GEOVET 2023

September 19th - 21st 2023 Silvi Marina, Teramo, Italy

Expanding boundaries: Interdisciplinary geospatial research for the One Health Era

Abstract Book

Edited by

Annamaria Conte, Carla Ippoliti, Lara Savini

Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Teramo, Italy (IZS-Teramo)

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September 19th - 21st 2023 **Silvi Marina, Teramo, Italy**

Expanding boundaries: Interdisciplinary geospatial research for the One Health Era

Abstract Book

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GEOVET 2023

INTERNATIONAL CONFERENCE

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Expanding boundaries: Interdisciplinary geospatial research for the One Health Era

Abstract Book

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Opening Ceremony

Distinguished guests and speakers, dear colleagues,

as Director General of the IZS-Teramo, veterinary public health institute for Abruzzo and Molise, I am extremely proud to extend a warm welcome to all of you at this international scientific conference, which is finally taking place in Italy, thanks to the opportunity provided by the GeoVet Community.

This event deeply promotes the multidisciplinary approach and the interaction among different technical and scientific domains, as established by the One Health paradigm, which is the heart of our mission.

Founded in 1941, the IZS-Teramo provides scientific and technical support to competent authorities in Italy and abroad on issues related to public health, animal health and animal welfare, food hygiene and food safety, and environmental protection.

According to our mandate, we have invested and continuously invest to produce knowledge and design innovative solutions to face the most pressing health issues stimulating trans-disciplinary collaboration on a global scale.

To reach this goal jointly, it is essential that we exchange each other backgrounds and identify together future perspectives.

Over the course of these three days, 150 experts, scientists, researchers, policymakers, and stakeholders will share knowledge and insights on innovative tools, data analysis, and visualization in support of Animal Health, Public Health, and Food Safety. I am sure there will be fruitful discussions, the emergence of innovative ideas, and the creation of lasting and robust partnerships. Through them, we can provide a relevant contribution to the protection of humans, animals and the environment worldwide.

I'd like to express my heartfelt gratitude to the conference organizers, who have dedicated their time and passion to the success of GeoVet2023 and to all of you, participating in this event. We, in synergy, have the unique opportunity to make a tangible difference. I wish you a productive meeting, hoping you thoroughly enjoy this special location.

Thank you for your attention.

Nicola D'Alterio
Director General
IZS-Teramo, Italy

Opening Ceremony

Dear guests, colleagues and friends,

It is a privilege to open this 8th edition of GeoVet which over two decades has enlarged and enriched its community.

From Veterinarians to engineers, from biologists to mathematicians, this diversity reflects one of the central tenets of this conference: addressing the health challenges requires commitment and contributions from every field. And our role and responsibility are to explore and discover novel tools and solutions to address them.

In the upcoming days, we will delve into a wide range of topics, including geospatial data analysis, network analysis, and artificial intelligence. We will share groundbreaking research, and engage in meaningful discussions that will shape the trajectory of future collaborations and, why not, future GeoVets.
Through presentations, posters, and interactions, we will build a bridge between Science and Policy, helping to pave the ground for synergy and open dialogue. We have received many contributions and through the three-minute poster presentations, our aim is to provide as many scientists as possible with the opportunity to share their research. Awards will be given to the 4 best student posters to acknowledge and encourage their research efforts.

We will host the roundtable "GeoVet science into practice for One Health" in which the GeoVet and Scientific Community will meet representatives from leading international organizations. These dialogues will explore the symbiotic relationship between science and policy-making, emphasizing how each can fortify the other.

We will also share some enjoyable moments, which represent important opportunities to forge new partnerships and exchange ideas! A webApp is available: authorizing the notification, you can receive last minute messages about the conference organization and leisure time schedule.

I want to thank the authorities and the sponsors who are present here today. Your support and encouragement serve as a driving force behind the success of initiatives like GeoVet. And a special thank you to the entire organizing committee that made the realization of this great event possible.

Once again, I extend my warmest welcome to each and every one of you, I really hope we will spend three wonderful days together.

Annamaria Conte
Chair of the GeoVet 2023 Conference
Head of Statistics and GIS Unit of the National Reference Centre for Epidemiology
IZS-Teramo, Italy

Abstract book of the
GEOVET 2023 INTERNATIONAL CONFERENCE
edited by Annamaria Conte, Carla Ippoliti, Lara Savini

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Summary

GEO 2023 VET
INTERNATIONAL CONFERENCE

Session 1

From Science to Policy: GIS and One Health integration

Chair: **Michael Ward**

K01 The challenges of real-time science communication and decision support in a pandemic context: building the plane instruments after take-off

Marius Gilbert[1]

1 - Spatial epidemiology Lab (SpELL), Université Libre de Bruxelles, Belgium

Abstract

The Covid-19 pandemic took most countries by surprise with relatively little preparedness in terms of equipment, disease diagnostic tools, or decision-support systems. Based on the experience of being at the forefront of the Covid-19 pandemic management in Belgium, the talk will describe and discuss the most important challenges in terms of public communication and decision support. More specifically, the talk will address the multiple consequences of a low general proficiency in health sciences in the public and decision makers, the difficulty in handling rapidly changing data and knowledge while maintaining good levels of trust, the critical need to carefully organize the much-needed scientific debate, and the overall conditions of an effective collaboration between scientists, decision makers and the media in the context of a crisis.

S01 Communication Breakdown – Of disease clusters, a trillium and One Health

Olaf Berke[1]

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Keywords: Disease cluster, Geographic epidemiology, One health, Philosophy of science, Spatial statistics

Abstract

One health is a concept and an approach to promote the health of human and animal populations in a shared and healthy environment. This interdisciplinary endeavour requires collaboration across professions and a common language. Geographic epidemiology is concerned with the identification of spatial patterns of health related states and events in a population defined via the boundary of the study area. Such spatial patterns (trend, cluster and clustering) require clear definition to be meaningful in science communication. However, the term "disease cluster" has been defined in the literature in various and rather different ways. When geographic epidemiology is unable to make sense of its own concepts it is questionable how respective research results can benefit one health. The goal of this study is to clarify the concept of disease cluster within geographic epidemiology.

Examples of disease cluster definitions from the literature will be compared. The term disease cluster will be semantically distinguished from similar concepts: clustering, hot spot and outbreak. The epidemiological triangle of causation (agent, host and environment) will be used to conceptualize geographic epidemiological data analysis. The semantics and statistical meaning of expectation and prediction will be reviewed and play a key role.

The true meaning of a disease cluster will be identified as embedded within the well-known Besag-York-Mollié (BYM) regression model. All the spatial patterns identifiable from the BYM model will be conceptualized in a new paradigm: the geographic epidemiological trillium of causation.

The concept of a disease cluster is clarified and a definition proposed. The paradigm of the geographic epidemiological trillium will help guiding causal epidemiological research. And researchers will be equipped to ask more precise questions and communicate their results more clearly to those who need to know.

R01.1 The use of spatial metrics to select regions for enhanced bovine tuberculosis control measures in Ireland

Jamie Tratalos[1], Guy McGrath[1], Jamie Madden[1], Simon More[1]

1 - Centre for Veterinary Epidemiology and Risk Analysis, University College Dublin, UK.

Keywords: Regionalization, bovine tuberculosis, movement networks, spatial analysis, risk-based trading

Abstract

Regionalization, the use of stricter disease and wildlife management controls in certain areas, has been proposed as a method to bring about the eradication of Bovine Tuberculosis (bTB) in Ireland. We used spatial Information to compute metrics for the selection of counties within Ireland where such stricter controls could be applied. Counties were ranked based on cattle demographics, bTB prevalence, farm fragmentation, movement network measures, information on badger abundance and control, and the predicted impact of risk based trading on cattle sales.

Herd fragmentation was measured as the percentage of herds with land outside of the county and also the percentage of land fragments whose home farm was in another county. These two metrics closely matched each other for a given county, but they varied considerably between counties, from 1% to 24%. Movement network information was combined with a herd risk model based on network metrics, badger abundance and herd and environmental characteristics to evaluate the proportion of moves which would be deemed high-risk under a risk-based trading regime. This would result in up to 53% of a county’s cattle sales and 42% of its herds being affected. This was compared to a more conservative approach which may be more practical to implement, which was based purely on the test history of each herd. This second approach resulted in a much smaller number of trades being potentially restricted. Wildlife metrics related to badger control and vaccination also varied considerably between counties. We also used information on cattle market sales to calculate cattle market catchment areas, as an alternative to counties a candidates for regionalized control.

These results will be used by the Irish government to select candidate areas for stricter bTB control measures.

R01.2 Poultry intensification and emergence of Highly Pathogenic Avian Influenza

Maria Fernanda Vincenti Gonzalez[1], Marie-Cécile Dupas[2], Jean Artois[2], Madhur Dhingra[3], Simon Dellicour[2], Marius Gilbert[2]

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3 - Senior Animal Health Officer, Food and Agriculture Organization (FAO), Italy

Keywords: Avian Influenza, poultry intensification, conversions, spatio-temporal models

Abstract

The global spread of Highly Pathogenic Avian Influenza (HPAI) following the emergence of the Goose/Guangdong H5N1 subtype in 1996 in China has raised concerns regarding its mechanisms and ecological niches. In that context, our study investigates the impact of poultry intensification on HPAI incidence, an aspect that has so far received limited attention (Gilbert et al., 2018). Specifically, we aimed to analyze the impact of global intensification of poultry production in the occurrence of Low Pathogenic Avian Influenza (LPAI) to Highly Pathogenic (HPAI) conversions and to predict the probability of conversion events at the country level.

We compiled a dataset of HPAI conversions from 1959 to 2022 (Dhingra et al., 2017), focusing on primary emergence reports while excluding secondary spread within epidemics. Poultry distribution data was obtained from the Gridded Livestock of the World (GLW). Generalized linear mixed models (GLMM) and Integrated Nested Laplace Approximation (INLA) were used to predict conversion events based on proxy variables for poultry intensification: poultry density, output/input ratio (animal production efficiency), and the total stock of poultry.

Our preliminary results show that the large majority of the detected conversion events took place in high-income countries (with highly intensified poultry production systems). Europe remained the center of conversions with n=18 followed by USA with n=9. In Europe, the UK, Germany, The Netherlands, and Italy depict the highest probability of having at least one conversion event. Finally, the output/input ratio showed to be the best predictor of conversion events.

This study highlights the overlooked relationship between poultry intensification and the emergence of HPAI. The concentration of conversion events in high-income countries with intensified poultry production systems suggests their susceptibility to HPAI. Further research will be needed to

comprehensively examine the poultry intensification pressures on avian influenza emergence and develop effective intervention measures. These findings might provide valuable insights for policymakers, public health officials, and the poultry industry to mitigate the risks associated with intensified poultry production and safeguard global public health and poultry industries.

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R01.3 Precision epidemiology in practice: applications to better prevent and control endemic diseases in the US swine industry

Beatriz Martínez-López[1], Maria Jose Clavijo[2], Rebecca Robbins[3], Carlos Gonzalez-Crespo[1], Jose Pablo Gomez[1], Ruwini Rupasinghe[4], Xin Liu[5]

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3 - Pig Improvement Company (PIC), Hendersonville, TN, USA
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5 - Computer Science Department, University of California, Davis, CA, USA

Keywords: user-friendly tool, decision-support system, geospatial modeling, network analysis, dashboard

Abstract

Similar to precision medicine or precision public health, precision veterinary epidemiology uses high-resolution data (from genome to phenome and beyond) to get further insights of the epidemiological problem and support the timely selection of customized interventions to specific groups of animals, farms or productions systems that are more adequate to address their specific needs. This approach requires Big Data that are not only genetic (both at host and agent level), but also include animal and environmental characteristics, management practices, biosecurity measures and animal movements at a farm and production system level.

This precision epidemiology concept is based on the novel development, application and operational accessibility of advanced data mining and machine learning approaches that effectively evaluate the complexity and multi-level nature of the epidemiological problem and that, in combination with decision support platforms, facilitates the timely analysis, visualization, communication and sharing of information to support decisions at population level and achieve global herd/farm/system optimization.

In this work we illustrate how we are using precision epidemiology in the swine industry using the Disease BioPortal platform to empower veterinarians and farmers through advanced data-driven analytics & customized dashboards to more proactively manage animal health. Our approach combines multiple analytical tools such as geographic information systems, phylogenetics, network analysis and machine learning models to dynamically analyze the distribution of disease over space and time and create predictive models adapted to epidemiologically changing scenarios. But finally, this complex

process needs to be translated in clear and simple visualizations of results or risks which can be easily interpreted by the final users (i.e. field veterinarians, production managers, diagnosticians, etc.). We will show how users can evaluate risks for animal collectives and support real-time responses in changing scenarios, which may include, for example, from the emergence of an outbreak in an area to changes on vaccination strategies or commercial policies.

Although we believe precision epidemiology will vertically contribute to the overall animal health, animal welfare, farm productivity/sustainability and revenue in the livestock industry; its application is in its infancy and it still requires critical advancement and substantial changes in the way we collect, standardize, integrate, share and use data in veterinary medicine. We share our experience addressing some of these challenges and provide some recommendations and future directions.

R01.4 How to combine spatio-temporal information and Danger theory for animal disease surveillance?

Bahdja Boudoua[1], Manon Richard[1], Mathieu Roche[2], Maguelonne Teisseire[1], Annelise Tran[2]

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2 - CIRAD, France

Keywords: Danger theory, Dendritic cells algorithm, Event-Based Surveillance, Spatio-temporal data, Risk factors

Abstract

Event Based Surveillance (EBS) systems such as HealthMap, Promed and PADI-web are used daily to detect outbreak events reported in web articles. Once the articles are collected, these systems rely on human moderation, and implement supervised classification algorithms to classify articles according to their relevance (Valentin et al., 2020). Applying such supervised methods can be challenging, as epidemiological datasets have an imbalanced class distribution, and because the annotation task, which is critical to the success of these models, can be expensive and time consuming. Another important limitation of EBS systems is that the drivers of disease transmission (e.g. disease characteristics, environmental and epidemiological risk factors) are not always found in textual data and are therefore not taken into account by EBS systems (Kim & Ahn, 2021).

In this context, we propose an unsupervised approach that relies on the spatio-temporal information of the reported epidemiological events, to classify articles while taking into account the environmental factors associated with disease onset through risk mapping. This method, called EpiDCA, is an adaptation of the Dendritic Cells Algorithm (DCA), inspired by the danger theory (Greensmith et al., 2008). EpiDCA is characterized by expert-defined parameters, making it applicable to different diseases and environmental contexts. The proposed method was first tested and evaluated using PADI-web and HealthMap datasets related to avian influenza (AI) in Asia between 2018 and 2019, and a suitability map for AI produced for the same area. To measure the accuracy of the model, we calculated the precision, recall and F-score. EpiDCA achieved a very good performance with an F-score of 0.70 and 0.90 for an imbalanced and a balanced dataset respectively. The results confirmed that considering disease risk factors is a good approach in event classification. EpiDCA was then compared with state-of-the-art supervised machine learning methods and appeared to be competitive.

To test the robustness of the method we then applied EpiDCA for the same disease (AI) in a different geographical context. We used PADI-web dataset related to AI in France between 2022 and 2023 and

the corresponding risk map. In this case, events were reported at different levels of spatial granularity (country, region, department and city, from the lowest to the highest granularity). The consistent results confirmed that this method is robust, and the best performance in terms of precision, recall and F-score was observed when events were reported at the department level.

In the future, additional tests will be conducted on different datasets and case studies (a cross-border disease such as African Swine Fever, and a vector-borne disease such as West Nile fever disease) to evaluate the genericity of the proposed method.

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Session 2

Exploring Novel Data Sources and Operational Tools

Chair: **Guy McGrath**

S02 Mapping global coldspots of veterinary capacity

Nicola G. Criscuolo[1], Yu Wang[1], Thomas P. Van Boeckel[1]

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Keywords: accessibility, allocation, coldspots, geospatial modeling, veterinarians, web-scraping

Abstract

Maps have been instrumental in prioritizing interventions against infectious diseases of global importance (Reich & Haran, 2018). In human medicine, high-resolution maps have helped to quantify the burden of diseases such as malaria and dengue. Similarly, in animal health, mapping efforts have focused on diseases such as Avian Influenza, Rift Valley Fever, or antimicrobial resistance, which pose threats to the livelihoods of those who raise animals for subsistence.

However, mapping the accessibility of veterinary care has received relatively little attention thus far. Veterinarians are at the forefront of defense against animal and zoonotic diseases (Bellemain, 2013). Yet, efforts to map the distribution of veterinarians have primarily concentrated on regional or provincial levels within a limited number of countries. Although crucially important, these efforts can overshadow important heterogeneities in access to veterinary care in countries currently transitioning from subsistence farming to commercial farming, which have also been suggested to be the most vulnerable to disease emergence.

In the past decade, online platforms enabled users to locate veterinarians based on postal codes or addresses (Royal College of Veterinary Surgeons, 2023). The purpose of these platforms is to match patients with veterinarians working in their vicinity. Whilst not primarily intended for public health, these platforms are an unprecedented opportunity to get insights into the fine-scale distribution of veterinarians, the factors driving that distribution, and supplement existing national-level data sources on veterinary capacity.

In this study, we predicted and mapped the global distribution of veterinarians at the 10x10 km^2 resolution using a global address book of veterinarians assembled from online sources. Specifically, we used web-scraping techniques and queried online web maps to collect the locations of 303,745 veterinarians across 115 countries. These locations were modeled through a Log-Gaussian Poisson Regression model implemented in a Bayesian framework provided by the Integrated Nested Laplace Approximation (INLA). By comparing the distribution map of veterinarians with density maps of animals

raised for food we mapped regions where animals are more than 1 hour away from veterinarians. The 91.3% of these regions, referred to as “veterinary coldspots”, were found in low- and middle-income countries. Finally, we furtherly identified, for 103 countries, the geographic locations where veterinary services should be scaled up to maximize access to care for animals raised for food.

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R02.1 Anthropogenic and environmental factors associated with koala deaths occurring through vehicle collisions and dog attacks in South East Queensland, Australia

Mark Stevenson[1], Ravi Dissanayake[2], Viviana Gonzalez-Astudillo[3], Rachel Allavena[3], Joerg Henning[3]

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Keywords: koala, death, mortality, Australia, spatial analysis

Abstract

Populations of the iconic Australian koala are under constant decline. Their deaths are associated with the rapid and extensive urbanisation and fragmentation of koala habitat. Using citizen science data on observed koala mortalities in South East Queensland, we quantified the association between environmental, infrastructural and demographic factors and the two leading causes of koala deaths, vehicle collisions and dog attacks. We achieved this objective using two modelling approaches: a Poisson point process model to identify factors increasing the intensity of a given cause-specific mortality and a case-control design to estimates the odds of a given cause of death compared to all other causes of death.

The intensity of koala deaths (that is, the expected number of koala deaths per square kilometre) from vehicle collisions was negatively associated with distance to primary roads, whereas the intensity of koala deaths from dog attacks was positively associated with dog population density. While these results were expected, the value in these analyses arose from the ability to identify specific areas where there was an excess of cause-specific mortality risk after known risk factors had been accounted for.

