Giorgio Guzzetta[3]

[1] University of Padua, Italy [2] Istituto Nazionale di Fisica Nucleare, Sezione di Padova, Italy [3] Fondazione Bruno Kessler, Trento, Italy [4] Istituto Superiore di Sanità, Rome, Italy

The coexistence of drug-susceptible and drug-resistant bacterial strains at different levels in neighboring geographies has been usually modelled at the country or federal state level, under homogeneous mixing assumptions. Here, we leverage multi-layer data on antibiotic resistance sentinel surveillance, antibiotic consumption in hospitals and the community, and hospital admission, discharge, and transfers, to reproduce the inter-regional heterogeneity of third-generation cephalosporins (3GC) resistant *Escherichia coli* in Italy in 2019–2023. We implemented a metapopulation model representing 19 Italian regions and 2 autonomous provinces, explicitly incorporating hospitalization dynamics and inter-regional coupling via commuting and hospital transfers. Transmission dynamics followed an established ecological model supporting the coexistence of drug-susceptible and resistant strains. We calibrated the model to routine antimicrobial resistance surveillance data in 2019, under the assumption of epidemic equilibrium, and validated predictions of temporal changes in resistance in 2020–2023, associated with dynamic regional antibiotic consumption rates. We additionally evaluated the impact of counterfactual scenarios, assuming homogeneous antimicrobial consumption across Italian regions. The model estimated that >90% of all new 3GC-resistant carriers arise from community transmission. Hospitals were amplifiers of resistance, with one-third of new 3GC-resistant carriers in hospitals being attributed to antibiotic-mediated selection. If all regions adopted the lowest 3GC consumption rates observed across Italian regions, the national proportion of 3GC-resistant *E. coli* would decrease from 33% to 14% in hospitals and from 17% to 5% in the community, with an estimated burden reduction for resistant infections of 60–65%. However, regional differences would still be partially maintained due to heterogeneities in transmission rates and inter-regional coupling. Our findings suggest that, although 3GC-resistant *E. coli* colonizations emerge mainly from transmission in the general community, hospitals have a disproportionate role in selecting and amplifying resistance. Antimicrobial stewardship actions in hospitals and in the community may produce large benefits towards reducing the burden of 3GC-resistant infections.

KEYWORDS *E. coli*, ecological coexistence, geographic variability, antimicrobial stewardship, hospital dynamics

Effectiveness of interventions to reduce MRSA carriage in a pediatric hospital

Alfredo De Bellis[1], Carmen D'Amore[2], Benedetta Zama[2], Elisa Cappelli[2], Chiara Mastrogiuseppe[3], Stefano Merler[1], Massimiliano Raponi[2], Giorgio Guzzetta[1], Marta Ciofi Degli Atti[2]

[1] Fondazione Bruno Kessler, Italy [2] Ospedale Pediatrico Bambino Gesù, Italy [3] Humanitas University, Italy

Methicillin-resistant *Staphylococcus aureus* (MRSA) can be carried asymptomatically or cause invasive infections. Assessing the impact of infection prevention and control (IPC) interventions on MRSA carriage among hospitalized children is essential to limit the associated disease burden. We developed an individual-based model of MRSA transmission to reproduce observed carriage rates in units implementing MRSA screening and related IPC protocols, including pediatric intensive care units (PICUs), neonatology (including neonatal intensive care unit, NICU), and cardiology. The model was informed by data on patient movements (admissions, discharges, units transfers) and IPC interventions such as nasal swab screening, contact precautions, and mupirocin decolonization. We used the calibrated model to assess transmission dynamics and the epidemiological impact of different screening strategies. MRSA carriage at admission was estimated at 3–9% in PICUs, 8–9% in neonatal units, and about 2% in cardiology and NICU. The mean reproduction number was 0.57 (95%CrI: 0.41–0.71), with highly heterogeneous transmission: 70% of carriers did not transmit MRSA, while 10% accounted for 60% of hospital-acquired colonizations. These superspreaders had longer hospital stays (mean 81 days) compared to the remaining 90% (mean 30 days). Removing IPC interventions would increase the reproduction number to 1.01 (95%CrI: 0.68–1.38), corresponding to a 44% reduction in transmission due to implemented IPC. Biweekly screening of all patients would reduce colonizations incidence by 33%, increasing tests by 56%. Targeted testing of highest-risk individuals using machine learning (ML) classifiers can achieve similar reductions with only a 20% increase in tests. Differences in carriage prevalence at admission across units suggest heterogeneity in patient risk factors. MRSA transmission may be driven by a small group of superspreaders with prolonged hospital stays. Transmissibility in the hospital remained below epidemic threshold and was substantially reduced by IPC measures. Targeted screening based on ML classifiers could significantly improve the cost-benefit ratio.

