Identify signs and drivers of zoonotic diseases emergence and digital data resources for Epidemic Intelligence

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IDENTIFY SIGNS AND DRIVERS OF ZOONOTIC DISEASES EMERGENCE AND DIGITAL DATA RESOURCES FOR EPIDEMIC INTELLIGENCE

Book of abstracts

EDITED BY
Annapaola Rizzoli, Floriana Marin, Roberto Rosà

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MOOD hybrid workshop

IDENTIFY SIGNS AND DRIVERS OF ZOONOTIC DISEASES EMERGENCE AND DIGITAL DATA RESOURCES FOR EPIDEMIC INTELLIGENCE

28-29 September 2022
Science Museum MUSE-TRENTO (Italy)

In the great acceleration era of the Anthropocene, the emergence of zoonotic pathogens including those with high pandemic potential is occurring at a faster rate than in any precedent historical phase. The scientific evidence demonstrates that emergence is preceded by a combination of driving factors and events which span from global environmental changes (i.e. climate change, biodiversity loss, land use) to changes at the local scale in socio-economical conditions, food habits and cultural trends. Seven major anthropogenic drivers of zoonotic disease emergence have been identified by UNEP: the increasing demand for animal protein, unsustainable agricultural intensification, increased use and exploitation of wildlife, unsustainable utilization of natural resources accelerated by urbanization, land-use change and extractive industries, travel and transportation, changes in food supply chains and climate change.

Epidemic intelligence aims at the early identification of potential health threats to improve timely detection and awareness of infectious disease events at the earliest stage of their emergence. Therefore, the identification and surveillance of the drivers and conditions which are recognized to promote the emergence and spread of infectious diseases are crucial to provide public health systems with bio-ecological data and early warning digital signals. Defining, for each disease, the subset of "core" drivers and signals associated with their capacity to emerge and spread along with the cataloguing of their related digital data sources available, would provide the basis for the establishment of an integrated drivers of infectious diseases digital data surveillance system. This approach would provide an innovative tool, useful for analysts, public and veterinary health agencies and decision-makers to define in which conditions the probability of infectious disease emergence and spread is high, and timely identify events with such high probability, therefore, triggering more timely and targeted surveillance, prevention and interventions actions since the pre-emergence phase.

These and other topics will be the subject of the 2 days MOOD 2022 hybrid workshop. This workshop will provide a forum for showcasing current research and findings in the field as well as for identifying critical questions and future research challenges including the provisioning of

new tools and data for Epidemic Intelligence and highlighting the inter-disciplinary approaches needed to meet them under the One Health umbrella. The scientific program will be organized in 5 sessions with plenary lectures by invited speakers followed by presentation from MOOD and other EU funded project partners and expert, with opportunities for personal interaction and discussion. Other side events and interview to speakers and guests will be organized to disseminate the key messages rising from this workshop through various channels and media.

COMMITTEES

Scientific committee

Annapaola Rizzoli, Fondazione Edmund Mach - Research and Innovation Centre, Ecohealth Lab, San Michele all'Adige (TN), Italy

William Wint, Environmental Research Group Oxford Ltd, c/o Department of Biology, Mansfield Road, Oxford, OX13ZS, UK

Roberto Rosà, University of Trento - C3A, Centre for Agriculture, Food and Environment, San Michele all'Adige (TN), Italy

Giorgio Guzzetta, Center for Health Emergencies, Fondazione Bruno Kessler, Trento, Italy

Luca Busani, Istituto Superiore di Sanità, Roma, Italy

Organizing committee

Annapaola Rizzoli, Fondazione Edmund Mach - Centro Ricerca e Innovazione, San Michele all'Adige (TN), Italy

Gonzalo Cervantes, Fondazione Edmund Mach - Centro Ricerca e Innovazione, San Michele all'Adige (TN), Italy

Floriana Marin, Fondazione Edmund Mach - Centro Ricerca e Innovazione, San Michele all'Adige (TN), Italy

Alberto Mattedi, Fondazione Edmund Mach - Centro Ricerca e Innovazione, San Michele all'Adige (TN), Italy

Federica Spimpolo, MUSE - Museo delle Scienze, Trento, Italy

Lorena Celva, MUSE - Museo delle Scienze, Trento, Italy

PROGRAM

28th September 2022			
Morning session – h. 08:30-12:00			
Registration	Welcome and opening speech	Plenary presentation 1	Plenary presentation 2

Time		
8.30-9.00 am	Registration	
9.00-9.30 am	Welcome and opening speech	Dr.ssa Annapaola Rizzoli (FEM), Dr.ssa Elena Arsevska (CIRAD), Prof. Mario Pezzotti (FEM), Dr. Michele Lanzinger (MUSE), Dr Stefano Merler (FBK), Dr.ssa Valentina Perrotta (PAT), Dr. Giancarlo Ruscitti (PAT), Dr Francesco Pizzo (APSS)
9.30-10.30 am	Plenary presentation 1: Science and pre-emergent prevention Chair Dr Heidi C. Hauffe	Prof. Peter Hudson
10.30-11.00 am	Coffee break	
11.00-12-00 am	Plenary presentation (on-line)2: Tracking and real-time risk assessment of emerging viruses: lessons learned from the COVID-19 pandemic Chair Dr Heidi C. Hauffe	Prof. Marion Koopmans
12.00-13.00	Lunch break	

28th September 2022		
Afternoon session – h. 13.00-18.35		
Session 1: Cross cutting theme: Which drivers and how they affect disease emergence		
Session 1a: Climate and environment as drivers of infectious disease: the evidence	Session 1b: Biodiversity loss, wildlife conservation, host and pathogen traits	Session 1c: Socio-economical drivers of diseases emergence

Time		
13.00-14.50	Session 1a: Climate and environment as drivers of infectious disease: the evidence. Chair Dr William Wint	
13.00-13.25	What climate data are out there and which should you use for modeling	Keynote: Dr. William Wint
13.25-13.50	What needs to be done to climate drivers to make them model friendly?	Keynote: Dr. Donal Bisanzio
13.50-14.05	Untangling the seasonal drivers of zoonotic spillover from wildlife: Hendra virus dynamics in an Australian bat colony	Dr. Olivier Restif
14.05-14.20	Effect of hydrometeorological indicators on leptospirosis risk in Fiji: a modelling study	Dr. Eleanor M Rees
14.20-14.35	Ecological covariates affecting the risk of tick-borne encephalitis in the European continent	Dr. Francesca Dagostin
14.35-14.50	West Nile virus Lineage 2 overwintering in Italy	Dr. Giulia Mencattelli
14.50-15.10	Break	
15.10-17.25	Session 1b: Biodiversity loss, wildlife conservation, host and pathogen traits. Chair Dr. Valentina Tagliapietra	
15.10-15.35	Pathogens spillover: lesson learned from bat borne viruses	Keynote: Prof. Raina Plowright. Cornell University
15.35-16.00	Describing the diversity of tick-borne pathogens to understand their transmission routes and manage their emergence	Keynote: Dr. Xavier Bailly
16.00-16.25	Changes in bird migration pattern in relation to West Nile virus emergence in Europe	Keynote: Dr. Lorenzo Serra
16.25-16.40	Macroparasites as drivers of emerging disease	Dr. Joanne Lello
16.40-16.55	Merging ecology and technology: the capacity for detecting infectious diseases in wildlife using computer vision	Dr. Sarah Perkins
16.55-17.10	Prezode: Preventing zoonotic disease emergence	Dr. Benjamin Roche
17.10-17.25	Epidemiological intelligence for surveillance of animal health: monitoring mass mortality events in wildlife	Dr. Nicola Ferrari

17.25-17.50	Coffee break	
17.50-18.40	Session 1c: Socio-economical drivers of diseases emergence Chair Dr. Luca Busani	
17.50-18.15	Epidemiology of SARS-Cov-2 and public health indicators	Keynote. Dr. Stefano Merler
18.15-18.40	Gender and infectious diseases	Keynote. Dr. Anna Ruggieri
19.00-21.00	Aperi-dinner at MUSE	

29th September 2022
Morning session – h. 09:00-13:00

Plenary presentation 1	Plenary presentation 2	Session 2b

Time			
9.00-10.00	Plenary presentation 1: Harvesting the potential of big data for vector-borne disease outbreaks Chair Dr. Heidi C. Hauffe	Prof. Jan Semenza	
10:00-11:00	Plenary presentation 2: Spillover Surveillance and One Health Response: Understanding Emerging Zoonotic Threats in Real Time. Chair Dr. Heidi C. Hauffe	Prof. Emily Gurley	
11:00-11.30	Coffee break		
11.30-13:00	Session 2: Cross cutting theme: What methods and tool can be applied to drivers to provide early warning and rapid disease risk assessment?		
11.30-13.00	Session 2b: Automatic data acquisition via web-scraping Chair Dr. Maguelonne Teisseire		
11.30-11.55	How text-mining could improve epidemiological surveillance?	Keynote. Dr. Mathieu Roche	
11.55-12.20	Innovative Surveillance: ISID's Program for Monitoring Emerging Diseases (ProMED)	Keynote: Dr. Linda MacKinnon	
12.20-12.35	Contribution of epidemic intelligence to transparency and timeliness in reporting to the World Organisation for Animal Health	Dr. Paolo Tizzani	
12.35-12.50	Social tensions due to ASF and HPAI on Polish Twitter	Dr. Andrzej Jarynowski	
13.00-14.00	Lunch break		