The results of this research can be used to develop risk mitigation strategies and to enhance surveillance for dog attacks in high-risk areas, for example by conducting educational awareness programs, promoting registration of dogs and discouraging free roaming of dogs. In a similar manner, in high-risk areas for vehicular collisions, safe over or underpasses can be built to facilitate safe movement of koalas for road crossing or speed limits could be introduced to reduce the likelihood of koala deaths.

R02.2 Epidemic intelligence data and disease risk mapping: the case of Crimean-Congo haemorrhagic fever (CCHF)

Angela Fanelli[1], Johannes Christof Schnitzler[2], Marco De Nardi [3], Alastir Donachie[2], Ilaria Capua[4], Gianvito Lanave[5], Domenico Buonavoglia[5], Paula Caceres-Soto[6], Paolo Tizzani[6]

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6 - World Animal Health Information and Analysis Department, World Organisation for Animal Health, Paris, France

Keywords: Crimean-Congo haemorrhagic fever, digital data, EIOS, epidemic intelligence, risk mapping

Abstract

The Epidemic Intelligence from Open Sources (EIOS) (WHO, 2023) is a system used for scanning information from open sources to detect disease events. The initiative, led by the World Health Organization (WHO), was built on the "One Health, All Hazards principle".

This study uses the EIOS for complementing data collection of neglected diseases thus improving the understanding of their geographic extent and level of risk. A case study on Crimean-Congo Haemorrhagic Fever (CCHF) in the European Region is presented.

Data on CCHF occurrence (January 2012–March 2022) were retrieved using an algorithm to detect mentions of CCHF cases in humans or vectors. A Bayesian additive regression trees (BART) model (Chipman et al., 2010) was built to map the risk of CCHF occurrence. Thirty-three explanatory variables retrieved from WorldClim, ENVIREM and PROBAV_V2.2.1. Every predictor was rescaled at a resolution of 4 x 4 km, aligned, and reprojected to EPSG:4326-WGS84. For each pixel a posterior distribution of predicted probabilities with the associated 95% credible intervals (CI) was obtained. The most important variables were selected by initially fitting the model using all variables. An automated stepwise reduction algorithm with 50 iterations and 10 trees was used to eliminate the variables with the lowest importance and obtain the model with the lowest root mean square error (RMSE). The final model was run with the reduced variable set, 200 trees, and 1000 posterior draws after a burn-in of 100 draws.

Overall, a general decreasing risk trend from south to north across the entire European Region was

detected. The results show a positive association between all the temperature-related variables and the probability of CCHF occurrence, with an increased risk in warmer and drier areas. In particular, the Mediterranean basin and the areas bordering the Black Sea are the areas at the highest risk of CCHF occurrence under the current environmental conditions. The model performed well in terms of accuracy (AUC = 0.95), correct classification rate (CCR = 0.80), correct prediction of presences (sensitivity/recall = 0.99), correct prediction of absences (specificity = 0.79), true skill statistic (sTSS = 0.89), Cohen's kappa (skappa = 0.69), but the positive predictive value was low (precision = 0.31). The low precision means that the model predicts positive pixels where there are no actual observations of human cases or virus isolation from ticks. These are represented by the locations which are likely to be favourable for CCHF occurrence, but where the disease has yet to be reported.

This work demonstrates the potential of internet-based data accessed through the EIOS system to create a disease risk map. The case study presented may constitute a model to combine epidemic intelligence tools and advanced analytical approaches to detect and assess changes in disease distribution, allowing prevention and early mitigation of disease events of veterinary and public health importance.

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R02.3 Geospatial Methods for Reporting During the United States 2022-2023 Highly Pathogenic Avian Influenza (HPAI) Outbreak and Ongoing Emergency Response Preparedness

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Abstract

The 2022-2023 U.S. HPAI outbreak has affected an unprecedented 836 commercial poultry premises across 47 states. Mapping is being used extensively to aid in control and containment, as well as situational awareness and reporting to international trading partners. Due to the extent of the outbreak, the United States Department of Agriculture (USDA) has developed and employed numerous automated mapping methods for the first time in a U.S. animal health emergency to meet reporting and response needs. Daily Situation Report maps are delivered to all affected states using a secure GIS portal. An online operational dashboard reports current metrics (number and types of cases, affected counties, epidemiological curve, etc.) and maps to help inform policy and decision making. Confirmed HPAI detections in wild birds are displayed in a publicly available online mapping and reporting tool. Automation using Python scripting is critical to efficiently process data collected by field personnel and is used in each of these applications. These developments have enabled a small team of mapping professionals at the USDA Center for Epidemiology and Animal Health (CEAH) to provide critical map products, geospatial data, and more to a wide variety of audiences including internal responders, leadership, trading partners, researchers, and the public.

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Session 3

Climate, human and enviromental impact on animal health

Chair: **Annalise Tran**

K03 Decision-support tools to track and predict climate-sensitive infectious diseases at cascading spatial scales

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Abstract

Extreme climatic events, environmental degradation, unplanned urbanization, and socio-economic inequalities exacerbate the risk of infectious disease emergence, spread and transmission. For example, mosquito-borne diseases, such as dengue and malaria, are highly sensitive to climate variability and climate change. A warming climate can lengthen the transmission season and alter the geographical range, potentially bringing diseases to regions which lack either population immunity or strong public health infrastructure. More frequent extreme weather events, such as storms, floods, and droughts, also affect the timing and intensity of vector and water-borne disease outbreaks. Despite the health threats of rapid environmental change, we lack the evidence-base to understand and predict the impacts of extreme events and landscape changes on disease risk, leaving communities vulnerable to increasing health threats. This talk will focus on the past, present and future risks of emerging infectious diseases and describe the partnerships, data, and tools required to build climate resilience in climate change hotspots, including cities, the rainforest, highland areas, and small islands, to improve preparedness and response to emerging infectious disease threats and assist public health services adapt to climate change.

S03 Impact of climate change on soil-borne and vector-borne diseases

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Keywords: climate change, Vector-borne diseases, bluetongue, fasciolosis, animal health

Abstract

Vector-borne, water-borne and soil-borne diseases are climate sensitive. Temperature affects the development of arthropods and helminths. Rainfall provides suitable breeding sites for mosquitoes and suitable soil moisture conditions for the development of helminths on pasture. Climate change, through its impact on global temperature and weather extremes is already affecting the health of humans and animals directly, and will have indirect impacts on the transmission of vector-borne, water-borne and soil-borne diseases. Over the past decade, various mathematical risk models driven by climate change scenarios have been used to simulate and anticipate future changes in disease burden. This presentation will review recent advances in our understanding of the impact of climate change on vector-borne diseases affecting animals.

Bluetongue disease is a viral disease transmitted by *Culicoides* midges to ruminants. A Bluetongue epidemic significantly affected livestock in Northern Europe in 2006-07. Modeling research highlighted the impact of a heatwave on increased risk of Bluetongue disease transmission in Northern Europe. Future climate change could enhance this risk further over this region (Guis et al., 2012); however, the use of standard control zones and subsequent restriction of animal movements could mitigate such risk (Jones et al., 2019). *Fasciola hepatica,* also known as the common liver fluke, is a parasitic trematode that affects ruminants in Europe. *Fasciolosis* has large economical impacts on the livestock sector. The parasite requires the presence of a freshwater snail to complete its life cycle. Infectious metacercariae and the intermediate snail host are favoured by wet weather conditions and soil moisture on grassland. Modelling studies highlight that climatic suitability for fasciolosis increased during the 2000s over northern Europe. Recent trends are likely to continue in future. The liver fluke transmission season could lengthen by 3-4 months in some locations (Caminade et al., 2015). Other examples of climate sensitive animal diseases, such as lungworms and Rift Valley Fever, as well as other non-climatic drivers will also be discussed. Finally, future research directions for this field of research will be suggested**.**

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R03.1 Contribution of climate change to the emergence of West Nile virus in Europe

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Keywords: West Nile virus, Europe, ecological niche modelling, climate change attribution, future projections

Abstract

West Nile virus (WNV) is an important mosquito-borne pathogen in Europe and although the causal relationship between climate change and its emergence on the continent has been reported, it has not been formally evaluated. Here, we examine whether WNV establishment in Europe can be attributed to climate change. For this purpose, we train and project ecological niche models for WNV considering historical, future, and counterfactual climate data, the latter corresponding to a hypothetical climate in a world without climate change. We show an increase in the ecologically suitable area for WNV under the historical climate evolution, whereas this area remains largely unchanged throughout the last century in a no-climate-change counterfactual. Our analyses therefore point towards climate change as one of the major drivers of the increased risk of WNV circulation in Europe, and further allows discussing potential scenarios for the future evolution of the areas at risk.

R03.2 Reducing data collection costs through sensitivity analysis of spatial data in GLEAM

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Keywords: data collection, GLEAM, livestock, greenhouse emissions, sensitivity analysis, spatial analysis

Abstract

The United Nations Food and Agriculture Organization (FAO) has developed the Global Livestock Environmental Model (GLEAM), a spatial data framework for estimating greenhouse gas (GHG) emissions from the livestock sector. In addition to livestock distribution data, GLEAM incorporates five spatially distributed variables associated with nitrogen and methane conversion factors. These variables include maximum methane production capacity from manure, climate zones, temperature, and losses due to leaching from solid and liquid manure management. All based on the 2019 and 2006 guidelines from the Intergovernmental Panel on Climate Change (IPCC). GLEAM has been used by several countries to estimate the impact of GHG mitigation actions and report these as part of their Nationally Determined Contributions. This process necessitates the development of a country-level data collection plan, which requires significant financial and planning resources. This study examines the impact of variability in spatial parameters on direct emission estimates by developing a sensitivity index at global and country scales. The results highlight the value of incorporating sensitivity analysis when designing data collection efforts, to reduce associated costs.

R03.3 Predicting socioeconomic and intervention-related factors influencing the risk of vector-borne diseases using Demographic and Health Surveys; a case study of malaria

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Keywords: Demographic and Health Surveys, earth observation, spatial modelling, sub-Saharan Africa, risk mapping, vector-borne diseases

Abstract

Vector-borne diseases (VBDs) account for more than 17% of all infectious diseases, with an annual global burden of more than 700,000 deaths. In this context, disease risk maps are a key decision-making tool to target control interventions. Yet, these maps are often not sufficiently accurate, as they rarely capture all disease determinants. They usually rely on environmental factors that influence vector presence and vectorial capacity, e.g. climatic and land cover variables. However, socioeconomic factors, such as housing quality or education, and human behaviors, such as the use of preventive measures, are also known risk factors. Environmental and socioeconomic determinants are still rarely combined in prediction models. While environmental factors are commonly derived from satellite-based earth observation, socioeconomic factors are measured through household surveys, which are more time-consuming and challenging to collect. Demographic and Health Surveys (DHS) provide estimates of key demographic and health variables based on nationally representative samples. These include indicators of respondents' socioeconomic level (e.g. wealth index and education) and use of preventive measures for malaria (e.g. bed nets and indoor spraying). Geolocations for survey clusters are available, and these can be interpolated to create grids that can be further used in spatial models of VBDs. The production of interpolated surfaces of DHS indicators has been widely studied. However, studies do not reach a consensus on the modelling workflow to be used and different types of models have been implemented with different levels of complexity and information required as input. Overall, three types of approaches have been used: (1) spatial interpolation methods, (2) ensemble methods, and (3) Bayesian models. In this research, we focus on malaria as an example of VBDs, and we aim at comparing several methods for predicting DHS indicators influencing malaria risk.

We selected DHS indicators falling into two categories: socioeconomic variables and malaria preventive measures. Using kriging, random forest modelling and spatial Bayesian models (INLA-SPDE implementation), we modelled and predicted these indicators at a high spatial resolution across several sub-Saharan African countries. A set of predictors representing climate, land use and land cover was compiled for use in some of the models.

Different categories of DHS indicators required different modelling approaches; indicators of malaria prevention were best modelled by capturing the spatial autocorrelation pattern, while socioeconomic variables were best predicted with spatial predictors.

These findings highlight the need to test different modelling approaches when mapping human determinants of VBDs risk. Ultimately, these factors can be integrated into a single modelling framework with environmental factors to map malaria risk and identify key drivers. As DHS are conducted consistently in many countries, the methods used in this research are applicable beyond sub-Saharan Africa and could be replicated for other infectious diseases.

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Session 4

Spatial methods in ecology and epidemiology

Chair: **Marius Gilbert**

R04.1 Using joint species distribution models to improve predictions of co-infection in veterinary epidemiology

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Keywords: Co-infections, Joint Species Distribution, Modelling, Multivariate

Abstract

Predicting pathogen distributions is vital for risk assessment and disease control in wild and domestic animal populations. Co-infections are of particular clinical and epidemiological significance, as they can often be associated with increased disease severity and pathogen shedding, increasing both the burden of disease and the risk of spillover (Peel et al., 2019). Moreover, pathogens can also interact and affect the likelihood of subsequent infections (Fountain-Jones et al., 2019). Yet, when predicting pathogen distributions, research overwhelmingly focuses on single infections caused by individual pathogens. This univariate focus means that important biotic effects are often excluded in distribution models, affecting both the reliability of inferences and the accuracy of predictions. Multivariate models help overcome this hurdle by accounting for biotic associations between pathogens. To explore avenues for improving distribution modelling in veterinary epidemiology, our primary objective was to understand the wider use of multivariate models in co-infection research. From these findings, we make recommendations on how Joint Species Distribution Models could be used by veterinary epidemiologists.

To understand the wider use of multivariate models in co-infection research, we conducted a systematic review of the literature using a suite of terms relating to both multi-response models and co-infections. This yielded 746 unique peer-reviewed research articles. Using seven pre-defined exclusion criteria, we identified 75 peer-reviewed primary studies that jointly measured infection patterns with two or more endo-pathogens of humans or animals in natural environments. Only 27% studied co-infections in animal hosts. Using a generalised linear model to explore how model choice may vary with study goals and purpose (i.e. inference or prediction), we found a strong association between model choices and study goals. Studies that sought to predict the spatial distributions of co-infections typically employed multinomial models, ignoring pathogen associations. Clustering analysis based on study features and a citation analysis to investigate rates of knowledge exchange both

identified distinct clusters for multinomial versus multivariate model users. We conclude that biotic associations are often ignored when predicting co-infections and that there exists a lack of knowledge exchange among co-infection researchers with different research agendas. Moreover, we show the untapped potential for using Joint Species Distribution Models in veterinary epidemiology and how one can go about selecting the most appropriate model for complex data for improving predictions of co-infection distributions (Powell-Romero et al., 2023), as well as highlight the importance of interdisciplinary collaboration.

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R04.2 Combining key hazard- and exposure-related drivers to model the probability of occurrence of TBE human cases in Europe

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Keywords: Boosted regression trees, Disease mapping, Human cases, Species Distribution Models, Tick-borne encephalitis, Vector-borne diseases

Abstract

In the last decade, the number of Tick-borne Encephalitis (TBE) human cases reported in Europe has increased both in endemic and in non-endemic areas (European Centre for Disease Prevention and Control, 2022). The geographical occurrence of TBEv is fragmented with “foci of infection” (“hotspots”) that are difficult to identify and often vary in space and time (Dobler et al., 2011). To improve the capability to identify the European regions at high risk of outbreaks, we developed a spatio-temporal predictive model inferring the year-to-year probability of occurrence of TBE human cases in Europe.

We used data provided by the European Surveillance System (TESSy, ECDC) to infer the distribution of TBE human cases at the regional (NUTS3) level during the period 2017-2021. We included variables related to temperature, precipitation, land cover and ticks’ hosts presence to account for the natural hazard of viral circulation. We also used indexes based on recorded intensities of human outdoor activity in forests as proxies of human exposure to tick bites. We identified the yearly probability of TBE occurrence using a boosted regression tree modeling framework.

Areas with higher probability for transmission were identified in Central-Eastern Europe and along the coastline of Nordic countries up to the Bothnian Bay. Our results highlighted a westbound and northbound spread of TBE-positive regions throughout the years. Areas at higher risks are characterized by the occurrence of key rodent reservoir and cervid species, intense human recreational activities in forests, steep drops in late summer temperatures and high annual precipitation amounts.

The predictive accuracy of the model was assessed through internal and external validation (AUC = 0.84; CBI =0.98).

Our study provides an assessment of the European regions at risk of TBE human infections on a yearly basis. Our results can therefore be used to evaluate the yearly risk of occurrence of TBE human infections, at different spatial scales, and to support surveillance and prevention campaigns within endemic and potential new risk areas.

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R04.3 Reducing uncertainty in spatial analysis involving fragmentated farms

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Keywords: GIS, Farm fragmentation, bovine tuberculosis, contiguity

Abstract

Farm fragmentation refers to spatial disaggregation of a farm into smaller, often highly separated parcels of land. Ireland has a high proportion of fragmented farms; an issue not unique to Ireland. Spatial analysis of farms depends on assigning a location to the livestock. Where a farm is heavily fragmented, this becomes problematic and introduces uncertainty. With increasingly sophisticated analytical techniques, reducing this uncertainty is imperative. We explore techniques to quantify the extent and regional variation in fragmentation and the between-fragment distances of fragmented farms in Ireland. We then explore methodologies to help account for farm fragmentation in geospatial analysis and to assist in surveillance and field epidemiology.

Farms in Ireland are recorded on a Land Parcel Identification System (LPIS) allowing for interrogation by GIS. The most commonly used point representation of a farm is the centroid of the largest single fragment. However, laneways, roads, streams and other physical features break up farms on a GIS so they are not seen as a genuine spatial/epidemiological unit. Alternative spatial representations such as weighted centroid, geographic medians, density based clustering, etc. are useful but often place the estimated location outside of the actual farm. This becomes increasingly problematic as fragment separation distances become greater. To better represent farms split by local features, we utilised the Integrate tool (ArcGIS 10.7, ESRI Redlands CA) to allow same-farm boundaries to snap together across these features. For fragmented farms, the largest integrated fragment was assigned as 'home' and all other integrated fragments were assigned as 'away'. Distance metrics were calculated from 'home' to 'away' fragments creating a fragment profile.

A methodology to better describe contiguity between farms was devised. Integrated farm fragments were placed into 3 categories based on their relative size to total farm size; **A**=>50%, **B**=20%-50%, **C**=<20%. A scoring matrix was generated to define the relative importance of adjacency between fragments based on their size category; **A-A**=1, **A-B**=2, **B-B**=3, **A-C**=4, **B-B**=5, **C-C**=6.

A spatial profile was generated for farms based on the number of integrated fragments and the fragment-fragment distances. Summary metrics (and maps) were generated by County and by uniform hexagonal grid.

A Neighbourhood matrix was generated for all contiguous between-farm fragments and coupled with shared boundary distance. This was appended to additional farm information such as head count, stocking densities, Bovine Tuberculosis (bTB) testing history and farm enterprise type to assist in prioritising farm surveillance in bTB outbreaks.