KEYWORDS MRSA, pediatric hospital, nosocomial transmission, screening strategies, mathematical modelling

Patient transfers and heterogeneous hospital clearing capacity shape regional vulnerability of the French healthcare system to *C. difficile* infections

Marco Mancastroppa[1], Lucille Calmon[1,2], Shrichand Bhuria[3], Madhav Chaturvedi[4], Daniel Goseberg[5], Rany Octaria[6], André Karch[4], Tjibbe Donker[5], Laura Temime[6], Pascal Crépey[3], Vittoria Colizza[1]

[1] Sorbonne Université Modeling Outbreaks Center (SUMOC), France [2] ISI Foundation Institute for Scientific Interchange, Italy [3] Recherche sur les services et le management en santé, France [4] Institute of Epidemiology and Social Medicine, University Münster, Germany [5] University Hospital Freiburg, Germany [6] Laboratoire Modélisation, épidémiologie et surveillance des risques sanitaires, France

Clostridioides difficile infections (CDI) are a growing public health concern in middle- and high-income countries. In France, CDI incidence increased in hospital settings in recent years. Since CDI is commonly acquired in hospitals, its circulation within the healthcare system can be sustained by patient transfers, and persistence is facilitated by heterogeneity in hospitals' capacity to clear CDI. Accounting for these factors is necessary to estimate local risk of CDI circulation in the French healthcare system. To assess regional vulnerability to CDI, we reconstructed intra-regional patient-transfer networks. Using PMSI data (Programme de médicalisation des systèmes d'information), we detected CDI activity periods in French healthcare facilities, defined by overlapping CDI-associated hospital stays. We inferred their duration from hospital characteristics and obtained hospital-specific clearing rates as the inverse of these durations. Leveraging an SIS transmission model between hospitals, with recovery parametrized by these rates, we estimated the vulnerability to CDI of regional networks, as the inverse of the epidemic threshold [Valdano et al., PRL (2018)]. We finally assessed the impact of considering inter-region transfers, uniform clearing rates or undirected, unweighted and static patient-transfer networks.

Hospitals show heterogeneous CDI clearing rates shaping regional vulnerability: Corse and Île-de-France present the lowest risk, while Hauts-de-France and Grand-Est the highest. Regional vulnerability is positively correlated with the observed number of CDI diagnoses per hospital, providing empirical support for the vulnerability estimates. Results are robust to cross-border transfers; however, homogeneous clearing capacity or neglecting network characteristics reshapes regions' ranking (Kendall's τ=0.74 and −0.10).

Regional differences in CDI vulnerability result from the interplay of transfers and heterogeneity in hospital clearing rates, rather than either factor. Both should be considered when building vulnerability maps, since considering only one alter the spatial distribution of estimated vulnerability and the identification of regions where CDI persistence is harder to interrupt.

From Disease-Specific to Whole-Healthcare-System Simulations: Challenges in Integrated Modelling

Margherita Molaro

Imperial College London, United Kingdom

No abstract is available for this invited talk – the rest of this page is left for your notes.

Limitations in patient-transfer data introduce contrasting biases in estimates of nosocomial infection persistence across healthcare systems

Marco Mancastroppa[1], Lucille Calmon[1,2], Madhav Chaturvedi[3], Daniel Goseberg[4], Shrichand Bhuria[5], Rany Octaria[6], André Karch[3], Tjibbe Donker[4], Laura Temime[6], Pascal Crépey[5], Vittoria Colizza[1]

[1] Sorbonne Université Modeling Outbreaks Center (SUMOC), France [2] ISI Foundation Institute for Scientific Interchange, Italy [3] Institute of Epidemiology and Social Medicine, University Münster, Germany [4] Institute for Infection Prevention and Hospital Epidemiology, University Hospital Freiburg (UKF), Germany [5] Recherche sur les Services et le Management en Santé (RSMS - U1309), Arènes (UMR6051), France [6] Laboratoire Modélisation, Epidémiologie et Surveillance des Risques Sanitaires (MESuRS), France

