



Scientific Conference & Closing Event

Emerging infectious diseases in Europe: challenges and opportunities in data sharing and modelling of response for improved One Health

**26th and 27th
November 2024**

Istituto Superiore di Sanità
Rome, Italy
Viale Regina Elena, 299

BOOK OF ABSTRACTS



This work has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement MOOD N° 874850.

Welcome

Dear Colleagues,

On behalf of the Organizing Committee, it is our pleasure to invite you to participate in the international conference entitled:

Emerging Infectious Diseases in Europe: Challenges and Opportunities in Data Sharing and Modelling of Response for Improved One Health

This conference, co-organized by the French Agricultural Research Centre for International Development (CIRAD), the Italian National Institute of Health (Istituto Superiore di Sanità - ISS) and the Edmund Mach Foundation (FEM), will be held from **Tuesday 26 to Wednesday 27 November 2024** in **Rome**, Italy.

The conference marks the conclusion of the H2020 MOOD project ("Monitoring Outbreak events for Disease Surveillance in a Data Science Context"). Over two days, participants will explore current research and outcomes in the field of emerging infectious diseases, examine critical challenges, and discuss future directions. The event will also present innovative tools, data, and models for epidemic intelligence, all developed within the MOOD project, and emphasize the interdisciplinary efforts required under the "One Health" initiative.

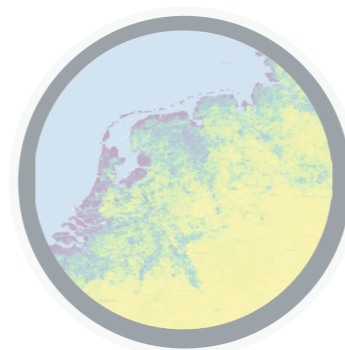
The scientific program will span two days:

- **November 26, 2024** will feature four major scientific sessions, including plenary and keynote lectures delivered by invited experts.

- **November 27, 2024** will highlight key scientific results from the MOOD project, including the MOOD platform and its associated tools. The day will conclude with a roundtable discussion involving representatives from the MOOD project, other EU-funded initiatives, and international organizations, addressing critical issues and future challenges in the field.

Yours sincerely,

The Organizing Committee



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Guest Speakers

Day 1: Scientific Conference

Maria Van Kerkhove



Dr. Maria Van Kerkhove is the Acting Director of the Department of Epidemic and Pandemic Prevention and Preparedness as well as the COVID-19 Technical Lead of the World Health Organization (WHO) and Head of the Emerging Diseases and Zoonoses Unit in the WHO's Health Emergencies Programme. Dr. Maria Van Kerkhove's work focused on zoonotic, respiratory and emerging/re-emerging diseases such as avian influenza, MERS, SARS, COVID-19, Ebola, Marburg, plague and Zika. Her research has focused on understanding and mitigating factors that are associated with transmission of zoonotic pathogens between animals and humans.

Session A: Respiratory transmitted pathogens (Influenza viruses, coronaviruses)

Birgitte Freiesleben de Blasio

Birgitte Freiesleben de Blasio is the Scientific Director at the Division of Infection Control at the Norwegian Institute of Public Health (NIPH) and holds a secondary professorship at the Department of Biostatistics, University of Oslo. With a background in physics, she leads the NIPH modelling team, focusing on research in surveillance, forecasting, and scenario analyses of infectious diseases of relevance for policy advice and social mixing behaviour related to the spread of infections.



Session B: Climate-sensitive infectious diseases in Europe

Joacim Rocklöv



Joacim is an eco-epidemiologist and modeller researching climate-sensitive infectious diseases. He obtained his PhD from Umeå University, Sweden. In the year 2021, he was awarded an Alexander von Humboldt Professorship endowed by the Federal Ministry of Education and Research in Germany. The chair at Heidelberg University is a bridge between the Heidelberg Institute of Global Health and the Interdisciplinary Centre for Scientific Computing. Joacim leads several larger international projects related to climate change, the environment, and health.

Alessandra della Torre



Alessandra della Torre (AdT) is Associate Professor of Parasitology at University SAPIENZA of Rome, where since year 2000 she coordinates the Medical Entomology research group at the Department of Public Health and Infectious Diseases. Since 2023 she coordinates the Research Node on Arthropod Vectors and Arthropod-transmitted Diseases of the INF-ACT project (MUR PNRR Extended Partnership initiative on Emerging Infectious Diseases), which gathers all Italian Research and Public Health Institution working on the topic.

Giovanni Savini



Giovanni Savini, head of the Public Health Laboratory at the IZS-Teramo, received his professional training in veterinary medicine at the University of Milan and completed his PhD in Epidemiology at Murdoch University, Western Australia. He then obtained a postgraduate specialization in Animal Health, Hygiene of Animal Breeding, and Their Products from the University of Pisa, Italy. In 2005, he was designated as a Bluetongue expert by the WOA, and the department he leads was recognized as WOA Reference Laboratory for Bluetongue (BT).

Session C: Antimicrobial Resistance

Tjibbe Donker



Tjibbe Donker is infectious disease modeller at the University Medical Center Freiburg, Germany, and group leader of the Quantitative and Predictive Infectious Disease Epidemiology group. His work includes the influence of patient referral networks on the spread of antimicrobial resistance (AMR), nowcasting and forecasting of epidemics, and the estimation of disease parameters from genomic data. He worked at the Dutch National Institute for Public Health and the Environment (RIVM), developing a novel way of looking at the spread of AMR by analysing the network of hospitals formed by patients exchanged between them.

Session D: Disease X and pandemic preparedness

Wanda Markotter



Prof. Wanda Markotter holds a PhD in Virology and started her academic career at the University of Pretoria (UP), South Africa, in 2004. She is currently the Director of the Centre for Viral Zoonoses, Department of Medical Virology, Faculty of Health Sciences. Since 2016, she has been a DSI-NRF South African Research Chair in Infectious Diseases of Animals (Zoonoses), and in 2021, she was also appointed as a Research Chair in People, Health and Places (One Health) at the Future Africa Institute at UP. She also served as the co-chair of the One Health High-Level Expert Panel (OHHLEP) advising the WHO, WOA, FAO and UNEP.

Niel Hens

Prof. Dr. Niel Hens (M) is a biostatistician and mathematical epidemiologist with over 18 years of experience in human epidemiology and an established international expert in infectious disease modelling. He is Full Professor in biostatistics, director of the Center for Statistics, co-director of the SIMD consortium, and director of the Data Science Institute (DSI, UHasselt) and Full Professor in biostatistics holding the scientific chair in evidence-based vaccinology at the Vaccine and Infectious Disease Institute (Vaxinfectio, University of Antwerp).



Brett Archer



Mr Archer is an Epidemiologist in the Surveillance Systems Department in the WHO Health Emergencies Programme. After undertaking medical science, public health and field epidemiology training, he has dedicated the past 15 years to strengthening public health intelligence for minimizing the impact of infectious diseases and outbreaks at state and national level in South Africa (NICD) and Australia (NCIRS, NSW Health, DHAC), regionally (WHO Regional Office for Africa), and now globally.

Day 2: Closing Event

Session A: From disease profiles to modeling and risk mapping

Didier Fontenille



Didier Fontenille is a medical entomologist from IRD, Montpellier, France. He spent 22 years in tropical countries in Madagascar, Senegal, Cameroun and Cambodia working on vector borne diseases, particularly malaria, Dengue, Chikungunya, Yellow fever, Japanese encephalitis, Rift valley fever. He is a member of COVARIS (Comité Français de veille et d'anticipation des risques sanitaires) and several international expert committees. He is now helping to structure research in France and at the University of Montpellier on 'One Health', climate change and vector-borne diseases issues.

Session B: Lessons learned on disease- X

Marisa Peyre



Marisa Peyre (Eng., Ph.D., HDR) is an epidemiologist and deputy director of ASTRE, the integrated health research unit in CIRAD. She specialized on the evaluation of health surveillance systems in developed and developing countries including community-based systems, on emerging zoonotic risks and on the strengthening of public-private partnerships. She provides expertise for international organisations (FAO, WOAAH, WB, PF). She is a co-founder and global science leader of the PREZODE initiative (Preventing Zoonotic Disease Emergence). She drives an international change in paradigm towards increased prevention of health risks using a bottom-up approach.

Session C: Data preparedness and innovative tools for improved EI in Europe

Paolo Tizzani



Dr. Paolo Tizzani is a veterinarian, graduated in 2000. From 2001 to 2015 he worked at the University of Turin (Italy) - Department of Veterinary Sciences. His research has mainly focused on the ecology and epidemiology of wildlife diseases. He obtained his PhD in Parasitology in 2007. He worked in several EU-funded projects on the control of infectious animal diseases. Dr Tizzani joined WOAAH (World Organisation for Animal Health) headquarters in Paris in 2015 as a Veterinary Epidemiologist. Dr Tizzani is currently working in the WOAAH Data Integration Department. He has authored or co-authored more than 100 peer-reviewed scientific articles in international journals.

Session D: Reaching out to users and impacts for Improved EI in Europe

Beate Conrady



Beate Conrady is a Full Professor in Veterinary Health-Informatics and -Economics and the leader of the Infectious Disease Epidemiology & Animal Health Economics Group (TIPTON Group) at the Department of Veterinary and Animal Sciences, at the University of Copenhagen. and sShe works for the FAO of the United Nations. Beate Conrady's main area of research is to help veterinary public health authorities make informed decisions in contingency planning.

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Tuesday, November 26th 2024 Istituto Superiore di Sanità, Rome, Italy and online

MOOD FINAL MEETING

Scientific Conference

REC

Emerging infectious diseases in Europe: Challenges and opportunities in data sharing and modelling of response for improved One Health

8.30 am	Registrations
9 am	Welcoming remarks by Prof. R. Bellantone (ISS), Dr. E. Arsevska (CIRAD, MOOD project coordinator), Dr. Annapaola Rizzoli (FEM)
9.15 am	Opening by Dr. Maria Van Kerkhove (WHO): Preparedness for current and future health threats
9.45 am	Session A: Respiratory transmitted pathogens (Influenza viruses, coronaviruses) Chair: Vittoria Colizza (INSERM) <ul style="list-style-type: none"> Keynote by Prof. Birgitte de Blasio (NIPH): The effectiveness of geographically targeted COVID-19 vaccination: Insights from agent-based and compartmental models for Norway Keynote by Dr. Patrizio Pezzotti (ISS): The role of surveillance and modelling in impact and risk assessment during emergencies: proofs of concept in the context of the covid-19 pandemic in Italy Keynote by Philippe Lemey (KU Leuven): Respiratory virus phylodynamics within MOOD
11 am	Coffee Break
11.30 am	Session B: Climate-sensitive infectious diseases in Europe Chair: Annapaola Rizzoli (FEM) <ul style="list-style-type: none"> Keynote by Prof. Joacim Rocklöv (Heidelberg University): Climate Change and Vector-Borne Diseases in Europe: Model and Data Challenges Keynote by Dr. Flavia Riccardo (ISS): Changing epidemiology of arboviruses in a changing climate: examples from human surveillance in Italy Keynote by Prof. Alessandra Della Torre (Sapienza – Università di Roma): Epidemiologically relevant bionomical parameters in invasive Aedes albopictus populations in Europe: do we know enough? Keynote by Giovanni Savini (IZS - Teramo): West Nile virus in Europe: Africa on the move
1 pm	Lunch Break

Tuesday, November 26th 2024 Istituto Superiore di Sanità, Rome, Italy and online

MOOD FINAL MEETING

Scientific Conference

REC

LIVE

2.15 pm	Session C: Antimicrobial Resistance Chair: Dr. Luca Busani (ISS) <ul style="list-style-type: none"> Keynote by Dr. Tjibbe Donker (Uniklinik Freiburg): Strengthening AMR control through hospital network analysis Keynote by Thomas van Boeckel (ETH Zurich): Antimicrobial Resistance in Animals Raised for Food, modelling approaches in Europe
3.15 pm	Coffee Break
3.45 pm	Session D: Disease X and pandemic preparedness Chair: Wim van Bortel and Esther van Kleef (ITM) <ul style="list-style-type: none"> Keynote by Wanda Markotter (UP): A One Health approach to prevent pandemics at the source Keynote by Niel Hens (Hasselt University): Modelling tools for pandemic intelligence: the next generation approach Keynote by Brett Archer (WHO): Advancing collaborative surveillance for health emergency prevention, preparedness, response and resilience (On line speech) Keynote by Thierry Lefrançois (CIRAD): Science-decision interface for a better anticipation and preparation to major health risks
5.15 pm	MOOD Platform session by Guy Hendrickx (Avia-GIS)
5.30 pm	Closing
7 pm	Official dinner

📅 Wednesday, November 27th 2024 📍 Istituto Superiore di Sanità, Rome, Italy and online