Farm fragmentation in Ireland was quantified and described through distance and neighbourhood metrics allowing for greater accuracy in application of exposure variables in geospatial analytics. In addition, they aid in prioritisation of epidemiological field investigations and contiguous surveillance for bTB and other transmissible diseases of livestock.

R04.4 Mapping bioclimatic suitability for cattle ticks in Ecuador

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Keywords: bioclimate, cattle ticks, distribution modelling, Species Distribution Models, suitability

Abstract

Hard ticks affect cattle in tropical and subtropical areas across the world. In Ecuador, the main species affecting cattle are *Rhipicephalus microplus* and the complex *Amblyomma cajennense* sensu lato. Both cause economic losses to cattle farmers by decreasing milk and meat production, and transmitting pathogens. They can indirectly affect human and environmental health, due to the toxicity of acaricides used to control ticks and acaricide residues. In Ecuador as in other countries, acaricide resistance in cattle ticks has become an acute problem in cattle management. Although several studies have modelled the distribution of *R. microplus* and *A. cajennense* s.l. worldwide and in South America, suitable models for Ecuador are still lacking. Ecuador's contrasted environment, spanning across the Andes, requires calibrating a specific model. The aim of this study was to model the distribution of *R. microplus* and *A. cajennens*e s.l. in continental Ecuador using Random Forest with 19 bioclimatic variables and vapour pressure deficit (CHELSA database). In total, 2895 farms were surveyed and georeferenced between 2012 and 2015. *R. microplus* was present in 38.51% and A. cajennense s.l. in 16% of farms. Cross-validation values for the Random Forest models were, for *R. microplus* and *A. cajenens*e s.l. respectively: accuracy = 0.97, 0.98, Sensibility = 0.97, 0.99, and Specificity = 0.96, 0.93. The final models included ten bioclimatic variables i.e. Bio 1, Bio14, Bio4, Bio12, Bio 13, Bio3, vapour pressure deficit max and min, Bio 2, and Bio 18. The predicted models showed the potential risk of the presence of *R. microplus* and *A. cajennense* s.l. distribution in continental Ecuador. We discuss the interest of these models for managing this issue at the national level, including through a better understanding of areas at risk, and better use of chemicals acaricide. This may be particularly important if cattle farming further develops in the Amazon region. We also discuss the challenge of focusing on the climatic envelope, while tick presence is also affected by management practices.

R04.5 Remote sensing as an additional tool for modelling spatiotemporal dynamics of questing Ixodes ricinus on Italian northwestern Alps

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Keywords: Ixodes ricinus, alpine landscape, Geographic Information System (GIS), remote sensing, spatio-temporal models, Bayesian modeling

Abstract

The distribution range of the tick *Ixodes ricinus* in Europe is expanding in latitude and altitude. Consistently, a rise in human cases of tick-borne diseases has been reported. Environmental and land-use changes, like the increasing abundance of wildlife and the abandonment of marginal territories, as well as the attenuation of winter temperatures and narrowing of the temperature range at high altitudes, led to the infestation of mountain areas previously not infested. In the Italian North-Western Alps, *I. ricinus* presence has been recorded above 1600m of altitude, and its abundance was related to altitudinal range and forest type. This study aims to re-evaluate previous records about questing *I. ricinus* nymphs distribution in relation with climatic and environmental factors.

Data from a previous study were employed (Garcia-Vozmediano et al., 2020). In the Susa valley, which stretches eastward for 80km from the French border to the city of Turin in the northwestern Italian Alps, 44 sites were selected. To collect ticks, from 2016 to 2019, the sites were sampled by dragging almost six times per year, from April to November. At sampling, temperature, relative humidity, weather condition and the presence of wildlife's traces were recorded along with exact geographic location and habitat characteristics. In addition to the five predictors previously measured on-site, we added ten measured from remote sensing. From digital terrain model, altitude, slope, and aspect were obtained. The Normalized Difference Vegetation Index (NDVI), which estimates vegetation coverage, and global horizontal irradiation, the sum of direct and diffuse solar irradiation, were included too. Weather conditions (minimum and maximum temperatures, saturation deficit, wind, and rainfall) were evaluated based on the *I. ricinus* survival range (Perret et al., 2000) and measured in the variable time spans preceding the sampling.

A spatio-temporal Bayesian LASSO model was implemented to select most relevant variables to explain

I. ricinus nymphs' distribution. Therefore, the model was fitted on a subset of 724 transects that ensured the most complete set of samplings on a subset of 29 sites.

Habitat, altitude, and wildlife were previously reported as key factors affecting ticks' density, but their relevance decreased when other variables were considered. Relative humidity and saturation deficit measured at sampling showed a non-linear effect on ticks' distribution but remained valid predictors. In addition, our model showed that nymphs' density is related to the global solar irradiation and adverse weather conditions during the days preceding the sampling.

The recent infestation of *I. ricinus* of high Alpine areas requires additional efforts to understand the complex adaptation mechanisms of this species to the environment. This study helps in the comprehension of the role of environmental and climatic factors and demonstrate how remote sensing variables can integrate data measured on-site.

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Session 5

Expanding boundaries of Remote Sensing

Chair: **Cyril Caminade**

K05 Infectious water-associated diseases: the role of the environment

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Abstract

The concept that our health is linked to air and water quality is not new. Nor is the idea that spatial patterns in disease outbreak could hold the key to solutions. What is new is the unprecedented access to spatially-resolved environmental data, thanks to space technology: whether they be satellite-based observations of our planet, or information from smart phones, through citizen science initiatives. Such streams of data open up new avenues for exploring the links between the environment and disease outbreaks. In this talk some applications of space technology for the study of water-associated diseases will be presented, drawing on our own work as well as that of others. However, when addressing such a complex problem, satellite technology can only provide a piece of the puzzle, at best. There is a need for scientists of various disciplines to work together with health practitioners and with the citizens in vulnerable areas, to enable effective and long-lasting solutions. Such thinking is embedded in the One Health concept of World Health Organization. They can also contribute to the Sustainable Development Goals of the United Nations, especially those that relate to water.

S05 Mapping Global Bushmeat Activities to Improve Zoonotic Spillover Surveillance

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Keywords: bushmeat, geospatial model, ensemble, regression trees

Abstract

Human populations that hunt, butcher, and sell bushmeat (bushmeat activities) are at increased risk for zoonotic pathogen spillover. Despite associations with global epidemics of severe illnesses, such as Ebola and Mpox, quantitative assessments of bushmeat activities are lacking. However, such assessments could help prioritize pandemic prevention and preparedness efforts.

We used geospatial models that combined published data on bushmeat activities and ecologic and demographic drivers to map the distribution of bushmeat activities in rural regions globally. We stacked the model predictions from Random Forest, Boosted Regression Trees, and Bayesian Additive Regression Trees, and used those as metacovariates for an ensemble model. We used a binomial logistic regression model in a hierarchical Bayesian framework with an intrinsic conditional autoregressive model (iCAR) to assemble the model predictions.

The resulting map had high predictive capacity for bushmeat activities (true skill statistic = 0.94). The model showed that mammal species richness and deforestation were principal drivers of the geographic distribution of bushmeat activities and that countries in West and Central Africa had the highest proportion of land area associated with bushmeat activities

These findings could help prioritize future surveillance of bushmeat activities and forecast emerging zoonoses at a global scale.

R05.1 How to integrate satellite-derived indicators into models of animal mobility?

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Keywords: remote sensing, spatial modelling, mechanistic model, animal movement, wildlife-livestock interface

Abstract

In a context of increasing anthropization at the interface between protected areas and rural communal areas in southern Africa, the multiplication of interactions between wildlife and livestock may generate conflicts such as competition for natural resources, predation, crop destruction by wildlife, or the risk of pathogen transmission. To better understand these potential contacts, we have developed a method combining remote sensing and spatial modelling to simulate the movements of domestic ruminants (cattle) and wild animals (buffaloes).

Water surfaces and vegetation, identified as the main drivers of movement for these ungulate species (Rumiano et al., 2020), were derived from a series of Sentinel-2 satellite images. The resulting maps were then integrated into a mechanistic model of collective movement of interacting individuals (Gregoire et al., 2003), applied to buffaloes (Rumiano et al., 2021) and cattle. The model, tested at three study sites in Zimbabwe, simulates herd movements, the location of contact zones and their seasonal dynamics.

Model results were compared with GPS collar location data from 34 individuals (16 buffalo and 18 cattle). The results show a high degree of spatial and seasonal variability in buffalo-cattle contacts in the three study areas, and a correspondence at landscape scale between the spatial extensions of modeled and observed contact zones. These results illustrate the potential of spatial modelling combined with remote sensing to simulate animal movements on a landscape scale, while offering possibilities for managing these interfaces through, for example, a coupling with epidemiological modelling, or the testing of different scenarios of changes (e.g., practices, environment, climate).

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R05.2 Use of Satellite Earth Observation to monitor aquaculture sites in coastal Abruzzo region, Adriatic Sea

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Keywords: Sentinel 2, chlorophyll-a, turbidity, Ocean color, aquaculture, Adriatic Sea

Abstract

Generally, river plume waters can be distinguished from seawater by differences in salinity, temperature, turbidity, suspended matter and dissolved organics. Optically active water constituents interact with light, and their reflectance can be measured using Satellite Earth Observation (SEO) (Lombardi et al., 2022).

When getting close to coastal zones, the effects of anthropogenic and natural activities on the sea require a finer observation scale than ready-to-use SEO-derived products. To get mapping products time series at high spatial resolution from SEO, local calibration of retrieval algorithms with *in situ* data is required to accurately estimate concentrations of near-surface parameters, although the collection of dedicated *in-situ* data is not easily available.

In this study, we calibrated regional algorithms based on Copernicus Sentinel-2 MultiSpectral Instrument (MSI) data with the value domain typical of the coastal area of central Adriatic Sea to build accurate estimates of turbidity and chlorophyll-a parameters.

The algorithm 'C2RCC' (C2X-Nets) (Brockmann et al., 2016) available in the Water Color Data Analysis System (WC-DAS) (Filipponi et al., 2021) was regionally (Abruzzo coast) calibrated with *ad hoc* collected data during 12 boat campaigns (years 2019-2020), in 20 sampling points distributed between Pescara river mouth and a mussel farm. We estimated and analysed mapping products time series at 10 m spatial resolution, related to turbidity (in FNU) and chlorophyll-a concentration (in mg/m3), from all available Sentinel-2 MSI satellite acquisitions in the period 01 July 2016 - 31 December 2021 (total of 589 observations).

On average, in situ data turbidity decreases and salinity increases when moving away from the coast. This general trend, expected when the softer and colder waters of the river mix with the saltier and warmer marine waters, is well captured by SEO imagery: turbidity values in the coastal waters (0-3

nautical miles NM) of Abruzzo region has mean value 4.48 FNU ± 1.58 standard deviation.
Chlorophyll-a mean value is 0.20 ± 0.04 standard deviation in 0-3 NM coastal waters of Abruzzo region, indicating oligotrophic waters.
There are many potential benefits of using SEO to support sea and public health as well as economic activities. For aquaculture purposes, SEO data provides (i) mapping of parameters at high spatio-temporal resolution to (ii) more accurately monitor environmental and sanitary conditions. Spatial analysis of SEO data helps in (iii) assessing the most suitable areas for aquaculture farming and can underlie Marine Spatial Planning. Furthermore, in combination with weather forecast, SEO data facilitates (iv) modelling in active forecasting systems and alert to timely intervene to safe production and mollusc quality.

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R05.3 How the scale of temperature measures affects the estimate of transmission of mosquito-borne diseases

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Keywords: Daily temperature variations, mechanistic model, WNV, Dengue, Malaria

Abstract

Vector-borne diseases account for more than 17% of all human infectious diseases and result in more than 700,000 deaths annually. A significant part of vector-borne diseases is caused by pathogens transmitted by mosquitoes, and include diseases as relevant as Malaria, Dengue, or West Nile Fever.

Mosquitoes are ectotherms; therefore, their physiology and life histories are driven by environmental temperature (Mordecai et al., 2013). Similarly, the processes involved in the transmission of mosquito-borne pathogens are highly dependent on ambient temperatures (Shocket et al., 2018). The relationship between those factors and the temperature is usually unimodal (i.e., once the minimum temperature needed for that factor is reached, the value of the factor increases until it peaks at an optimum temperature, and then decreases to zero at the maximum temperature). The transmission of mosquito-borne diseases can be quantified using the Basic Reproductive Number (R_0), which defines the number of cases of a disease that arise when one case is introduced into a totally susceptible population. An ideal approach to evaluate the relationship between the risk of transmission of mosquito-borne diseases and temperature is the R_0 equation.

The objective of our study was to quantify the effect that the precision with which temperature is measured (hours, days, months) has on the estimates of transmission of mosquito-borne diseases. In order to do that, we used mechanistic models to quantify the basic reproductive number (R_0), which we applied to different mosquito-pathogen combinations: West Nile virus (WNV) and *Culex pipiens*, dengue virus (DENV) and both *Aedes albopictus* and *Aedes aegypti* and *P. falciparum* malaria parasites and *Anopheles* mosquitoes. At the world level, the higher the precision, resulted in significantly smaller estimates of transmission and much larger transmission areas, and those results were consistent for different mosquito-pathogen combinations and for the different months of the year. However, when that effect was evaluated at a smaller spatial scale (i.e. climatic areas), spatio-temporal heterogeneities

were observed. For example, hourly rather than monthly temperatures tended to decrease the estimates of transmission in areas of tropical climate but increased them in areas of continental climate. While those effects were clearly different between climatic areas, they were consistent for the different mosquito-pathogen combinations within a climatic area.

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R05.4 Tick's suitability habitat maps and tick-host relationships in wildlife. A One Health approach based on multitemporal remote sensed data, entropy and Meta® population dataset in Aosta Valley, NW Italy

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Keywords: Earth Observation, Meta® Population dataset, One Health, Suitability maps, Ticks, Zoonotic pathogens

Abstract

Ticks represent a reservoir of zoonotic pathogens, and their numbers are increasing largely in wildlife. The development of Earth Observation (EO) missions and GIS-Remote sensing techniques have contributed to the enhancement of epidemiological data analysis capabilities providing new and potential tools for the surveillance of animal diseases (Estrada-Peña, 2002). Moreover, the correctly geomatic-based use and development of remote sensing and EO Data in veterinarian ordinary workflows is still under-exploited.

In this regard, to strengthen the use of free EO data in ordinary veterinarian analysis, this work aimed identifying the tick species most involved, their distribution in wild hosts and develop suitability habitat maps (SHM) in Aosta Valley (NW Italy) based on multitemporal EO data processed in Google Earth Engine providing also a risk assessment (Orusa et al., 2023). SHM were realized considering the following inputs: A) Growing Degree Ticks (GDT) computed from Land Surface Temperature from MOD11A1 by assigning a threshold, B) NDVI from MOD09GA involving the pixels satisfying the GDT

threshold, C) NDVI entropy, D) water surfaces distance, E) terrain features, F) Precipitation retrieved from WORLDCLIM/V1/BIO.

Clouds, shadows and defective pixels have been masked out in the EO data considered and monthly composites within the years 2020-2022 created. Since the data of the ticks have not been punctually geo-referenced, not allowing a multivariate regression analysis of the variables involved in the suitability map, to define the weight of each one, on the basis of the existing literature, the variables considered have been assigned the same weight and have been normalized. An ISODATA unsupervised classification–clustering algorithm was performed on B), and the separability of each class obtained was checked by computing the Jeffries–Matusita distances to compute than C).

Ticks were collected from hunted, injured, and found dead wild animals (*Sus scrofa, Capreolus capreolus, Rupicapra rupicapra, Cervus elaphus*), and they were identified to species level using taxonomic keys (Accorsi et al., 2022). Between September 2020 and December 2022, a total of 90 ticks were collected from 89 wild animals. *Ixodes ricinus* (93.4%) was the most prelevant tick species, followed by *Dermacentor marginatus* (5.5%) and *Dermacentor* spp (1.1%). In roe deer, *Ixodes ricinus* was the most frequent species founded, as *Dermacentor* spp., while in wild boar *Dermacentor marginatus* was the dominant species. Molecular analyses demonstrated the infection of ticks with *Anaplasma* spp., *B. burgdorferi* sensu lato, *Coxiella burnetii*, *Rickettsia* spp.

Finally, to assess population potential exposure to tick presence during the period investigated, the Meta® population dataset was considered by performing zonal statistics per each suitability class.

In conclusion this study shows the potentialities of Remote sensing and how the use of different information layers can allow a technological transfer to the veterinary sector according to a real One Health perspective.

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Session 6

Modelling for ASF emergency

Chair: **Paolo Calistri**

S06 Choice of Landscape Discretisation Affects the Rate of Spread in Wildlife Disease Models

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Keywords: disease spread modelling, land use, landscape discretisation, spatial models, voronoi tessellation, wildlife-livestock interface

Abstract

Research on the interplay between domestic animal and wildlife populations has gained momentum recently. African Swine Fever (ASF) is a highly infectious viral disease that is of particular interest due to ongoing outbreaks in Europe, where wild boar constitute a reservoir of disease spillover into domestic pigs.

It is theoretically desirable to model spread of the ASF virus through a wild boar population using a continuous-space model, where wild boar distribution is inferred from spatial mapping of the available habitat. Because continuous-space models are difficult to work with, these are typically approximated using discrete-space models, where the wild boar population is divided into patches within the landscape.

In this study, we investigate the epidemiological impact of different assumptions regarding the spatial discretisation of a wild boar population. We use a simulation study with a fixed population of wild boar within a fictional, homogeneous landscape. This landscape is discretised into patches using different methods. A deterministic compartmental Susceptible-Infected-Recovered (SIR) model is formulated to allow pairwise spread between each patch depending on a transmission matrix β, which is then fit using an ODE solver. The scenario is as follows: Two buffer zones are created with a large gap in between. An outbreak is started in one, and the time until the other buffer zone has crossed a certain prevalence threshold (τ) is recorded. This process is repeated on the same landscape, but with different discretisations of the landscape at different spatial resolutions. For each simulation, transmission between patches is controlled by a pairwise transmission matrix β.

We considered many correction factors for β that were hypothesised to re-scale overall transmission so that τ is independent of landscape discretisation choice. These included: scaling with respect to the diameter of the patch, exponential distance decay, normalising discrete distances, and normalising

using an integrated distance kernel. These corrections mask the inconsistency for some scenarios, but overall τ remains highly dependent on the choice of discretisation, suggesting that the underlying epidemiological process is impacted by the spatial discretisation. We also present an alternative method of formulating β, using pairwise proximity of artificially-created high-resolution lattice points that approximates transmission in continuous space. This yields a τ that is more robust to the details of landscape discretisation, so that the overall model results are less dependent on arbitrary decisions regarding size and shape of patches.