Patient transfers can sustain the spread of healthcare-associated infections across facilities, making their control a healthcare-system problem rather than solely a hospital-level problem. Data on patient transfers are needed to reconstruct the healthcare network and estimate its risk to the persistence of infections. However, available data have different resolution and coverage: in France a high-resolution nationwide healthcare network can be reconstructed, whereas in Germany only regional networks with partial patients' coverage are available. Such data limitations raise concerns about the extent to which estimates of the risk of sustained transmission can be considered reliable. In order to quantify these biases, we reconstructed several French healthcare networks under various aggregation and coverage assumptions, as well as partial regional German networks. We quantified how these data limitations affect estimates of the vulnerability of the hospital system to nosocomial infections, defined as the inverse of the epidemic threshold, accounting for the directionality, volume and evolution of patient transfers [Valdano et al. PLR (2018)]. Temporal aggregation systematically overestimates the ability of pathogens to persist across the healthcare system, increasing the estimated vulnerability by up to a factor 18. However, if the aggregation window is shorter than the average hospital clearing time, temporally aggregated data may provide robust vulnerability estimates. Incomplete observation has instead the opposite effect, systematically underestimating the risk of sustained transmission. By detecting only 34% of transfers, as in the German case, the estimated vulnerability is 3.6 times smaller than the estimate obtained using the full population coverage. Limitations in patient-transfer data can substantially bias estimates of healthcare-system epidemic risk, depending on population coverage and the relationship between data resolution and infection timescale. Quantifying these effects identifies when routinely available data remain informative and provides a basis for interpreting—and potentially correcting—biased risk estimates.

KEYWORDS data limitations, patient transfers, nosocomial infections, healthcare networks, France, Germany, bias, risk assessment, vulnerability, systemic risk, temporal network, resolution, coverage

Scaling up incomplete hospital admissions data for the construction of healthcare transfer networks

Madhav Chaturvedi[1], Shrichand Bhuria[2], Lucille Calmon[3,4], Daniel Goseberg[5], Marco Mancastroppa[3], Rany Octaria[6], Vittoria Colizza[3], Tjibbe Donker[5], Laura Temime[6], Pascal Crépey[2], André Karch[1]

[1] Institute of Epidemiology and Social Medicine, University of Münster, Münster, Germany [2] RSMS - U 1309, ARENES - UMR 6051, EHESP, CNRS, Inserm, Université de Rennes, Rennes, France [3] Sorbonne Université, INSERM, Sorbonne Public Health Institute, Sorbonne Université Modeling Outbreaks Center (SUMOC), Paris, France [4] ISI Foundation, Turin, Italy [5] University Hospital Freiburg, Germany [6] Laboratoire Modélisation, Epidémiologie et Surveillance des Risques Sanitaires (MESuRS), CNAM, Paris, France

Patient transfers between hospitals form an important pathway through which antimicrobial resistant bacteria (ARBs) can spread and persist within the healthcare system of a region, eventually spilling out into the general population. Modelling and understanding the patient transfer network within hospitals is thus vital to understanding and preventing the spread of ARBs within a region. Given data on all hospital admissions and discharges within a certain region, it is straightforward to create such a patient transfer network. However, such comprehensive data is not always easily available, and researchers may only have access to part of this data (for example, data from one health insurance provider). We investigated ways to upscale such incomplete admissions data to a dataset of similar size to the complete data, for the purposes of obtaining patient transfer networks that can approximate networks obtained using a complete admissions dataset. The approach used most commonly in the literature involves simply bootstrapping patient records from the incomplete dataset until the desired size is reached. We compared this bootstrapping approach to an approach we developed, which involves obtaining from the incomplete dataset a transition matrix which defines how likely an individual is to be transferred from one hospital to the other (either directly or indirectly via the community), and then generating the desired number of hospital records by simulating hospital stays as Markov chains using this transition matrix. We found that, although the Markov chain approach did not reproduce seasonal and holiday-related (re)admission patterns observed in empirical data as well as the bootstrapping approach, it was much less susceptible to biases in the subsequent analysis caused by the arbitrary left- or right-censoring of the empirical dataset induced when defining the period of interest of the study, as well as to other forms of selection bias.