MOOD FINAL MEETING

Closing Event REC LIVE

8.30 am	Registrations
9 am	Welcoming remarks by Dr. Elena Arsevska (CIRAD)
9.05 am	Session A: From disease profiles to modeling and risk mapping Chair: Dr. Tomislav Hengl (OGH) <ul style="list-style-type: none"> • Keynote by Claudia Cataldo (ISS): Integration of sex-gender analysis in One Health approach at human-animal-ecosystem interface • Keynote by Pachka Hammami (CIRAD): ArbocartoR: a simulation tool for decision support in the implementation of surveillance and control of mosquito-borne diseases • Keynote by Eimear Cleary, Shengjie Lai (SOTON): Optimizing the detection of emerging infections using mobility-based spatial sampling • Keynote by Maria Fernanda Vincenti (ULB): Insights into the Emergence and Spread of Highly Pathogenic Avian Influenza: Global risk mapping of HPAI cases and conversion events • Perspectives by Didier Fontenille (IRD): Anticipating and managing vector-borne diseases: a French (and European) vision
10.30 am	Coffee Break
11 am	Session B: Lessons learned on disease-X Chair: Anna Teresa Palamara (ISS) <ul style="list-style-type: none"> • Keynote by Andrea Bizzotto (FBK): Increasing situational awareness through nowcasting of the reproduction number • Keynote by Soushieta Jagadesh (ISID): Global Risk Mapping of Bat- and Rodent-borne Diseases: Insights for Preventing Disease X • Keynote by Esther Van Kleef (WHO): Modelling practices, data and dissemination needs for pandemic decision-making: a scoping review and survey-based modellers' perspective from the MOOD consortia • Keynote by Markus Neteler (Mundialis): The role of environmental covariates for disease outbreak monitoring • Perspectives by Marisa Peyre (CIRAD)
12.30 pm	Lunch Break

📅 Wednesday, November 27th 2024 📍 Istituto Superiore di Sanità, Rome, Italy and online

MOOD FINAL MEETING

Closing Event REC LIVE

1.30 pm	Session C: Data preparedness and innovative tools for improved EI in Europe Chair: Maguelonne Teisseire (INRAE) <ul style="list-style-type: none"> • Keynote by Giovanni Marini (FEM): Estimating the incidence and seroprevalence of West Nile virus in the avian population in Northern Italy • Keynote by Servane Bareille (ANSES): UTOPIA: a user-friendly tool to identify trade movements at risk when a disease emerges in a trading partner country • Keynote by Carlène Trevennec (INRAE): A new multisource surveillance tool for highly pathogenic avian influenza in mammals • Keynote by Mirco Cazzaro (IZS): Integrating Advanced Distance Metrics with Route Navigation Systems for Biosecurity in Livestock Transportation • Perspectives by Paolo Tizzani (WOAH): Harnessing Data and Tools for Effective Epidemic Intelligence: A WOAHPerspective on Enhancing Global Health Preparedness
3 pm	Coffee Break
3.30 pm	Session D: Reaching out to users and impacts for Improved EI in Europe Chair: Guy Hendrickx (Avia-GIS) <ul style="list-style-type: none"> • Keynote by Fanny Bouyer (GERDAL): Improving epidemic Intelligence in Europe: the challenging innovation process of the MOOD project • Keynote by Saeed Ahmad (TU): Preparing for the future: EPIET's role in training the next generation of epidemiologists for emerging infectious disease response in Europe • Keynote by Francesca Dagostin (FEM): A machine learning modelling framework for the assessment of tick-borne encephalitis risk in Europe • Keynote by Agnese Zardini (FBK): Estimating the potential risk of transmission of arboviruses in the Americas and Europe: A modeling study • Perspectives by Beate Conrady (UCPH): Enhancing Epidemic Intelligence in Europe through Advanced Computational Models for Sustainable One Health Actions
5 pm	Closing words: Jean-Baptiste Perrin, European Commission (HERA) <i>online speech</i> , Dr. Elena Arsevska, CIRAD (MOOD project coordinator), Nathalie Vachier, CIRAD (ASTRE research unit director - AnimalS health Territories Risks Ecosystems)
5.30 pm	Departures

Abstracts Tuesday, November 26th

Scientific Conference



Session A: Respiratory transmitted pathogens (Influenza viruses, coronaviruses)

The effectiveness of geographically targeted COVID-19 vaccination: Insights from agent-based and compartmental models for Norway

Birgitte Freiesleben de Blasio, Louis Yat Hin Chan, Francesco Di Ruscio, Jørgen Eriksson Midtbø, Gunnar Rø, Alfonso Diz-Lois Palomares, Jonas Kristoffer Lindstrøm, Anja Bråthen Kristoffersen, Geir Bukholm, Sara Sofie Viksmoen Watle, Lene Kristine Juvet, Jasper Littmann, Preben Aavitsland, Karin Maria Nygård, Are Stuwitz Berg, (Norwegian Institute of Public Health); Kenth Engø-Monsen (Telenor Research); Arnaldo Frigessi (University of Oslo); Solveig Engebretsen (Norwegian Computing Center).

In early 2021, with the limited initial supply of SARS-CoV-2 vaccines, health authorities worldwide had to enact priorities for mass vaccination campaigns. Most countries focused on reducing severe health outcomes by targeting high-risk groups, such as the elderly and immunocompromised, alongside protecting healthcare workers.

Norway, which has a low population density and where most people live in the southern and coastal regions, encountered significant regional variations in COVID-19 prevalence. Here, the Norwegian government, in addition to prioritising vaccines based on individual risk factors, also decided to implement a geographically targeted vaccination roll-out based on incidence rates. This two-step moderate-level vaccine redistribution aimed to reduce inequities in local transmission dynamics while ensuring ethical considerations and maintaining public trust.

In my talk, I will discuss the modelling approach used to support this decision, conducted by a team of researchers at the Norwegian Institute of Public Health (NIPH), the University of Oslo, Norwegian Computing Center and Telenor Research. The modelling approach utilised two models: (i) an individual-based model and (ii) a metapopulation model for Norway to increase the robustness of the results. The models were simulating the COVID-19 transmission from January through July 2021. The work to support policy decisions in 2021 was undertaken under high time pressure, with limited time for exploration and sensitivity analyses.

We later retrospectively analysed the impact of Norway's geographical vaccine prioritisation during the early roll-out phase. We compared it to national and optimal vaccine allocation strategies across various outcomes: infections, hospitalisations, ICU admissions and deaths. Overall, our models suggest that geographical prioritisation could have reduced health-related outcomes by 8% to 20% compared to a national strategy. Importantly, the optimal strategy varied depending on the specific outcome considered. The best strategy to minimise infections, hospitalisations, or ICU admissions was to allocate all available vaccine doses to fewer high-risk municipalities, comprising approximately one-fourth of the

population. In contrast to lowering deaths, a moderate level of geographic prioritisation, doubling doses for approximately one-third of the population, gave the best outcomes, balancing the trade-off between vaccinating younger people in high-risk areas and older people in low-risk areas.

Ultimately, we found that Norway's geographically targeted strategy was implemented too late to offer significant advantages over a national roll-out strategy, underscoring the importance of early implementation of geographic prioritisation for it to be effective.

The role of surveillance and modelling in impact and risk assessment during emergencies: proofs of concept in the context of the covid-19 pandemic in Italy

Patrizio Pezzotti, Flavia, Riccardo, Antonino Bella, Martina Del Manso, Alberto Mateo Urdiales, Massimo Fabiani, Chiara Sacco, Emmanouil Alexandros Fotakis, Daniele Petrone, Paola Stefanelli, Anna Teresa Palamara (*Department of Infectious Diseases, Istituto Superiore di Sanità*); Mattia Manica, Valentina Marziano, Piero Poletti, Giorgio Guzzetta, Stefano Merler (*Center for Health Emergencies, Fondazione Bruno Kessler*).

The COVID-19 pandemic was sudden with a rapid spread. Italy was the first European country to face its impact and established impelling public health measures with limited data availability. The Italian National Institute of Health (Istituto Superiore di Sanità, ISS) drove systematic and continuous expert interactions among epidemiologists, microbiologists, statisticians, and mathematical modelers whose studies have been pivotal in providing timely evidence-based insights to public health decision makers. During the pandemic alert phase (February 2020), epidemiologists and modelers performed scenario analyses of the impact of SARS-CoV-2 infections based on estimated transmissibility and severity in China. These scenarios were promptly provided to decision makers.

As the first autochthonous case was identified, data from the Italian surveillance system describing the epidemiological characteristics of COVID-19 cases and was used to estimate the basic reproduction number at regional level and to provide insights on at-risk groups.

The impact of the National lockdown was then evaluated. Data showed that it enabled the rapid reversal of the epidemic trend within 2 weeks in most Italian Regions, independently from the level of spread. Further analyses, based on cases ascertained in each Italian municipality with symptom onset before the National lockdown, highlighted that imposing isolation measures only on municipalities with at least ten cases would have left uncontrolled more than 75% of spillover transmission from the already affected municipalities. This data confirmed that national-wide restrictions were substantial to curb short-distance transmission of SARS-CoV-2 in the winter-spring of 2020.

Starting from April 2020, mathematical modelers and epidemiologists defined scenarios to establish the best reopening timeframe in light of specific activities (e.g. school re-opening). Simultaneously, a standardized weekly risk assessment tool was implemented for each Region and became one of the main components used to define, sub-nationally, the implementation of non-pharmacological measures. The impact of these measures was evaluated with positive results and the risk-assessment system itself was shown to reliably anticipate subsequent 3-week increases in hospitalization and mortality rates.

Since 2021, following the implementation of the vaccination campaign, several studies based on surveillance data, were performed to estimate vaccine effectiveness under the predominance of different virus variants, vaccination impact in terms of averted outcomes (e.g. deaths) and the bias related to case underreporting. Further collaborative studies provided further insights on:

- incubation period and generation time during waves characterized by different variants
- the advantage of Omicron compared with Delta variant in terms of transmissibility, but lower disease severity at population level
- changes of infection ascertainment ratio, infection hospitalization ratio, infection ICU ratio, and infection fatality ratio in five different periods associated with the dominance of the ancestral lineages and Alpha, Delta, and Omicron BA.1 variants
- Estimating SARS-CoV-2 transmissibility in Italy accounting for reporting delays.

Conclusion

The COVID-19 pandemic highlighted the need for a continuous interaction of different professionals over evolving key epidemiological questions. This interaction should be maintained in the interpandemic phases to strengthen collaborative surveillance and response approaches including preparedness towards flexible systems able to scale up and down interventions in response to mid to long-term epidemic crises.

Respiratory virus phylodynamics within MOOD

Philippe Lemey, Emanuele Gustani-Buss (*Department of Microbiology, Immunology and Transplantation, Rega Institute, KU Leuven – University of Leuven*); Chiara Poletto (*Department of Molecular Medicine, University of Padova*); Francesco Parino, Vittoria Colizza (*Sorbonne Université, INSERM, Institut Pierre Louis d'Epidémiologie et de Santé Publique - IP-LESP*); Moritz Kraemer (*Department of Biology, University of Oxford*).

Introduction

Respiratory viruses, such as influenza, RSV, and the novel coronavirus SARS-CoV-2, have significant impacts on global health due to their high morbidity and mortality rates. These viruses cause widespread illness, leading to millions of hospitalizations and deaths each year, particularly affecting vulnerable populations such as the elderly, young children, and those with pre-existing health conditions. The economic burden of respiratory viruses is substantial, encompassing healthcare costs, lost productivity, and broader societal impacts. Genomic epidemiology and phylodynamics play crucial roles in understanding and combating these viruses. By analyzing the genetic sequences of virus samples, researchers can reconstruct historical transmission patterns and track pathogen spread and evolution in near real-time.

Results and Discussion

In this talk, I will present the development and application of phylodynamic inference methods to respiratory viruses within the MOOD project. This includes collaborative research within MOOD to elucidate the invasion dynamics of Omicron BA.1 in the UK and the global circulation patterns of RSV. This work leverages computational approaches to integrate epidemiological and mobility data in phylodynamic reconstructions. Finally, I will highlight another MOOD collaboration that takes this integration another step forward by combining a dynamical model of global influenza spread (GLEAM), incorporating high-resolution demographic and mobility data, with a generalized linear model of phylogeographic diffusion that accounts for time-varying migration rates. This multiscale approach describes global influenza dynamics at different scales and has important implications to improve preparedness against respiratory virus epidemics.

Session B: Climate-sensitive infectious diseases in Europe

Climate Change and Vector-Borne Diseases in Europe: Data and Modelling Challenges

Joacim Rocklöv (*Heidelberg Institute of Global Health & Interdisciplinary Centre for Scientific Computing, Heidelberg University & Department of Public Health and Clinical Medicine, Section of Sustainable Health, Umea University*).

In this talk I will introduce how and what we know about the sensitivity of vector-borne diseases to climate variability and change. I will describe and contrast experimental evidence with empirical observations and data. I will further discuss the introduction and transmission of emergent vectors, hosts, and pathogens from a wider system perspective and the role of climate as a gatekeeper. I will further give examples of how mathematical process-based models and machine learning approaches are used and how they can be applied to study patterns and responses to these changes within this system. Finally, I will talk about the lack of consistent high-quality data across scales and how novel data streams hold potential to better understanding, surveillance and preparedness.

Changing epidemiology of arboviruses in a changing climate: examples from human surveillance in Italy

Flavia Riccardo, Antonino Bella, Martina Del Manso, Emmanouil Alexandros Fotakis, Giulietta Venturi, Marco Di Luca, Patrizio Pezzotti, Anna Teresa Palamara (*Department of Infectious Diseases, Istituto Superiore di Sanità*); Federica Ferraro, Francesco Maraglino (*Ministry of Health, Rome, Italy*); Ilaria Pati, Letizia Lombardini (*National Transplant Centre, Istituto Superiore di Sanità*).