In conclusion, we propose that the method of landscape discretisation should be regarded as a source of uncertainty that impacts disease spread, and as such should be treated as a hyper-parameter in epidemiological models involving wildlife. It is important to ensure that overall conclusions from such models are robust to landscape discretisation choice.

R06.1 Examining the Impact of Fencing on the Front Wave of African Swine Fever in the Korean Wild Boar Population

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Keywords: African swine fever, wild boar, front wave, fences, South Korea

Abstract

African Swine Fever (ASF) is a viral disease that affects both wild boar and domestic pigs. In recent years, this virus has spread rapidly across Europe and Asia, causing extensive damage to pig populations and related industries. In South Korea, the first notification in wild boar was made in October 2019 in the northern region bordering North Korea. Since then, the virus spread southward, leading to more than 2,800 reported cases in wild boar and sporadic outbreaks in domestic pig farms. To mitigate its spatial spread, Korean authorities built fences over 2,300 km. In this study, we aimed at evaluating the effectiveness and its heterogeneity of these fences in controlling the spread of ASF in South Korea, using the spatiotemporal distribution of ASF cases reported in wild boar between November 2019 – March 2023 in South Korea.

We first identified the main spatiotemporal clusters and selected only the front wave cases within each cluster. By examining these front wave cases, we estimated the spread rate (in km²/week) using trend surface analysis (Tisseuil et al., 2016). Finally, to evaluate the effectiveness of fencing on the spread of ASF, we created a null scenario by randomly redistributing front wave case locations as described in Dellicour et al. (2020). By comparing the observed patterns to the expected patterns from the null scenario, we were able to test whether fences effectively reduced the spatial propagation of the virus as well as the front wave velocity.

Among the total 2,661 wild boar cases reported in the study period, we identified nine clusters that included 691 front wave cases. We restricted our analysis to the 619 front wave cases from the four largest clusters. Overall, the front wave spread by 0.52km^2 per week at national level, with heterogeneous velocities calculated in each cluster, from 0.15 km^2/week to 0.99 km^2/week. For two out

of the four clusters studied, we found that the number of fence-crossing events was statistically significantly lower than under the null scenario, suggesting that fences reduced the propagation of the virus across the fences in these regions. However, we did not find any evidence for the two other clusters. Also, we did not find any statistical evidence suggesting that fences slowed down the front wave velocity.

We conclude that ASF virus in South Korea spread geographically at a faster rate than in other environmental contexts like Belgium (Dellicour et al., 2020) and that this geographical spread must be associated to specific determinants that are yet to be elucidated. The heterogeneous effects of fences can be explained by their spatio-temporal erecting patterns and environmental determinants. We highlight the crucial need to account for unobserved ASF virus diffusion when deciding where and when to place them.

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R06.2 Elucidating African swine fever transmission cycle dynamics at the domestic-wildlife interface. Multihost epidemic modeling in Romania

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Keywords: modeling, mechanistic, spatiotemporal, African swine fever, interface, transmission

Abstract

The global spread of African Swine Fever (ASF) poses an unprecedented threat to the swine industry. Mathematical modeling has proven useful for quantifying disease transmission and informing control strategies among domestic pigs and wild boars separately. Such models are sufficient for regions where ASF is restricted to a single ecological compartment, however for areas where spillover is suspected—as in Romania where there exists a predominance of low-biosecurity backyard pig holdings—a multihost approach is likely needed. To explain the spatio-temporal infection pattern of ASF in Romania, and to evaluate outcomes from alternative control strategies, a multihost individual-based mechanistic model was developed and parameterized to the period of initial disease spread: June to December 2018. Two types of domestic pig herds were considered in the model: low-biosecurity backyard farms and high-biosecurity industrial operations. Due to the ubiquity of backyard pig farming, each village was considered to be a single backyard farm with locations represented by village centroids. Industrial farms were also represented by their point coordinates. Wild boar presence was simulated via rasterized CORINE Land Cover data sized to estimated wild boar home-ranges, with wild boar presence modeled as a function of raster cell forest density. For initial parameterization, domestic pig herds iterated through susceptible (S), infectious-undetected (Iu), infectious-detected (Id), and recovered (R) states, while wild boar cells were considered to be perpetually infectious following infection, allowing only S-Iu-Id states. Model fitting was performed through Adaptive Population Monte Carlo, a means of approximate Bayesian computation. A total of 24 models were evaluated, with the observed epidemic dynamics being best explained through frequency-dependent transmission between domestic pig units, density-dependent transmission between wild boar cells and domestic pig units, and 2nd order adjacency spread between wild boar cells. Model outputs estimated that a median of 20% of domestic pig unit infections came from wild boar sources, and 30% of wild boar infections came from domestic pig units

(https://www.veterinariaitaliana.izs.it/index.php/GEOVET23/article/view/3244/1406). Further, our model estimates that the majority of interhost transmission events occurred during periods of undetected circulation. Alternative control strategy outcomes were evaluated through comparing final epidemic size and relative host contribution, with the biggest decrease in epidemic size occurring through a combination of increasing wild boar surveillance with aggressive local environmental sanitation following initial case detection, and instituting village-wide culling upon ASF case detection in a domestic pig. These results help advance our collective understanding of multi-host pathogen spread to inform animal health policy.

R06.3 Spatially explicit agent-based modeling as a tool in aiding African swine fever mitigation and eradication in Thailand

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Keywords: African swine fever, Agent-based model, Animal movement, Disease spread model, Thailand

Abstract

African Swine Fever (ASF) is a highly contagious viral disease of swine with exceptionally high mortality in domestic pigs. Due to the lack of effective vaccine and treatment at present, the socioeconomic impact losses caused by the virus to the swine industry across the globe is very high (Blome et al., 2020). Many studies have shown that disease modeling and forecasting can provide valuable information on the overall disease impact and can be used as guideline for decision makers to evaluate their disease surveillance and control programs (Beaunée et al., 2023; Mur et al., 2018). With the recent arrival of ASF in January 2022 in Thailand, a spatially explicit agent-based model has been constructed to support the surveillance and control strategies for ASF within the country.

In this study, we used a fine scale grid with detailed pig demographic and pig movement data in Thailand to evaluate the spatio-temporal dynamics of ASF at local and national level. Our model aimed to estimate the impact of the disease under diverse interventions such as stamping out, movement restrictions, compartmentalization, and early detection. We estimated the total number of infected farms, number of infected areas and duration of the outbreak under diverse epidemiological scenarios.

Our model estimates that reducing the average days to detection from 21 to 14 days will reduce the overall epidemic impact by 43%. Our results provide high resolution information about the regions with higher impact and the complex disease spread networks developed. These results will be used to support and improve the current ASF eradication efforts in Thailand and can be easily adapted to other transboundary animal diseases or regions under different epidemiological settings.

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R06.4 Spatial analysis to inform African Swine Fever spread modelling in Laos

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Keywords: African swine fever, clusters, disease spread model, pigs, Lao PDR

Abstract

African Swine Fever (ASF) was first reported in Laos in June 2019, when an incursion caused 150 village outbreaks across all Provinces and territories. Despite stamping out control measures, ASF virus (ASFV) spread rapidly. Understanding the rate of disease spread and the infectious period of ASFV at the village level is necessary to accurately model this disease in the smallholder system which exists in countries such as Laos. However, such parameter estimates are scarce. The aim of this study was to estimate key epidemiologic parameters to enable modelling of ASFV spread in Laos.

Data were collected on ASF outbreaks reported and confirmed via PCR testing during the period 1 June 2019 to 1 January 2020. Information included outbreak date or date of first report, and village location. The latter was used to determine latitude and longitude coordinates.

To estimate disease spread parameters, the Approximate Bayesian Computation Sequential Monte Carlo (ABC-SMC) technique was used to validate simulated disease parameters against the reported ASF outbreaks using a compartmental disease model. A prior for between-village transmission was based on ASFV outbreaks between smallholder farms in Uganda, represented as a gamma distribution. For the latent (mean, shape) and mean infectious periods, various estimates based on experimental and field studies from published studies were used.

A critical assumption is homogenous mixing within the modeled population. To better meet this assumption, the outbreak data were analysed to identify likely spatiotemporal clusters; these clusters were assumed to represent the occurrence of linked, village spread of ASFV.

The final dataset contained 150 outbreak villages representing all Provinces in Laos. Six spatiotemporal clusters were identified. The size of these clusters ranged from 4 to 14 case villages, radii 16 to 153km and period 0 to 22 days.

The mean estimated latent period was 5.82 to 5.95 days across the clusters, the mean village infectious period 61.53 to 67.70 days, and mean β 0.19 to 0.51. The R_0 ranged from 13.06 to 31.06 across the clusters. Simulated outbreaks utilising the estimated transmission parameters struggled to match the observed data in clusters in which fewer than ten outbreaks occurred or where all outbreaks were reported over only one to two days.

Spatio-temporal analysis can be used to improve ASFV transmission parameter estimation, thus improving outputs from disease spread models. However, this study demonstrates that the value provided by such approaches can be limited by the surveillance data that is available.

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Session 7

Artificial intelligence for One Health

Chair: **Rowland Kao**

K07 Issues and challenges in fair and robust AI models

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Abstract

Artificial Intelligence (AI) and Deep Learning have emerged as revolutionary technologies that have transformed various industries and are driving innovation across the globe. However, as AI and Deep Learning continue to evolve and find applications in numerous domains, they face several significant challenges and issues. One of the foremost challenges is the reliance on data, especially the quality and quantity of data. AI and Deep Learning models are heavily dependent on large datasets for training and fine-tuning. Weak annotations and biases in the data can lead to profound consequences, affecting the performance and fairness of these systems. Moreover, the availability of different sources of data to be integrated in a common AI model is crucial to let the AI model to mimic real complex systems. The talk will explore all these challenges, delve into the pressing issues related to weak annotations and biases in data, shedding light on their implications for the development and deployment of AI technologies in society, and propose some strategies to address them.

S07 Shade from Space: Utilizing Satellite Imagery to Assess Shade Provision on New Zealand Dairy Farms

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Keywords: Deep Learning, Satellite Imagery, Spatial Epidemiology, Climate Change, Animal Welfare, Heat Stress

Abstract

As climate adaptation strategies gain importance, mitigating heat stress in livestock, particularly in New Zealand's dominant pasture-based farming system, is crucial. Studies have documented the positive effects of shade provision in mitigating heat stress, leading to increased rumination, milk production, and improved welfare in dairy cows (Blackshaw & Blackshaw, 1994; Bloomberg & Bywater, 2007; Fisher et al., 2008). Our project, "Shade from Space," employs high-resolution (30cm) Maxar Satellite 4-band imagery and deep learning algorithms to automate shelter identification and shade quantification on dairy farms. The overarching goal is to optimize shelter and shade provision on a national scale, ensuring maximum accessibility for livestock during peak heat loading times.

Our pixel-classification model identifies trees and categorizes them into broad classifications: individual deciduous and coniferous trees, riparian, NZ native bush, grouped trees, and shelterbelts. We isolate each tree crown in grouped trees using individual tree crown techniques. The model generates data on tree location, classification, average canopy diameter, and footprint raster. Tree heights are inferred from regional growth curves for each classification. We then apply a ray-shading model to estimate the projected shade based on the position and angle of the sun at different times of the year for each tree.

To validate our model, we collected field data from eight farms, covering 239 trees. Technicians logged tree locations, delineated the shade extent using GPS, and captured images for future model refinement through enhanced speciation/classification. The ray-shading model was applied concurrently to assess our shade coverage model's predictive accuracy at the date and time of field capture.

Looking to the future, we aim to refine our model using field data to improve classification granularity, extend our shelter identification to man-made shelters, and optimize shade estimations considering factors like terrain and paddock use. Alongside these goals, we face challenges such as streamlining workflows for efficient, cost-effective satellite imagery acquisition and managing computing

requirements for a larger-scale rollout. We also plan to evaluate the cost-benefit trade-off of lower-resolution, cheaper imagery against model accuracy and effectiveness. Despite these challenges, we are confident that our innovative methodology will significantly enhance our understanding and management of heat stress in livestock farming in NZ amid evolving climatic conditions.

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R07.1 Earth Observation-based Self Organising Map for Northern Africa regions

Luca Candeloro[1], Carla Ippoliti[1], Susanna Tora[1], Markus Metz[2], Laura Amato[1], Romolo Salini[1], Valentina Zenobio[1], Paolo Calistri[1], Nicola D'Alterio[1], Alessandro Ripani[1], **Annamaria Conte**[1]

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Abstract

The global climate is undergoing relentless change. While it is a complex phenomenon with difficult-to-predict full-scale impacts, its influence on the emergence of diseases, especially vector-borne diseases (VBDs), is widely acknowledged. Therefore, comprehending our landscape and examining its potential shifts over time due to alterations in climatic and environmental factors becomes crucial.

In the framework of the WOAH project "Defining Ecoregions and Prototyping an EO-based Vector-borne Disease Surveillance System for North Africa (PROVNA)," we have identified ecoregions across North Africa, sharing similar environmental and climatic characteristics and which can serve as a pivotal foundation for enhancing surveillance systems and early warning system for vector-borne viruses.

Selected EO data products for the period 2018-2022 (Land Surface Temperature Day and Night - LSTD and LSTN, Normalised Difference Vegetation Index - NDVI, Soil Moisture - SM, Normalised Difference Water Index - NDWI, Rainfall - RF) at 250 meters/16 days resolution have been collected, aggregated, and standardized at a season/year level. We used the (super)SOMs method (an unsupervised neural network clustering method) to get a topology-preserving map, transforming a complex high-dimensional input space into a simpler low-dimensional (typically two-dimensional) discrete output space. The resulting map is easy to interpret and can be used for classifying new (both in space and time) observations.

A stratified random sampling, preserving the spatial and temporal variation of the environmental factors, was used to half the ~3 hundred million pixels of the entire extent and to create the dataset to train the SOMs.

An RGB colorization was applied to the trained (super)SOM map (a hexagonal grid made up of 40x40 neurons for 20,000 epochs) to further improve its readability with respect to the input environmental variables averages (the red channel was assigned to LSTD and LSTN, the green channel to NDVI and NDWI and the blue channel to RF and SM). Finally, the affinity propagation clustering algorithm was applied to the map's neurons (1.600) to group them and get the number of distinct ecoregions.

The map clustering was in the end used to classify all of the pixels and to get yearly classification rasters.

The proposed approach allows to apply the SOMs algorithm to EO data for a very large area, classifying landscape (and its temporal evolution) while preserving high spatial resolution and at the same time getting an immediate interpretation of similarity. This model will effectively support Competent Authorities in North Africa to identify locations where applying surveillance activities (while optimising financial, material and human resources) for identifying potential viruses in the area such as Rift Valley Fever which pose a threat for the entire Mediterranean region, including Europe.

R07.2 Predicting spatially explicit swine premises using deep learning and aerial imagery to improve disease monitoring and surveillance

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Keywords: convolutional neural networks, Deep Learning, disease transmission, livestock, surveillance

Abstract

Accurate farm geolocations are essential for disease outbreak surveillance and monitoring, and for developing spatial epidemiological models that evaluate distance-dependent transmission processes across different farm types. Farm geolocation data is often not available, which leads to assumptions of the spatial distribution of livestock premises; potentially resulting in over/underestimation of transmission rates, misleading model predictions, and limited interpretation of epidemic dissemination dynamics (Sellman et al., 2020). Here, we developed a convolutional neural network (CNN) model to i) identify individual swine barns from non-barn features (e.g., residential homes, commercial buildings), with the objective of ii) developing a rule-based filtering method to calculate the area and the aspect ratio of swine barns and combine this information with farm metadata (pig capacity, farm type) to iii) predict farm types and population size.

High resolution aerial imagery from a 22,369 x 13,457 pixel extent was obtained from the National Agriculture Imagery Program (NAIP) (USGS, 2022), and used to generate 1,148 raster tiles with dimensions of 512 x 512 pixels. We constructed a binary mask consisting of 118 known swine barns, which we incorporated into the raster tiles as an additional raster band. Raster tiles were split as 60% for training and 20% for validation, and testing a ResUnet CNN model (Diakogiannis et al., 2020), respectively. Model performance was evaluated by examining the accuracy of the classification of barn and non-barn features.

The CNN model was able to accurately identify swine barns from non-barn features with an accuracy of 80% in a swine production region of the United States. Additionally, the fractional predicted probability of the "barns" class, recognized open space between barns and nearby waste lagoons as a high probability of belonging to a swine barns.

We were able to successfully predict swine barn geolocations using aerial images and deep learning with an accuracy of 80%. We also obtained valuable contextual information regarding environmental, demographic, and structural properties of swine barns and the surrounding areas, which we will be incorporating as we continue to refine our model. Once the best model is identified, our aim is to use this model to predict different swine farm types, and their corresponding population size. Results obtained from this work will enable researchers and policymakers to better understand the distribution and spatial arrangement of swine farms, and aid in the development of accurate spatial epidemiological models. This information is crucial for the identification of high-risk areas, potential sources of disease transmission, tailoring disease control strategies, and evaluating their effectiveness.

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R07.3 Forecasting West Nile Virus Circulation through Sentinel and Landsat Imagery and Graph Neural Networks

Angelo Porrello[1], Carla Ippoliti[2], **Lorenzo Bonicelli**[1], Federica Iapaolo[2], Daniela Morelli[2], Federica Monaco[2], Simone Calderara[1], Annamaria Conte[2]

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Keywords: Deep Learning, Graph Neural Networks, Landsat, Sentinel, Remote Sensing, Satellite imagery, Self-Supervised Learning, Zoonosis, West Nile virus

Abstract

The West Nile Virus (WNV) infection represents one of the most common mosquito-borne viral zoonosis. Its circulation is highly influenced by climatic and environmental variables influencing vector proliferation and virus replication (Paz & Semenza, 2013). Several statistical models have been developed to predict WNV circulation. Beyond this, the recent massive availability of Earth Observation data, coupled with the continuous advances in the field of Artificial Intelligence, offers new valuable opportunities in modelling animal diseases or vector population dynamics (Porrello et al., 2019).

In the work presented herein, we seek to forecast WNV circulation by supplying Deep Neural Networks (DNN) with high-resolution multi-band Copernicus Sentinel-2 and Landsat-8 imagery. While aggregated indices (e.g. NDVI) have been extensively shown to hold environmental and climatic features, here we let the DNN learn directly from raw spectral bands.

While previous DNN approaches analyze each geographical site independently (Porrello et al., 2019), we propose a spatial-aware approach that includes the characteristics of close sites. Specifically, we build upon Graph Neural Networks to aggregate features from neighbouring locations, while considering their mutual environmental relations. In particular, for each site, we measure their difference in Land Surface Temperature and Surface Soil Moisture - acquired from Copernicus Sentinel-3 and Sentinel-1 respectively - as well as their geographical (Haversine) distance. Moreover, we take into account the temporal factors that characterize the spread of the virus by injecting time-related information directly into the model.

To prove the merits of our proposal, we design an experimental setting that combines satellite imagery with “on-the-ground observations”, i.e. the veterinary cases detected in Italy in the years 2017-2019

and reported in the National Disease Notification System of the Italian Ministry of Health, as described in Candeloro et al., 2020.