Data-Driven Infection Risk Forecasting in Hospital Contact Networks: Integrating Mechanistic Compartmental Models with Graph Neural Networks

Yamil Vindas[1], Alban Bornet[1], Mohamed Abbas[2], Damien Geissbühler[3], Jose F. Rodrigues-Jr[4], Douglas Teodoro[1]

[1] University of Geneva, Switzerland [2] University Hospital of Geneva, Switzerland [3] Max-Planck-Institute for the Science of Light, Germany [4] University of São Paulo, Brazil

Background & motivation. Hospital-acquired infections and antimicrobial-resistant pathogens spread through time-varying contact networks involving patients, healthcare workers, and clinical environments[1]. Early identification of high-risk patients can support targeted infection prevention and control (IPC). Temporal and space-time-and-memory graph neural networks (GNNs/STM-GNNs) can model such networks[2], but standard deep learning lacks mechanistic disease constraints and interpretability. **Methods.** We introduce an Epidemiology-Informed Graph Neural Network (EIGNN) combining graph learning with compartmental models (SIR, SEIR, SEIRD-NS) to predict patient-level state transitions and infection risk, while estimating epidemiological parameters (e.g., transmission/recovery rates and basic reproduction number). We evaluate two physics-informed paradigms: AutoDiff, minimizing continuous-time residuals via automatic differentiation[3], and ODE-NSP, predicting next states using discrete-time hazard equations and a differentiable physics layer with learnable epidemiological parameters. EIGNN also applies biological transition masking and monotonicity constraints, to penalize forbidden state transitions. **Results.** Across 1-, 3-, and 7-day horizons, we evaluated three datasets: HUG-COVID[2] (282 patients, 52 nosocomial cases, 135 days), SocioPatterns[5] pseudo-synthetic contacts, and a synthetic 236-bed *Clostridioides difficile* hospital simulation (Murcia)[6]. Across several GNN backbones, EIGNN variants reached up to 98.46% AUC-ROC, while improving calibration at longer horizons. In addition, EIGNN recovered biologically plausible epidemiological parameters for the HUG-COVID dataset consistent with clinical baselines, including a recovery period of approximately 12 days. **Clinical relevance.** By embedding mechanistic disease dynamics in dynamic contact networks, EIGNN links scientific modeling with actionable IPC decision support and prospective scenario analysis, enabling simulation of patient cohorting, staff assignments, antibiotic stewardship, or social distancing interventions before deployment in hospital networks.

REFERENCES [1] Liu & Dickter, Gastrointest Endosc Clin N Am, 2020 [2] Geissbuhler et al., Artificial Intelligence in Medicine, 2025 [3] Raissi et al., J Comput Phys, 2019 [4] Myall et al., Lancet Digit Health, 2022 [5] Génois & Barrat, EPJ Data Sci, 2018; Vanhems et al., PLoS ONE, 2013 [6] Kim et al., Sci Rep, 2023

Dynamic graph machine learning for early detection of antimicrobial resistant infections from acute care data

Oskar Fraser-Krauss[1], Mauricio Barahona[2]

[1] Department of Mathematics, Imperial College London, United Kingdom [2] Imperial College London, United Kingdom

Predicting infection risk in real time is paramount to preventing its spread. Incorporating information on patients' contacts and co-location can improve individualised risk stratification beyond patient characteristics alone. Furthermore, hospital-acquired infections contribute to the burden of antimicrobial resistance (AMR), highlighting the need for approaches that can identify patients at increased risk of infection and support timely infection prevention and control interventions. Electronic health records (EHRs) provide a rich source of patient information, but translating these temporally evolving data into representations suitable for dynamic graph machine learning remains challenging. We present a framework for generating patient-level dynamic graph representations capable of being deployed in real time. We construct network graphs in which edges represent within- and between-hospital ward movements, while node features comprise microbiology and virology test results and patient demographics. These dynamic graph representations are provided as input to the EvolveGCN model, which learns from changes in network structure and patient-level features across successive time points. The model generates patient-specific infection-risk probabilities, enabling risk estimates to be updated in real time based on patient co-location and movement. We implemented the framework using data from 1,995,905 hospital inpatients admitted to a UK National Health Service hospital group (Imperial College Healthcare NHS Trust), comprising four major hospitals, since January 1, 2015, including 3,466,105 ward movements. Our approach demonstrates the feasibility of leveraging routinely collected EHR and clinical laboratory data to bridge the gap between complex dynamic graph theory and real-time clinical decision support. Ultimately, this framework provides data-driven infection risk prediction to support infection prevention and control teams in identifying patients at increased risk, enabling timely interventions to reduce nosocomial transmission and inform strategies to limit the spread of AMR.