Introduction/Background

Arboviruses include diverse viral pathogens that are transmitted in nature by the bite of arthropod vectors. These include zoonotic diseases like West Nile Virus (WNV) where humans are accidental hosts of an enzootic cycle between wild birds and mosquitoes, and diseases like dengue (DENV) whereby transmission occurs with a human-mosquito-human cycle in the absence of other reservoir hosts.

Several factors influence the human epidemiology of arboviruses. These include the presence and density of vectors, the presence of reservoir hosts and/or the frequency of incoming viraemic hosts and specific weather conditions that may allow transmission. Temperature is a particularly relevant factor as it impacts on vector breeding and on the extrinsic incubation of these pathogens within the vectors. Warming temperatures are recognized as elements that could increase the extension and intensity of arbovirus transmission in the EU.

Material and Method

In Italy, arbovirus surveillance is regulated by a five year national plan that addresses both endemic (WNV, tick-borne encephalitis-TBE and Toscana virus-TOSV) and emerging travel-related/sporadic (e.g. DENV, Chikungunya-CHIKV, Zika virus-ZIKV) arboviral diseases, in alignment with EU case definitions. Reporting of acute human infections by Regions/Local units at national level ensures immediate warning of national actors involved with regional authorities in confirmation and response actions, including the safety of substances of human origin (SoHO). Historical data allows to compare trends and assess changes in the epidemiology of these diseases.

Results

Endemic WNV has geographically expanded in Italy since its first emergence in 1998 with an increase in the number of affected areas and the occurrence of years of substantially increased incidence in human infections peaking at 330 neuro-invasive cases and 51 deaths in 2022. These years were characterized by extreme weather anomalies, including exceptionally high temperatures, and with increases in the incidence of other arboviruses in Italy including the endemic sand-fly borne TOSV (peaking at 152 neuroinvasive cases also in 2022).

As of July 2024, there has been a substantial increase in travel-related DENV infections diagnosed in Italy contextually to the global increased incidence of this disease.

We also documented two local transmission events of CHIKV, in 2007 and 2017, and five local transmission events of DENV in 2020 and 2023, all in the warmer months, in a context of widespread presence of *Aedes albopictus* and of incoming travel-related acute infections.

Discussion

The epidemiology of arboviral diseases is influenced by multiple factors impacting the ecology of these viruses and their vectors. In Italy, we are observing changes in the epidemiology of several arboviral infections in humans with the extension of transmission areas of endemic viruses, epidemics in years with weather anomalies, and the appearance of sporadic local transmission of viruses previously exclusively travel related. These epidemiological changes are redefining how arboviruses are being monitored and contrasted in Italy with investment in One-Health oriented early warning systems and strengthened SoHO safety measures.

Conclusion

The incidence of arboviral infections in humans is expected to increase in the EU. In Italy, the existence of a robust, one-health national plan and the close collaboration of different professionals at central et local level have proved to be key tools; however, there is a need to strengthen collaborative surveillance and response approaches including preparedness towards flexible systems able to scale up interventions in response to epidemics.

Epidemiologically relevant bionomical parameters in invasive *Aedes albopictus* populations in Europe: do we know enough?

Alessandra della Torre (*Dipartimento di Sanità Pubblica e Malattie Infettive*).

Introduction/Background

Predicting risk of vector borne diseases' introduction and spread are instrumental to increase preparedness and optimizing control measures. Epidemiological models of vector-borne diseases include vector-related variables as well as variables related to the pathogens within the vector, and both strongly affects the predictions. However, in the cases of arboviruses transmitted by the invasive species *Aedes albopictus* in Europe, many of these parameters are only partially quantified, especially for endemic ecotypes. The Medical Entomology group of Sapienza University is focused on studying the biology and behaviour of *Ae. albopictus* in Italy in order to provide data to feed models thus allowing more precise and evidence-based predictions. Here, some of the most relevant results so far obtained are summarized.

Material and Method

We here focus on our past and most recent efforts to assess:

- 1- the host-feeding habits, by sticky-trap collections and analysis of origin of blood-meal in fed females;
- 2- the dispersal, by Mark-Release-Recapture (MRR) experiments using sticky-traps;
- 3- the absolute abundance, by Latin-square experiments exploiting MRR data to assess the capture rate or widely used BG-Sentinel Traps;
- 4- the longevity, by development of a novel approach based on Mid-Infrared Spectrometry coupled with Supervised Machine-Learning (MIRS+SML);
- 5- the relationship between eggs collected by ovitraps and adult abundance assessed by Human Landing Catches.

Results

We found that: 1-*Ae. albopictus* in Italy has generalist feeding habits, and that 2- the flight range of 90% of the population of blood-fed females exceed 200 m. We: 3- assessed the heterogeneous effectiveness associated with different trap types in collecting *Ae. albopictus* and predicted estimates of its absolute density; 4- obtained high accuracy in age-estimation of semi-field reared adults; and 5- showed that predictions of adult females based on egg collections varies among sites due to local condition varying across space and time.

Discussion and Conclusions

Further studies in this field by novel cutting-age approaches will allow a deeper understanding of *Ae. albopictus* bionomics and phenology in Europe and improve epidemiological models. Other relevant parameters that need to be assessed in the next future will be discuss

West Nile virus in Europe: Africa on the move.

Giovanni Savini, G. Mencattelli, R. Rosà (*University of Trento*); A. Silverj, A. Rizzoli (*Research and Innovation Centre, Fondazione Edmund Mach*); F. Monaco, L. Teodori, A. Leone, G. Savini (*Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise Giuseppe Caporale*); M.H.D Ndione, M.M. Diagne, O. Faye (*Institut Pasteur*).

West Nile Virus (WNV), now known as Orthoflavivirus nilense, is the most widely distributed zoonotic arbovirus in the world. A member the new classified genus Orthoflavivirus within the Flaviviridae family, WNV is known to cause neurological symptoms in both humans and animals and is currently regarded as a significant public health concern globally. The virus is perpetuated in nature through an enzootic cycle that involves competent mosquitoes and a diverse range of reservoir bird species. First identified in Africa in 1937, WNV has since spread across the globe primarily through migratory birds. Europe serves as a crucial resting and transit area, as well as a final destination, for many long- and short-distance migratory birds originating from the African continent. The annual migrations of these birds have facilitated the introduction and dissemination of various WNV strains, particularly those from lineages 1 (WNV L1) and 2 (WNV L2), which are the most prevalent among the eight lineages identified to date.

In recent years, we have endeavoured to uncover the spatial and temporal viral dynamics of two lineages of WNV between Africa and Europe. By integrating epidemiological studies with molecular, phylogenetic, and phylogeographic analyses, our research has shown a complex behaviour of WNV L1 clade 1A which seems to have originated in the 1900s, likely in a region between North and West Africa. From this area, it spread in two opposite directions, towards East (Egypt) and West (Senegal) of Africa, and from the latter to Northern Africa (Morocco) and then Europe (Spain, France, Italy). Interestingly, our study also highlighted sporadic back re-introductions of this lineage between Europe and Africa. Additionally, our findings suggest that the common ancestor of the WNV L2 strains likely emerged between the 18th and 19th centuries in South Africa. From there, it was introduced to Hungary in 2004 and, subsequently, spread throughout Europe, where are now intensively circulating.

The study also revealed that WNV L1 and L2 strains travel along two ideal corridors that connect Africa and Europe, aligning with the two primary Afro-Paleartic migratory flyways. These varying pathways of dissemination likely shaped the evolutionary history of the two lineages, highlighting the crucial role that different bird species play in the transcontinental spread of WNV.

Session C: Antimicrobial Resistance

Strengthening AMR control through hospital network analysis

Tjibe Donker (*Institute for Infection Prevention and Hospital Epidemiology, Medical Center, University of Freiburg*).

A growing body of evidence shows that hospital networks formed by patient movements (or transfers) influence the spread of hospital-associated pathogens and antimicrobial resistance. The spread of these pathogens through the hospital network poses a considerable challenge for infection prevention and control, because a disease outbreak in one hospital has the potential to become the problem of all hospitals. This makes it more difficult to control these pathogens than if each hospital would have been its own little island. However, we can also use the structure of the hospital networks to our advantage.

I will present how knowledge about the structure of the hospital network can help us combat antimicrobial resistance, by moving away from the traditional view where individual hospitals are solely responsible for the problems within their own walls. Through differentiation of infection prevention and control investments, targeted placement of sentinel sites, and creating network-based incentives for searching affected patients, we can more efficiently (and more effectively) tackle the spread of AMR. I will further show some of the implemented health care policies (partially) based on knowledge of the hospital network, and discuss some of the challenges that come with it.

Antimicrobial Resistance in Animals Raised for Food, modelling approaches in Europe

Thomas Van Boeckel (*ETH Zurich*).

Since the 1950s, the global increase in demand for meat has driven the Use of antimicrobial drugs in agriculture. This practice has led to the development of antimicrobial resistance (AMR) in animals and food products with potentially harmful consequences for agricultural productivity, and human health. In the context of the MOOD project, we explored the use of geospatial models as well as disease dynamics model to document trends in resistance and identify potential policy interventions for AMR. In Europe, to determine refine current estimates of the geographic distribution, we combined 33,802 country-level AMR prevalence estimates with 2,849 local AMR prevalence estimates from 209 point-prevalence surveys across 31 countries. We produced geospatial models of AMR prevalence in *Escherichia coli*, nontyphoidal *Salmonella*, and *Campylobacter* for cattle, pigs, and poultry. We summarized AMR trends by using the proportion of tested antimicrobial compounds with resistance >50% and generated predictive maps at 10 × 10 km resolution that disaggregated AMR prevalence. For *E. coli*, predicted prevalence rates were highest in southern Romania and southern/eastern Italy; for *Salmonella*, southern Hungary and central Poland; and for *Campylobacter*, throughout Spain. Our findings suggest that AMR distribution is heterogeneous within countries and that surveillance data from below the country level could help with prioritizing resources to reduce AMR. We also considered the effect of taxes on veterinary antimicrobials to reduce antibiotic consumption, and antimicrobial resistance. Taxation can be applied flatly across all antibiotic classes, targeted to single antibiotic classes, or scaled based on resistance in each class, so called "differential" taxation. Taxation could also maximize the average number of antibiotics with a resistance prevalence of under 25% and potentially generate annual global revenues of 1 billion US\$ under a 50% taxation to current prices of food-producing animal antibiotics. Differential taxation was also able to maintain a high availability of antibiotics over time compared to single and flat taxation strategies, while also having the lowest rates of intervention failure and highest potential revenue across all taxation strategies.

Session D: Disease X and pandemic preparedness

A One Health approach to prevent pandemics at the source

Wanda Markotter (*University of Pretoria, Centre for Viral Zoonoses*).

One Health is an integrated, unifying approach that aims to sustainably balance and optimize human, animal and plant health and ecosystem, recognising that it is closely linked and interdependent. Global anthropogenic change is a key driver of infectious disease emergence and spread and can increase disease burdens in humans, animals and plants, leading to biodiversity loss and the degradation of ecosystem function in a complex and interconnected manner. Disease spill-over events, subsequent outbreaks, and pandemics may arise, particularly when multiple factors driving disease emergence converge. Conventional disease surveillance has been organised within silos by sector, with separate surveillance systems focusing on the health of humans and animals and very rarely including drivers of disease emergence. There is a need to develop One Health systems that involve and coordinate multiple sectors, disciplines, and communities to tackle risks and threats in a coordinated and timely manner. One Health surveillance would include surveillance for known and unknown pathogens but also surveillance of drivers of disease emergence to provide an alert system for increasing risk of spill-overs, combined with the more traditional disease-based surveillance. This presentation will outline the principles of such an approach and discuss specific examples relevant.

Modelling tools for pandemic intelligence: the next generation approach

Niel Hens, Leonardo Angeli, Constantino Pereira (*University of Antwerp*).

Understanding the role of different age groups in virus transmission is crucial for managing respiratory virus outbreaks, such as COVID-19. This study focuses on SARS-CoV-2 transmission in Belgium from November 2020 to February 2022, using a next-generation matrix approach integrated with social contact data and simulations of population susceptibility. A longitudinal analysis of the reproduction number (R_t) perturbations revealed shifting transmission dynamics across age groups.

Initially, adults aged 18-60 years were the primary transmission drivers from November to December 2020, while children contributed minimally. However, this shifted with the reopening of schools and the emergence of the Alpha variant in early 2021, where children under 12 years old became key contributors. Stricter public health measures in March 2021 temporarily reduced the role of adults aged 18-30. The Delta variant, which emerged in mid-2021, increased transmission by adults aged 18-40, with a resurgence in children's influence observed in the fall of 2021.

This research highlights the importance of considering age-specific transmission dynamics, particularly in light of evolving social contact patterns and the emergence of new variants of concern. The methods employed, including R_t perturbation analysis, provide a valuable framework for understanding transmission shifts and informing public health policies. By accounting for changes in susceptibility and social interactions, this study offers key insights into optimizing age-targeted interventions throughout different phases of the pandemic.

Science-decision interface for a better anticipation and preparation to major health risks

Thierry Lefrançois (CIRAD); Bruno Lina (HCL, Hospices Civils de Lyon); Brigitte Autran (Sorbonne University, President of COVARS).