29th September 2022		
Afternoon session – h. 14.00-17.30		
Session 2: Cross cutting theme: What methods and tool can be applied to drivers to provide early warning and rapid disease risk assessment?		
Session 2a: Innovative modelling methodologies that enable risk modelling and mapping	Plenary presentation 3	Closing

Time	
14.00-16.05	Session 2: Cross cutting theme: What methods and tool can be applied to drivers to provide early warning and rapid disease risk assessment?
14.00-16.05	Session 2a: Innovative modelling methodologies that enable risk modelling and mapping Chair: Dr. Giorgio Guzzetta and Prof. Roberto Rosà
14.00-14.25	Source-sink epidemic dynamics shaping COVID-19 pandemic waves	Keynote. Dr. Vittoria Colizza
14.25-14.50	The context specific emergence and spread of novel SARS-CoV-2 VOCs	Keynote. Dr. Moriz Kraemer
14.50-15.05	Drivers of West Nile virus human transmission risk in Europe	Dr. Giovanni Marini
15.05-15.20	EO data and Deep Learning methods to map Culex pipiens distribution in central Italy	Dr. Carla Ippoliti
15.20-15.35	Early warning of WNV human cases issued from a climate-dependent epidemiological model operating in a probabilistic framework	Dr. Ioannis Kioutsioukis
15.35-15.50	Global spatiotemporal pattern and potential drivers of influenza decline during the COVID-19 pandemic	Dr. Chiara Poletto
15.50-16.05	Local vs nationwide restriction against COVID-19 pandemic in France between September 2020 and June 2021	Dr. Chiara Sabbatini
16.05-16.30	Coffee break	
16.30-17.30	Plenary presentation 3: Broad-spectrum countermeasures in response to early spillover events Chair Dr. Heidi C. Hauffe	Prof. Hector Aguilar- Carreno
17.30	Closing	

Plenary presentation 1

Science and pre-emergent prevention

Prof. Peter Hudson

Willaman Professor of Biology, Center for Infectious Disease Dynamics, Pennsylvania State University, State College, Pennsylvania, USA

Keywords: Pre-emergent intelligence, spillover prevention, wildlife diseases

Our understanding of outbreak dynamics reveals that even without a large R0, many emerging infections have short generation times and spread at a rate that would escape much of our pandemic prevention schemes. Indeed, we now know there are social limitations when rolling out protective responses including vaccines and anti-virals. As such I argue that pre-emergent intelligence is essential to preventing future pandemics and we need both rigorous science that bridges multiple disciplines. I will discuss some successes and failures and provide insights, ideas about ecological countermeasures that emerge from studies of pathogen spillover between free-living wildlife systems and wildlife and humans.

Plenary presentation 2

Tracking and real-time risk assessment of emerging viruses: lessons learned from the COVID-19 pandemic

Prof. Marion Koopmans

Erasmus Medical Centre, Department of Viroscience, Rotterdam, The Netherlands

Keywords: COVID-19, real time risk assessment

Abstract not available.

SESSION 1: CROSS CUTTING THEME: WHICH DRIVERS AND HOW THEY AFFECT DISEASE EMERGENCE

What climate data are out there and which should you use for modeling?

William Wint

Environmental Research Group Oxford Ltd, c/o Department of Biology, Mansfield Road, Oxford, OX13ZS, UK

Keywords: Covariates, dataset, modelling

Background. Modelling human and animal diseases, whether using spatial or mathematical techniques, require not only some form of disease data, but also information on the factors that are likely to affect the occurrence of the disease i.e. the drivers or covariates. These drivers may include climatic, environmental, demographic, or socioeconomic data, as well as the distributions of vectors and/or hosts distributions without which the diseases cannot occur. The most frequently used are climatic datasets, perhaps because they are the ones most frequently evaluated and reported in the published literature. The variety and volume of such data accessible to modelers becomes ever more daunting, and few non specialists are aware of the huge range of possibilities available. This is especially true of climate data. This presentation provides an overview of what climate data can be found, which may be more suited disease modelling than others, and sets out some of the ways that the data can optimized for use in disease models.

Methods and findings: The superstars of the climate covariates are probably temperature and rainfall and as a result there are many sources of such data available – most obviously based on either remotely sensed satellite imagery or derived from

weather station data. Each type has their pros and cons in terms of timeliness, accuracy, and thematic diversity and accessibility. Most of these data are available as time series covering decades, which itself presents the problem of which precise variable to choose – mean, maximum, a specific date, and so on. Some techniques to provide time series summaries and bioclimatic indicators relevant to disease modelling are discussed. In these days of climate change awareness, it is obvious that climate covariates are readily projected and widely available. These data are both complex and very diverse, and there are some pitfalls and problems to be negotiated when choosing the projection data to use in models – which are briefly outlined. One of the key challenges in the provision of climate covariates is the requirement to standardize the data so that it is compatible with other covariate datasets thar comprise the required driver suite for disease modelling. A brief overview is provided of the standards that should be applied to spatial climate data when added to the covariate suite provided to disease modelers. Despite the huge volumes of data that are available, some are notably and perhaps surprisingly missing. Such gaps are illustrated and discussed, and some suggestions provided of what the priorities might be in filling the current gaps in covariate data provision.

Discussion. Climate datasets are essential as inputs to disease models, and given the proliferation of datasets and sources, choosing and acquiring the ones that are most appropriate to a particular analysis is not necessarily straight-forward. A number of suggestions are provided to assist the selection process and to choose processing needed to optimize climate inputs for disease modelling.

What needs to be done to climate drivers to make them model friendly

Donal Bisanzio, DVM, PhD

RTI International, Washington, DC, 20005, USA

Background. During the last decades, climate data have become widely available and easy to access. As a result, researchers studying the effect of climate on disease transmission dynamics can obtain data from several sources. These sources provide data covering different spatial and temporal scales created with several methods. For

example, historical climate data such as temperature and precipitation results from ground observations (weather stations) or remote sensing surveys (satellite images). Researchers can also access forecasting climate data that are the product of advanced climatological models, predicting the climatic characteristics of future years on a global scale. However, even though access to climatic data has become easier, they cannot be used 'out of the shelf', but after some post-processing methods. This presentation aims to describe analytical methods to process climate data to add them as variables in different modeling frameworks. The presentation will also provide suggestions on how to include climatic factors in models to investigate their relationship with disease transmission dynamics.

Methods and findings. To include climate data as model covariates, researchers need to reshape the raw data to make them suitable for their modeling needs. Climatic data must be vetted, corrected, and aggregated before being used as model covariates. The post-processing methods can differ depending on the type of data and their spatio-temporal characteristics. Researchers can apply various analytical methods to obtain model covariates for their studies. At the same time, researchers should also explore different modeling approaches to investigate the relationship between climatic factors and disease outcomes. Besides the classical linear relationship, researchers should apply non-linear modeling frameworks. These modeling methods can capture the temporal lag of the covariate effect that characterizes the impact of climate on diseases.

Discussion. Although availability and access to climatic data have widely increased, knowing analytical approaches to building strong models including climatic covariates is crucial for investigating the relationship between climate and disease transmission dynamics.

Untangling the seasonal drivers of zoonotic spillover from wildlife: *Hendra virus* dynamics in an Australian bat colony

Aaron Morris[1], Alison Peel[2], Tamika Lunn[3], Emma Glennon[1], Hamish McCallum[2], Raina Plowright[4], Olivier Restif[1]*

* Presenting author

[1] Department of Veterinary Medicine, University of Cambridge, Cambridge, UK
[2] Griffith School of Environment, Griffith University, Brisbane, Queensland, Australia
[3] Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas, USA
[4] Department of Public and Ecosystem Health, Cornell University, Ithaca, NY, USA

Background. Understanding the circulation and shedding of pathogens within wildlife populations is central to the prediction of zoonotic spillover risk. For bat-borne zoonotic viruses, the drivers of spillover have been the subject of two decades of speculation, but evidence remains scarce. One theory which is gaining increasing empirical recognition, particularly for paramyxoviruses, is that bats harbour persistent infections which reactivate seasonally in response to processes that affect host immunity. Direct evidence for recrudescence of latent infections is difficult to obtain for wild bats, and data limitations have restricted our ability to validate dynamical models with different structures and ascertain infection risk.

Methods and findings. In this study we fit mechanistic models to data on Hendra virus serology and shedding in Australian flying foxes, collected longitudinally in one colony over a year. We provide new evidence for the recrudescence hypothesis in bat henipavirus infections, by showing that immune and virus shedding dynamics of Hendra virus are best described by compartmental models that include seasonal reactivation of latent infections. Models that had a faster transition from the latent (L) to infectious (I) state in winter – aligning with the hypothesis that Hendra virus shedding is driven by nutritional stress from reduced food resources in winter – more closely replicated empirical patterns of virus shedding.