KEYWORDS antimicrobial resistance, dynamic graphs, machine learning, nosocomial infection, electronic health records

Antibiotics as infrastructure for civilization

Kevin Outterson(remote presentation)
Boston University School of Law, United States

No abstract is available for this invited talk – the rest of this page is left for your notes.

Estimation of hospital catchment populations from patient flows in France

George Shirreff[1], Cécile Chauvel[1], Jean-Sebastien Casalegno[2], Philippe Vanhems[2], Cédric Dananché[2], Abdesslam Redjaline[3], Karim Tazarourte[1], Marta C. Nunes[2]

[1] Université Claude Bernard Lyon 1 - Faculté des sciences, France [2] Hospices Civils de Lyon, France [3] Centre Hospitalier Le Corbusier, Firminy, France

Background. Estimating the burden of community-acquired disease from hospital data requires appropriate definition of the population from which patients are drawn. Patient flows between residential areas and healthcare facilities provide an opportunity to derive catchment populations while also characterising networks through which patients access care. **Methods.** Catchment populations were estimated for hospitals throughout France using a proportional flow approach. National data on hospital use and patient residence were accessed from the Agence Technique de l'Information sur l'Hospitalisation (ATIH). For each administrative area, we calculated the proportion of patients attending each hospital, and combined this with population data to estimate hospital-specific catchment populations. We examined variation by age, geographic resolution, and type of hospital visit and major diagnostic category. For one large hospital group (Hospices Civils de Lyon, HCL), we compared these estimates with data on emergency visits, and data from a retrospective cohort of respiratory infections. **Results.** Catchment populations varied substantially by hospital group, reaching approximately 4 million per year for Assistance Publique – Hôpitaux de Paris. Catchment distributions reflected geographic proximity and hospital scale but frequently extended across administrative boundaries, illustrating the overlapping nature of healthcare utilisation networks. Catchment size also varied widely across diagnostic category, with specialised services drawing patients from considerably larger populations. Emergency department catchments were smaller than those based on hospitalisations. For the HCL, estimated catchment distributions closely corresponded to the residential information of patients observed in the respiratory cohort. **Conclusions.** This study demonstrates the consistency of the proportional flow framework when applied to data on hospital usage. Catchment populations for each hospital group and individual hospital in France were determined which providing denominators for incidence estimation, but also quantify the interconnectedness of healthcare populations. This could support analyses on how overlapping hospital catchments influence the burden of hospital-acquired infections and antimicrobial resistance.

KEYWORDS catchment population, catchment area, patient flow, proportional flow, denominator, hospital admission, respiratory infections

Regional structuring of healthcare networks, and their shared AMR problems

Tjibbe Donker

Medical Center – University of Freiburg, Germany

Shared patients between hospitals provide potential transmission routes of antimicrobial resistant (AMR) micro-organisms between hospitals. As a result, the structure of the network formed by these shared patients influences the dissemination of AMR on local, regional, and national levels. Because these healthcare networks have a clear regional structuring, the dissemination of AMR can be expected to follow a clustered dynamic.

By describing the genetic diversity of MRSA ST22, as well as the occurrence of different resistance mechanisms in Carbapenemase-Producing *Enterobacterales* (CPE), we study the effect of regional clustering in the English hospital network on the dissemination of these AMR micro-organisms. These results are compared to both geographical and administrative boundaries to determine to what extent the network influences their distribution.

MRSA ST22 isolates submitted by hospitals within network clusters are genetically more similar than those submitted from hospitals in different clusters. Random assignment of hospitals to different clusters always resulted in worse inter-cluster genetic separation of the isolates. CPE isolates showed clear association with the hospital network clusters. For both MRSA and CPE, the regional structure of the hospital network provided a stronger association than the administrative boundaries.

Hospitals within regional clusters share their AMR problems with each other, while borders between these clusters form a barrier for AMR dissemination. AMR infection prevention and control, as well as surveillance, need to take this effect into account. Elevated rates of AMR in one hospital within the cluster may quickly affect other hospitals within the cluster. A joint regional AMR prevention and control strategy based on the hospital network structure is therefore advisable.