By means of both qualitative and quantitative results, we show that our proposed Multi-Adjacency Graph Attention Network (MAGAT) consistently leads to higher performance than classical Machine Learning and Deep Learning baselines, especially when paired with an appropriate pre-training stage.

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Session 8

Network analysis for transmission pathways

Chair: **Beatriz Martínez-López**

K08 Emergent infection disease problems under environmental land management

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Abstract

The world is experiencing environmental change which is unprecedented in its speed, geographical reach and severity. At the same time, biodiversity loss is in many ecosystems near catastrophic and food security a growing worldwide concern. Both long terms trends and individual system shocks have already been shown to have far-reaching implications for global health. In response, actions over land management to respond to those threats must be equally drastic and our decisions in the short term will have far-reaching implications for decades to come. These conditions are also already known to influence the emergence of new infectious disease threats. In turn, infectious diseases have the capacity to derail our efforts to respond to these challenges. Here, I shall discuss some of the issues involved, and present some preliminary investigations into the impact of how spatial coordination of land management decisions and infectious disease risks impact the potential for infectious diseases to affect wildlife and livestock.

S08 Landscape Connectivity and travel corridors routes for predicting the spread of ASF in European wild boar

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Keywords: African swine fever, disease spread modelling, landscape connectivity, corridors, habitat patches, probability connectivity, spatial analysis, wild boar

Abstract

African Swine Fever (ASF) is an infectious and highly fatal disease affecting wild and domestic swine. It is rapidly spreading worldwide and there is a pressing need for tools that help to identify areas to prioritize monitoring and prevention measures. In Europe, wild boars are the main driver of local spread, transmission, and maintenance of the disease in endemic areas, and also an introduction into ASF-free countries. Landscape connectivity studies are the main discipline to analyze wild species dispersal networks, and it can be an essential tool to predict dispersal wild boars' movements and the associated potential ASF spread with holistic and successful disease management. In this study, we aimed to integrate structural and functional wild boar connectivity predictions with their population abundance and ASF notifications to calculate the impact of wild boars' infection across Europe.

First, for the connectivity analyses we defined the available habitat patches, which represent the suitable areas of wild boar habitat. *Second*, the landscape surrounding the habitat patches was characterized by a resistance surface, measuring the difficulty level of moving through each land cover class of the landscape. *Third*, we estimated the most favorable routes or corridors of movement for wild boar between habitat patches with the least-cost path algorithm; obtaining the least accumulated resistance between each pair of habitat patches. *Fourth*, based on the probability of connectivity (PC) index used by the Conefor software (which measures the overall habitat connectivity of a landscape), we identify the most important areas to apply ASF spread control and surveillance measures using two risk indicators: the impact factor (how much the infection of each habitat patch and corridor would potentially affect the whole wild boar network), and the risk factor (the threat of infection of each habitat patch from already affected habitat patches). Furthermore, we tested the accuracy of the risk of infection comparing the results with the temporal distribution of ASF cases from 2019 to July 2022.

Our findings highlighted that the impact and risk factors were generally higher in Europe's central and eastern regions. Additionally, the impact factor was 31 times higher on habitat patches that actually were infected the next year, proving the utility of the proposed approach and the key role of wild boars' movements in ASF spread. This early warning system tool and network analysis can aid to identify important areas for ASF management and locate the potential routes/corridors of the international spread of the disease to other countries by the natural movements of wild boar. Also, it is a useful tool to implement cost-effective active surveillance and preventive measures in the framework of the European wildlife health surveillance program for ASF disease.

R08.1 Multihost foot-and-mouth disease dissemination model: why using just cattle data neglects the disease spread potential and covered transmission routes

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Keywords: disease control, epidemiological model, Transmission pathways, disease spread modelling

Abstract

Foot-and-mouth disease (FMD) infects multiple food-animal species and disseminates among ungulate species. FMD is known to disseminate through a combination of within-host and between-host dynamics. Several single-species FMD transmission models have been used to simulate outbreaks and examine the effects of control actions to mitigate outbreaks, however, often focusing on individual food animal species such as cattle. Our multi-species and multiscale (metapopulation and between-farm dissemination driven by animal movement and farm-to-farm distance) compartmental stochastic model accounts for births, deaths, and species-specific transmission dynamics. Our model outputs included the number of secondarily infected animals and farms, the role of animal movement and between-farm distances as transmission pathways, and the effectiveness of countermeasure actions. Our results demonstrated that after 20 days of FMD dissemination without any control actions, all the species were infected, and the median number of infected farms was eight. The spatial proximity was the predominant route associated with bovine infection, while in swine, it was linked with animal movements.

Furthermore, the median distance between seeded, and secondary infections was 5.77 km, with the highest spatial dissemination reaching 695.40 km. The simulated control strategy results showed that depopulating 12 farms and vaccinating 15,000 farms daily after 20 days of silent FMD dissemination would contain 93.4% of epidemics, with a median of, nine infected farms within 54 days after implementing control actions. In conclusion, our model highlights the need for multispecies FMD transmission models, especially in regions where multiple species are raised on the same premises.

R08.2 Integration of spatial and network analysis to undercover community exposure to zoonotic vector-borne diseases: the example of Ross River Virus during the COVID19 lockdown in Brisbane Australia

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Keywords: geospatial model, network analysis, Vector-borne diseases

Abstract

Ross River Virus (RRV) infection is the most incident arbovirus disease in Australia. Despite the significant human health burden of RRV, the ecological characteristics of putative exposure sites to RRV infected mosquitos are not fully understood. In this study, we aimed to ascertain the most likely sites of RRV exposure and their characteristics for individuals residing in the RRV notification hotpots of the Greater Brisbane Region.

We analysed all reported RRV notifications geolocated to the household level for the period prior, during and after the Queensland COVID19 lockdown (January 2020 to July 2020). We first used geospatial cluster detection methods to identify RRV notification hotspot areas for each study period. We then harvested mobile-phone data for users in the areas of residence of the identified RRV notification hotspots. Using network analysis, we estimated the areas in Greater Brisbane that were more connected and the average time people spent in green areas during the lockdown period. Using a Zero-inflated Poisson model, we estimated associations between RRV notifications and environmental data and population movement.

During the study period, a total of 993 RRV cases were notified with geolocation in Greater Brisbane, resulting in an annual case rate of 66.1 cases per 100,000 people and we identified a total of 22 RRV geospatial clusters. Our analysis of movement data involved 9 million movements from hotspots areas of residence of RRV cases. We found that areas with high degree centrality measures had a significant higher incidence of RRV (p-value <0.05). Additionally, we noticed a slight increase in time spent walking in green areas across the study period, while the time spent in green areas was lower in the pre-

lockdown phase, averaging at 11.4 minutes per week. Further, we observed that areas with a higher percentage of vegetation cover had a higher RRV incidence (p-value <0.01).

This study provides strong evidence RRV exposure was likely to occur in urban areas, specifically locations with higher vegetation coverage than the target areas identified in this study (e.g. urban green areas). This information can be used as an evidence-base regarding changes to current surveillance protocols and the deployment of mosquito control and surveillance strategies to areas where the community in high-risk areas tend to spend more time outdoors.

R08.3 On the interaction between bovine and bubaline trade network in epidemic spreading

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Keywords: Bovine Trade Network, Bubaline Trade Network, Q-Fever, Social Network Analysis

Abstract

The Italian cattle movement network has been extensively studied in the literature (Bajardi et al., 2011) while the Italian buffalo network has not been investigated. Throughout the peninsula there are several farms that breed buffaloes and more than 60% of these also breed cattle. Such situation highlights potential transmission of pathogens between the two species. In order to study the interaction between the two networks we considered a pathogen, *Q-Fever*, that can infect both species and also humans. It is a dangerous disease for humans, but, since it is usually asymptomatic in animals, it is often neglected. This pathogen is widespread among cattle and buffaloes in Campania region (Ferrara et al., 2022).

We want to study if the buffalo network can support the diffusion of the pathogen and spread it to the cattle network through those farms that breed both species. To do this, we consider a SIS model. Since the diagnosis is complicated and usually carried out at herd level, the epidemiological units of our model are the farms. An infectious farm is a farm where at least one animal is infectious.

A susceptible farm that receives animals from an infectious farm will also become infectious according to a defined probability of infection.

We randomly infect a small subset of the buffalo farms (0.05% of all the farms), and then simulate the diffusion of the pathogen using real movement data between 2017 and 2020, aggregated by week. Given the above considerations, we considered a low probability of "healing" among the farms, 0.1%.

In Table 1 (https://www.veterinariaitaliana.izs.it/index.php/GEOVET23/article/view/3247/1405) we can observe the results of 100 different simulations for different infection probabilities.

From this analysis, it can be concluded that the interaction between the buffalo and the cattle network is not negligible. Indeed, the buffalo network may support the spread of a pathogen and is able to

spread it within the cattle network through those farms that breed both species. Further work could include a more in-depth study of both the buffalo network and the interaction between the two species in the multidimensional network. In addition, improving the model by considering surveillance in the cattle network might be interesting to observe the impact that the buffalo network would have by itself.

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R08.4 Development and application of a network model to understand the epidemiological and economic burden of an aquaculture disease outbreak under different control strategies

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Keywords: aquaculture, trout, network, fishing, freshwater

Abstract

Aquatic animal diseases cause high mortality, threatening biodiversity, and food security, resulting in substantial economic impact to aquaculture and recreational fishing industries. Tools such as mathematical models and computer simulations are valuable for predicting the potential spread and impact of disease, thereby informing evidence-based, cost-effective management policy and decision making.

The AquaNet-Mod is a modelling tool used to simulate the spread of disease across a network of connected sites representing the aquaculture industry, in this case the trout aquaculture and inland fishery industry in England and Wales. Each site is considered a single epidemiological unit, and disease can spread between sites via four transmission mechanisms: live fish movements, river-based transmission, short distance mechanical transmission and distance independent mechanical transmission. The connectivity between sites is based upon real-world data gathered as part of the Competent Authority's statutory monitoring. Following the seeding of infection, sites transit between three disease states: susceptible, clinically infected and sub clinically infected, according to defined criteria. Disease spread can be interrupted by the application of disease mitigation measures and controls such as contact tracing, culling, fallowing and surveillance. The model also incorporates economic costs to affected sites and the Competent Authority associated with infection and controls, allowing the cost of an outbreak to be estimated and compared between control scenarios.

Here we present AquaNet-Mod outputs for Viral Haemorrhagic Septicaemia (VHS), a freshwater salmonid disease listed by WOAH and in the UK. Simulations showed that, intuitively, controls which reduced the total number of infected sites reduced the overall epidemic costs. In particular, the model demonstrated that the current disease controls in England and Wales resulted in the lowest total number of infected sites, on average, and that contact tracing was both effective at reducing the spread of disease through the network and relatively low cost. The merit of this model for evaluation of disease spread and the cost-effectiveness of controls, in the context of policy, is discussed.

R08.5 Movenet: a toolkit facilitating the use of livestock movement networks in veterinary public health

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Keywords: anonymisation, data flows, livestock movement data, network analysis, software, transmission modelling

Abstract

Commercial livestock movements are an important factor in the spread of infectious diseases of livestock such as African swine fever (ASF). The analysis of these movements can provide valuable intelligence for emergency preparedness: network analysis can determine a movement network's effectiveness at transmitting infection and the relative importance of different holdings and connections, and incorporating detailed movement data into transmission models can improve the accuracy of predictions such as outbreak size. However, the effective use of livestock movement data is fraught with challenges. On the data side, commercial sensitivity concerns can inhibit data sharing between relevant actors. On the analysis side, network and modelling studies require resources, time and expertise that may be in short supply. We have developed Movenet, a toolkit that addresses these challenges and simplifies the effective use of livestock movement data in veterinary public health.

Movenet is an R package that facilitates the use of livestock movement data in two ways:

1. To improve the potential for collaborative data sharing by addressing commercial sensitivity concerns, Movenet provides data owners and data managers with a variety of options to make livestock movement data less identifiable: holding identifiers can be substituted (pseudonymised); holding geographical coordinates can be jittered in a density-dependent manner; and movement dates and weights can be modified by addition of random noise or by rounding. Modified datasets can be viewed and downloaded in various formats. The authors encourage users to consider that data modifications may impact the results of any analyses, and to seek an appropriate balance between identifiability of data and accuracy of results. To this end, Movenet provides users with the opportunity to compare the effects of various data modifications on network measures and model predictions.
2. To facilitate the effective use of (real or modified) movement networks in risk assessment,

> Movenet provides researchers and decision-makers with a quick entry into social network analysis of livestock movement data. Movenet produces a standardised, downloadable report, with a range of tables and figures displaying metrics relevant to disease spread. The report includes basic network properties such as the number of active holdings and edges (overall and over time), static network analysis of (monthly or yearly) snapshots, temporal analysis including ingoing and outgoing contact chains (reachability), and component analysis. A basic guide to interpretation is also provided. An equivalent quick entry into transmission modelling using livestock movement data is currently in development.

Movenet is freely downloadable, open-source software (https://github.com/digivet-consortium/movenet). An accompanying interactive app is also available, which makes the package functions accessible to users who are not confident in R, or who prefer graphical user interfaces.

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Session 9

Genetics and Bioinformatics

Chair: **Olaf Berke**

S09 Landscape phylogeography — using viral gene sequences to compare and explain the heterogeneous spatial dynamics of virus epidemics

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Keywords: molecular epidemiology, continuous phylogeography, landscape phylogeography, environmental factors, RNA viruses, seraphim

Abstract

Recent advances in genomics, mathematical modelling and computational biology have enabled evolutionary approaches to become a key component in studying of viral infectious diseases. The use of evolutionary approaches offers many advantages compared to traditional epidemiological methods; for example, they can reconstruct the demographic history of an entire epidemic even when surveillance data are sparse or non-existent, they require only a small number of sampled pathogens, and they can detect linkages among infections in time and space that may not be evident otherwise. Even over short time scales, viruses can accumulate significant diversity, resulting a genomic imprint of the ecological impact on transmission dynamics. By statistically analyzing the genetic differences among viruses sampled from a population, we can reveal the underlying processes that govern viral transmission. Yet, a major challenge in this field is to develop methodologies to formally test the effect of environmental factors on pathogen transmission and evolution. Over the last years, we have addressed this challenge by developing tools in landscape phylogeography, a field at the interface between spatial and molecular epidemiology and that aims to relate phylogenetic informed movements to environmental factors. Specifically, we here present new methods that we developed and applied to investigate the impact of environmental factors on the dispersal velocity, dispersal direction, or dispersal frequency of viral lineages. In particular, we have applied those new analytical approaches to investigate the external factors having impacted several epidemics of public and one health importance like, e.g., the Ebola virus outbreak in West Africa (2014-16; Dellicour *et al.* 2018), the circulation of Rabies virus in different regions and host species (Dellicour et al., 2019), and the West Nile virus invasion in North America (Dellicour et al., 2020). For instance, our analyses have demonstrated that announcements of border closures were followed by a significant but transient effect on international virus dispersal during the 2014-16 Ebola virus outbreak, and that West Nile virus lineages tended to disperse faster in areas associated with higher temperatures. With our latest developments in the field

of landscape phylogeography, we illustrate how to go beyond historical reconstructions and exploit spatially-explicit phylogeographic reconstructions to formally test epidemiological hypotheses.

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R09.1 Development of an operational tool for genomic and phenotypic surveillance of antimicrobial resistance: applications for swine pathogens in the United States

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Keywords: Antimicrobial resistance, Dashboard, Genomic surveillance, Phenotypic surveillance, Swine pathogens

Abstract

The increasing emergence of resistant bacteria to the existing antimicrobials and the lack of developing novel antimicrobials have created a global health emergency. Intelligent real-time surveillance is the key prerequisite to informed policy decisions and evidence-based interventions to tackle antimicrobial resistance (AMR) and enhance antimicrobial stewardship. Here, we present new capabilities of the Disease BioPortal platform (https://bioportal.ucdavis.edu), which allows users to generate interactive dashboards to facilitate the visualization and analysis of AMR patterns in swine farms in the United States in near real time. Production systems, veterinary clinics, or diagnostic laboratories can easily integrate their AMR phenotypic (e.g., Minimum Inhibitory Concentration -MIC- values) and/or genotypic (e.g., whole genome sequences) confidential data using APIs or manual uploads. Genomic surveillance is a valued addition to phenotypic surveillance of AMR and provides insights into the resistance mechanisms, AMR evolution, and population dynamics at different spatial and temporal scales. The putative genetic determinants of resistance (e.g., AMR genes) are identified using CARD v3.1.0 (including only perfect and strict paradigms) and ResFinder (90% minimum identity and length coverage) databases (Alcock et al., 2020; Florensa et al., 2022). Heatmaps and donut charts are generated to visualize the distribution of AMR genes at various production scales (individual animal, farm, production system, etc.). AMR prevalence is observed dynamically at multiple spatial and temporal scales using space-time-visualizations and phylogeographic methods (i.e., Nextstrain). Further, various spatial and temporal analyses (e.g., time-series analysis, Scan statistics) are incorporated into the Disease BioPortal dashboard to identify important resistance trends. We illustrate the value of this tool for several use cases using de-identify datasets for *Streptococcus suis* in the United States to identify resistance trends and improve antimicrobial stewardship. Ultimately, this tool

better informs us on how we might approach prevention and control of resistance.

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R09.2 Geographical isolation in an interconnected world: application of phylodynamic and phylogeographic methods for the investigation of Porcine circovirus type 4 history

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Keywords: epidemiology, evolution, origin, PCV-4, phylodynamics, phylogeography

Abstract

Over the years four porcine circoviruses (PCVs) species have been discovered, which apparently share common epidemiological trajectories. In particular, PCV-2 and PCV-3 species, better known for their pathogenicity and economic impact, despite being reported as emerging new viruses, were thereafter proved to have been circulating undetected over several decades in domestic pigs.

The detection of PCV-4 in China in 2019 (Zhang et al., 2019) and retrospectively in samples from 2012, demonstrates a circulation for at least 10 years in Chinese domestic pigs, reminding PCV-2 and -3 scenarios. However, the current restricted distribution in China, South Korea, Malaysia and Thailand, and the lack of detection in Italy, Spain and Colombia (Franzo et al., 2020, Vargas-Bermudez et al., 2022), apparently suggest a recent origin, thus conflicting with what demonstrated for the ubiquitous PCVs-2 and -3.

The present study aims to investigate PCV-4 apparent geographical confinement and address questions about its actual epidemiology and emergence.

Phylogenetic, phylodynamic, and phylogeographic analyses were performed on PCV-4 sequences with adequate metadata available in GenBank to reconstruct its history, migration paths and evolution.