Discussion. This study demonstrates the potential role of seasonal forcing on within-host ecological processes, and supports suggestions that seasonal events other than birth pulses, may be driving infection and shedding. Mechanistic incorporation of seasonal forcing on immune dynamics, as developed in this study, will be an important addition to future models of infection in Hendra virus and bat-virus systems more broadly, and has the potential to improve prediction of zoonotic spillover risk.

Effect of hydrometeorological indicators on leptospirosis risk in Fiji: a modelling study

Eleanor M Rees

Department of infectious diseases epidemiology, London School of Hygiene and Public Health

Background. Leptospirosis is a zoonotic disease which occurs in tropical and subtropical regions around the world. Leptospirosis is endemic in Fiji, with cases occurring year round and frequent sporadic outbreaks. These outbreaks often coincide with periods of heavy rainfall and flooding, however, the relationship has not yet been well characterised in this region. In this study, we aimed to quantify the effects of different hydrometeorological and climatic indicators, and particularly precipitation indicators, on leptospirosis risk in Fiji between 2006 and 2017. *Methods and findings*. We used a Bayesian hierarchical mixed-model framework to explore the impact of different precipitation indicators, temperature, and measures of El Niño Southern Oscillation (ENSO) on leptospirosis cases in Fiji over a 12-year period. We found that total precipitation over a six week period was the best precipitation indicator, with increased total precipitation leading to increased leptospirosis risk. La Niña periods (as measured by Sea Surface Temperature in region 3.4) were associated with increased leptospirosis risk. Finally, minimum temperature when included with the other variables, was found to be slightly associated with leptospirosis risk, with warmer temperatures resulting in increased risk. *Discussion*: The results from this study improve our understanding of how hydrometeorological and climatic factors contribute to outbreaks of leptospirosis in Fiji. Combined with the knowledge of demographic and spatial risk factors of leptospirosis, this can allow for a precision public health framework which can allow for more effective public health preparedness and response, targeting interventions to the right person, place and time.

Does high habitat diversity reduce the risk of TBE in Europe?

Francesca Dagostin[1],Valentina Tagliapietra[1], Giovanni Marini[1], Duccio Rocchini[2,3], Marco Cervellini[2,4], Claudia Cataldo[5], Maria Bellenghi[5], Scilla Pizzarelli[6], Rosaria Rosanna Cammarano[6], William Wint[7], Neil S. Alexander[7], Markus Neteler[8], Julia Haas[8], Timothée Dub[9], Luca Busani[5], Annapaola Rizzoli[1]

[1] Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige (TN), Italy
[2] BIOME Lab, Department of Biological, Geological and Environmental Sciences, Alma Mater Studiorum University of Bologna, Bologna, Italy
[3] Department of Spatial Sciences, Faculty of Environmental Sciences, Czech University of Life Sciences Prague, Praha-Suchdol, Czech Republic
[4] School of Biosciences and Veterinary Medicine, University of Camerino, Italy
[5] Centre for Gender-specific Medicine, Istituto Superiore di Sanità, Rome, Italy
[6] Knowledge Unit (Documentation, Library), Istituto Superiore di Sanità, Rome, Italy
[7] Environmental Research Group Oxford Ltd, c/o Dept Zoology, Oxford, United Kingdom
[8] Mundialis GmbH & Co. KG Koelnstrasse 99, 53111 Bonn, Germany
[9] Department of Health Security, Finnish Institute for Health and Welfare, Helsinki, Finland

Keywords: Tick borne encephalitis, biodiversity, habitat diversity, statistics, modelling, Europe

Background. Tick-borne encephalitis (TBE) is a severe neurological disease caused by the TBE virus (TBEv), a flavivirus transmitted in Europe mainly by ticks of the *Ixodes ricinus* complex. The natural transmission cycle occurs in foci and is enhanced by complex interactions occurring between vectors and several key hosts, which are strongly connected to the features of their habitat. Here, we aimed to evaluate the effect of habitat diversity on the pattern of TBE infections in Europe, at different spatial scales, and gain insights on whether TBE control is among the ecosystem services yielded by biodiversity.

Methods and findings. To assess the current distribution of TBE in the European continent, we computed TBE incidence (data provided by the European Surveillance System: TESSy), averaged between 2017 and 2020, at the regional spatial level for ten different countries. We then statistically assessed the relationship between TBE incidence and the maximum value of habitat richness index in each region, evidencing

a "diluting" effect of habitat diversity. To check whether our findings hold at a finer spatial scale, we performed a literature search and retrieved data of TBEv detections in ticks and hosts in Italy and Finland, aggregated at municipality level, and eventually explored how habitat diversity affects the local probability of TBEv occurrence.

Discussion. In the current context of global biodiversity loss, recent efforts (mostly focused on Lyme disease) were made to understand the effect of biodiversity on disease transmission, with divergent conclusions. In our study, we used a novel variable, the habitat richness index, to understand how varying levels of habitat diversity affect TBE risk in Europe. We performed our analysis at two different spatial scales (regional to urban), responding to the need for a broad and scale-dependent understanding of the relationship between diversity and disease.

West Nile virus Lineage 2 overwintering in Italy

Giulia Mencattelli[1,2,3]*, Roberto Rosà[1,2], Federica Iapaolo[3], Valentina Curini[3], Liana Teodori[3], Giovanni Marini[1], Federica Monaco[3], Giovanni Savini[3], Annapaola Rizzoli[1]

*Presenting author

[1] Research and Innovation Centre, Fondazione Edmund Mach, 38098 San Michele all'Adige (TN), Italy
[2] Center Agriculture Food Environment, University of Trento, 38098 San Michele all'Adige (TN), Italy
[3] Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, 64100 Teramo, Italy

Keywords: West Nile virus; Winter circulation; alternative transmission routes

Background. Since its first outbreak occurred in Italy in 1998, West Nile virus (WNV) has caused an increasing number of disease cases in humans and different animal species, especially wild birds and horses. Currently, the Country has recorded one of the highest, number of cases in Europe so far. The establishment of a national surveillance plan has, allowed to collect, epidemiological and molecular data held at the National Reference Lab in Teramo.

Methods and findings. The whole and partial genome sequences of the Italian WNV strains have been compared by phylogenetic analysis. The high strain identity and the

yearly circulation in certain areas of the country, strongly support the hypothesis of WNV endemic circulation and overwintering in local host and mosquito populations.

Discussion. Clinical sign of WNV infection have been reported in birds, especially raptors, during the coldest season, when *Cx. pipiens* mosquitoes, the main WNV vectors, are usually not active. However, the occurrence of different biotypes of *Cx. pipiens - Cx. molestus*, which are active all year round, might be one of the mechanisms allowing WNV winter transmission in Italy. Another transmission route could take place through oral infection after predation or necrophagy by raptors and scavenger bird species. Several studies have in fact demonstrated the occurrence of persistent chronic infection in birds and rodents, supporting this hypothesis. Further research is therefore needed to better understand the role of different bird and mosquito species in favoring winter transmission of WNV in Italy.

Pathogens spillover: lesson learned from bat borne viruses

Raina K. Plowright[1], Peggy Eby[2,3,4], Alison J. Peel[3], Andrew Hoegh[5], Wyatt Madden[6], John R. Giles[7], Peter J. Hudson[8]

[1] Department of Public and Ecosystem Health, Cornell College of Veterinary Medicine, Cornell University, Ithaca, New York, USA
[2] School of Biological, Earth, and Environmental Sciences, University of New South Wales, Sydney, Australia
[3] Centre for Planetary Health and Food Security, Griffith University, Nathan, Australia
[4] Center for Large Landscape Conservation, Bozeman, Montana, USA
[5] Department of Mathematical Sciences, Montana State University, Bozeman, Montana, USA
[6] Department of Microbiology and Cell Biology, Montana State University, Bozeman, Montana, USA
[7] Institute for Health Metrics and Evaluation, University of Washington, Seattle, Washington, USA

[8] Center for Infectious Disease Dynamics, Pennsylvania State University, State College, Pennsylvania, USA

Background: Bats are hosts of human pathogens that have pandemic potential, including coronaviruses, henipaviruses, and filoviruses. Bats are also key pollinators, seed dispersers, and insect consumers and may be sensitive to environmental change.

Methods and findings: Over the past four years, we have been sampling bats on multiple continents to understand the factors that drive pathogen shedding and spillover. At the same time, we have been collecting and analyzing long-term data on land use change, bat ecology, bat behavior, and henipavirus spillover events. Here, we present our data on Hendra virus in Australia. We combine climate, landscape, and bat behavior datasets in Bayesian network models to predict clusters of spillover events and understand the mechanistic connections among environmental change, bat behavior, and spillover. We find that bat virus shedding is more likely during stressful conditions and from populations that have been displaced to novel habitats. Clusters of spillover events occur after food shortages when no native food is available.

Discussion: Our work indicates that ecological stressors may trigger the cascade of events that leads to spillover of bat pathogens to humans. We consider how to proactively prevent spillover by addressing the upstream factors that drive the transmission of pathogens from animals to humans.