Inference and control of antimicrobial-resistant organisms in hospitals

Sen Pei

Columbia University, United States

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Evidence for patterns of colonization risk in the nationwide hospitalized patient network in France

Shrichand Bhuria[1], Lucille Calmon[2], Madhav Chaturvedi[3], Laura Temime[4], André Karch[3], Tjibbe Donker[5], Vittoria Colizza[6], Pascal Crépey[1]

[1] RSMS - U 1309, ARENES - UMR 6051, EHESP, CNRS, Inserm, Université de Rennes, Rennes, France [2] Institut Pierre Louis d'Epidémiologie et de Santé Publique, France [3] Institute of Epidemiology and Social Medicine, University Münster, Münster, Germany [4] Laboratoire Modélisation, Epidémiologie et Surveillance des Risques Sanitaires (MESuRS), Paris, France [5] University Hospital Freiburg, Freiburg, Germany [6] Sorbonne Université, INSERM, Institut Pierre Louis d'Épidémiologie et de Santé Publique, IPLESP, Paris, France

Patient movement within and between hospitals creates a complex hospital network that facilitates the spread of antimicrobial-resistant bacteria and contributes to healthcare-associated infections. Yet most national-scale studies infer spread from aggregated hospital-to-hospital patient sharing, leaving patient-to-patient contact pathways and the role of routine patient mobility in shaping colonization risk poorly characterized. Using France's 2023–2024 national hospital-discharge data, we reconstructed a temporal patient-based network of 10.4 million patients across 1,408 acute-care hospitals, comprising 326.6 million overnight ward co-location interactions. We simulated colonization over 365 days on the observed day-by-day temporal network using a stochastic susceptible-colonized-susceptible model, with a mean colonization duration of 180 days. We used national carbapenemase-producing *Enterobacterales* (CPE) surveillance data to calibrate differences in transmission risk across clinical settings. Across 2,000 simulations initiated on randomly selected dates in 2023, we calculated patient-level colonization probabilities and summarized risk across patients' residential areas, wards, and hospitals. We further assessed hospital-level consistency between simulated risk and recorded CPE occurrence. Simulated risk was highly heterogeneous across patients and care settings. When mapped by place of residence, hospital-associated colonization risk showed strong spatial clustering in both urban and rural areas. Multivariable regression analyses identified patient- and hospital-level characteristics associated with heterogeneity in simulated colonization risk. Sensitivity analyses varying initial seeding and colonization duration showed that relative risk patterns remained highly stable. This nationwide framework shows how patient mobility and ward co-location patterns can reveal patterns of hospital-associated colonization risk and could support pathogen-specific surveillance and intervention evaluation.

KEYWORDS antimicrobial resistance, healthcare-associated infections, mathematical model, colonisation risk, patient-based network, temporal network

Modelling pathogen spread and control across a regional patient-sharing network

Elise Hodbert[1,2], Laura Temime[3,4], Gabriel Birgand[1,5]

[1] Cibles et Médicaments des Infections et de l'Immunité - UR 1155, France [2] Laboratoire Modélisation, épidémiologie et surveillance des risques sanitaires, France [3] PACRI unit, Institut Pasteur, Conservatoire national des arts et métiers, Paris, France [4] Modélisation, épidémiologie et surveillance des risques sanitaires (MESuRS), Conservatoire national des arts et métiers, Paris, France [5] Mission PRIMO de surveillance nationale de l'antibiorésistance en soins de ville et secteur médico-social, France

Background and aims. Patient transfers connect healthcare facilities which can facilitate the spread of multidrug-resistant organisms. Most patient-sharing networks have focused on hospitals, despite the potential role of nursing homes as reservoirs. We aimed to characterize a patient-sharing network including nursing homes in the Pays de la Loire region, develop a transmission model of ESBL-producing *Enterobacterales* (ESBL-E), and assess control strategies for an emergent highly transmissible pathogen. **Methods & results.** Using French national healthcare data from 2017–2023, we reconstructed annual directed weighted networks linking 603 healthcare facilities and nursing homes through direct patient transfers. Network density increased from 0.012 in 2017 to 0.016 in 2023, with increasing transfers from nursing homes to general and university hospitals. Seven geographically structured communities were identified. Centrality analyses identified eight facilities remaining among the ten most central throughout 2017–2023, including both university hospitals, five general hospitals and one private clinic. We developed a stochastic metapopulation model with susceptible-colonised-susceptible dynamics within facilities, coupled to observed transfers and community admissions and discharges. Facility-type-specific transmission rates were calibrated against ESBL-E incidence from surveillance data. The calibrated model reproduced observed incidence across facility types, supporting its ability to capture regional transmission dynamics. We then simulated introduction of a more transmissible emerging pathogen and extended the model to include quarantine and facility-level alert. We compared baseline with strategies triggered by cases detected in nursing homes, rehabilitation facilities, or hospitals. Colonised patients transferred from alerted facilities were quarantined on admission to receiving facilities. Preliminary results suggest that nursing home-triggered alerts tended to reduce final prevalence across facility types. **Implications.** This framework combines patient-sharing network analysis with a data-calibrated transmission model to identify key facilities for surveillance and explore targeted quarantine strategies for emerging resistant pathogens.