A total of 97 sequences were included in the data set: 88 were detected in 10 different Chinese provinces, 4 in South Korea, 3 in Thailand, and 2 in Malaysia. The achieved alignment and phylogenetic trees showed a certain genetic stability between strains over time, and congruent results were obtained for different genomic regions. Additionally, the evolutionary rate is of the same order of magnitude of PCV-3. The analysis of viral population dynamics, similarly to other PCVs, suggests an ancient origin followed by persistent but undetected circulation in the swine population. Based on these

results and others PCVs history/epidemiology a wider distribution than the one currently shown in literature was expected. On the contrary the geographical clustering, and the low number of clearly supported migration rates among Chinese provinces respectively showed by phylogenetic and phylogeographic analysis are compatible with the geographical isolation suggested by the detection of PCV-4 in Asia only and its absence in pivotal swine farming countries such as Italy and Spain. The contradiction with the hypothesis of an ancient viral origin is challenging to be explained, although the currently scarce number of available sequences, the limited number of studies performed outside Asia and the short timespan considered may be also involved.

This study provides an example of the application of genetic methods as instrumental tools to improve the understanding of pathogens' epidemiology, geographical relations, and emergence. In presence of larger-scale geographical data, genetic and spatial methods may act in synergy to better investigate the presence of spatial patterns, and to monitor, predict and thus better control the spreading of animal infectious diseases.

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R09.3 Unravelling the epidemiology of Mycobacterium bovis in North Cameroon using genomic, environmental and demographic data

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Keywords: bovine tuberculosis, GIS, One Health, Phylogeography, whole genome sequences, Zoonotic pathogens

Abstract

In recent years, the increased availability, efficiency and reliability of genomic reading techniques, such as whole-genome sequencing (WGS), has significantly increased the amount of information we can use to study infectious diseases. Consequently, it has improved the precision of epidemiological inferences for pathogens like *M. bovis*. As a consequence, novel methods have been developed to combine spatial explicit data and pathogen's genome to understand the impact of the landscape on epidemic spread in space and time (Dellicour et al., 2016).

In this study, we used WGS to gain insights into the epidemiology of *M. bovis* in Cameroon, a developing country where the pathogen has been reported for decades. Ninety-one high-quality sequences were obtained from tissue samples collected in four abattoirs located in the North of the country (Egbe et al., 2017). Sixty-four of these had complete metadata including, information on the geolocation of the herd the cattle were coming from. We tested the maximum credibility trees generated with the software Beast 1.10.4 against several spatial explicit factors: land cover, road network, population and cattle density, altitude.

Our findings suggested that *M. bovis* in Cameroon is slowly expanding its epidemiological range over time, therefore endemic stability is unlikely, as it was previously hinted by other studies in the literature (Awah-Ndukum et al., 2012). The most recent common ancestor was dated in the 1950s, and after an initial slow spread, a sudden jump in space to cover the entire study area was dated during the late 1960s. As previously reported (Egbe et al., 2017), most of the *M. bovis* genetic diversity was detected in

the Adamawa and North region. The simultaneous prevalence of *M. bovis* in co-located cattle and humans highlights the risk of zoonotic transmission.

The spatial analysis suggested that percentage of land covered by forest and the altitude might have played a role in facilitating *M. bovis* spread in the area. While the former could be a proxy for wild species presence, the latter result could be due caused by the presence of agropastoral communities living in these regions uplands. Thanks to such rearing practices, cattle from different herds mingle together, increasing the number of potential infectious contacts, thus facilitating spread.

In conclusion, we showed how using genomic tools combined with geographical information can improve our understanding of livestock diseases ecology and spread patterns. This is of paramount importance in contexts where data about animal populations and their movements are scarce, which could hamper the usefulness of tools like epidemiological mechanistic models. Adopting genomic tools as part of surveillance would vastly improve our understanding of disease transmission processes and, therefore, control strategies.

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R09.4 West Nile Virus in Europe: a return ticket to Africa

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Keywords: West Nile virus, Infectious diseases, phylogeny, phylogeography, evolution, epidemiology, Africa, Europe, Italy

Abstract

West Nile virus (WNV) is an arthropod-borne virus belonging to the *Flavivirus* genus and *Flaviviridae* family, which is currently considered a serious public health problem worldwide. The virus, first identified in Africa in 1937, is characterized by at least eight different lineages. WNV lineages 1 (L1) and 2 (L2), often associated with cases of encephalitis in humans and horses, are by far those most widespread in Europe and the Mediterranean basin. These two lineages are endemic in many Italian regions.

In this study, we have tried to uncover the spatial and temporal viral dynamics of the two lineages between Africa and Europe. By integrating epidemiological studies with molecular, phylogenetic, and phylogeographic analyses, we showed that there is a strong viral connection between the two continents, supported by birds crossing international boundaries while migrating through the African-Eurasian flyways. According to the data analysis, WNV L1 clade 1A seems to originate in the 1900s between North and West Africa. It moved forward and backward through Senegal, Morocco, and Western-Mediterranean European countries. WNV L2 strains now circulating in Europe and Africa likely originated between the 18th and the 19th century in South Africa from where it was introduced into Hungary in 2004 and then spread throughout Europe. Our study also gave an insight of the dynamics of the viral circulation in Italy, demonstrating the endemic presence of WNV L1 and L2 in part of Italy supported by resident wild birds and vector competent mosquitoes mainly belonging to the *Culex* genus, and the existence of a continuous transmission of the two strains between Western-Mediterranean countries, supported by short distance migratory birds. It also showed the presence of genetically stable WNV L2 strains in Italy with continuous circulation throughout the time, and characteristic silent periods observed for WNV L1 in the country, with unnoticed circulation lasting

sometimes for more than 10 years thanks to overwintering mechanisms supported by bird-to bird, rodent-to bird, or mosquito-to bird transmission routes.

In conclusion, from this study it clearly appears that WNV L1 and L2 have had different eco-epidemiological and genetic evolutionary features with L1 exhibiting complex behaviour and genomic heterogeneity, while L2 being characterised by homogeneity and less inclination to spread. We stress the crucial importance of an integrated surveillance system between Africa and Europe to monitor both the introductions and circulation of avian emerging zoonotic diseases in the two continents.

R09.5 Antimicrobial resistance in food animals: priority drugs maps to guide global surveillance

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Keywords: antimicrobial resistance, disease mapping, one health, spatial epidemiology, surveillance

Abstract

Antimicrobials are life-saving drugs used to treat infections. However, the majority (73%) of antimicrobials sold globally are used in animals raised for food (Van Boeckel et al., 2017) . Antimicrobial resistance (AMR) in food animals is a growing threat to animal health and potentially to human health. In resource-limited settings, allocating resources to address AMR, as for any disease of global importance, can be guided with maps. However, in low- and middle-income countries (LMICs), attempts at documenting trends in AMR so far relied on summary metrics of resistance across antimicrobial classes. This is a major limitation for potentially taking targeted actions on individual antimicrobial classes.

Here, we mapped AMR prevalence of 7 antimicrobials in E. coli and Salmonella across LMICs, using a geospatial model with data from 1,169 point prevalence surveys. We also developed a novel approach, named co-resistance contextual models, to predict the antimicrobial with the highest probability of its resistance exceeding 50% in the future (2.8 to 6.9 years) at each location on the map. This approach exploited correlations of resistance between antimicrobials to predict the resistance profiles that will most likely occur in the future, producing a map of priority antimicrobials for AMR surveillance.

Hotspots of AMR were predicted in southern and eastern China, Iran, Turkey, northeastern India, southern Brazil, and southern Chile. The highest resistance prevalence was for tetracycline (55%, average across LMICs) and the lowest was for ciprofloxacin (25%). In Africa and South America, 87% locations were associated with penicillins or tetracyclines crossing 50% resistance in the future. In contrast, in Asia, 71% locations were associated with penicillins or sulphonamides, because resistance to tetracyclines has already exceeded 50% in 84% of locations across Asia. Our maps could help to adapt policies to local epidemiological context across LMICs, and provide policy makers with targets –geographic locations and priority drug classes- where scaling up surveillance could carry the greatest benefits.

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Session 10

Spatio-temporal surveillance and modelling

Chair: **Mark Stevenson**

R10.1 Disentangling the role of wild bird species in Avian Influenza transmission to poultry

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Keywords: BART, bridge species, HPAI, ornithocoenosis, wild birds, wild-domestic interface

Abstract

Migratory waterfowl are widely acknowledged as the primary source of avian influenza (AI) virus introduction into poultry. However, recent studies have challenged the assumption of direct interactions between waterfowl and poultry, revealing a more complex interface (Shriner&Root, 2020; Verhagen et al., 2021). While waterfowl are crucial for maintaining and amplifying AI viruses in nature, other species may function as the actual bridges for introducing AI into the poultry sector (Caron et al., 2015). However, the nature of this wild-domestic interface remains elusive, leaving gaps in understanding which species play the bridging role.

An ornithocoenosis study was conducted in northern Italy between January and December 2019, in the area with the highest occurrence of Highly Pathogenic AI (HPAI) outbreaks during the 2017-2018 H5N8 epidemic. The study focused on ten poultry farms: five fattening turkey, four laying hen, and one duck premises. Three census transects were established within one kilometre from each farm, and visited biweekly, while two camera-traps per holding were installed adjacent to the sheds. A Bayesian Adaptive Regression Trees (BART) approach was adopted to define a series of Species Distribution Models (SDM) to predict the favourability of species detected by camera-trapping. These results were then input as geographical raster layers into further BART-SDMs to produce risk maps for AI and determine which wild bird species significantly contributed to the occurrence of the 2017-2018 H5N8 HPAI outbreaks in northern Italy.

The transect survey revealed a marked diversity despite the environmental and climatic homogeneity, with approximately 150 species detected. However, only 41 of these were also observed by camera-trapping in proximity to the farms, suggesting a fragmented community. The likelihood of observing an AI outbreak resulted positively associated with the presence of *Ardea alba*, *Bubulcus ibis*, *Columba livia* and *Phasianus colchicus*, and negatively with the *Falco peregrinus*, *Phoenicurus phoenicurus* and *Picus*

viridis. In particular, the contribution of pheasants to the probability of observing AI outbreaks was likely due to the release of birds for repopulation or hunting, which might create bridges between wild and domestic populations. The tendency of released game birds to seek out anthropized areas, such as poultry farms, in search of food, further corroborates the hypothesis.

The study shed light on the intricate interface between wild birds and poultry in the dynamics of AI spread. Our results stressed the need to account for the role of both aquatic and non-aquatic bird species in the introduction and/or inter-farm spread of AIVs, emphasising the potential risks associated with wetland proximity and the impact of human activities, such as releasing game birds, on the risk of disease spread (Shriner&Root, 2020). These findings may be used to inform targeted surveillance activities and prevention strategies to mitigate the AI threat in domestic birds.

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R10.2 Estimating the coverage of slaughterhouse surveillance for bovine tubercolosis

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Keywords: coverage, surveillance, bovine tuberculosis, network analysis, slaughterhouse

Abstract

Slaughterhouse surveillance plays a key role in disease detection, especially for zoonotic diseases such as Bovine Tuberculosis (bTB). Premises are under slaughterhouse surveillance if a sufficient number of their animals reach slaughterhouses in order to detect an outbreak. Since the probability of detecting an outbreak is dependent on the number of animals sent to slaughterhouses, total number of animals in the farm, and the prevalence of disease, premises that send animals directly to abattoirs might not be under surveillance, while premises that do not send animals directly to abattoirs might be (through indirect contacts). Therefore, social network analysis is essential to estimate the coverage of one of the main strategies for the surveillance of bTB and could help identify the premises and/or regions that are within the reach of this strategy and those that are not. This study aimed to evaluate the coverage of the Bovine Tuberculosis slaughterhouse surveillance in a state of Brazil. We used a two-year animal movement database, hypergeometric distribution, social network analysis, and stochastic simulations to estimate the probability that at least one infected animal of a premises would reach a slaughterhouse. We considered that premises are under slaughterhouse surveillance if this probability is at least 80%. Results showed that 45% of premises and 86.5% of cattle were covered by the slaughterhouse surveillance in the state. These results can be used to identify regions and premises that are not within the reach of this strategy, prompting stakeholders to develop other surveillance components to fill the gap. Results could also be integrated with the probability of detecting bTB lesions in slaughterhouses to estimate the sensitivity of a slaughterhouse surveillance system. This approach can also be adapted to estimate the coverage of slaughterhouse surveillance for other diseases.

R10.3 Modelling transmission of Avian Influenza in wild birds using a spatiotemporal cellular automata model

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Keywords: Avian Influenza, risk mapping, spatiotemporal, mechanistic, disease spread model

Abstract

Within the last 10 years, Denmark has faced an increasing number of Avian Influenza cases in wild birds and outbreaks on poultry farms, emphasizing the need to update national avian influenza prevention and control strategies. Highly Pathogenic Avian Influenza (HPAI) is transmitted over long distances by migratory wild birds, and wild birds can further spread the disease locally via their aggregation in suitable areas. With a coastline of more than 8,000 km, Denmark is an important stopover for migratory birds. Bird species belonging to the order *Anseriformes* have been the most commonly reported Avian Influenza virus positive species in recent years in Denmark.

This study aims to improve the understanding of HPAI transmission in migratory wild birds by developing a stochastic spatiotemporal epidemiological model. The model will predict HPAI prevalence in selected wild bird species over one year simulated period and identify hotspots and high-risk periods of transmission.

To date we have rasterized Denmark into 10 by 10 km grid cells. We have then combined 5 years of national and citizen science weekly count data on bird populations for five common bird species (two swan species, two geese species and one duck species) in each grid cell and extrapolated to grid cells with unknown counts using geographical and temporal variables and generalized linear mixed model regression. Following this, we built a mechanistic simulation model including three weekly steps; temporal migration of birds, a susceptible-infectious-removed (SIR) model with environmental transmission, and disease transmission due to bird dispersal between grid cells. The model will be parameterized using published data, expert opinions and literature estimates. Calibration and sensitivity analysis of main parameters, such as the infectious period and virus shedding rate of different bird

species, will be implemented once the model is complete.

Preliminary results were obtained using model simulations for one iteration. The model outputs identified high-prevalence areas and periods, and the changes in simulated prevalence for the study period was compared to reported HPAI incidence in passively surveyed wild birds. We intend to use the spatio-temporal model to evaluate the risk of HPAI virus transmission and help Danish farmers and veterinary authorities to allocate resources to prevent potential outbreaks.

R10.4 Spatial distribution of poultry farms using point pattern modelling: a methodology to address disease transmission risks

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Keywords: disease spread modelling, poultry intensification, spatial clustering, point processes, geospatial model

Abstract

The distribution of farm locations and sizes is paramount to characterize disease spread patterns. With some regions undergoing rapid intensification of livestock production, resulting in increased clustering of farms in peri-urban areas, measuring changes in the spatial distribution of farms is crucial to design effective interventions. However, those data are not available in many countries, their generation being resource consuming.

Here, we develop a farm distribution model (FDM), which allows predicting locations and sizes of poultry farms in countries with scarce data. It combines (i) a Log-Gaussian Cox process model (LGCP) simulating the farm distribution as a spatial Poisson point process with logarithm varying intensity, conserving the level of clustering of spatial points patterns, and (ii) a random forest (RF) model simulating farm sizes (i.e. the number of animals per farm). Spatial predictors were used to calibrate the FDM on intensive broiler and layer farm distributions in Bangladesh, Gujarat (Indian province) and Thailand.

The LGCP and RF models yielded realistic farm distributions in terms of spatial clustering, farm locations and sizes, while providing insights on spatial analysis of the poultry production systems and spatial clustering drivers. Finally, we illustrate the relevance of modelling realistic farm distributions in the context of epidemic spread by simulating pathogen transmission on an array of spatial distributions of farms. We found that farm distributions generated from the FDM yielded spreading patterns consistent with simulations using observed data, while random point patterns underestimated vulnerability to epidemics. Indeed, spatial clustering increases vulnerability to epidemics, highlighting the relevance of

spatial clustering and farm sizes to study epidemic spread.

As the FDM maintains a realistic distribution of farms and their size, its use to inform mathematical models of disease transmission is very relevant for regions where these data are not available.

R10.5 Assessing the risk of arbovirus outbreaks in non-endemic regions

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Keywords: early-warning modelling, spatial epidemiology, Vector-borne diseases, Spatiotemporal risk assessment model

Abstract

The threat posed by mosquito-borne viruses (arboviruses) causing Dengue (DENV), Zika (ZIKV), Chikungunya (CHIKV), Yellow Fever (YFV), among other widespread viral infections, represent a global public health concern. In European countries, like Spain, Italy, or France, factors such as global warming, increased human mobility (locally and globally across different latitudes where such diseases are endemic), the presence and spreading of invasive mosquitoes (such as *Aedes albopictus*), and the existence of confirmed non-autochthonous viremic cases have the potential to cause significant disease outbreaks in disease free regions, as it was reported in France where autochthonous Dengue cases have been recently identified.

Here, we introduce a quantitative method for risk assessment of outbreaks of diseases susceptible to transmission by *Aedes mosquitoes* in a non-endemic area. Our proposed method is built on the basis of a mathematical model we developed: a modified version of the standard SIRUV compartmental model (that couples the human and mosquito dynamics), adapted to meet the specific features of non-endemic areas. By using only the latest entomological data (related to the vector abundance), epidemiological data (confirmed imported and autochthonous cases) and population statistics (population density census), the risk can be estimated and different epidemiological scenarios can be evaluated. Finally, a GIS dashboard has been implemented (using data from the Basque Country, Spain), envisioned as a prototype tool to inform and guide the decision-making by the public health authorities.

R10.6 Surveillance data and early warning models of highly pathogenic avian influenza in East Asia, 2020-2022

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Keywords: Highly pathogenic avian influenza, early-warning modelling, endemic-epidemic modelling, disease transmission, wild and domestic birds, East Asia

Abstract

Avian influenza poses a problem for animal welfare and potentially also for public health. In recent years, the numbers of disease outbreaks and cases of highly pathogenic avian influenza (HPAI) virus infection throughout the world has increased, resulting in many poultry flocks being culled. Preventive actions require timely knowledge of high-risk infection periods. Thus, there is an increasing need for early warning systems.

We utilized readily available data from the World Organization for Animal Health and the Food and Agriculture Organization of the United Nations on HPAI H5 detections in wild and domestic birds together with a time-series modelling framework (Meyer et al., 2014) to predict HPAI detections within East Asia. This framework decomposes time series data into endemic and epidemic components, and we have previously used it successfully to model HPAI in Europe. We tested multiple model formulations, including seasonality, long-distance versus short-distance transmission, and covariates (coastline length and area of wetlands).

Due to data constraints, we were only able to fit a model for Japan and South Korea for the years 2020-2022, as these two countries consistently reported outbreaks during the study period. We divided each country into regions based on geography and local administrative areas. The best performing model included seasonality in both the endemic and epidemic components, and covariates as offsets in the endemic component. Due to data constraints, we did not differentiate between H5 subtypes. The model was fitted to all HPAI records with good overall agreement. Interestingly, we found a clear cyclic seasonal component in the predicted occurrence of HPAI, whereas our previous model for Europe for the same time period predicted occurrence during the summer period as well, i.e., less cyclic seasonality. The model predicted that most reported detections (79.3%) were epidemic in nature and were dominated by within-region transmission (55.5%). Of the reported detections, 20.7% was

described as endemic transmission in the model, which could represent transmission from migratory birds coming from regions and countries not included in our study and/or endemic H5 HPAI virus circulating within the included regions.