Using the diversity of tick-borne pathogens to understand their emergence

Xavier Bailly[1,2]

[1] Université de Lyon, INRAE, VetAgro Sup, UMR EPIA, 69280, Marcy l'Etoile, France
[2] Université Clermont Auvergne, INRAE, VetAgro Sup, UMR EPIA, 63122, Saint-Genès-Champanelle, France

Background. Tick-borne diseases are a significant risk to public and veterinary public health. The emergence of tick-borne pathogens depends on the distribution of hosts and vectors as well as opportunities for contact with humans. The distribution of pathogen diversity in hosts and ticks illustrates the species combinations favorable to different pathogen variants. However, it remains difficult to determine quantitatively how the structure of host and vector communities influences the evolution of the frequency of the different circulating variants.

Methods and findings. The distribution of pathogen diversity in ticks and human cases can be used to identify pathogen genotypes more frequently associated with human cases. A limitation of these approaches is the difficulty in differentiating the effect of exposure to variants and the intrinsic ability of variants to infect humans on the observation of differential associations.

Discussion. The use of spatialized data, based for instance on citizen science and crowdsourcing, might help to overcome some of the current limitations in understanding the emergence of tick-borne diseases. Beyond the study of current epidemiological situations, these advances should facilitate the anticipation and monitoring of tick-borne disease risk due to global changes.

Changes in bird migration patterns in relation to West Nile virus emergence in Europe

Lorenzo Serra[1], Gaia Bazzi[1], Jacopo G. Cecere[1], Simona Imperio[1], Andrea Marcon[1], Riccardo Nardelli[1], Simone Pirrello[1], Roberto Ambrosini[2]

[1] Area Avifauna Migratrice, Istituto Superiore per la Protezione e Ricerca Ambientale, 40064 Ozzano Emilia,BO, Italy
[2] Department of Environmental Science and Policy, University of Milan, Via Celoria 26, 20133 Milan, Italy

Background. Bird migrations have evolved under the selective pressures of seasonality of trophic resources. Being highly mobile at every geographical scale and rapidly adapting to environmental changes, birds gave major scientific evidence of the

rapid effect of climate change on migratory patterns. A seasonal advancement of the timing of prenuptial migration and of the start of breeding season have been observed in some Palearctic and Nearctic species since the early 1990s. Bird ringing data offers a unique opportunity for studying bird movements, and recent improvements in analytical techniques of ringing recoveries led to statistically sound tools for mapping seasonal movements, migratory connectivity and geographical shifts in breeding and wintering areas.

Methods and findings. We present and discuss the results of some recent studies based on bird ringing data showing that European bird populations are rapidly adapting their migration patterns and morphological traits in order to face environmental modifications induced by global warming. Observed changes in bird ecology possibly affecting the circulation of the West Nile virus include: a) timing of arrival/departure of (infected) birds from/to Africa, b) shifts in wintering and breeding areas, c) length of stay (presence) in Europe of trans-Saharan migrants, d) frequency of multiple clutches, e) proportion of birds moulting feathers in or near the breeding area before post-nuptial migration; f) proportion of the non-migratory component of partially migrant populations/species, e) population trends.

Discussion. Even if available bird population size estimates have strong limits mainly due to under sampling and analytical biases, there is evidence that trans-Saharan migrant populations are decreasing and synanthropic /resident species are increasing. Therefore, particular attention should be paid to the demographic trends of some resident bird populations in order to understand the intra-European circulation of the West Nile virus.

Macroparasites as drivers of emerging disease

Joanne Lello[1], Roberto Rosà[3], Adam Konecny[2], Giovanni Marini[2], Stan Marée[1], Heidi Hauffe[2]

[1] School of Biosciences, Cardiff University, CF10 3AX, Cardiff, UK;
[2] Fondazione Edmund Mach, Centro ricerca e innovazione, Via Mach, 1 38010 San Michele all'Adige (TN), Italy;
[3] Center Agriculture Food Environment, University of Trento, San Michele all'Adige (TN), Italy

Backgorund. Wildlife are the major source of viral and bacterial emerging infections. The majority of wild animals will be concurrently infected with chronic microparasitic infections. Many macroparasites have the capacity to control host population dynamics. Conversely, microparasites are generally driven by the dynamics of their host populations. Macroparasite control of host dynamics therefore represents a potential indirect mechanism of interaction between macroparasites and emerging / potentially emerging infections.

Methods and findings. Here we demonstrate that the dynamics of hantavirus in wild mice *Apodemus flavicollis*, are driven by the dynamics of a common macroparasite of these mice, the helminth *Heligmosomoides polygyrus*. We demonstrate this effect through a combination of statistical and mathematical models validated using empirical data collected from the Trentino region of Northern Italy. We subsequently use the mathematical model to explore the effect of helminth perturbation on the viral dynamics, demonstrating that relatively limited changes in helminth numbers can profoundly alter viral dynamics.

Discussion. As this mechanism of macroparasite-emerging disease interaction is generic, it is likely to occur in a multitude of natural systems and future predictions of disease emergence should therefore consider this wider parasite community perspective

Merging ecology and technology: the capacity for detecting infectious diseases in wildlife using computer vision

Sarah Perkins[1], A. Olsen[1], C. Jones[2], P. Rosin[2], J. Cable[1]

[1] School of Biosciences, Cardiff University, Cardiff, UK
[2] School of Computer Science and Informatics, Cardiff University, Cardiff, UK

Keywords: Wildlife disease, AI, computer vision

Background. Wildlife diseases play a role in species extinctions, spillover of pathogens to humans (zoonoses), and can threaten food security (e.g., wild fisheries). Systematic monitoring of infectious diseases in wildlife, however, is sparse. For the majority of wildlife, disease goes undetected, yet understanding where, when and why wildlife diseases occur is essential for safeguarding biodiversity, agricultural resources as well as animal and public health. Artificial Intelligence (AI) could offer a new tool by which to fill the knowledge gap. Many images are shared publicly on social media with no scientific intent, but those images can be a rich source of important ecological data. Indeed, the emerging field of 'iEcology' uses these large online resources to generate ecological insights but is relatively unharnessed in the field of infectious diseases, despite significant data availability.

Methods and findings. Here, we review the potential for computer vision to be used as a tool for wildlife disease monitoring by quantifying the number and type of wildlife diseases that have visible symptoms and so are suitable for detection via an image. Secondly, we assess the image availability associated with these diseases on open access photo-sharing platforms. We find computer vision-detectable diseases are most commonly caused by fungi, and/or ectoparasites and over 40% of diseases with visible symptoms are available within online photo-sharing sites, thereby offering the potential to fill a monitoring gap*.

Discussion. Although AI could offer a step change in disease monitoring, challenges remain in developing the field. A significant volume of verified images (i.e., confirmed disease) must be available for optimal training of an AI pipeline to accurately detect any given disease. Subsequent long-term monitoring also requires a rich dataset, for which targeted citizen science data collection may provide an optimal approach to wide-scale disease monitoring.

Prezode: Preventing zoonotic disease emergence

Benjamin Roche

Infectious Diseases: Vector, Control, Genetic, Ecology and Evolution (MIVEGEC); Centre for Ecological and Evolutionary Research on Cancer (CREEC); Centre IRD de Montpellier 911, Avenue Agropolis BP64504, 34394 Montpellier cedex 5, France

Background. One of the greatest burdens on human health and livelihoods is caused by the epidemic and endemic zoonoses. Preparedness and responses strategies are crucial in mitigating the impact of diseases but not sufficient. Prevention, i.e. interventions needed to mitigate risk and reduce the likelihood or consequences of spillover events at the human/animal/ecosystem interfaces, are therefore needed.

Methods and finding. Based on the idea that it is necessary to strengthen actions to prevent the emergence of infectious diseases, in the spirit of a prevention/preparedness/response continuum, the PREZODE initiative was launched during the One Planet Summit in 2021. Through an unprecedented co-construction process, with the organisation of more than 25 workshops that mobilised a community of 1,500 actors from nearly 150 different countries, the PREZODE community is building a strategic agenda that will identify research and operational needs. During its co-construction process the PREZODE community identified over 300 critical research and actions priorities that must be tackled to efficiently prevent zoonotic disease emergence.

Discussion. The initiative gathers more than 150 members, including 11 governments. It will launch its first operational actions with core funding from France in 2022 in a spirit of synergy building. With its operationalisation in 2022, PREZODE becomes 1) a tool to launch new and build synergies between existing research and developments programs, 2) a dynamic platform for sharing innovative knowledge and 3) a resource center for decision-makers enabling the implementation of risk-reduction policies and actions to reduce pandemic risks.

Epidemiological intelligence for surveillance of animal health: monitoring mass mortality events in wildlife

Nicola Ferrari[1]*, Mariana Delgado[2], Lesa Thompson[2], Jenny Hutchison[2], Paolo Tizzani[2]*

[1] Department of Veterinary Medicine and Animal Sciences – Università degli Studi di Milano, Italy
[2] World Organisation for Animal Health - WOAH

Keywords: syndromic surveillance; emerging diseases; EIOS

Background. In recent years, an increase in the trend of threat emergence has been observed at the human/animal/ environmental interface. Emerging diseases represent one of the main threats; 61% of emerging infectious diseases are zoonotic, and of those 75% have emerged from a wildlife source. Wildlife-borne emerging diseases play a major role for public health. This situation supports the impelling need to set up adequate surveillance plans at country, regional and international level, aimed at the early detection of potential emergence of health threats in wildlife. Due to the diversity of wildlife species in the world, the prioritisation for active and passive surveillance in domestic animals, and the lack of appropriate wildlife health surveillance, many circulating pathogens emerging and / or reemerging are overlooked. In this context, targeted surveillance, which focuses on specific pathogens—besides being expensive and logistically demanding—can miss emerging or unknown pathogens that can impact public health.