KEYWORDS regional interfacility network, nursing homes, metapopulation model, ESBL-producing *Enterobacterales*, emerging pathogen

Modelling and targeted control of healthcare-associated infections in regional healthcare networks

Konrad Sakowski

Institute of High Pressure Physics, Polish Academy of Sciences, Poland

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The patient trajectories forming healthcare networks

Tjibbe Donker, Daniel Goseberg
University Hospital Freiburg, Freiburg, Germany

Hospital network analysis provides a powerful tool in the study of the spread of antimicrobial resistance (AMR). While each patient movement forms a potential transmission route between hospitals, the total flow of patients is a strong indicator for the risk of an AMR outbreak in one spreading to the next hospital. However, hospital network reconstruction is traditionally done based on single-step patient movements, disregarding any previous hospital admissions in the patient's healthcare trajectory We studied the contribution of individual patient trajectories on the structure of the healthcare network in Baden-Württemberg, Germany, by tracking admission motifs in the trajectories. These motifs are formed by three consecutive admissions, thus containing two between-hospital movements. This results in five possible motifs, which we compared based on length of stay, time between admissions, and their occurrence over link weights. The largest part of the motifs was formed by three admissions to the same hospital (AAA, 51%), with the other four possible motifs being approximately equally prevalent (9.5% - 13.6%). Loop motifs (ABA) showed the highest proportion of direct transfers (21.8%), followed by motifs containing three different hospitals (ABC, 14.2%). Patients tended to keep the same motif during their entire trajectory, particularly for AAA motifs. Strong inter-hospital links in the hospitals network were dominated by ABA and AAB motifs, while weaker links showed higher proportions of ABC motifs. Admission motifs are not uniformly distributed over the hospital network, nor over the patient population. As a result, hospital network analyses based on single-step patient movements may over-estimate the probability of hospital-associated pathogens, such as AMR, to spread between different parts in the network. As patients are more likely to return to previously visited hospitals than new ones, they are more likely to return any hospital-acquired pathogens to already affected hospitals than spread it to new institutions.

KEYWORDS network reconstruction, motifs

Patterns of Patient Contact and Transfer Across Clinical Settings in the French Hospital System: Potential Pathways for Pathogen Dissemination

Pascal Crépey[1], Shrichand Bhuria[1], Rany Octaria[2], Marco Mancastroppa[3], Lucille Calmon[4], Madhav Chaturvedi[5], Daniel Goseberg[6], André Karch[5], Tjibbe Donker[6], Vittoria Colizza[7], Laura Temime[8]

[1] RSMS - U 1309, ARENES - UMR 6051, EHESP, CNRS, Inserm, Université de Rennes, Rennes, France [2] Laboratoire Modélisation, épidémiologie et surveillance des risques sanitaires (MESuRS), Conservatoire national des arts et métiers, Paris, France [3] Sorbonne Université Modeling Outbreaks Center (SUMOC), France [4] Institut Pierre Louis d'Epidémiologie et de Santé Publique, France [5] Institute of Epidemiology and Social Medicine, University Münster, Münster, Germany [6] University Hospital Freiburg, Freiburg, Germany [7] Sorbonne Université, INSERM, Institut Pierre Louis d'Épidémiologie et de Santé Publique, IPLESP, Paris, France [8] Laboratoire Modélisation, Epidémiologie et Surveillance des Risques Sanitaires (MESuRS), Paris, France