The COVARS is a scientific committee which was implemented in France following the covid-19 scientific council, to help the government in anticipating and monitoring health risk with a One Health approach. One of the major report released in 2024 was focused on health risks which could occur in the next 5 years and induce a major impact on health system in France mainland and remote territories. Known and unknown infectious disease risks (pandemic respiratory diseases, vector borne diseases...) were estimated against the probability of occurrence and the epidemiological and clinical consequences considering the counter measures available. Environmental risks, including climate change, biodiversity loss and pollution were also considered as already impacting health system either directly or by aggravating infectious disease burden. Recommendations regarding research, innovation and monitoring were provided to the government to better anticipate and be prepared to these risks through an holistic and intersectorial collaboration.

MOOD Platform Session

Science-decision interface for a better anticipation and preparation to major health risks

Guy Hendrickx (Avia-Gis).

The MOOD (Monitoring Outbreak Events for Disease Surveillance) platform is an innovative and comprehensive tool designed for epidemiological surveillance, addressing the challenges posed by global environmental and climatic changes on emerging infectious diseases and antimicrobial resistance (AMR) in Europe. Developed by Avia-GIS with funding from the European Union's Horizon 2020 research and innovation program, the platform aims to enhance risk assessment, monitoring, early detection, and analysis of disease trends in a One-Health context.

Platform Capabilities – The MOOD platform provides access to an extensive array of standardised environmental and co-variate data, including administrative layers, demographic and socio-economic information, and diverse environmental datasets such as altitude, daylight, hydrography, land cover/use, precipitation, temperature, and vegetation indices. This wealth of data supports the creation and querying of time series graphs, comparison and configuration of data layers, and extraction of data for model building.

A distinctive feature of the MOOD platform is its integration with PADI-web, an automated disease information extraction tool based on event-based surveillance (EBS) data, and other public disease data sources. Users can access, import, and work with a variety of disease datasets (including their own), enhancing their ability to perform comprehensive epidemiological analyses.

Target Users – The MOOD platform is designed to cater to a wide range of users involved in public health and epidemiological research, including:

- Public Health Agencies: Organizations responsible for disease surveillance and control, benefiting from enhanced monitoring and risk assessment capabilities.
- Animal Health Agencies: Entities focusing on zoonotic diseases and their impact on animal health, utilizing the platform for early detection and monitoring.
- Data Scientists: Professionals analysing large datasets to extract meaningful insights, leveraging the platform's advanced analytical tools and data visualization capabilities.
- Social Scientists: Researchers examining the societal impacts of diseases and interventions, using the platform's data to inform their studies.
- Epidemiologists: Experts studying the distribution and determinants of diseases within populations, utilizing the platform for detailed epidemiological investigations.
- End-Users: A diverse group including policymakers, researchers, and other stakeholders who interact with the platform for various purposes related to disease surveillance and public health.

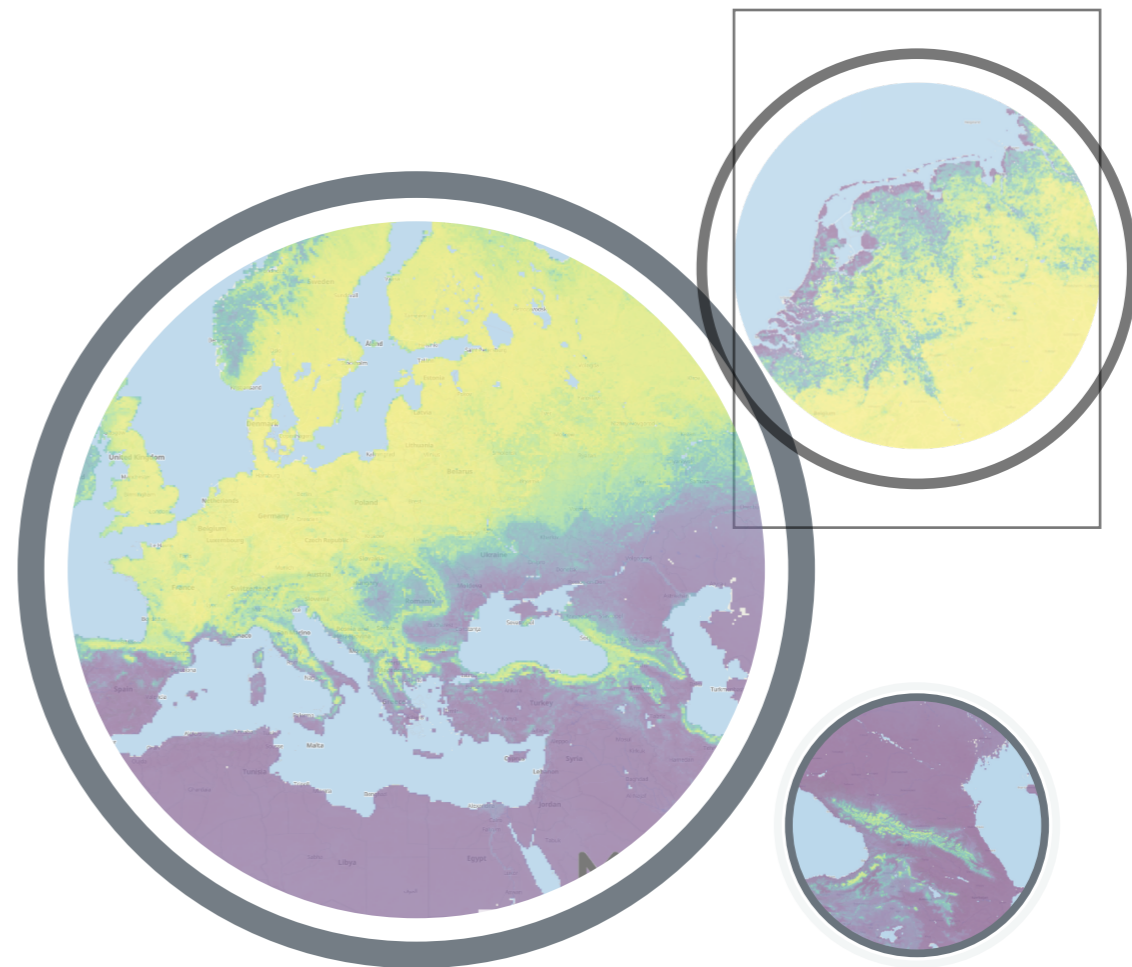
Uniqueness – The MOOD platform stands out among existing epidemiological surveillance tools due to several unique features:

- **Comprehensive Data Access:** Unlike many platforms that provide limited datasets, MOOD offers extensive access to a wide range of standardised environmental and socio-economic data.
- **Integrated Disease Database:** The integration with PADI-web and easy link to other public disease data sources allows users to work with a variety of disease datasets, enhancing their analytical capabilities.
- **Multi-Source Data Linking:** The platform links epidemiological data from both official (indicator-based surveillance) and unofficial (event-based surveillance) sources, providing a comprehensive overview and enabling detailed comparisons
- **Epidemiological Focus:** Specifically designed to address the impacts of environmental and climatic changes on infectious diseases, MOOD provides targeted tools for risk assessment and monitoring within a One-Health framework.
- **Advanced Analytical Tools:** MOOD provides sophisticated tools for text-mining, normalization, risk mapping, and data visualization, enabling users to perform in-depth analyses and build custom models

In conclusion, the MOOD platform is a versatile, data-rich tool that significantly enhances the capabilities of various stakeholders in public health and epidemiology, offering unparalleled data access, integration, and analytical tools compared to other platforms.

Abstracts Wednesday, November 27th

Closing Event



Session A: From disease profiles to modeling and risk mapping

Integration of sex-gender analysis in One Health approach at human-animal-ecosystem interface.

Claudia Cataldo, Luca Busani (*Center for Gender-specific medicine, Istituto Superiore di Sanità*).

Introduction

One Health is an integrative and systemic approach to sustainably balancing and optimizing the health of people, animals, and ecosystems. It recognizes that the health of humans, domestic and wild animals, plants, and ecosystems is closely linked and interdependent. Integrating gender analysis in One Health policy allows for a transversal, holistic, and transdisciplinary point of view. Gender is defined as roles and behaviors determined by the social context learned and adopted by men and women, which leads to different identities and roles considered suitable for each. Sex and gender differences can modulate the dynamic of infectious diseases through biological, social, economic, and environmental drivers, including animal reservoirs and arthropod vectors for some diseases. These interactions reflect socioecological systems.

In the framework of the MOnitoring Outbreak events for Disease surveillance in a data science context (MOOD) project, prototype infectious diseases such as Chikungunya, Tularemia, and Leptospirosis were analyzed to identify exposure scenarios in which sex-gender-related drivers interact with animal reservoirs and environmental drivers in the ecosystem.

Material & Methods

A comprehensive literature search selected studies with quantitative data on disease, sex-gender, behaviors, activities, animal, vector and environmental covariates. The selection was restricted to Europe in the last 20 years. The results were: Tularemia:1806 articles,193 included (Animals: 69, Vector: 45, Humans: 23, Environment: 43). Chikungunya 1165 articles, 65 included (Humans: 14, Vectors: 12, Environment : 5). Leptospirosis 1045 articles, 95 included (Animals: 57, Humans: 31, Environment: 27). Of the 353 included papers, 26 were analyzed to identify gender-related exposure scenarios (6 for Chikungunya; 13 for Leptospirosis and 7 for Tularemia)

Results

Chikungunya exposure scenario involved elderly males for their attitude toward staying outdoors during prevalent mosquito vector activity and near mosquito breeding and resting sites. Another individual risk factor was the poor use of insect repellents. Leptospirosis exposure scenario was characterized by adult males engaged in recreational activities in contaminated freshwater or professionally exposed to

infected animals, animal products, contaminated soil or water. Another individual risk factor was having uncovered wounds/abrasions. Tularemia exposure scenario involved adult males in outdoor activities who came into contact with infected animal species (hares, in particular) and/or infected vectors (mosquitoes and ticks). Another individual risk factor was the consumption or use of contaminated water.

Discussion and Conclusion

The scenarios highlighted the gender-related activities, behaviors and social roles that modified the risk of infection between men and women, considering the contexts, the community and the whole ecosystem. Gender analysis is important to maximize One Health's potential. It provides a lens for analyzing, preventing, and mitigating risks at the human-animal-ecosystem interface, identifying target groups more effectively.

ArbocartoR: a simulation tool for decision support in the implementation of surveillance and control of mosquito-borne diseases

Pachka Hammami (UMR Animals, Health, Territories, Risks, and Ecosystems - Astre, Department of Biological Systems - Bios, French Agricultural Research and International Cooperation Organization for Development - CIRAD, Université de Montpellier); Andrea Apolloni (UMR Animals, Health, Territories, Risks, and Ecosystems - Astre, Department of Biological Systems - Bios, French Agricultural Research and International Cooperation Organization for Development - CIRAD); Ewy Ortega (UMR Animals, Health, Territories, Risks, and Ecosystems - Astre, Department of Biological Systems - Bios, French Agricultural Research and International Cooperation Organization for Development - CIRAD, Ministère de l'agriculture et de l'alimentation, Direction générale de l'alimentation - DGAL); Elena Arsevska (UMR Animals, Health, Territories, Risks, and Ecosystems - Astre, Department of Biological Systems - Bios, French Agricultural Research and International Cooperation Organization for Development - CIRAD); Renaud Marti, Maxime Lenormand, Annelise Tran (UMR Territoires, Environnement, Télédétection et Information Spatiale - TETIS, INRAE, AgroParisTech, CIRAD, CNRS)

Introduction/Background

The recent expansion of invasive Aedes mosquito species has raised significant concerns regarding the potential emergence of arboviruses in new regions, such as dengue, Zika, and chikungunya. While these threats are influenced by unpredictable factors, the emergence and spread of vector-borne viruses largely depend on vector and host populations, their movement patterns, introduction scenarios, and the efficacy of vector control measures. Despite advances in our understanding, there is still a need to more accurately predict and mitigate the risk of arbovirus outbreaks in new areas colonized by Aedes mosquitoes. Modeling serves as a powerful tool to better understand the mechanisms behind viral emergence and to explore various epidemiological scenarios. To address these challenges, arbocartoR, a modeling tool was developed by CIRAD under the H2020 MOOD project.

Material and Methods:

The tool is based on a compartmental model using a mechanistic approach that incorporates both biological observations and behavioral processes. It combines deterministic and stochastic algorithms to simulate (i) the population dynamics of two Aedes species, Aedes albopictus and Aedes aegypti, based on local environmental conditions such as temperature, precipitation, and breeding sites, and (ii) the transmission dynamics of Aedes-borne viruses following an introduction, accounting for the responsiveness and effectiveness of vector control strategies.

Results: The simulations provided by arbocartoR yield crucial insights into the population dynamics of the mosquitoes and the progression of viral transmission under different scenarios. These results enable the evaluation of control strategies by analyzing the interplay between vector population dynamics, virus

introduction events, and the local conditions. Key indicators generated by the model help guide targeted vector control interventions and public health surveillance efforts.

Discussion: Through its detailed simulations, arbocartoR supports the exploration of epidemiological scenarios, enabling a better understanding of the potential risks posed by Aedes-borne virus outbreaks. By integrating biological and environmental factors, the tool aids in anticipating possible outbreaks and optimizing vector control measures. Additionally, the ability to account for both stochastic (random) events and deterministic processes ensures that the model can accommodate real-world variability in viral emergence and transmission.