Methods and findings. Event-based surveillance, including syndromic surveillance, which analyses unusual health events and disease-related signs as mass-mortality events, or unusual morbidity and/or mortality may facilitate early detection and rapid reaction. The WHO has developed a system called EIOS (Epidemiological Intelligence Open Source) that scans around 15,000 sources in the web every 5 minutes. The World Organisation for Animal Health (WOAH) has implemented this system in its daily active search activity since 2017. In particular, the system is used to monitor most of the WOAH-listed diseases. Since March 2022 a specific algorithm has been created to scan unusual morbidity and mortality events in wildlife, and the system has been used to collect and screen around 8,000 media news items. Unusual events such as the mass mortality of elephants (*Loxodonta africana*) in Botswana in 2020 may have been detected early and assessed, preventing not only the spread of disease but on occasions (as in this example) protecting species with high biodiversity values.

Discussion. The large amount of data provided by epidemiological intelligence activities in real time raises new challenges such as the development of appropriate algorithms tailored to detect spatio-temporal aberration in detection of wildlife diseases. Moreover, epidemiological intelligence, based on web scanning, can be highly sensitive but poorly specific. Therefore, this approach needs to be integrated with other systems, such as official reporting, supervised screening, and verification by field epidemiologists, as well as WOAH Members, thus developing a participatory surveillance".

Epidemiology of SARS-Cov-2 and public health indicators

Stefano Merler

Center for Health Emergencies, Bruno Kessler Foundation, Trento, Italy

Background. Solid estimates of the incubation period, the relative susceptibility to infection, the reproduction number, which in turn depends on the generation time, the risk of developing symptoms and of progressing to critical disease, the infection fatality ratio in individuals infected with SARS-CoV-2 are key to interpreting COVID-19 dynamics and defining effective control strategies.

Methods and findings. Estimates of key parameters were obtained by performing cohort studies in China and Italy. These cohort studies analyzed quarantined case contacts. Contacts were tested for SARS-CoV-2 infection and monitored for symptoms and clinical outcome. Bayesian inference models were used for the reconstruction of the transmission links. In early 2020, the incubation period was estimated at 5.2 days (95%CI: 1.8–12.4). Children 0 to 14 years of age were less susceptible to severe infection than adults 15 to 64 years of age (odds ratio 0.34, 95%CI: 0.24–0.49). The mean serial interval was estimated at 5.1 days (95%CI: 1.3–11.6) in China and 6.6 days (95%CI: 0.7–19) in Italy. In Lombardy, the epicenter of the epidemic in Italy, the reproduction number was estimated at 2.6 in Pavia (95% CI: 2.1–3.2) to 3.3 in Milan (95% CI: 2.9–3.8). The proportion of infected persons who developed symptoms ranged from 18.1% (95% CI: 13.9–22.9) among individuals younger than 20 years to 64.6% (95% CI: 56.6–72.0) for those aged 80 years or older. Among infected individuals older than 60 years, 6.6% (95% CI: 5.1–8.3) developed critical disease. The infection fatality ratio was 0.43% (95%CI: 0.21–0.79) for individuals younger than 70 years and 10.5% (95% CI: 8.0–13.6) for older individuals. Most of these estimates changed over time because of interventions and emergence of virus variants.

Discussion. Contact tracing data were key to estimate critical parameters shaping SARS-CoV-2 epidemiology. In turn, these estimates were used to inform dynamical

models of disease transmission and to define effective control strategies. The lack of solid estimates for some of these key parameters since the emergence of the Alpha variant has weakened our understanding of SARS-CoV-2 epidemiology. Contact tracing data should be considered as a fundamental component of surveillance systems, to improve preparedness against future emergencies.

Gender and infectious diseases

Anna Ruggieri

Center for Gender Specific Medicine, Istituto Superiore di Sanità, Rome, Italy

Keywords: viral infections; sex differences; immune response

Background. Recent studies have highlighted sex differences in the prevalence and susceptibility to several viral infections, as in the case of Hepatitis B and C viruses, HIV, West Nile Virus infection, that are more prevalent and intense in male than in female infected patients. However, the course of viral infections is frequently worse in women than in men, expecially during reproductive years, although the mortality is often higher in male patients than in female ones. The recent Covid pandemic has identified sex as a major risk factor for SARS-CoV-2 infection, as men have higher risk (about twice) of developing severe disease and to undergo complications, including acute respiratory distress syndrome (ARDS), intensive care unit admission and death, compared to women. Factors affecting the observed sex differences in response to viral infections, also including COVID-19, have not been completely disclosed. However it is known that women usually mount stronger immune responses towards pathogens than men, developing higher innate and adaptive immune responses than males. As a consequence, women have reduced susceptibility to viral infections but are more prone to develop increased symptoms compared to male infected patients. Both genetic/epigenetic mechanisms and sex hormones, that differentially modulate the immune responses, could contribute to the sex disparity in response to infections.

Methods and findings. Our group conducted studies aimed to assess the mechanisms underlying the sex bias in COVID-19 outcome and to identify circulating non-invasive sex-specific prognostic markers of COVID-19 severity and progression. Our data show that some biomarkers could be predictive for both males and female patients and others only for one sex. Angiotensin1-7 plasma levels and neutrophil count predicted

the outcome of ARDS only in females, whereas testosterone plasma levels and lymphocytes counts only in males.

Discussion. In conclusion, a gender approach is urgently needed in order to personalize management of virus infected patients, including COVID-19 patients . The assessment of prognostic validity of biomarkers for viral infection pathogenesis and disease severity based on sex/gender-related variables, will contribute to obtain precision of diagnosis, cure and prevention toward a sex personalized approach in medicine.

Harvesting the potential of big data for vector-borne disease outbreaks

Jan C. Semenza and Joacim Rocklöv

Heidelberg Institute of Global Health, University of Heidelberg, Im Neuenheimer Feld 205, 69120 Heidelberg, Germany

Background. Large data sets from a variety of sources lend themselves to be computationally analyzed for pattern recognition, time trends, predictive and behaviour analytics. They have been extensively used by social media companies for sureillance and marketing purposes, but less so by public health for monitoring of disease prevalence and spread. Historically, public health surveillance has used electronic health records for ongoing, systematic collection, analysis, interpretation, and dissemination of data to guide interventions. More recently, Google or Wikipedia internet search queries have been applied to anticipate influenza epidemics but failed to anticipate the first wave of the influenza A(H1N1) pandemic outbreak in 2009. Here we discuss how big data could be used to disentangle drivers of vector-borne disease outbreaks and predict their spread.

Methods and Findings. In a first case study, we discuss how big data can be used to monitor the introduction and spread of the 2017 chikungunya outbreak in Europe. Conceptually, the outbreak can be divided into 2 distinct phases: The first phase is importation of the chikungunya virus via a viremic person into a virus-naive

population. For this phase, we used air passenger volume from large-scale aviation data to estimate journeys from areas with active chikungunya transmission as a measure of the force of introduction of the virus into the outbreak zones in Europe. For the second phase, the establishment of autochthonous transmission in Europe, we used near–real-time geocoded Twitter data (velocity) to quantify human mobility patterns to define areas potentially at risk. In a second case study where human mobility plays less of a role, we discuss how big data can be used to disentangle abiotic and biotic factors considered to be determinants of West Nile virus (WNV) epidemiology. We show how machine learning algorithm, can be used for classification and regression tasks to differentiate and rank the most important eco-climatic parameters of WNV outbreaks in Europe on a regional scale. We show eco-climatic drivers of the preceding year, and of the first half of the current outbreak year, can be used to predict WNV-outbreaks in advance for the latter half of the year.

Discussion. Big data can help to pinpoint areas at risk for the introduction and dispersion of vector-borne diseases. For the chikungunya outbreak, areas at greatest risk were those in close proximity to the original outbreaks and several larger metropolitan areas. The trajectory and sustained spread of vector-borne diseases can be anticipated with predictive modeling in real time. The WNV framework had an ability to even forecast a WNV-outbreak for the entire transmission season ahead of time. These studies suggest that big data should be an indispensable tool for the prevention and control of vector-borne diseases in Europe.

Spillover Surveillance and One Health Response: Understanding Emerging Zoonotic Threats in Real-Time

Emily S Gurley

Department of Epidemiology, Bloomberg School of Public Health, Johns Hopkins University, Baltimore, Maryland, USA

Keywords: One Health; Surveillance; Spillovers

Background. Historically, the public health response to emerging zoonoses has been reactive rather than proactive, with efforts to contain transmission only after a pathogen has spilled over and is being transmitted between people. Surveillance investments to catalogue viruses in wildlife represent a more proactive approach but have not meaningfully improved our ability to stop spillovers.