The modelling framework used in this study produced a model that was able to predict H5 HPAI detections in Japan and South Korea on a weekly basis and could be utilized by decision makers to predict periods with higher risk of HPAI within these countries. If possible, future modelling studies should obtain more data from other Asian countries to create a combined model for Asia/Oceania. Given enough surveillance data, future studies could also focus on modelling the specific HPAI genotypes and clades; this would potentially improve predictive ability and timeliness, as well as clarify endemic and epidemic components of HPAI occurrence.

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R10.7 A raster-based compartmental model combining the host's density and movements, driven by vector suitability

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Keywords: Compartmental model, VBD, Suitability maps, SNA, shortest path

Abstract

Vector-borne diseases cause significant veterinary and public health burdens as they widely re-emerge in affected areas or emerge in new healthy areas. Understanding, predicting, and mitigating the spread of vector-borne disease in diverse hosts and geographic areas are modeling objectives still to be explored. Many scientific studies are focused on developing predictive models for vector distribution and suitability to identify high-risk transmission areas and plan disease prevention and control strategies (Nguyen et. al., 2023; Saucedo & Tien, 2022; Leta et al., 2019).

Vector distribution is driven by climatic, geographic, and environmental factors (such as temperature, precipitation, and altitude), and understanding its presence and abundance is fundamental to planning effective prevention and control strategies. Additionally, the movements of infected susceptible hosts are crucial, as they let the disease reach farthest, unaffected areas.

In this study, we combine information on vector suitability and host movement data in a raster-based compartmental epidemiological model to predict disease occurrences and critical management areas. The proposed approach incorporates network analysis features to model the health status of a location (pixel), considering both host movements and proximity-based contagion due to vector-suitable conditions. The model focuses on the "suitable paths", the shortest paths weighted on the vector's suitability, linking sources of infection to susceptible hosts within an area.

We used a case study to show the application of this theoretical model and demonstrate the practical utility of this approach in informing mitigation strategies: the Bluetongue Virus serotype 4 (BTV4) epidemic, that occurred in the Sardinia region in 2017.

This research offers valuable insights into the dynamic interplay between network analysis, vector suitability, host density, and host movements, enhancing our ability to predict and manage vector-

borne diseases effectively. These findings are essential for public health planning and disease control strategies in a changing global environment.

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Poster Session

Geospatial Data to Support Veterinary Avian Flu Surveillance in the Autonomous Province of Bolzano (Italy)

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Keywords: Avian Influenza, Fowl, GIS, H5N1, Surveillance, Veterinary Public Health

Abstract

The domestic fowl population in the Province of Bolzano, 520,000 inhabitants, northern Italy (Alps), currently amounts to approx. 156,700 heads (domestic poultry, turkeys and ducks, i.e. *Gallus gallus*, *Meleagris gallopavo, Anas platyrhynchos domesticus*) at a total 207 farms, very few of which hold over 5000 birds. Currently, the province is not a high-risk area for Avian Influenza (EFSA et al. 2023). Although major migratory routes cross the province, there are few wetlands serving as wintering sites for wild bird species. However, there are small rural poultry farms for private consumption throughout the province and, albeit at low density, several commercial farms containing laying hens, broilers, turkeys and species of lesser economic importance. On average, these farms, also due to consumer attention to animal welfare, offer outdoor access. Free-ranging birds leaving the coop increase the risk of Avian Influenza infection through contact with wild fowl. In addition, the need for commercial farms to source poultry flocks exposes them to diseases introduced from other regions or European countries with higher infection risks.

Given the need to implement the government's annual Avian Influenza surveillance plan and the decrees concerning biosecurity at poultry farms, it is essential to monitor Veterinary Public Health interventions and to practise outbreak preparedness.

Until present, no Avian Influenza cases have been reported in the province; however, cases are being reported in all neighbouring provinces (IZS 2023, July 12). Between 24/02 and 02/03/2023, three cases of H5N1 in Black-headed Gulls (*Chroicocephalus ridibundus*) only 50 km from the provincial borders further substantiated the risk of an Avian Influenza introduction (IZS 2023, July 13).

The project aimed to provide local veterinary services with a tool for more effective, close monitoring of

disease emergence.

GIS data of all registered poultry farms were collected with details at municipality level, adding geospatial data of sites with the largest waterfowl concentrations and linking them to information about each farm (bred species, number of heads) using ArcGIS Desktop (Version 10.5). The farm coordinates were collected alphanumerically and imported to the map as a point layer. Lakes and biotopes were georeferenced using orthophotos from 2020. The river line layer was delimited by an initial and an end point, which were indicated. The coordinate system used is ETRS89 UTM zone 32N (EPSG: 25832).

Five different geographic distribution maps were prepared for the entire territory and distributed to the veterinary services of the four health districts. An information seminar was organized to inform both veterinarians and poultry breeders. At present, browsable online versions are being explored.

With respect to emergency preparedness, response and management regarding Avian Influenza, geographic information systems should be considered an important additional tool for the Veterinary Public Health sector and routinely used in One Health strategies.

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Time trends and forecasting of antimicrobial use and minimum inhibitory concentration for Salmonella spp. in chicken production

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Keywords: Antimicrobial resistance, Minimum inhibitory concentration, Poultry, Salmonella spp.

Abstract

Antimicrobial resistance (AMR) is a major concern for "One Health". Any use of antimicrobials can potentially contribute to the spread of multidrug-resistant bacteria. Antimicrobial use (AMU) in food animals is projected to increase over time. Thus, it is important to monitor AMU and changes in the efficacy of antimicrobials. The objectives of this study were to determine (i) AMU over time in chicken production in Canada, (ii) to examine the advantages of using minimum inhibitory concentration (MIC) data to characterize temporal trends in AMR and (iii) to forecast the AMR to commonly used antimicrobials in *Salmonella* spp. from chicken production.

Farm-level data, including AMU and other farm management practices, were collected by the Canadian Integrated Program for Antimicrobial Resistance (CIPARS). Using CLSI guidelines, *Salmonella* spp. were isolated and susceptibility tested using broth microdilution. Statistical analysis was performed to determine the effect of AMU and management factors on MIC over time. Important risk factors included in the generalized linear model were selected by LASSO regression. The ability to predict subtle changes on MIC over time was compared using two different models (i) logistic and (ii) multinomial regression. The best model fit was determined by Akaike information criteria. Forecasting for the effect of AMU on AMR over time in *Salmonella* spp. was performed using ARIMA model.

Overall, AMU in chickens has decreased over the last decade. However, the use of some antimicrobials has fluctuated over time. The effect of time was most evident on the use of streptomycin, sulfamethoxazole, and tetracycline. In terms of AMR, there was decrease in the MIC's of streptomycin and sulfamethoxazole and an increase in tetracycline over time. Both logistic and multinomial regression models showed similar results on the effect of AMU and time on MIC, however, the multinomial model was more sensitive to subtle MIC time trends. We found that the use of lincosamides-aminocyclitols or third generation cephalosporins contributed to tetracycline resistance. Forecasting model results

suggest that if antimicrobials continue to be used at the current rate tetracycline resistance will continue to increase in *Salmonella* spp. isolated from Canadian chicken farms in the next 4 years.

Reduction in AMU in chicken production mitigates AMR in *Salmonella* spp., an important pathogen for human and animal health. Analyzing the AMR surveillance data by multinomial model is more accurate than logistic regression in detecting early subtle changes in MIC's. Continued monitoring of AMU and AMR is necessary to evaluate the effect of measures to reduce AMU on food production and safety and to preserve the efficacy of antimicrobials to treat infections.

What can we learn from phylogeographic analyses of SARS-CoV-2?

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Keywords: discrete phylogeography, continuous phylogeography, SARS-CoV-2, COVID-19

Abstract

In the field of molecular epidemiology, genetic analyses of pathogens are used to complement traditional epidemiological methods in various ways. For instance, genetic analyses offer the possibility to infer linkages between infections that are not evident without analysing viral genomes. In particular, the development of phylogeographic methods has enabled to reconstruct dispersal history of epidemics in a discretised or on a continuous space, using only a relatively limited number of viral sequences sampled from known locations and times. Since the beginning of the COVID-19 pandemic, phylogeographic analyses have been conducted to reconstruct the dispersal history of SARS-CoV-2 lineages at global and more local spatial scales. I here illustrate the interest of phylogeographic inference by presenting analytical approaches that we implemented and applied to address some specific questions related to the epidemiology of SARS-CoV-2: the relative importance of introduction events to establish local transmission chains (e.g. at a country level), the impact of international travels during European summer holidays 2020 on the resurgence of COVID-19 in Europe, the invasion dynamic of the Alpha variant that emerged in England, and the variant-specific dispersal dynamics of SARS-CoV-2 in New York City. In these recent studies, we specifically aimed to go beyond historical reconstructions and further exploit phylogeographic reconstructions to formally test epidemiological hypotheses.

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Beyond mapping hotspots: using geospatial models to guide surveillance against antimicrobial resistance in animals.

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Keywords: Antimicrobial Resistance, Surveillance, China, Spatial Uncertainty, Spatial Allocation, Species Distribution Models

Abstract

The rise of antimicrobial resistance (AMR) in food animals is a growing threat for animal health, and potentially for human health. China, as the world's largest user of veterinary antimicrobials could play a pivotal role in leading the international response to AMR, and maps of AMR could help coordinate this response (Zhao et al., 2021). Here, we used geospatial models to identify regions where future surveillance effort could be targeted in priority.

We extracted resistance rates from 446 point-prevalence surveys on *Escherichia coli*, *Salmonella*, *Campylobacter*, and *Staphylococcus aureus*. We mapped the proportion of drugs tested with resistance rates higher than 50%. The uncertainty map associated with these predictions was used to identify locations where surveillance efforts could be intensified in the future. We calculated an index of 'necessity for additional surveillance' - the product between uncertainty in AMR level and animal densities- to identify locations where 50 surveys could be conducted such as to minimize uncertainty on future AMR levels in China. We computed both exact and approximate solution for the spatially optimal allocation of surveys to improve AMR surveillance in China.

In China, AMR levels were the highest in the east and lowest in the southwest. Regions that would benefit the most from increased surveillance were the southwest (21/50 surveys) and northeast (11/50 surveys). Using geographically targeted surveillance could reduce uncertainty of AMR level by 104% compared with an equal surveillance effort across administrative divisions. Our findings help outline priorities for AMR surveillance in China, and identify where future surveys could best improve the accuracy of AMR maps.

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Beyond contact rate for assessing pathogen transmission: implementing a movement-driven model in exposure risk inference

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Keywords: contact networks, epidemiological model, shared infections, spatial disease dynamics, telemetry, wildlife-livestock interface

Abstract

Interactions between individuals from different species are highly relevant in the transmission of pathogens in multi-host systems. In this regard, we can distinguish between direct interactions, which involve contact, and indirect interactions, mediated by the environment or vectors. Various technologies have been employed to study animal interactions, such as proximity loggers, GPS tracking devices and/or camera traps. However, the subsequent analysis of these data to estimate risk transmission is often reduced to interaction rates and the probability of transmission given interaction. Thereby, a continuous spatio-temporal process is simplified and discretized, overlooking the influence of interaction characteristics and the pathogen's relationship with the host and the environment.

In this study, we applied a novel movement-based model that considers the interaction duration -by means of the number of GPS locations where the interaction occurs and the time interval between them-, the temporal window between consecutive locations of different individuals, a continuous pathogen decay in the environment until its survival period in the environment is fulfilled, and the excretion and acquisition rates of each host species. Therefore, each interaction has unique characteristics, and consequently, a unique transmission risk. Using animal tuberculosis (*Mycobacterium tuberculosis* complex) as disease example, we analyzed GPS data from 54 collared

wild (15 red deer [*Cervus elaphus*], 7 fallow deer [*Dama dama*] and 12 wild boar [*Sus scrofa*]) and domestic animals (8 pig and 12 cattle) in two management systems in Spain where this disease is prevalent: a national park and an area with extensive free-ranging pig and cattle farms. We considered an interaction to occur within the GPS error margin (12 or 26 meters, depending on the GPS device) and a pathogen survival period in the environment of 4 to 12 days, depending on the area and season. We compared the results with those obtained for the same data in previous studies based just on the quantification of interaction rates. As a result, wildlife species identified as most involved in pathogen transmission to livestock differed between the two approaches, particularly in the national park. Among the three considered wild species, fallow deer had the highest interaction rate with livestock according to the traditional approach, but with the new approach, wild boar took the lead as posing the highest transmission risk to livestock. These results indicate that failing in considering the specific conditions of each interaction can imply a misidentification of key species in pathogen transmission. In addition, we found that wildlife poses a greater risk to livestock than livestock to wildlife in both studied systems, emphasizing that disease control measures should be implemented in wild populations in addition to those already established for livestock.

GrapeTree integration with spatio-temporal data visualization: a holistic understanding of diseases and the transmission pathways

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Keywords: Geographic Information System (GIS), Genomic sequencing technology, GrapeTree, Infectious diseases, Transmission pathways, Spatial-temporal analysis

Abstract

Understanding transmission pathways of infectious diseases plays a crucial role in enabling effective surveillance and outbreak response. Recent advancements in genomic sequencing technology have led to an enormous data volume that can provide valuable insights into the spread of infectious diseases. GrapeTree (Zhou et al., 2018) is a fully interactive tree visualization program for investigating phylogenetic trees plus associated metadata that facilitates the analyses of large numbers of allelic profiles and supports interactive visualizations of large trees, allowing the manipulation of both tree layout and metadata. However, the current capabilities are limited in terms of conducting spatio-temporal analyses due to the lack of the integrated Geographic Information System (GIS) as well as a data visualization system across time. This study aims to address this limitation by developing a web application that integrates GrapeTree with GIS and a temporal visualization system, thereby enhancing its potential.

We leveraged the potential of GrapeTree enabling spatio-temporal analysis of disease transmission. The web application allows users to upload genomic data and metadata, including spatial and temporal data, visualized in the form of a minimum spanning tree. The tree can be manipulated to highlight different aspects, such as transmission pathways or genomic diversity. Effective management of geographic coordinates and temporal data of each sample allows to display them reflecting the selection in the tree on the map and vice versa, and reproducing a timelapse visualization both in the map and in the tree.

The developed web application offers an intuitive and user-friendly interface for the visualization and comprehension of infectious disease transmission pathways. Integrating GrapeTree with GIS and temporal data visualization functionalities, enables the joint analysis of genomic, spatial and temporal data, yielding a more holistic understanding of disease transmission. In particular, timelapse

functionalities allow us to visualize and highlight the spread of an outbreak.

The integration of GrapeTree with GIS in this web application constitutes a valuable tool for the surveillance and operational early warning systems of infectious diseases, offering insights into potential outbreak sources and transmission pathways. The application is a fundamental integration in GenPat (https://genpat.izs.it), and in Cohesive Information System (Di Pasquale et al., 2022) (https://cohesive.izs.it) as an interactive dashboard implementing data results from bioinformatic analyses and currently it is used for displaying analyses carried out through Reportree (Mixão et al., 2023). The tool is fully Open Source and available at https://github.com/genpat-it/grapetree-gis. It is also feasible to utilize it directly from the browser without requiring any installation.

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Multicriteria geospatial analysis of the risk of avian influenza in Cuba

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Keywords: Avian Influenza, Spatial-temporal analysis, risk factors, surveillance

Abstract

Influenza A viruses, especially because of their capacity for genetic reassortment and mutagenesis as RNA viruses, and the possibility of cross-species transmission, are considered among the most challenging viruses that threaten human and animal health. The persistence of Highly Pathogenic Avian Influenza A (H5N1) virus and the emergence of multiple novel Avian Influenza viruses in Asia, the Americas, and Europe in 2022 raised concerns in the global community about their pandemic potential (Mosaad et al., 2023). This work aimed to identify opportunities for improvements in the active surveillance system for avian influenza established in Cuba. Risk factors associated with the occurrence of the disease (Leon et al., 2009; Steven et al., 2013; Ferrer et al., 2013) were used to perform a geospatial multi-criteria analysis with a resolution of one km^2. Additionally, the existence of contiguous areas between poultry farms (< 3 km^2) where the spread of the causal agent could be favored in case of introduction was taken into account. As a result, areas with a very high risk of occurrence were identified, either by exposure or by spread, which was sometimes favored by the contiguity between commercial poultry farms. Accuracy and management of the risk of spread are of great importance because they are often the main determinant of the magnitude of the epidemic. It is concluded that there are strategic and highly important areas where significant resources should be prioritized to strengthen biosecurity surveillance and early warning.

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The Phylodynamics of SARS-CoV-2 Delta and Omicron Variants between 2021 and 2022 in Kuwait

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Keywords: Delta Variant, Evolutionary Epidemiology, Genomic Surveillance, Omicron Variant, Phylodynamics, Phylogeography, SARS-CoV-2

Abstract

The rapid emergence and spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has resulted in unparalleled public health and economic implications worldwide. In Kuwait, the virus was first detected in February 2020, after which it rapidly spread and caused over 600 thousand infections, reinfections, and over 2500 deaths until early 2023. While the pandemic has passed its emergency stage and been declared endemic, continuous molecular surveillance for rapidly evolving pathogens like SARS-CoV-2 is critical for early intervention efforts, as the emergence of new variants is the most essential component in shaping the dynamics of the pandemic. Thus, the main objective of this study is to investigate and compare the variant-specific evolutionary epidemiology of all the Delta (B.1.617.2 and descendant lineages) and Omicron (B.1.1.529 and descendant lineages) complete genome sequences collected between 2021 and 2023 in Kuwait. Here, we reconstructed, traced, and compared the two variants' demographic, continental phylogeographic origins, and the role of sex and age in shaping their transmission history between infected patients using a discrete-trait Bayesian phylodynamic analytic pipeline. We found that the Delta variant had a higher evolutionary rate than the Omicron variant. While both variants went through periods of sequential growth and decline, likely linked to air travel, intervention measures and the development of natural immunity. Our results indicate that the delta variant and descendant lineages were frequently introduced into Kuwait from Asian countries between mid-2020 and early 2021, while those of the Omicron variant were most likely from Africa and North America between late 2021 and 2022. For Both variants, our between-patient discrete-trait analysis revealed statistically significant (Bayes Factors > 1000) asymmetric unidirectional and intense transmission routes from adult patients aged between 20 and 50 years on one side and patients aged less than 20 and older than 50 years on the other. In contrast, no significant evidence was found for the role of sex in shaping the evolutionary transmission history of both variants between males and females. Our analysis highlighted the importance of implementing risk-based genomic surveillance programs to uncover important epidemiological aspects of SARS-CoV-2 that may improve the efficiency of future decision-making related to allocating intervention resources toward relevant

emerging variants. Finally, we discuss the importance of unifying molecular surveillance efforts in humans and companion animals to improve the inferences derived from our phylodynamic models.