Conclusions: arbocartoR offers a comprehensive tool for simulating the dynamics of Aedes mosquitoes and the transmission of associated arboviruses. It provides actionable insights to improve preparedness and response to mosquito-borne disease outbreaks, helping to anticipate and mitigate the spread of viruses like dengue, Zika, and chikungunya. By guiding vector control and surveillance efforts, arbocartoR supports the development of more effective public health strategies.

Optimizing the detection of emerging infections using mobility-based spatial sampling

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Introduction/Background

Timely and precise detection of emerging infections is imperative for effective outbreak management and disease control. Human mobility significantly influences the spatial transmission dynamics of infectious diseases. Spatial sampling, integrating the spatial structure of the target, holds promise as an approach for testing allocation in detecting infections, and leveraging information on individuals' movement and contact behavior can enhance targeting precision.

Material and Method

This study introduces a spatial sampling framework informed by spatiotemporal analysis of human mobility data, aiming to optimize the allocation of testing resources for detecting emerging infections. Mobility patterns, derived from clustering point-of-interest and travel data, are integrated into four spatial sampling approaches at the community level: human contact intensity (HCI), human flow intensity (HFI), case flow intensity (CFI), and case transmission intensity (CTI). We evaluate the proposed mobility-based spatial sampling by analyzing both actual and simulated outbreaks, considering scenarios of transmissibility, intervention timing, and population density in cities.

Results

Leveraging inter-community movement data and initial case locations, the proposed Case Flow Intensity (CFI) and Case Transmission Intensity (CTI)-informed spatial sampling enhances community-level testing efficiency by reducing the number of individuals screened while maintaining a high accuracy rate in infection identification. Furthermore, the prompt application of CFI and CTI within cities is crucial for effective detection, especially in highly contagious infections within densely populated areas. The findings underscore the potential enhancement in the performance of community-level testing through thoughtful consideration of initial confirmed case locations and mobility patterns within and between communities.

Discussion

Both HCI and HFI tend to sample areas with high human activity, which may not necessarily align with the areas where cases are present due to timely public health interventions. This mismatch can lead to resource inefficiencies and hinder testing efficacy. Consequently, spatial sampling approaches that integrate human mobility data with epidemiological insights in the early stages of an outbreak can significantly enhance infection detection efficiency. In this regard, the CFI and CTI approaches, which consider both inter- and intra-community movements of initially affected populations in communities with cases, demonstrated superior performance compared to other geospatial sampling methods.

Conclusions: With the widespread use of human mobility data for infectious disease responses, the proposed theoretical framework extends spatiotemporal data analysis of mobility patterns into spatial sampling, providing a cost-effective solution to optimize testing resource deployment for containing emerging infectious diseases.

Insights into the Emergence and Spread of Highly Pathogenic Avian Influenza: Global risk mapping of HPAI cases and conversion events

Maria F. Vincenti-Gonzalez, Marie-Cécile Dupa, Simon Dellicour, Marius Gilbert (*Spatial Epidemiology Lab (SpELL) Université Libre de Bruxelles (ULB)*); Jean Artois (*Department of Productions in Agriculture. CRA-W - Centre Wallon de Recherches Agronomiques*); Madhur Dhingra (*Food and Agriculture Organization of the United Nations*); William Wint (*Environmental Research Group Oxford Ltd, Department of Biology*); Guy Hendrickx, Cedric Marsboom (*Avia-GIS, Agro-Veterinary Information and Analysis*).

Background: Highly Pathogenic Avian Influenza (HPAI) poses significant global concerns due to its high mortality rates and economic impacts on both poultry and wild water birds. Since the emergence of the Goose/Guangdong H5N1 subtype in 1996 in China, HPAI outbreaks have surged, presenting critical challenges worldwide. These two studies aimed to elucidate the environmental and anthropogenic factors driving HPAI incidence before and after 2020 and to analyze the impact of global poultry intensification on the conversion of Low Pathogenic Avian Influenza (LPAI) to HPAI.

Material and Methods: We first investigated the environmental drivers of increased HPAI cases, particularly H5N1 and H5Nx strains, by assessing shift in ecological niches and predicting at-risk areas using boosted regression trees (BRT). HPAI occurrence data before and after 2020 were analyzed, and the predictive accuracy of our models was evaluated using various cross-validation techniques. Key environmental predictors included densities of intensive chicken populations, human density, distance to water, and land cover variables. Additionally, we compiled a dataset of HPAI conversions events from 1959 to 2022, focusing on primary emergence reports. Generalized Linear Mixed Models (GLMM) and Integrated Nested Laplace Approximation (INLA) were used to predict conversion events based on proxy variables for poultry intensification such as poultry density, output/input ratio and total stock of poultry.

Results: Our findings revealed that models based on spatial cross-validation methods demonstrated higher predictive capabilities, particularly for H5N1 in domestic birds, with high AUC values. Risk maps indicated significant suitability for HPAI spread in Europe, Asia, and North and South America, with notable expansions post-2020. Additionally, diversity indices for avian species involved in HPAI outbreaks showed increased diversity post-2020, particularly among marine birds. The analysis of poultry intensification showed that the majority of detected conversion events occurred in high-income countries with highly intensified poultry production systems, particularly in Europe and the USA. The output/input ratio was identified as the best predictor of conversion events.

Discussion: The results from both studies underscore the critical role of anthropogenic and environmental factors in HPAI dynamics, providing valuable insights for targeting surveillance and control measures. This study enhances the understanding of HPAI transmission, aiding in the formulation of effective prevention strategies globally.

Conclusions: Both studies provide valuable insights into the drivers of HPAI, aiding in the formulation of effective prevention strategies. The critical role of environmental and anthropogenic factors, poultry intensification, and recent shifts in wild (marine) bird ecology in HPAI emergence necessitates continued research to comprehensively examine these pressures. These findings are crucial for policymakers, public health officials, and the poultry industry in safeguarding global public health and the poultry sector.

Session B: Lessons learned on disease-X

Increasing situational awareness through nowcasting of the reproduction number

Andrea Bizzotto, Giorgio Guzzetta, Valentina Marziano, Piero Poletti, Mattia Manica, Agnese Zardini, Stefano Merler (*Center for Health Emergencies Bruno Kessler Foundation*); Martina del Manso, Alberto Mateo Urdiales, Daniele Petrone, Andrea Cannone, Chiara Sacco, Massimo Fabiani, Antonino Bella, Flavia Riccardo, Patrizio Pezzotti (*Department of Infectious Diseases, Istituto Superiore di Sanità*); Filippo Trentini (*Covid Crisis Lab Bocconi University*); Marco Ajelli (*Laboratory for Computational Epidemiology and Public Health Department of Epidemiology and Biostatistics Indiana University School of Public Health*).

Background

Real-time estimates of the reproduction number (R_t) are essential in monitoring and responding to infectious disease outbreaks. R_t represents the number of secondary infections generated by an infected individual and is commonly estimated from case incidence curves. However, intrinsic delays between infection and reporting in surveillance databases present formidable challenges for the real-time estimation of R_t .

Material and Method

We propose a simple method to estimate R_t in real-time by nowcasting the incidence curve at any date of analysis using information on data consolidation delay from previous weeks. We validated our method using COVID-19 epidemiological surveillance data collected in Italy between May 1, 2020, and December 31, 2021. We retrospectively assessed the absolute error between the reference values of R_t estimated from consolidated incidence curves (ground truth) and i) R_t estimated from surveillance data available at the time of the analysis (net R_t); ii) R_t based on nowcasted incidence curves (nowcasted R_t).

Results

When estimating R_t at 13 days before the date of analysis, the median absolute error was 0.032 (95% confidence interval, CI: 0.001-0.275) for net R_t and 0.019 (95%CI: 0.001-0.257) for nowcasted R_t . When referring to 8 days before the date of analysis, the error for net R_t increased to 0.104 (95%CI: 0.029-0.346) while that for nowcasted R_t was 0.037 (95%CI: 0.002-0.277).

Discussion

Compared to net R_t , nowcasted R_t at 8 days was closer to ground truth in 87% of cases and was better able to detect transitions to periods of epidemic growth, providing an earlier warning by between 5 and 22 days.

Conclusions

Our method offers a generally applicable tool for public health response planning by improving both the timeliness and accuracy of R_t estimates during epidemic outbreaks.

Global Risk Mapping of Bat- and Rodent-borne Diseases: Insights for Preventing Disease X

Soushieta Jagadesh (*ISID, France*); Claudia Cataldo, Busani Luca (*Istituto Superiore di Sanità*); Wim Van Bortel, Esther Van Kleef (*Institute of Tropical Medicine*); Willy Wint (*Environmental research group, University of Oxford*); Maxwell Julia (*ISID, USA*); Rizzoli Annapaola (*Research and Innovation Centre, Fondazione Edmund Mach*); Arsevska Elena (*CIRAD*).

Background: The unknown Pathogen X capable of causing Disease X, a disease with epidemic or pandemic potential, is likely to be a virus capable of zoonotic spillover, given that many emerging infections in humans are caused by viruses from wildlife. Bat- and Rodentborne diseases are the most likely candidates. Control and prevention of such outbreaks are lacking at a global and regional scales, in comparison to vector-borne diseases. Mapping the distribution of these Bat- and Rodent-borne diseases and studying the drivers that influence their emergence and spread would benefit the prevention and control of future Disease X.

Material and Method: We used a multistep procedure to model the geographical distribution of bat-borne and rodent-borne diseases, which included: Collating occurrence datapoints from a systematic literature search; Preparing environmental and demographic covariates; Fitting separate disease distribution models; Conducting ensemble modeling for both bat-borne and rodent-borne diseases; Calculating the uncertainty of disease risk in Europe.

Results: The resulting map had high predictive capacity for Bat- and Rodent-borne diseases (true skill statistic = 0.93, 0.96 respectively). The Bat-borne disease model showed that precipitation and bushmeat activities were its principal drivers, while the distribution of Rodent-borne diseases was influenced by deforestation, population density, and minimum temperature. The distribution of batborne outbreaks was mainly restricted to Africa (78.3% of total area) followed by Asia (17.5%). While countries in South America (46%) and Europe (17.3%) had the largest area associated with rodent-borne diseases. Our results demonstrate that although the risk of emergence of bat-borne diseases is low in Europe, the probability of a rodent-borne disease outbreaks remains significant.

Discussion: The results provide a valuable foundation for public health policies. The global maps of bat-borne and rodent-borne disease distributions offer a visual tool for global health agencies to prioritize surveillance and intervention. The uncertainty maps highlight regions where data quality or model predictions are less certain, guiding future research and data collection efforts in Europe. Identifying high-probability areas allows for focused resource allocation, enhancing disease prevention and control efforts. The insights into environmental and socio-economic drivers can inform multi-sectoral approaches, integrating ecological conservation, urban planning, and public health strategies.

Conclusions: The comprehensive geospatial analysis of bat-borne and rodent-borne disease outbreaks provides critical insights into the global distribution and also have direct implications for managing Disease X. Understanding the environmental and socio-economic factors that drive zoonotic disease outbreaks can aid in identifying potential hotspots for Disease X, enabling proactive measures and rapid response strategies. By improving surveillance and intervention efforts in high-risk areas and data collection in areas of high uncertainty, we can enhance global preparedness and reduce the risk of Disease X.

Modelling practices, data provisioning, sharing and dissemination needs for pandemic decision-making: a scoping review and survey-based modellers' perspective

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Introduction

The COVID-19 pandemic posed significant challenges to public health systems worldwide. Advanced outbreak analytics proved at the core of governmental pandemic decision-making globally. We assessed the evolution of modelling practices, data usage, data lacking, and the uptake and nature of interactions between modellers and decision-makers throughout the pandemic. Hence, this study aimed to provide directions for investments in surveillance systems, and modelling at the science policy interface for future pandemic preparedness

Methods

We conducted a two-stage semi-quantitative survey administered in July 2023 among modellers involved in a large multi-partner and multi-country epidemic intelligence consortium. We used descriptive statistics and cross-tabulation to analyse responses across early, mid-, and later-pandemic phases.

Results

Our sample included 64 contributions from 11 institutions in four European countries. The scope of COVID-19 modelling shifted from understanding epidemic dynamics in the early phases to evaluating non-pharmaceutical interventions and vaccination impacts in later phases. Traditional data sources such as case line lists and incidence data were widely used, while non-traditional data, notably real-time social contact and behavioural surveys, were frequently reported as lacking. Interactions with decision-makers were frequent and often directly informed modelling scope, especially in later phases. Code sharing at the time of publication was not common place, with less than half of the studies providing open access code at time of publication.

Discussion

This work highlights the evolving needs of pandemic modelling. The frequent reporting of missing notably non-traditional surveillance data, even two years into the pandemic, underscores a need for reviewing sharing practices and a rethinking of sustainable data collection from non-public/governmental providers. Enhanced collaboration between modellers and decision-makers was crucial for effective pandemic response. Future efforts should focus on addressing data gaps, supporting open access to code, and strengthening collaborative approaches to improve preparedness for future pandemics.

The role of environmental covariates for disease outbreak monitoring

Markus Neteler, Julia Haas, Lina Krisztian, Markus Metz (*Mundialis GmbH & Co. KG*); William Wint (*Environmental Research Group Oxford - ERGO*).