Methods and findings. In this talk, we will present a vision for a proactive approach to identification and investigation of spillovers to improve our ability to mitigate their public health risk. Surveillance for spillovers should be focused on patients presenting to clinical care facilities to ensure that the data are actionable. A hospital-based approach has limitations because it could miss many human infections but identifying a pathogen in a human is the most straight forward way to provide evidence to support public health action. Patients with febrile illness and a history of relevant occupational or animal exposures should be targeted for screening. In order to identify emerging zoonotic infections in the patients, we must have fast, high-throughput screening tests for the viral families of greatest interest. Currently available tests are either slow, too expensive, or complicated to be done on large numbers of patients in the field. The expansion of RT-PCR diagnostics during the pandemic could be leveraged to create real-time assays for viral families. Quick diagnosis of the clinical case is imperative for being able to understand 1) whether or not other cases are occurring, 2) whether or not the infection is being transmitted between people, and 3) how the initial spillover(s) occurred. As soon as a spillover is detected, local, multi-disciplinary One Health teams should be ready to respond to look for cases occurring in the community, conduct backwards and forwards contact tracing, sample animals that live in the case's community and any animals that the case had contact with before onset of illness, and gather community perspectives about transmission. Additional biological specimens should be collected from the patient so that the infecting pathogen can be fully characterized. Risk factor data should be collected, including from controls, even if the number of cases is very small since the data on exposures can accumulate over time until there are sufficient observations for analysis.

Discussion. These activities are rarely, if ever, conducted quickly and collaboratively to gather real-time intelligence about spillovers because it is logistically difficult to have these teams trained and ready to move quickly to respond as spillovers infrequently occur. There are cultural and logistical barriers in forming these One Health teams and donors have little interest in funding activities when the number of spillovers that will be detected is unknown. To overcome these barriers, we must make One Health science and collaboration mainstream, such that all clinical

surveillance activities are linked with One Health teams. If we can overcome the technological, logistical and cultural barriers to real-time spillover identification and investigation, we will be truly prepared to respond quickly to emerging threats and learn about how spillovers occur so that they can be prevented in the future. Our proposed strategy has the added benefit of also being able to quickly identify and investigate cases resulting from laboratory exposures or intentional release of novel pathogens.

SESSION 2: CROSS CUTTING THEME: WHAT METHODS AND TOOL CAN BE APPLIED TO DRIVERS TO PROVIDE EARLY WARNING AND RAPID DISEASE RISK ASSESSMENT?

> *Session 2b: Automatic data acquisition via web-scraping*

How text-mining could improve epidemiological surveillance?

Mathieu Roche

CIRAD, UMR TETIS, Montpellier, France

Keywords: Event-based surveillance, Text mining, Data science

Background. The ability to identify emerging and re-emerging diseases is challenging for the health domain. In this context, event-based surveillance (EBS) gathers information from heterogenous data sources, including online news articles. EBS systems integrate text-mining methods to deal with huge amounts of textual data. Text mining aims at discovering new information from textual datasets (i.e. corpus).

Methods and findings. This talk focuses on the use text-mining and multidisciplinary approaches in order to mine news data dealing with the health domain. These data science approaches are integrated in an EBS system called PADI-Web (Platform for Automated extraction of Disease Information from the web). PADI-Web dedicated to animal health surveillance tackles disease-based and symptom-based surveillance. To address these issues different text-mining methods associated with labeled textual datasets are integrated in the main steps of EBS systems: data acquisition, information retrieval (i.e. identification of relevant texts), epidemiological information extraction, information to communicate to end-users. In our work, specific methods are proposed to extract epidemiological events in multilingual news.

First, a fine-grained classification enables to highlight texts dealing with "Outbreak declaration" (i.e. sentence classification). Second, a group of epidemiological information (i.e. locations, hosts, symptoms, etc.) is automatically extracted in relevant documents.

Discussion. Based on these approaches, different strategies and associated algorithms are proposed and discussed for improving EBS systems.

Innovative Surveillance: ISID's Program for Monitoring Emerging Diseases (ProMED)

Linda C. MacKinnon

International Society for Infectious Diseases (ISID) Brookline, MA 02446 USA

Keywords: Innovative Surveillance, One Health, Emerging Infectious Diseases

Background. Back in 1994, a team of infectious disease experts established a program to leverage burgeoning communication networks, new research methodologies, and engaged subject matter experts to quickly identify and report infectious disease outbreaks to the international community. As a flagship Program of the International Society for Infectious Diseases (ISID), we have thousands of daily subscribers in 170+ countries and operate a round-the-clock internet-based surveillance service to identify emerging and re-emerging infectious disease outbreaks across humans, animals, and the environment – ProMED Moderators. Fundamentally, ProMED's goal was to identify outbreak events before they had the chance to cause significant harm.

Methods and Findings. Over its many years, ProMED has provided the first report on numerous outbreaks, as well as alerts for 'requests for information' to better understand disease cluster detection. Had ProMED not sent the first alerts about these impactful events to the world at large, response efforts would have been delayed, resulting in more infections, further spread, and increased mortality. ProMED consistently beats platforms that rely on automation alone, and our subject matter commentary highlights the importance of each report - a feature that cannot be replicated with artificial intelligence.

Discussion After 28 years, ProMED operates at the speed of infectious disease outbreaks. However, now is the time to shift from surveillance to prediction. Years of

historical data makes ProMED the ideal platform for a deep learning infrastructure, generating relationships between disparate data points, identifying previously unseen insights, and turning outbreak data into powerful visualizations. When this deep learning infrastructure is linked with augmented intelligence (AI) capabilities, the possible advancements in infectious diseases are unprecedented. Beyond identifying outbreaks after they have emerged, ProMED hopes to begin to forecast where they are most likely to appear. By linking our tagged outbreak data to other datasets, we can understand and monitor drivers of infectious disease emergence to intensify our surveillance efforts in at-risk communities. Epidemic and pandemic mitigation efforts can preserve the hard-won health advancements made over the past decades while reducing the infectious disease burden in low-resource settings. We'll explore new developments with ProMED and within the ever challenging pandemic and epidemic intelligence arena to stay ahead of the curve and find the 'needle in the haystack' before it takes hold on a population level.

Contribution of epidemic intelligence to transparency and timeliness in reporting to the World Organisation for Animal Health

Paolo Tizzani

World Organisation for Animal Health – WOAH, Paris, France

Keywords: Epidemic intelligence, WOAH, West Nile virus

Background. West Nile virus (WNV) is maintained in nature in a complex enzootic cycle between mosquitoes and birds. Epidemiological models have been used to estimate the best timing for intervention and to predict human cases in space and time. With time, epidemiological models for WNV have improved and have contributed to better understanding of the complex transmission cycle of WNV.

Methods and findings. MIMESIS (spatial dynaMIcal Model for wESt nIle viruS) is a climate-dependent spatial epidemiological model (Angelou et al., 2021). The model is calibrated for the human cases observed in Greece since 2010. The implementation of MIMESIS in predictive mode requires the assessment of meteorological and epidemiological uncertainty. The former is obtained from the ECMWF's ensemble of

seasonal forecasts while the latter is estimated from an ensemble model developed per se. The predictive skill of the forecasts issued in May is investigated for the years 2019, 2020, 2021. The seasonal risk level at the municipality scale, measured from the composite index CSI which considers all aspects of the event forecast (hits, misses, false alarms), demonstrates increasing values as the simulated probability of infection increases. This pattern is consistent across all examined years. The forecast version of MIMESIS exhibits critical success for the cases with probability of infection exceeding the level of 30% in 2020 and 70% in 2019 and 2021. Overall, using the ECDC definition for WNV, the level of 70% represents an accurate "projected" risk level 5.

Discussion. Our results suggest that the seasonal forecasts issued from a climate-dependent epidemiological model for WNV, operating in a probabilistic framework with the right share between climatic and epidemiological uncertainty, have considerable predictive potential. The predictions, issued in May, were proved accurate for all years provided the forecast probability was exceeding a certain threshold. Those early warning predictions can assist the surveillance systems with targeted control actions.

Social tensions due to ASF and HPAI on Polish Twitter

Andrzej Jarynowski

IBI Wrocław/Aidmed Gdańsk/Institute of Biometry and Veterinary Epidemiology, Berlin, Germany

Keywords: Twitter, sentiment analyses, ASF, HPAI

Background. Epizootics show a widely destructive effect on livestock production, but also cause tensions between various groups of interest. Pre-existing social conflicting matters of the animal production conditions has been manifested in reconfiguration of social relations in regions affected by ASF and HPAI among others by strengthening the tendency to issue farm animal protection in the general population (mostly urban) and "hijacking" profitability and cultural values of farmers. Such a structural configuration facilitates mobilisation of own groups of interest and ends up with conflict between animal breeders, far-right, agricultural parties, Christian organisations as well as opposing, government, pro-European opposition and

ecological organisations. A) Case study ecologists: Series of national-wide protests started January 2019 with protests against wild boar depopulation. In turn, in several Polish cities animal right defenders organised demonstrations against hunters and government plans of wild boars depopulation and as a way to slow down the spread of ASF. B) Case Study farmers. On the other hand, farmers call for significant reduction of the wild boar population. In September 2020, the governing party (Law and Justice) proposed the so-called "Five for Animals" which attempted to extend animal rights, but at the same time it impacted a number of sectors of Polish agriculture. Moreover, the feeling of abandonment (by the state) and powerlessness (for instance due to ongoing outbreaks of ASF and HPAI) led to massive protests.