Background. Patient co-location within hospital wards creates opportunities for pathogen transmission, while subsequent transfers may transport this risk across clinical units and healthcare facilities. However, national-scale studies rarely characterize both ward-level contact structure and patient movement across clinical settings. We aimed to describe patient contact and transfer patterns in the French hospital system and identify structural pathways relevant to potential pathogen dissemination. **Methods.** We used French national hospital-discharge data (PMSI-MCO). Using 2023 data, we reconstructed a directed, weighted, temporal ward-based transfer network in which nodes represented medical units and edges represented direct same-day transfers between consecutive ward episodes of the same patient. Transfers were characterized by ward type, broad clinical group, and within-versus inter-hospital movement. Using 2023–2024 data, we also reconstructed ward-level patient co-location networks within major clinical groups based on overnight stays. Age-specific matrices described relative pairwise co-location frequency and mean overlap duration between co-located age pairs. **Results.** The ward-transfer network included 1,889,077 transferred patients, 3,227,740 transfer events, 373,766 directed ward-to-ward connections, 24,178 medical units, and 1,428 hospitals. Overall, 80.4% of transfers occurred within hospitals and 19.6% between hospital sites. Transfer patterns differed markedly across clinical settings. Emergency and short-stay units accounted for 30.8% of outgoing transfers, whereas adult medicine received the largest proportion of incoming transfers. Within-hospital movements reflected pathways linking emergency, medicine, surgery, and critical-care settings, while inter-hospital transfers showed distinct bridging patterns concentrated in specific ward types. Age-specific co-location matrices revealed substantial heterogeneity across clinical groups in contact frequency and overlap duration. **Conclusions.** Patient co-location and transfer patterns are highly structured and heterogeneous across clinical settings. Combining ward-level contact structure with patient-transfer pathways provides a framework for identifying settings that may facilitate local pathogen exposure and broader dissemination across healthcare facilities. This approach highlights care-pathway features that may inform interventions against nosocomial pathogen spread.

KEYWORDS antimicrobial resistance, ward-level network, clinical pathways, patient colocation

Summary and perspectives

Gabriel Birgand
Nantes University Hospital, France
Introduced by Laura Temime.

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List of participants

Registered participants and invited speakers, as of 11 October 2026.

Ait Bouziad, Karim
Cnam

Apolloni, Andrea
ANSES

Aupépin, Chloé
Conservatoire national des arts et métiers

Baye, Lina
Faculty of medicine

Bennoura Bouchiba, Karim
Institut Pasteur

Bertola, Tommaso
University of Padova & Fondazione Bruno Kessler

Bhuria, Shrichand
EHESP Rennes

Birgand, Gabriel
Nantes University Hospital, France

Bizzotto, Andrea
Institut Pasteur

Bracher, Johannes
Karlsruhe Institute of Technology

Calmon, Lucille
INSERM

Chaturvedi, Madhav
University of Münster

Colizza, Vittoria
Epicx Lab

Cozzolino Cangiano, Claudia
Sorbonne Public Health Institute, SUMOC

Crépey, Pascal
EHESP Rennes

De Bellis, Alfredo
Fondazione Bruno Kessler

Deng, Qi
York University

Donker, Tjibbe
Institute for Infection Prevention and Hospital Epidemiology, Medical Center University of Freiburg

Fraser-Krauss, Oskar
Imperial College London

Garal, Marie-Rachel
Medical Center – University of Freiburg, Germany

Givehchi, Saeed
Faculty of Environment, University of Tehran

Guijarro Matos, Ana
Université de Montpellier

Guzzetta, Giorgio
Fondazione Bruno Kessler

Hodbert, Elise
Conservatoire National des Arts et Métiers

Hodgetts, Timothy
Independent Researcher

Karch, André
University of Münster, Germany

Kociurzynski, Raisa
Medical Center - University of Freiburg

Latif, Fatima
Sonographer, Cardiff, United Kingdom

Leclerc, Quentin
Conservatoire National des Arts et Métiers

Mancastroppa, Marco
Sorbonne Université Modeling Outbreaks Center (SUMOC), Sorbonne Université, INSERM, Sorbonne Public Health Institute

Maurin, Aurélie
Conservatoire national des arts et métiers

Mengoni Noritake, Leon
Bruno Kessler Foundation (FBK)

Molaro, Margherita
Imperial College London, United Kingdom

Octaria, Rany
Cnam

Opatowski, Lulla
Institut Pasteur / UVSQ / INSERM

Otero, Sofia Myrup
Statens Serum Institut

Outterson, Kevin
Boston University, United States

Pei, Sen
Columbia University, United States

Price, Trevor
Newcare Institution

Robotham, Julie V.
UK Health Security Agency / University of Oxford, United Kingdom

Roudakian, Kamyar
INSERM

Roustit, Manon
INRAE

Sakowski, Konrad
Institute of High Pressure Physics, Polish Academy of Sciences, Poland

Shirreff, George
Université Claude Bernard Lyon 1

Syaban, Satria Nur
Laboratoire MESuRS, Conservatoire des arts et métiers

Temime, Laura
Cnam

Vindas, Yamil
Université de Genève



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