Accurately predicting and monitoring of disease outbreaks requires robust data on environmental factors that influence disease dynamics. The MOOD (Monitoring Outbreak Events for Disease Surveillance) project aims to improve outbreak surveillance by integrating environmental covariates derived from Earth Observation (EO) data into disease surveillance systems. The creation and provision of essential covariates linking environmental conditions to disease spread will improve the predictive power of outbreak models. Work Package 3 (WP3) focused on the standardisation and integration of numerous datasets to support the modelling activities of WP4 and to enhance the disease surveillance capabilities of the MOOD platform. The main objectives of WP3 include the acquisition, processing and integration of covariate and disease data, data standardisation and archiving of critical data resources.

WP3 focused on the identification, collection and standardisation of spatial and covariate datasets. The creation of environmental covariates from high-resolution geospatial and EO data played an important role, as they are critical for understanding and predicting the spread of vector-borne diseases. Using data from multiple satellite platforms, mundialis and ERGO extracted variables such as land cover types, vegetation indices (e.g. NDVI), surface temperature, precipitation patterns, water body extent and others. A major achievement of WP3 is the development of data processing pipelines that transform heterogeneous datasets into unified formats, improving their usability for MOOD researchers and the wider scientific community. These covariates have been processed using open source geospatial tools to ensure consistency and interoperability. Covariates have been generated at different spatial and temporal resolutions to suit different disease models, and are made available through a geospatial infrastructure that supports real-time analysis and visualisation. The team's work on data standardisation and integration has

significantly enhanced the capabilities of the MOOD platform. By ensuring that spatial and covariate data are accessible, interoperable and standardised, the team supported the project's goal of improving pathogen detection and response systems. Selected datasets have been published on Zenodo.org as well. The creation of environmental covariates is a critical contribution to the MOOD project, significantly improving the ability to monitor and predict disease outbreaks.

The open data and open source approach ensures that these covariates can be widely used, providing a sustainable method to support global health surveillance systems. These efforts highlight the importance of robust data frameworks to inform epidemiological research and public health decision-making, providing valuable resources beyond the life of the project. Future efforts will focus on maintaining and updating these datasets and tools to ensure they remain at the forefront of disease surveillance technology.

Session C: Data preparedness and innovative tools for improved EI in Europe**Estimating the incidence and seroprevalence of West Nile virus in the avian population in Northern Italy**

Giovanni Marini, Roberto Rosà (*Research and Innovation Centre, Fondazione Edmund Mach*); Alex De Nardi, Francesco Menegale, Andrea Pugliese (*Department of Mathematics, University of Trento*); Ilaria Dorigatti (*MRC Centre for Global Infectious Disease Analysis, Department of Infectious Disease Epidemiology, Imperial College London*); Marco Tamba, Luca Gelmini, Alice Proserpi, Mattia Calzolari (*Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia-Romagna "B. Ubertini"*); Piero Poletti (*Center for Health Emergencies, Fondazione Bruno Kessler*).

Background/Introduction

West Nile virus (WNV) is one of the most threatening mosquito-borne pathogens in Italy where hundreds of human cases were recorded during the last decade. Here, we estimated the WNV incidence in the avian population in the Emilia-Romagna region (northern Italy) through a modelling framework which enabled us to eventually assess the fraction of birds that present anti-WNV antibodies at the end of each epidemiological season.

Material and methods

We fitted an SIR model to ornithological data, consisting of 18,989 specimens belonging to Corvidae species collected between 2013 and 2022: every year from May to November birds are captured or shot and tested for WNV genome presence.

Results

We found that the incidence peaks between mid-July and late August, infected corvids seem on average 17% more likely to be captured with respect to susceptible ones and seroprevalence was estimated to be larger than other years at the end of 2018, consistently with the anomalous number of recorded human infections.

Discussion and Conclusion

Thanks to our modelling study we quantified WNV infection dynamics in the host community, which is still poorly investigated despite being its importance for virus persistence. To the best of our knowledge, this is among the first studies providing quantitative information on infection and immunity in the bird population, yielding new important insights on WNV transmission dynamics.

UTOPIA: a user-friendly tool to identify trade movements at risk when a disease emerges in a trading partner country

Servane Bareille, Céline Dupuy, Viviane Hénaux (*University of Lyon, French Agency for Food, Environmental and Occupational Health & Safety - ANSES, Epidemiology and Surveillance Support Unit*).

When a foreign country declares the emergency of an animal disease, its trading partners want to assess if animals or products of animal origin potentially carrying this pathogen have been imported into their country. The investigation of trade movements using the regulatory European database TRACES-NT can meet this need. However, these data are complex, with many fields designed for border inspections, and the querying procedures can be laborious. Their analysis is long and a source of errors through misuse. We developed a dashboard for rapid analysis of TRACES-NT data to evaluate the risk of direct or indirect disease introduction to France related to emergency notifications in foreign countries. Its name is UTOPIA, for User Tool for Outbreak Prevention and Introduction Assessment. UTOPIA was built in close collaboration with end users (French Epidemic Intelligence team, ANSES, French ministry of agriculture). Animals and animal products traded from a source country to European countries, including France, were categorized according to product type and species using the international Combined Nomenclature. The goods' route was established, and European countries that can act as staging points between the country where the disease emerged and France were identified. Epidemiological features of diseases were used to filter out goods that may carry the pathogen according to species and product types. Ten regulated diseases, selected with future end-users, were pre-registered in UTOPIA. However, users have also the possibility to provide epidemiological information on non-listed diseases. Users also specify the place and the time of the suspicion or confirmed outbreak to define the period at risk to be considered. In addition, information on the disease situation in the region of its emergence was retrieved from WAHIS and data on susceptible animals were extracted from FAOSTAT and Eurostat.

The main output is a table showing certificates information of all import movements of animals or animal products potentially carrying the pathogen. A spatialized network graph shows movements between cities from the foreign country to France, with the location of declared outbreaks in the background. In addition, the tool provides graphs on the number of susceptible animals raised in the foreign country, as well as information on its main commercial partners of the sector. All these outputs give users a comprehensive overview of the situation.

UTOPIA allows users with TRACES-NT access to easily generate tables and figures to meet their needs. Currently it only considers introductions through declared imports and not through illegal imports or via wildlife or vectors. It comes with a guide for making queries and specifying underlying hypotheses. UTOPIA provides rough information about at-risk trade movements that need to be interpreted carefully by experimented users. UTOPIA improves data preparedness to respond quickly to emergency notifications when partner countries declare the emergence of an animal disease. It will be used to help with epidemiological surveillance and investigations in France and could be easily adapted for other European users.

A new multisource surveillance tool for highly pathogenic avian influenza in mammals

Carlène Trévenec (*INRAE, Montpellier*); Pierre Pompidor (*LIRMM, Montpellier*); Samira Bououda, Julien Rabatel, Mathieu Roche (*CIRAD, Montpellier*).

Introduction/Background

The multisource surveillance tool (MUST) is a new platform for collecting, gathering, and visualizing different sources of information related to health events and highly pathogenic avian influenza in mammals (HPAIM). MUST-AI constitutes the first part of the MUST tool, which centralizes health information relating to cases of HPAIM since January 1, 2021, and comes from 3 different notification sources: an official notification source confirmed by public health institutions (i.e., WAHIS) and two other alternative unofficial sources that collect events from online media (PADI-web) and expert networks (ProMED). MUST-AI is designed to provide a comprehensive view of various events.

Material and Method

Owing to the use of natural language processing algorithms, MUST-AI collects and visualizes HPAIM events from ProMED Mails and from PADI-web articles. MUST-AI is based on four main components, a map, some search criteria, a list of events, and a distribution chart. The extraction quality of various strategies used by PADI-web have been evaluated in terms of recall and precision, based on official events reported in the WAHIS database and some cases reported in published articles as gold standards for HPAIM cases.

Results

Two PADI-web strategies have been selected. The events associated with these strategies will be integrated into MUST-AI according to the location of interest and the goal of surveillance (sensitivity vs. specificity).

Discussion

MUST-AI, collects automatically unstructured data from ProMED and PADI-web and extracts valuable information, to make comparison and to complete official data. We highlight the relevance of integrating events from two strategies of PADI-web. A merging option has been designed to analyze and merge similar events based on certain criteria, even if they were published by different sources.

Conclusion

This communication presents new approaches for data fusion and experiments to assist epidemic intelligence teams in producing early-warning messages and summaries on emerging events, such as HPAIM. In our future work, we plan to improve spatial entity recognition in texts and the impact of the final results obtained.

Integrating Advanced Distance Metrics with Route Navigation Systems for Biosecurity in Livestock Transportation

Mirco Cazzaro, Paolo Mulatti, Francesca Scolamacchia, Nicola Ferrè (*Istituto Zooprofilattico Sperimentale delle Venezie*).

Introduction/Background

Infectious diseases among livestock are significantly influenced by the geographical and infrastructural contexts of farm locations. Conventional epidemiological models often use Euclidean distances, which fail to capture real-world complexities such as road accessibility and geographical barriers. This research introduces a sophisticated computational tool designed to incorporate multiple distance metrics, offering a more comprehensive analysis of potential disease transmission pathways among livestock.

Materials and Methods

We developed an advanced tool capable of calculating six distinct types of distances: Euclidean, Haversine, route, route with elevation, orographic/elevation, and cost/friction. Tailored to include various environmental and man-made factors affecting disease spread, such as terrain orography, road networks, and land use patterns, the tool is implemented through Python scripts and embedded in a user-friendly web application. This setup allows users to upload farm locations and obtain detailed distance matrices, enhancing the basis for epidemiological analysis.

Results

The initial development phase has yielded a robust tool that generates comprehensive distance matrices from user-uploaded datasets of farm locations. Python scripts utilize computational libraries to handle diverse distance calculations efficiently, with a particular focus on complex metrics like orographic and route distances with elevation. Preliminary testing has focused on algorithmic accuracy and computational efficiency, ensuring the tool's reliability across various types of distance calculations.

Discussion

While the tool significantly enhances the analytical framework for veterinary epidemiology by incorporating diverse distance metrics, its real potential lies in future applications. The planned correlation of these distance metrics with epidemiological data aims to uncover which factors most significantly impact disease spread. Should the outcomes align with existing research suggesting that routes critically influence disease transmission, this would justify further robust development of a prototype we have already built. This comprehensive route navigation system is designed to strategically manage animal movements, avoiding buffer areas around infected farms, thereby reducing the risk of disease transmission.

Conclusions

This tool not only advances the field of veterinary epidemiology by enabling broader analyses of

disease spread but also sets the stage for critical follow-up projects. The development of this tool and the preliminary prototype of our comprehensive route navigation system exemplify our commitment to integrating innovative technologies into disease management strategies. By validating which distances most impact disease spread, particularly if route distances are confirmed as critical, we aim to robustly develop and enhance our navigation system. This will significantly improve biosecurity in livestock transportation, directly contributing to the control and prevention of infectious diseases in agricultural settings.

Session D: Reaching out to users and impacts for Improved EI in Europe

Improving epidemic Intelligence in Europe: the challenging innovation process of the MOOD project

Fanny Bouyer (*Groupe d'Expérimentation et de Recherche: Développement et Actions Locales (GERDAL)*); Pierrine Didier (*VetAgro Sup, Marcy l'Etoile*); Henok Tegene, Viviane Hénaux (*University of Lyon - ANSES, Laboratory of Lyon, Epidemiology and support to Surveillance Unit*); Claudio Proietti (*CIRAD, DIMS*); Elena Arsevska (*CIRAD, Astre*).

Background/introduction

The amount and breadth of data available for European epidemic intelligence (EI) systems, as well as the methods to manage and analyze these data, are constantly increasing. The MOOD project has implemented a co-creation process aiming at enhancing the effective use of these data and methods through user-oriented numeric tools and services. A user needs assessment realized at the inception of the project has brought the practitioners' perspective into the process.

Material and methods

A monitoring of the co-creation process and outcomes has been implemented from december 2020 to december 2023 and was based on: meetings with partners to review the impact pathway, 24 interviews with partners, 3 interviews with external participants, registration of the participation of practitioners to MOOD exchanges, 28 online questionnaires about the perceptions of the modules, 6 Key-Performance Indicators, analysis of MOOD reports of meetings and testing sessions.

Results

The initial user needs assessment highlighted multi-dimensional expectations that we gathered around three axes of intervention: i) stronger peer networking, ii) better data integration and data access, and iii) access to semi-automatic tools for detection, monitoring, and assessment of epidemic risks. The initial strategic choices (open access or open source tools; pre-defined human resources of the consortium and research tasks) and challenges faced by the MOOD project (sanitary context of Covid-19 pandemics; sharable datasets; duration of the project) led to a prioritization of the users' needs to be addressed. In addition, MOOD management strategy, including monitoring and evaluation, was built and adapted upon the participatory development and review of the project impact pathway, a flexible and visual representation of the project logic model including the expected mid and long-term impacts. Qualitative monitoring of the co-creation process and outcome-oriented approaches allowed us to identify the key organizational and operational issues concerning the project organization, scientific goals, communication, and involvement of consortium partners and users, which impact the project quality and effectiveness bringing generic

lessons learned. The collective thinking to shift from the tools' development to the building of the platform was an important piece of the learning loops. The exchanges with practitioners have allowed to integrate the concerns of the practitioners into the internal discussion among partners. The last step of testing the platform allowed identifying 3 main expectations from the potential users that will be key to fully reach the expected outcomes: solving of the technical bugs, improvement of the guidance materials and long-term sustainability of the platform (with maintenance of the tools and updating of the data).