Methods and findings. We have collected 9739 tweets between 1-31.10.2020 in Polish language with hashtag #ProtestRolników (farmers protest) and 5285 retweets with #ASF language also in Polish from 19.12.2018 to 18.01.2019. We primarily applied Social Network Analysis (SNA) of the Internet media users connected via their tweets sharing activities. Moreover, our investigation was extended by time series analysis as well as NLP techniques such as sentiment analysis and keyword analysis. A) Ecological protests have been massively discussed by mainstream media and the general population constitute a general component linked closely to ecological activists clusters.B) Animal breeders' protest communication has a highly modular and hierarchical structure with farmers as a general component, but with clear boundaries between internet communities and opinion leaders. There was only a small presence of the general public (i.e. mainstream media) in the discourse. Tweeting activity concentrates around late mornings (the time after post sunrise grooming of animals).

Discussion. Level of optimism (text sentiment) among farmers was significantly higher than animal rights defenders- probably due to a feeling of unity. Level of verbal aggression is opposite, which suggests that language repertoires differ.

Source-sink epidemic dynamics shaping the Fall 2020 COVID-19 pandemic wave in France

Vittoria Colizza

INSERM & Sorbonne Universite, Paris, France

Keywords: COVID-19; pandemic wave; dynamics

Background. Spatially and temporally heterogeneous COVID-19 pandemic waves mask non-local dynamics of case importations that are not captured by surveillance, limited to local indicators such as the time-varying reproductive number Rt.

Methods and findings. Using high-resolution co-location records from Facebook and COVID-19 case surveillance, we define an analytical metapopulation framework yielding a spatially coupled reproductive number connecting the 94 departments of mainland France. We expose source-sink dynamics that, through case importations mainly from the south-east of France, shaped the rise of the second wave in the country in the Fall 2020. We validated these source locations directly with rising incidence of cases in the destination areas, confirming the ability of our approach to detect early signals of importation. Our findings have implications for targeting surveillance and anticipating the areas at higher risk of early resurgence.

The context specific emergence and spread of novel SARS-CoV-2 VOCs

Moritz Kraemer

Department of Zoology at the University of Oxford; Martin Programme on Pandemic Genomics

Keywords: SARS-CoV-2, VOCs, invasion dynamics

Background. The SARS-CoV-2 variants of concern spread globally, causing resurgences of COVID-19 worldwide. They emergence in the UK on the background of a heterogeneous landscape of immunity and relaxation of non-pharmaceutical interventions. I will discuss the use of multiple data streams in quantifying the introduction to and regional dissemination of SARS-CoV-2 across England in the context of changing travel and social restrictions. Methods and findings. Through analysis of human movement, contact tracing, and virus genomic data, we found that the geographic focus of expansion shifted rapidly from the original location of emergence to a more global pattern. In England, lineages of new VOCs are often introduced >1,000 times. We find that hotel quarantine for travelers reduced onward transmission from importations for the Delta variant for example; however transmission chains that later dominated England's Delta wave were seeded before travel restrictions were introduced. Increasing inter-regional travel within England drove Delta's nationwide dissemination, with some cities receiving >2,000 observable lineage introductions from elsewhere. Subsequently, increased levels of local population mixing, not the number of importations, were associated with faster relative growth. Discussion. Invasion dynamics depended on spatial heterogeneity in contact patterns, and our findings will inform optimal spatial interventions to reduce transmission of current and future variant of concern.

Drivers of West Nile virus human transmission risk in Europe

Giovanni Marini[1], Andrea Pugliese[2], William Wint[3], Neil S. Alexander[3], Annapaola Rizzoli[1], Roberto Rosà[1,4]

[1] Research and Innovation Centre, Fondazione Edmund Mach, 38098, San Michele all'Adige (TN), Italy
[2]. Department of Mathematics, University of Trento, 38123, Trento, Italy
[3]. Environmental Research Group Oxford, c/o Department of Zoology, Mansfield Road, Oxford, UK
[4] Center Agriculture Food Environment, University of Trento, 38098, San Michele all'Adige (TN), Italy

Background: West Nile Virus (WNV) is one of the most recent emerging mosquito-borne pathogens in Europe where each year hundreds of human cases are recorded. Here we present a relatively simple technique to model WNV force of infection (FOI) in the human population through normal density functions.

Methods and Findings: We collated WNV human case-based data reported to the European Surveillance System from 15 European Countries. We modeled WNV FOI for each considered region and year through normal curves whose free parameters, namely average, variance and a rescaling factor, were calibrated to observed cases. Finally, we investigated a posteriori, through regression models, how such parameters are associated to a set of climatic, environmental and demographic covariates. Our modelling approach fits observed epidemiological curves quite well. We found that FOI magnitude is positively associated with spring temperature and larger in more natural areas while FOI peak timing is negatively related to summer temperature. Unsurprisingly, FOI is estimated to be greater in regions with a larger fraction of elderly people, ho are likely to experience more severe infections.

Discussion. Our results confirm that temperature plays a key role in shaping WNV transmission in Europe and provide some interesting hints on how human presence and demography might affect WNV burden. Our modelling approach, simple yet reliable, could be easily adopted for further epidemiological investigations when other sources of data are scarce and for similar vector-borne infections.

EO data and Deep Learning methods to map *Culex pipiens* distribution in central Italy

Carla Ippoliti[1], Lorenzo Bonicelli[2], Stefano Vincenzi[2], Silvio Gerardo D'Alessio[3], Alessio Di Lorenzo[1], Susanna Tora[1], Angelo Porrello[2], Simone Calderara[2], Matteo De Ascentis[3], Michela Quaglia[3], Maria Goffredo[3], Annamaria Conte[1]

[1] Statistics and GIS Department, Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, 64100, Teramo, Italy
[2] AImageLab, University of Modena and Reggio Emilia, 41121, Modena, Italy
[3] Entomology Department, Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, 64100, Teramo, Italy

Background. *Culex pipiens* mosquitoes are important vectors of emerging and re-emerging diseases in Europe, and it is able to adapt to a wide variety of environments. In the last 20 years, studies on vector distribution models have grown exponentially. Nowadays, the ever-increasing abundance of Earth Observation (EO) data, in combination with new Artificial Intelligence (AI) techniques, offers enormous opportunities for vector-borne disease investigations. Aim of this work is of explaining the spatial distribution of *Culex pipiens* in Abruzzo and Molise regions, the integration of field entomological data, highly detailed remotely sensed imagery and newly innovative artificial intelligence algorithms.

Methods and findings. To establish a ground-truth, three season campaigns of field catches were carried out in 2019, 2020 and 2021, and the presence/absence of *Culex pipiens* in about 50 sites were collected on a biweekly basis between May and November. The site locations were chosen in a variety of climatic and environmental conditions. To these real data, pseudo-absence catches were added, assuming vector absence in December and January. The total database was thus made up of 2301 records. The presence/absence (labels or annotations) of *Culex pipiens* in each entomological collection was paired with multi-spectral images acquired through the optical devices onboard the Sentinel-2A and 2B satellites of the Copernicus programme. Patches of 224x224 pixels of 20 meters spatial resolution were extracted around each site and for each revisit time. The dataset was split in training (80%) and

test (20%) so that all the images of the same site could only belong to one of the two datasets, thus avoiding misleading results. A stratified 5-fold technique was applied, preserving the proportion of positive/negative labels between train/test datasets. To solve the binary classification task, we applied a Deep Convolutional Neural Network (DCNN) and evaluated three models: the baseline exploited a single multi-band image; the second one integrated the baseline with the spatial relationships among sites through a Graph Neural Network (GNN) aggregation method; the third model focused on extracting temporal patterns from a history of ten multi-spectral images. In all models, a final classification layer delivered the probability of each site being positive or negative (presence/absence of *Culex pipiens).* The baseline model reached an F1 score of 79%, which was increased up to 84% with the GNN. In the third approach, we extracted the embedding for each image and applied an attention module, which computes a weighted average of instances. This model had an F1 score of 82%.

Discussion. This work describes a successful synergy between entomological field activities, the use of Sentinel 2 and DL. The methodology adopted can be extended to the national territory and to other vectors, to support the Ministry of Health in the surveillance and control of vectors and the diseases they transmit.

Early warning of WNV human cases issued from a climate-dependent epidemiological model operating in a probabilistic framework

Ioannis Kioutsioukis

Laboratory of Atmospheric Physics, Department of Physics, University of Patras, Grecia

Keywords: West Nile virus, early warning, MIMESIS

Background. West Nile virus (WNV) is maintained in nature in a complex enzootic cycle between mosquitoes and birds. Epidemiological models have been used to estimate the best timing for intervention and to predict human cases in space and time. With time, epidemiological models for WNV have improved and have contributed to better understanding of the complex transmission cycle of WNV.