Discussion

Finally, we discuss how collective thinking based on the review of the impact pathway is useful to better identify the probable impact, based on evolving hypotheses and risks and what are the useful paths of work to fully reach the targeted impact after the end of the project.

Preparing for the future: EPIET's role in training the next generation of epidemiologists for emerging infectious disease response in Europe

Saeed Ahmad, Fahmeeda Idrees (*Tampere University*).

Introduction

The rise of emerging infectious diseases (EIDs) presents ongoing challenges to public health systems worldwide, necessitating robust and agile responses. The European CDC Fellowship Program, known as the European Programme for Intervention Epidemiology Training (EPIET), is crucial in equipping epidemiologists with the skills necessary to tackle these threats. This study examines how EPIET's comprehensive training framework prepares the next generation of epidemiologists for effective response to EIDs, emphasizing the integration of data sharing, response modelling, and One Health approaches.

Material and Method

This study employs a mixed-methods approach, combining quantitative analysis of program outcomes with qualitative insights from interviews and focus group discussions. Data sources include EPIET curriculum and training materials, deployment records of EPIET graduates during EID outbreaks, and surveys and interviews with EPIET alumni, mentors, and public health officials. Quantitative data was analyzed to assess the deployment, activities, and impact of EPIET graduates in recent EID responses. Qualitative data was coded and thematically analyzed to capture detailed experiences and perspectives on the training program's effectiveness.

Results

Preliminary results indicate that EPIET graduates play pivotal roles in the response to various EIDs across Europe. Key contributions include conducting over 260 outbreak investigations and managing contact tracing for more than 150,000 individuals across multiple EID events. Graduates utilized advanced data analysis techniques and tools, such as electronic registries, to enhance real-time data collection and epidemiological modelling. They implemented risk assessments and strengthened border health measures at major entry points during disease outbreaks. Additionally, EPIET-trained epidemiologists played critical roles in coordinating and supporting vaccination campaigns, administering over 1.8 million doses in collaboration with local health authorities. These efforts significantly improved data-driven decision-making, outbreak control and public health communication, thereby mitigating the impact of EIDs on public health systems.

Discussion

The findings highlight the efficacy of the EPIET program in preparing epidemiologists for complex and dynamic EID responses. The program's focus on data-driven decision-making, integrated surveillance systems, and cross-disciplinary collaboration equips graduates with essential competencies for

modern public health challenges. Furthermore, the incorporation of One Health principles ensures that EPIET-trained epidemiologists are prepared to address the interconnectedness of human, animal, and environmental health.

Conclusions

EPIET's robust training framework is instrumental in developing a highly skilled epidemiological workforce capable of managing EIDs effectively. By fostering competencies in data sharing, response modelling, and One Health approaches, EPIET contributes significantly to the resilience and preparedness of public health systems in Europe thus promoting global health security.

A machine learning modelling framework for the assessment of tick-borne encephalitis risk in Europe

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Introduction

Caused by the tick-borne encephalitis virus (TBEV), tick-borne encephalitis (TBE) is a zoonotic disease that can cause severe neurological symptoms. Despite the availability of a vaccine, it remains a public health concern in Europe, with an increasing number of reported human cases and new hotspots of virus circulation, also in previously non-endemic areas. To geolocate and predict new areas at risk of human TBE infections, we developed a spatio-temporal predictive model to infer the year-to-year probability of human TBE occurrence across Europe at the regional and municipal administrative levels.

Materials and methods

We derived the distribution of human TBE cases at the regional (NUTS-3) level during the period 2017-2022 using data provided by the European surveillance system (TESSy, ECDC), while the distribution of human TBE cases at the municipal level during the same years was obtained using data from five European countries (Austria, Finland, Italy, Lithuania, and Slovakia). We modelled the probability of TBE occurrence at regional and municipal levels using a boosted regression trees approach, including the most critical variables affecting TBE risk: climate, land cover, presence of tick hosts to account for the natural hazard of virus circulation, forest road density and human population density as proxies for the probability of human exposure to tick bites.

Results

Our study highlights a significant rising trend in the probability of human infection with TBE in north-western and south-western European countries and show that areas at high risk of TBE are characterised by the presence of key tick host species, intense human recreational activity in forests, steep drops in late summer temperatures and high annual precipitation.

Discussion

Our study provides a framework for the annual assessment and identification of European regions and municipalities at risk of human TBE infection, based on epidemiological and ecological data collected during the period 2017-2024. The results show a continuous westward, northward, but possibly also south-westward shift of TBE risk areas. Being based on lagged covariates, our approach can also be used to predict risk areas one year in advance, providing a multi-scale perspective to improve our understanding and prediction of short-term variations in the spread of tick-borne encephalitis in Europe.

Conclusions

Our study provides an assessment of the European regions at risk of TBE human infections on a yearly basis. As TBE range is spreading westwards, northwards, and to higher altitudes, our results will be used to support surveillance and prevention campaigns within endemic and potential new risk areas.

Estimating the potential risk of transmission of arboviruses in the Americas and Europe: A modeling study

Agnese Zardini, Francesco Menegale, Andrea Gobbi, Mattia Manica, Giorgio Guzzetta, Valeria d'Andrea, Valentina Marziano, Stefano Merler, Piero Poletti (*Bruno Kessler Foundation*); Filippo Trentini (*Bocconi University*); Fabrizio Montarsi, Gioia Capelli (*Istituto Zooprofilattico Sperimentale delle Venezie*); Beniamino Caputo, Angelo Solimini, Alessandra della Torre (*University of Rome La Sapienza*); Cecilia Marques-Toledo, Mauro M. Teixeira (*Federal University of Minas Gerais*); André B.B. Wilke, Marco Ajelli (*Indiana University School of Public Health*); Roberto Rosà, Andrea Pugliese (*University of Trento*); Giovanni Marini, Daniele Arnoldi, Annapaola, Rizzoli (*Fondazione Edmund Mach*); Ana Pastore y Piontti, Alessandro Vespignani (*Northeastern University, Boston*); John C. Beier (*University of Miami*).

Background

Estimates of the spatiotemporal distribution of different mosquito vector species and the associated risk of transmission of arboviruses are key to design adequate policies for preventing local outbreaks and reducing the number of human infections in endemic areas. In this study, we quantified the abundance of *Aedes albopictus* and *Aedes aegypti* and the local transmission potential for three arboviral infections at high spatiotemporal resolution in areas where no entomological surveillance is available.

Material and Method

We developed a model to quantify the daily abundance of *Aedes* mosquitoes, leveraging temperature and precipitation records. The model was calibrated on mosquito surveillance data collected in 115 locations in Europe and the Americas. Model estimates were used to quantify the reproduction number of dengue virus, Zika virus, and chikungunya in Europe and the Americas.

Results

In areas colonised by both *Aedes* species, *A. aegypti* was estimated to be the main vector for the transmission of dengue virus, Zika virus, and chikungunya, when compared with *A. albopictus*. Our estimates highlighted that these arboviruses were endemic in tropical and subtropical countries. A non-negligible potential risk of transmission was also estimated for Florida, Texas, and Arizona (USA). The broader ecological niche of *A. albopictus* could contribute to the emergence of chikungunya outbreaks and clusters of dengue autochthonous cases in temperate areas of the Americas, as well as in Mediterranean Europe.

Discussion and conclusions

Our results provide a comprehensive overview of the transmission potential of arboviral diseases in Europe and the Americas, highlighting areas where surveillance and mosquito control capacities should be prioritized.

Perspectives Sessions

Anticipating and managing vector-borne diseases: a French (and European) vision.

Didier Fontenille (*IRD*).

Like all countries, France, including its overseas territories, is facing major climatic, environmental and societal changes. These changes modify the risks of emergence and transmission of infectious diseases to humans, animals and plants.

The French Human Health Risk Surveillance and Anticipation Committee (COVARS) has assessed these risks for vector-borne diseases (VBD) affecting humans, taking into account epidemiological and clinical risks, control measures and impacts, for the next 5 years.

The conclusions show that the risk of major Exceptional Health Situations linked to VBD is mainly linked to mosquito-borne arboviruses (dengue fever and West-Nile virus infection), with a different distribution between mainland and overseas France. Three other arboviruses diseases - Zika, Chikungunya (mosquitoes) and Crimean-Congo hemorrhagic fever (ticks) - pose a lesser but still serious risk. Finally, tick-borne encephalitis, rift valley fever and Lyme disease could also see their level of risk change as a result of climate change and other environmental factors. For dengue and WN fever, COVARS has made detailed recommendations for surveillance and control that can be applied to other European countries.

Harnessing Data and Tools for Effective Epidemic Intelligence: A WOAHPerspective on Enhancing Global Health Preparedness

Paolo Tizzani, Jenny Hutchison (*WOAH Data Integration Department*).

The World Organisation for Animal Health (WOAH) is an intergovernmental organisation established in 1924, and since its foundation its main role has been to prevent the international spread of animal diseases. WOAHP recognized the importance of proper data quality, improved data analysis, and the development of new and advanced tools to reduce the risk of spread and impact of health threats, with a specific attention on animal threats

Taking into account the presentations made during the session, the WOAHP's contribution aims to provide reflections and perspectives on the results achieved by the MOOD projects and beyond, in the field of data preparation and the use and implementation of innovative tools for improved epidemic intelligence in Europe and at the global level. The results of the MOOD project presented in the session highlighted the importance of integrating 'traditional' epidemiological approaches and epidemic intelligence activities with advanced analyses (e.g. molecular, phylogenetic and phylogeographic analyses to study the evolution of WNF) and innovative tools (e.g. the MUST multisource surveillance tool) to improve the efficiency

and performance of epidemic intelligence. However, an effective epidemic intelligence system relies not only on the collection, monitoring and analysis of health threats, but also on a solid base of additional and complementary information to support risk assessment. In this latter context, the results presented on the UTOPIA tool to identify at-risk trade movements, or on the Advanced Distance Metrics with Route Navigation Systems for Biosecurity in Livestock Transport, clearly highlighted the importance of having solid data and analysis available to take decisions to anticipate, prevent and/or control health events.

From the perspective of an intergovernmental organisation dealing with animal health, while we recognise the importance of improved data analysis and advanced tools, we should also remember that they can only be truly effective if they are built on a solid foundation. There is still work to be done to homogenise the way data is collected and standardised, and to establish a common reference and terminology that will allow organisations working in human, animal and environmental health to share information, speak the same language, and work together effectively. To be effective, data and require that people are able to use them to their full potential, so the human factor and capacity building must always be considered. Finally, geographical differences and the capacity of individual countries with different available resources need to be taken into account when considering the possibility of extending some experiences beyond high-income countries. The WOAHP recognised the importance of collaboration in the field of epidemic intelligence between institutions (international, regional, national) dealing with animal, human and environmental health and research institutions to ensure a proper link and exchange between scientific approaches and their practical application in reducing health threats.

Enhancing Epidemic Intelligence in Europe through Advanced Computational Models for Sustainable One Health Actions

Beate Conrady (*Department of Veterinary and Animal Sciences, University of Copenhagen*)

In today's rapidly changing environment, national institutions responsible for animal and public health security can no longer rely solely on traditional disease reporting mechanisms and risk assessment strategies that are not equipped to detect emerging hazards. Epidemic Intelligence (EI) encompasses a range of activities aimed at conducting rapid risk assessments of unexpected health events. EI focuses on early identification of potential health hazards, verifying disease incursions in new areas, and assessing acute, serious, or endemic diseases. This is achieved through the development of computational models that assist national risk assessors and managers in understanding the epidemiological consequences of disease spread and in recommending public health mitigation strategies.

This talk will use case studies to demonstrate how the goal of Epidemic Intelligence (EI)—specifically, to complement traditional surveillance systems by integrating indicator-based and event-based monitoring with existing datasets and understanding the interconnectedness between systems through a One Health approach—can be achieved.

Poster Session

Large-scale Interdisciplinary Alliance on Nature-based SoLutions and Health: Indicators, Inequality and Innovation

Marina Treskova, Cassia Rocha Pompeu, Joacim Rocklöv (*Heidelberg University*).

Introduction/Background

Nature-based Solutions (NbS) are instrumental in European climate change mitigation and adaptation strategies. Through creating ecosystems, NbS can have positive and negative impacts on the health of people, animals and the environment, i.e. co-benefits and unintended consequences. As NbS are increasingly integrated into policy and implemented on the ground, it is urgently needed to adopt evidence-based approaches to their design and implementation, which minimize maladaptation and mislabeling practices, particularly in the health domain.

Material and Method

The LILY project focuses on NbS impacts on health (NbSHealth) and addresses:

1. the lack of a comprehensive framework outlining health outcomes and underlying pathways,
2. gaps in NbS-Health indicators,
3. vulnerability and inequality,
4. NbS-Health monitoring,
5. NbS-Health gaps in NbS platforms.

LILY will engage scientists, implementers, stakeholders, and community in participatory approaches and produce

1. a conceptual NbS-Health framework,
2. best-practice guidelines for spatio-temporal NbS-Health indicators considering vulnerability and inequality,
3. recommendations on novel data streams and methodology for indicator-based monitoring and evaluation,
4. a network and data platform for proficient information sharing.