Methods and findings. MIMESIS (spatial dynaMIcal Model for wESt nIle viruS) is a climate-dependent spatial epidemiological model (Angelou et al., 2021). The model is calibrated for the human cases observed in Greece since 2010. The implementation of MIMESIS in predictive mode requires the assessment of meteorological and epidemiological uncertainty. The former is obtained from the ECMWF's ensemble of seasonal forecasts while the latter is estimated from an ensemble model developed per se. The predictive skill of the forecasts issued in May is investigated for the years 2019, 2020, 2021. The seasonal risk level at the municipality scale, measured from the composite index CSI which considers all aspects of the event forecast (hits, misses, false alarms), demonstrates increasing values as the simulated probability of infection increases. This pattern is consistent across all examined years. The forecast version of MIMESIS exhibits critical success for the cases with probability of infection exceeding the level of 30% in 2020 and 70% in 2019 and 2021. Overall, using the ECDC definition for WNV, the level of 70% represents an accurate "projected" risk level 5.

Discussion. Our results suggest that the seasonal forecasts issued from a climate-dependent epidemiological model for WNV, operating in a probabilistic framework with the right share between climatic and epidemiological uncertainty, have considerable predictive potential. The predictions, issued in May, were proved accurate for all years provided the forecast probability was exceeding a certain threshold. Those early warning predictions can assist the surveillance systems with targeted control actions.

Global spatiotemporal pattern and potential drivers of influenza decline during the COVID-19 pandemic

Chiara Poletto

INSERM, Sorbonne Université, Pierre Louis Institute of Epidemiology and Public Health, Paris, France

Keywords: Influenza, spatio-temporal pattern, drivers

Background. The COVID-19 pandemic has been associated with a sharp influenza decline. Timing, extent of the decline and its link with governmental interventions

against COVID-19 were described for certain countries or regions. Limited work so far addressed the phenomenon at the global scale. We provided a global cross-country comparison of the influenza decline between March 2020 and September 2021 and investigated its potential drivers.

Methods and findings. From the GISRS FluNet database we computed the influenza decline with respect to the 2015-2019 period by country and trimester. We used machine learning techniques - random forests and Classification And Regression Trees (CARTs) - to identify predictors of the influenza decline among countries' demography, weather, pandemic preparedness, COVID-19 incidence, and COVID-19 pandemic response variables, and to classify countries-trimesters based on these predictors. We found that the most important predictors of the influenza decline were COVID-19 incidence and pandemic preparedness as measured by the Infectious Disease Vulnerability Index. Among the Covid-19 response variables, reduction of international flights and workplace presence (from Google Global Mobility Reports) had higher importance than the extent of governmental interventions (from Oxford COVID-19 Government Response Tracker). The regression tree identified interpretable groups of countries-trimesters. Spring 2020 trimesters of Europe and North America clustered together, showing limited influenza decline despite the severe restrictions. For the rest of the period, countries-trimesters with low influenza decline were in the tropics and had low pandemic preparedness, COVID-19 incidence and strength of COVID-19 response. Conversely, countries-trimesters were in temperate regions, with high pandemic preparedness, high COVID-19 cases and stringent social restrictions had strong influenza decline. A separate group, formed by four zero-Covid countries, had the lowest influenza level.

Discussion. The spatiotemporal influenza decline was heterogeneous and showed a complex association with COVID-19 response variables depending on the sociodemographic context and stage of the COVID-19 pandemic. Zero-Covid countries maintained record-low levels of influenza with strict border controls and close-to-normal social activity. This supports the importance of global travels as a driving force of influenza epidemics. The study shows the power of regression trees techniques for gaining insights from the integration of extensive and diverse data sources.

Local vs. nationwide restrictions against COVID-19 pandemic in France between September 2020 and June 2021

Chiara E. Sabbatini[1], Giulia Pullano[2], Laura Di Domenico[1], Stefania Rubrichi[3], Shweta Bansal[2], Vittoria Colizza[1]

[1] INSERM, Sorbonne Université, Pierre Louis Institute of Epidemiology and Public Health, Paris, France
[2] Department of Biology, Georgetown University, Washington, DC, USA
[3] Orange Labs, Sociology and Economics of Networks and Services (SENSE), Chatillon, France

Background. The first winter of COVID-19 pandemic saw the emergence of the first variant of concern (B.1.1.7 or Alpha variant) characterized by an advantage in transmissibility and severity. As mass vaccination campaigns were just starting to roll out, countries adopted different approaches to large-scale restrictions to manage the rise of cases through spring 2021. France applied national interventions in the form of a second lockdown in the fall 2020, followed by a long-lasting curfew in the winter, and by a third lockdown in the spring 2021. Other countries, for example Italy, adopted regionally-based lockdowns with a tiered system.

Methods and findings. Using cell-phone mobility data integrated in a metapopulation model fitted to French epidemiological data, we compared the efficacy and social cost of applied interventions in France with alternative regionally-based restrictions. We show that there exist ranges of thresholds for triggering and releasing regional lockdowns yielding both lower hospitalizations and fewer days of closure. Results are robust also in presence of compensatory behaviors adapting to locally targeted restrictions.

Discussion. Our findings help inform the design of effective strategies for future emergencies.
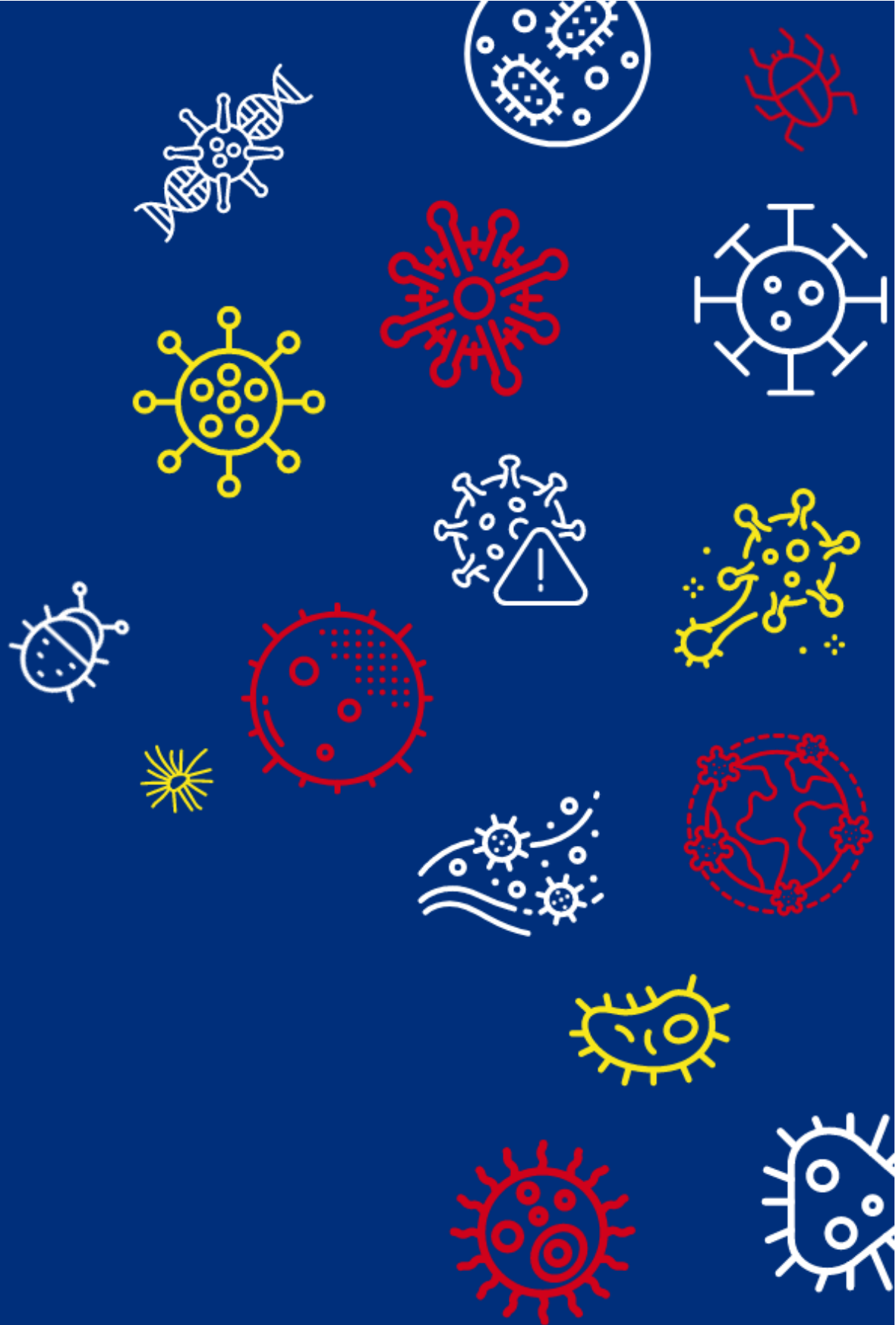
Broad-spectrum countermeasures in response to early spillover events

Hector Aguilar-Carreno

Multi-Director, Cornell PACE and Rising Stars Programs, Department of Microbiology and Immunology, College of Veterinary Medicine, Cornell University

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