Discussion

LILY will empower young scientists through summer schools, knowledge exchange workshops, and arranging the first NbS-Health conference. The outcomes will be translated into policy briefs, materials for Lancet Countdown, EU-Horizon projects and clusters, and public dissemination. LILY commits to excellence and innovation through co-production among scientists and stakeholders, transdisciplinarity, One Health concept, Exposure-Vulnerability-Risk framework, and inclusive and gender balance approaches in its governance.

Evaluating the Impact of the ECDC One Health Framework on Emerging Infectious Disease Surveillance in Europe

Saeed Ahmad (*Tampere University*); Fakhra Ikhtlaq (*University of Birmingham*).

Introduction

The European Centre for Disease Prevention and Control (ECDC) has implemented a One Health Framework designed to unify efforts across the European Commission, EU agencies, and Member States to address emerging infectious diseases (EIDs). This approach fosters cross-sectoral collaboration to enhance the interoperability and coordination necessary for preventing and controlling communicable diseases. This study evaluates the impact of the ECDC One Health Framework on improving EID surveillance and response in Europe, with a particular focus on the integration of multi-sectoral data and its effect on public health outcomes.

Material and Method

A mixed-methods approach was utilized, combining quantitative analysis of EID surveillance data with qualitative insights from key stakeholders. Data sources included ECDC surveillance reports, cross-sectoral collaboration records, and interviews with public health officials, veterinarians, environmental scientists, and ECDC staff. Quantitative data were analyzed to assess changes in EID detection rates, response times, and outbreak containment success before and after implementing the One Health Framework. Qualitative data were thematically analyzed to understand stakeholder perceptions and experiences regarding the framework's impact.

Results

The implementation of the ECDC One Health Framework resulted in significant improvements in EID surveillance and response. Detection rates of EIDs increased by 28%, response times decreased by 35%, and outbreak containment success improved by 22%. Enhanced data sharing and integration across sectors facilitated early warning systems and real-time surveillance, significantly contributing to more effective and coordinated responses. For instance, the use of electronic registries allowed for the collection and analysis of over 150,000 health records, improving data-driven decision-making. Additionally, stakeholders reported improved collaboration and communication between human health, animal health, and environmental sectors, which were critical in addressing EIDs' complexities.

Discussions

The findings underscore the significant positive impact of the ECDC One Health Framework on EID surveillance and response in Europe. The framework's emphasis on cross-sectoral collaboration and data integration has proven effective in addressing the multifaceted nature of EIDs. However, challenges

remain in achieving seamless coordination and resource allocation across different sectors. The experience from the COVID-19 pandemic and other recent outbreaks highlights the necessity of a well-prepared health workforce equipped with advanced epidemiological skills and supported by robust digital health systems.

Conclusions

The ECDC One Health Framework has significantly strengthened EID surveillance and response capabilities in Europe, demonstrating the value of a holistic and integrated approach. By fostering cross-sectoral collaboration and enhancing data sharing, the framework has improved public health outcomes and preparedness against future EID threats. The lessons learned from the implementation of this framework are invaluable for resilient health systems.

AI²: Artificial Intelligence supported phylodynamic spatio-temporal analysis of Avian Influenza outbreak in mammals in Europe

Andrzej Jarynowski (*Wroclaw Medical University*); Alisa Sergeeva, Vitaly Belik (*Free University of Berlin*).

Background

A/H5N1 epizootic in cats in Poland in Spring-Summer 2023 was investigated. Environmental, surveillance and social media data on various driving factors were collected real-time enabling effective modeling of the disease spread.

Methods

Data and methods triangulation were applied based on:

1. 30 positive cases (with RNA sequences) and 27 negative cases from WOAHI reference lab (geolocalized and with a timestamp),
2. 87 suspected cases submitted by animal owners (participatory epidemiology),
3. daily time series of: (i) Google queries for Avian Influenza (AI), cats disease and cats deaths, as well as (ii) mentions of cat/cats and AI in social and traditional media. Other factors such as distance to water or abundance/migration of birds is considered. To evaluate the phylogenetic distance between strains detected in cats, other mammals and birds from a period 2022-2024 worldwide, bioinformatics was used, such as BLAST, SNP-calling, building of a phylogenetic tree for each gene of AI.

Results

Positive cases form a chain-like structure both on bird migration paths and close to the high abundance of waterbird nesting sites (verified by comparison of the average nearest neighbor distance and betweenness clustering of positive case vs. controls). A/H5N1 was already probably circulating in cats in the second half of May in regions bordering with Ukraine (a month before the first confirmed case). There are at least 2 – eastern and western Poland – separate introductions of viruses according to k-mean and DBSCAN clustering. The hemagglutinin (HA) gene shared SNPs with 2022-2024 bird and mammal strains from Africa and Europe. Polymerase-binding protein 1, 2 (PB1, PB2) displayed two subpopulations in cats and mutations found in Polish birds and chickens. The matrix protein (MP), nucleocapsid protein (NP), nonstructural protein (NS), acidic protein (PA) mutations were found in European wild birds and Polish chicken strains. All avian influenza genes clustered with 2022 African wild bird strains, particularly from Egypt, and some with a 2021 Saratov strain.

Discussion

Bioinformatics and spatio-temporal analysis identified two subpopulations of A/H5N1 in cats without typical mammalian adaptation mutations. Key genes had mutations common in wild birds and chickens from Poland and broader regions. This suggests that the virus from cats was closely related to strains circulating

in wild birds in Africa and Europe and have been silently circulating in Eurasia and Africa for some time before in an unknown mammal population (maybe rodents?).

Conclusions

Common outbreak investigation of veterinary and sanitary inspection revealed multiple gaps in emerging new zoonotic threats. Veterinarians in the USA, coping with a similar spill-over (Spring 2024), knew (because of Polish experience among others) that cats can be a sentinel of avian influenza in mammals, as well what kind of obstacles can appear in investigation and infection control duties. Thus, use of unconventional data and infodemic management should be incorporated into surveillance and risk assessment as similar events might happen in Europe in the future.

The application of WebGIS to manage Avian Influenza

Giacomo Nalesso, Clara Tassinato, Guido Di Martino, Simone Rizzo, Matteo Mazzucato, Claudia Casarotto, Luca Martelli, Diletta Fornasiero, Francesca Scolamacchia, Vittoria Tregnaghi, Grazia Manca (*Istituto Zooprofilattico Sperimentale delle Venezie*).

Background/Introduction

Avian Influenza (AI) has historically been a major threat for Italian poultry production, especially in the northeast due to the high poultry population density and the proximity to vast wetlands located along the Black Sea–Mediterranean and the East Atlantic migratory flyways. These factors led to heavy and persistent infections with AI viruses. Beyond impacting the industry and consumers, AI outbreaks also come at a great cost to governments and the general public.

Material and Methods

To improve AI management, the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) developed different tools, including:

1. a data warehouse that integrates poultry farms data with diagnostic test results derived from a Laboratory Information Management System (LIMS), geospatial information and outbreak data;
2. a data manager dedicated to managing AI outbreak data (e.g. date of suspect, date of cleaning and disinfection, etc.);
3. a management system to support and store the documents during the outbreaks, and (iv) a WebGIS tool called IZSVeGIS Avian Influenza (IZSVeGIS-AI) that supports the decision-making process behind the application of specific control measures.

Results

Information accessible through the WebGIS tool allows monitoring the evolution of the epidemiological situation in real time. Among the main functionalities of this tool there is the visualization of risk and restricted zones, and the possibility to measure the distance between farms through a distance buffer. To each suspected, confirmed or extinct outbreak extra information are readily available (e.g. poultry species kept, productive type, housing date and poultry company). In addition, the IZSVeGIS-AI tool allows to identify the areas that have been confirmed by the health authority (restricted zones).

Discussion and Conclusion

By integrating data from different sources, it is easier for veterinary authorities to make decisions during AI outbreaks and share it with the involved stakeholders, which can be granted by direct access to the tool with specific privileges. In the future, the IZSVeGIS-AI could be further expanded to provide supplementary information for each poultry holding, such as vaccination status or biosecurity score level.

A Comparative Analysis of Predictive Models for *Aedes albopictus* Dynamics

Daniele Da Re (*Edmund Mach Foundation*), Marharyta Blaha, Roberto Rosà (*University of Trento*) Alessandro Albieri, Marco Carrieri (*Centro Agricoltura Ambiente "Giorgio Nicoli", Crevalcore*) Cyril Caminade (*International Centre for Theoretical Physics*) Kamil Erguler (*The Cyprus Institute*) Adolfo Ibanez Justicia (*Centre for Monitoring of Vectors*) Hammami Pachka (*Centre de coopération internationale en recherche agronomique pour le développement*) William Wint (*University of Oxford*) Agnese Zardini (*Bruno Kessler Foundation*).

Introduction/Background

The invasive mosquito *Aedes albopictus* presents a significant public health challenge due to its potential to spread arboviruses. Understanding and predicting its abundance and seasonality is crucial for effective vector control and public health strategies. Over the past 20 years, various predictive models, both correlative and mechanistic, have been developed. However, a comprehensive comparison of these models to assess their strengths and limitations has been lacking, which is essential for improving predictive accuracy and developing effective intervention strategies.

Material and Method

We reviewed and tested eight different modelling approaches to estimate the abundance and seasonality of *Ae. albopictus*. These included both correlative models, which rely on statistical relationships between observed mosquito populations and environmental variables, and mechanistic models, which simulate the biological processes governing mosquito dynamics. The evaluation criteria focused on the beginning, peak, and end of the seasonal activity of the species. Additionally, the feasibility of integrating multiple models into an ensemble approach to enhance prediction capabilities was evaluated.

Preliminary Observation

Initial observations suggest that each modelling approach has distinct strengths and limitations. Correlative models appear to perform well in data-rich environments, while mechanistic models seem to offer valuable insights into the biological processes of mosquito dynamics. The potential of ensemble models to combine predictions from multiple individual models indicates possible improvements in accuracy and reliability, especially in diverse environmental settings.

Discussion and Conclusions

Advancements in modelling approaches for *Ae. albopictus* dynamics represent a significant step forward in vector control and public health strategy development. By comparing and integrating different models, we aimed to improve predictive capabilities, which are crucial for mitigating the growing threat of vector-borne diseases. Future research should focus on refining these models, expanding data collection efforts, and exploring the integration of additional environmental and biological variables to further enhance prediction accuracy and utility in public health applications.

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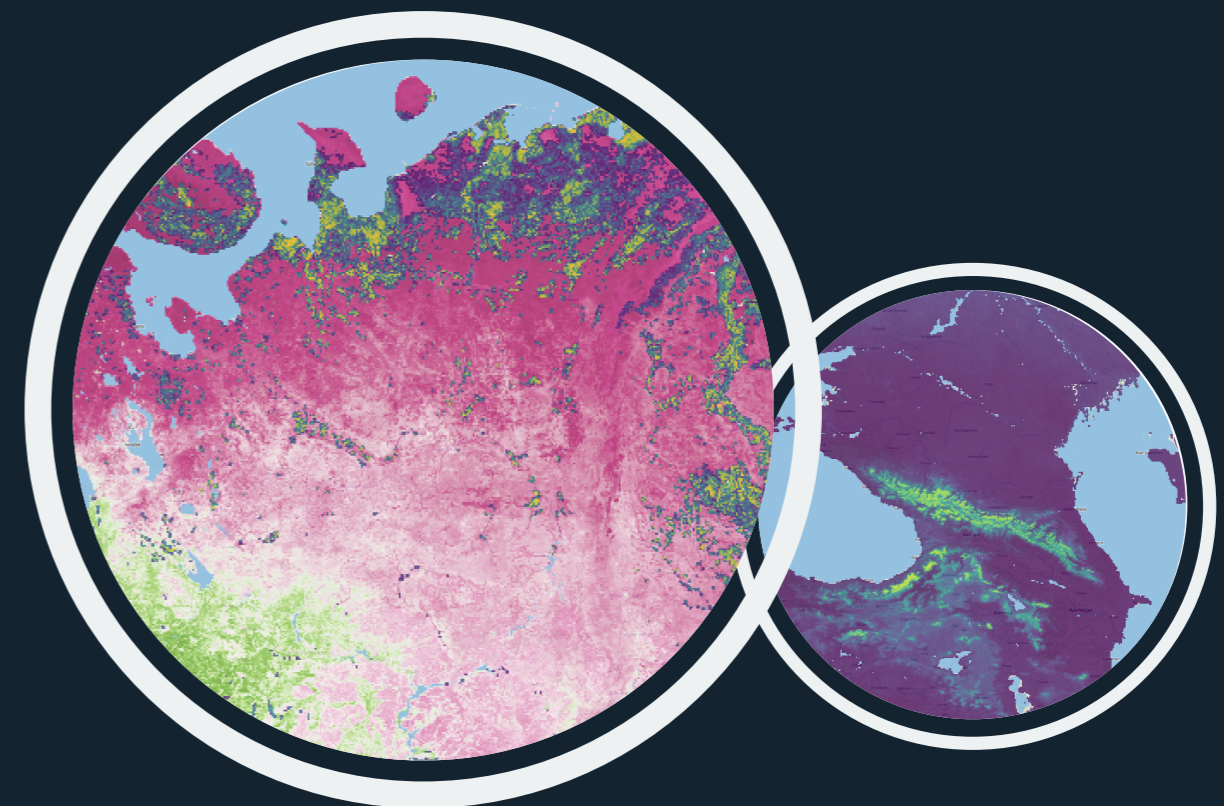
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