The development and impact of an online bovine TB system for GB - information bovine TB (ibTB)

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Keywords: M Bovis, bTB, Bio-security, Web Mapping

Abstract

www.ibTB.co.uk plots the location of all cattle herds in England and Wales affected by Bovine Tuberculosis (bTB) in the last 10 years. It was developed as a tool to inform farmers about the bTB risks in their area and help them take proportionate steps to reduce the threat to their herds.

Prior to its launch in 2015, information on bTB incidents was viewed as personal, confidential and not to be shared. There was therefore limited information available to farmers about local bTB risks and to support livestock purchasing decisions. However, in 2015 Defra and the Welsh Government (WG) in consultation with the farming industry decided that releasing bTB data was integral to their long-term strategies for the eradication of bTB and in line with their open data policy (#OpenDefra).

To enable the sharing of bTB data, both Defra and the WG needed to change legislation (their respective TB Orders) to allow the publishing of information on bTB affected herds. Once these legislative hurdles were overcome, the decision was made to create a spatial mapping system - Defra and WG had seen the benefits of various internal Geographical Information Systems (GIS) already in use. The specification for ibTB was underpinned by two key principles. a) The data published should be accurate, timely and contain no personal information and b) The system should be simple to use, and should be searchable by the farm identifier (County Parish Holding) and postcode.

In 2018 the development team held a series of meetings with farming groups across England and Wales to better understand their requirements for ibTB and in particular to assess the system's suitability as a portal for information to support Informed Responsible Trading (IRT). As well as confirming that ibTB was an appropriate tool for the display of IRT information, the survey identified distinct requirements for several subsets of users, such as farmers in high and low bTB risk areas, veterinarians and TB advisors. These requirements have been distilled into a series of staged system improvements, which were released in tranches up to October 2021.

The impacts of ibTB are difficult to gauge, because as an open access site, there is currently no way of tracking users and linking to their other bTB data to see if it is affecting their behaviours and reducing their herd's risk of contracting bTB. Usage of the system has steadily increased over time and now stands at around 800 hits/day. The link to ibTB via a major cattle trading app provides about half the traffic, which shows that the system is being used to inform farmer trading.

Clusters and risk factors of bovine tuberculosis in a Mexican state

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Keywords: Geographic Information System (GIS), spatial epidemiology, cattle, Mycobacterium bovis

Abstract

Bovine tuberculosis (bTB) is a chronic infectious disease widely distributed in the cattle population in Mexico, a campaign against bTB was officially stablished in 1996, but up to now few and isolated epidemiological studies of the disease have been carried out in the country. Information on the status of bovine tuberculosis in SLP available from academic studies and public data is limited, and no attempts have been made to characterize the spatial distribution of bovine tuberculosis in the state to date. A better understanding of the disease spatial distribution and the factors associated with increased risk is required to implement more effective control measures.

A cross-sectional study based on bTB testing on >1,600 herds in two regions of San Luis Potosi state, Altiplano and Huasteca, during 2018-2021 was conducted for the identification of spatial clustering and of bTB risk factors using the scan statistic test and multivariable logistic regression models.

The proportion of herds with at least one reactor was 17.9% in Altiplano and 38.6% in Huasteca, with one high risk cluster present in each region, that comprised 27.7% and 57.4% of the positive herds. Larger herds (>20 animals) and those included in the spatial cluster were exposed to a significantly increased risk of having at least one reactor in both regions.

Results demonstrated the presence of certain herds exposed to higher risk depending on their size and location in both regions, suggesting similar patterns of transmission; these findings can be used to further investigate how the disease spreads in San Luis Potosi

Spatial modelling *Aedes caspius* (Pallas 1771) and *Aedes vexans* (Meigen 1830) distribution in the Po Plain (Northern Italy)

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Keywords: Aedes caspius, Aedes vexans, Geostatistics, Kriging, Machine Learning, surveillance

Abstract

In this work, we analyse the abundance data collected in the frame of West Nile Virus (WNV) surveillance in northern Italy (Po Plain) by 292 CO2-baited traps to evaluate the distribution and density of two non-target mosquito: *Aedes caspius* (Pallas 1771) and *Aedes vexans* (Meigen 1830). We applied two different approaches of spatial analysis (geostatistical and machine learning) which gave congruous results. Both species are more abundant in the middle of Po plain, near Po River, but distribution was different. *Ae. caspius* was more abundant in the east and west areas, *Ae. vexans* in the middle area of Po plain. This work demonstrated the importance to maintain and improve entomological surveillance of WNV, with an adequate sampling effort.

Best options to apply MCDA in an environmental context

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Abstract

Multi-criteria decision analysis (MCDA) is a sub-discipline that blends spatial geographic data and its weighting, to transform them into a decision map. It is for the most part used in land suitability, epidemiological risk area assessment, and environmental studies.

The scope of the study was to describe how MCDA has been used in an environmental context in the last five years. The research questions of the study are: (i) what are the most used MCDA methods in the environmental context? (ii) what kind of criteria are used to create maps? (iii) what are the most used MCDA methods based on the available criteria?

We conducted a rapid literature review, which followed the Cochrane guidance. The methodology included five steps: (i) elaboration of the research question; (ii) identification of peer-reviewed articles published from January 1st, 2018, to March 6th, 2023; (iii) definition of criteria for the inclusion and analysis; (iv) charting of the information obtained; (v) summarizing and reporting the results.

The rapid review search identified 1364 articles. After duplicate elimination, 1362 abstracts were screened for relevance and pertinence. 91 full-text articles were assessed for eligibility. Finally, 21 articles were included in the review. The articles concern communicable diseases (13), natural disasters (4), vectors (2), and environment (2). The most used MCDA methods in the articles are the analytic hierarchy process (AHP), weighted linear combination (WLC), and fuzzy logic (FL). Eight articles use more than one method to create maps. The criteria used to create maps were divided into eight sectors: human, animal, animal reservoir, vector, ecological, physical, climate, and socioeconomic. The types of criteria used are human population, animal, and vector density; animal reservoir density and distribution; landcover and NDVI; distance and characteristics of water/soil; temperature, humidity, rainfall; knowledge, and Provincial Gross Domestic Product (PGDP).

AHP is the most used method when criteria from all eight groups are present, often in combination with FL and/or WLC. The data are collected with satellite, ground sensors, interviews, or field observations but they may also be density or socio-economic related. AHP is primarily used for satellite and density data, WLC just for density data, and FL for density data as well as for data collected with satellite,

ground sensors, and field observations. Socio-economic data and the ones collected with interviews are not widely used. The most used methods for sensitivity analysis are enumeration and One-at-a-time. For validation, the most used method is field validation.

Identifying the most used MCDAs and the types of data required will allow us to use MCDAs properly. This method will help identify the drivers that most lead to zoonotic outbreaks to support planning, decision-making, and prioritizing areas for targeted prevention interventions.

Spatial and temporal analysis on the impact of ultra-low volume indoor insecticide spraying on *Aedes aegypti* household density

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Keywords: Aedes aegypti, dengue, Vector-borne diseases, vector control, ultra-low volume, intervention

Abstract

Aedes aegypti is the primary vector for several arboviruses that can cause widespread epidemics, such as Dengue and Zika. This mosquito feeds primarily and frequently on humans, and is well adapted to the urban environment, where it has successfully established itself in many areas throughout the tropics and subtropics. Ultra-low volume (ULV) indoor insecticide spraying has been shown to be effective at reducing Ae. aegypti density for short periods of time (Gunning et al., 2018), however the spatial extent of the vector control effect along the margins of a treated area is unclear, as is the potentially reduced effect of incomplete spray coverage within the treated area. In this study, we characterize the impact of pyrethroid ULV indoor spraying on the Ae. aegypti population within households in relation to the spray events occurring in the proximity of that household in time and space. Improved understanding of the duration and the distance of the effect of a spray intervention on Ae. aegypti populations can better inform planning the coverage and frequency of sprays needed during vector control interventions, as well as modeling efforts that contrast different vector control strategies.

This project uses data from two large-scale experiments that involved six cycles of indoor pyrethroid spray applications in the Amazonian city of Iquitos, Peru (Gunning et al. 2018). We developed spatial multi-level models to disentangle the reduction in Ae. aegypti numbers that resulted from (1) recent ULV treatment of a specific household and (2) ULV treatment of households in the neighboring area. We compared the fit of models including different weighting schemes for the spray effect, based on different temporal and spatial decay functions to understand lagged ULV effects.

Our results suggest that the effect of a spray event in a house wanes over time following a gaussian decay, with a spray that occurred between 9-30 days ago having half the effect of a spray that occurred the day before. In addition, we found that the reduction of Ae. aegypti density is mainly

determined by time since the most recent spray event, with no significant explanatory value added by the cumulative effect of multiple past sprays. Our results also indicate that the reduction of the Ae. aegypti in a house is due to spray events occurring in that same house, with no significant effect of sprays occurring in adjacent houses or the neighboring area. In summary, the reduction of Ae. aegypti in a house is determined mainly by the time since the last spray intervention in that same house. Together, our results suggest that increased coverage rather than increased frequency of sprays should be the priority of indoor vector control programs.

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Does landscape play a role in the canine leptospirosis epidemic in Sydney?

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Keywords: canine leptospirosis, companion animal, landscape, reservoir, urban environment

Abstract

Beginning in 2017, cases of canine leptospirosis started to be reported from the City of Sydney council area, the highly urbanized centre of the Greater Sydney Area, Australia (Griebsch et al., 2022). Prior to this, the most recent cases had been reported in 1976. The reasons for the appearance of canine leptospirosis after a period of more than 30 years of absence are unknown. Some suggested reasons included local construction activities, flooding events, and rodent problems (Gong et al., 2022). The aim of this research program is to identify the drivers of the current canine leptospirosis epidemic in Sydney, and specifically the role played by the urban landscape.

To date, using passive surveillance of veterinary practices, case ascertainment has been carried out. Using demographic information generated by dog registration and microchip data, the population at-risk has been modelled. Statistical areas have been used to calculate disease incidence. For each of these areas, information on a range of urban landscape factors have been extracted; these include parks, recreational areas, water bodies, vegetation coverage, and housing density.

Between 2017 and 2023, 20 cases of canine leptospirosis have been detected in the two central local government areas of Sydney and Inner West. The greatest number of cases (n=8) were detected in 2019. Cases were reported from a total of 18 out of 906 statistical areas. Clustering of cases was identified in an area on the periphery of the central business district of Sydney in 2019. Both a statistical area matched case-control study analysis and an area-based incidence Poisson regression are being used to identify the landscape factors associated with canine leptospirosis.

Most of our knowledge of landscape factors that influence leptospirosis outbreaks and epidemic are derived from the human literature and are often anecdotal. Results of the current study are expected to assist dog owners and veterinarians to control and prevent canine leptospirosis within this region.

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Production of risk maps for ASF at a local level through the analysis of relevant epidemiological data

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Keywords: African swine fever, domestic pigs, risk factors, risk map, wild boar

Abstract

African swine fever (ASF) poses a significant threat to the global pig industry, with the disease having gradually expanded over the past decade worldwide. Once introduced to the wild boar population, the virus can establish itself, making it challenging to control it across extensive geographical areas. To facilitate the implementation of effective control measures, it is advantageous to classify administrative units based on the risk of ASF virus introduction and transmission. However, it should be noted that a key limitation in implementing control actions involving wildlife is the lack of detailed data on wild populations.

In this study, we classified the municipalities of Lombardy and Emilia-Romagna regions (Northern Italy) by evaluating the following parameters: i) the risk of ASF spread in the pig sector (low, medium, high), determined as a combination of pig density (number of holdings and heads) and pig movements (Tamba et al., 2020); ii) a habitat suitability index (HSI) for wild boar (ranging from 0 to 10), calculated as the geometric mean of suitability values assigned to land cover, elevation and slope (Qin et al., 2015); iii) the density of hunted wild boar per km^2; iv) the presence of protected natural areas. The HSI and wild boar density were categorized into three classes, as the risk of ASF spread, so that the three parameters can be summed. The low risk class was assigned to HSI values ≤2 and to densities ≤1; the medium risk class to HSI values between 2 and 6, and densities between 1 and 4; the high risk class to HSI values >6 and densities ≥4. To the three classes were assigned increasing score of 0 (low), 0.5 (medium) and 1 (high). The sum of these scores at Municipality level was multiplied by 1.5, if a protected natural area is present.

The final score ranged between 0 and 4.5, and the corresponding risk classes were defined as follows: low (score ≤1), medium (score ≤2), and high (score is >2). The 1836 municipalities included in this study were classified as follows in terms of risk: 161 (9%) were classified as high risk, 248 (14%) as medium and 1427 (78%) as low. We noted that for Emilia-Romagna, the municipalities (330) were relatively evenly distributed across the three risk classes (about 33% in each class). Municipalities with higher or

medium risk were concentrated in the hilly part of the region, with some exceptions in the lowlands due to a high presence of pig holdings.

This classification system appears to be useful for prioritizing intervention measures to control the wild boar population and/or improve biosecurity and surveillance in pig holdings.

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The model-driven approach to zone geospatial standardisation – the GeoZone project

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Keywords: Data product specification, ISO/TC211, Process model, Requirements analysis, WOAH collaborating centre, Zoning

Abstract

WOAH Terrestrial Code (hereafter Code), defined a zone as “a part of a country defined by the Veterinary Authority, containing an animal population or subpopulation with a specific animal health status with respect to an infection or infestation for the purposes of international trade or disease prevention or control” (WOAH, 2021). However, in the Code there is no indication on how to represent zones geographically. From a GIS perspective, what is missing in the Code specifications are the zone geospatial data model, including application schema, data content, data quality level, geospatial data accuracy, referencing information type and data structure type. The GeoZone project aims to develop a zone geospatial model for implementation by 182 WOAH Members. This study describes the model-driven approach used to develop the GeoZone geospatial data specification.

The organisational model is an abstraction of the RM-ODP framework (SO/IEC 10746-3:2009), which allowed for the early identification of issues relevant to data specification in the process. The goal was to identify numerous issues before implementation.

The framework consisted of five main threads:

(i) Requirements are defined through use-case scenarios, who, in their turn described with user-story narratives, including a template for use-case definition and a specification checklist. These documents

assisted discussions between the domain experts from WOAH Collaborating Centres (CC) and GIS experts. The discussion's result was documented in the requirements model.

(ii) GIS experts used ISO 19131 to draft the zone geospatial Data Product Specification (ISO 19131:2007). GIS experts gained a comprehensive understanding of the relevant zones. This understanding was documented via an application schema using the UML as conceptual schema language, following ISO 19100 profiling. This application schema became the core of the specification.

(iii) With WOAH CC domain experts' support, the initial draft of the zone geospatial data product specification was integrated with various sections including scope, identification, content, structure, reference systems, quality, delivery and metadata.

(iv) The data specification results will be tested in a pilot study, to verify its applicability and sustainability.

(v) A "technical guidance" document will be created to support Members in implementing the standard, considering the complexity of the data product specification for the non-experts.

The Zone Geospatial Data Specification document has been created and will be presented to WOAH for consideration and feedback.

To establish a sustainable zone geospatial data model for WOAH, the experts of the seven WOAH CC followed an RM-ODP framework with two distinguishing features. Firstly, it follows a cyclic approach, gradually enhancing system definition and implementation based on expressed requirements. The other feature is a set of anchor point milestones, ensuring stakeholder commitment to achievable system solutions.

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Combining Geographical Information System (GIS) and innovative devices (GPS and drones) for a new strategy to monitor and control the micro-epidemiology of cystic echinococcosis in grazing areas of southern Italy

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Keywords: Echinococcosis, canids, geospatial data, GPS, drones

Abstract

Cystic echinococcosis (CE) is a parasitic zoonosis of public health importance caused by the larval stage of the cestode *Echinococcus granulosus*. CE has a worldwide distribution but exhibits the highest prevalence in communities where pastoral activities predominate, as the Mediterranean areas (Deplazes et al., 2017). The lifecycle of *E. granulosus* involves canids as definitive hosts and a broad spectrum of mammals, including humans, as intermediate hosts. A pivotal role in the transmission of echinococcosis is played by dogs (especially sheep dog and stray dogs of rural areas), due to their ability to wander freely in pastoral areas and prey on slaughtered livestock (Wang et al., 2022). In this context, the combined use of Geograpghical Information Systems (GIS) and innovative devices (e.g., GPS, drones), represent a useful tool for the development of innovative strategies to control CE. Recently, the delivery of baits containing praziquantel on the grazing areas using GPS and Unmanned Aerial Vehicles (UAV), proved to be an effective approach to treat stray dogs in areas endemic for alveolar echinococcosis caused by the larval stages of *Echinococcus multilocularis* (Yu et al., 2017).

The spatial analysis performed in this study aimed to design a new CE control strategy based on a thorough investigation of the micro-epidemiology of CE and the treatment of potentially infected definitive hosts, combining the use of GIS and innovative devices (GPS, drone, camera trap).

In 5 farms positive to CE, the movements of sheep and sheepdogs were tracked for 1 month, using 15 GPS devices applied to the animals. Multiple ring buffers and standard deviational ellipses were generated to estimate the size and the spatial distribution of the grazing areas. Punctual positions were fixed on the risk areas and medicated baits laced with Praziquantel were released by the UAV to

deworm stray dogs.

Spatial patterns of the animal positions and the areas of the pastures with highest risk of access by potentially infected animals, were identified. A drone payload was designed on purpose for the release of medicated baits and spatial sampling criteria to improve deworming actions were introduced.

The study shows that the use of GPS collars is more effective than the traditional geospatial approach for accurate identification of the micro-epidemiological channels of the spread of CE, and allows to improve the rationalization of the resources needed to control CE infection. In addition, the results of the study confirmed that the combined use of geospatial technology and innovative devices might be a useful method to interrupt the *Echinococcus* lifecycle and to reduce the spread of the disease.

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Geographic Information System for surveillance and disease response in aquatic animal health management – The Aquae Strength project

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Keywords: Aquaculture, Feature catalogue, GIS methods, WOAH collaborating centre

Abstract

Geographic information requires special modelling and analysis methods (Luaces et al., 2005) . GIS technicians base the selection of data modelling and application methods on many factors including the available software, aim of the application, and, most of all, the user's level of training and examples from the literature (Maguire D.J., 1991). Despite the increased interest in GIS as a tool for aquaculture, often, knowing what GIS is still does not necessarily translate into using it effectively. Aim at supporting the planning and management of GIS projects in aquaculture, the WOAH project, Aquae Strength, has a specific work package for developing and implementing a capacity-building framework available for GIS technicians. Therefore, developing GIS projects could be exploited by veterinary services in surveillance and disease response in the aquaculture domain.

The Aquae Strength work package includes three groups of activities:

- Structured training courses. Specific training courses will present an empirical approach to implement GIS technologies to be exploited by veterinary services in surveillance and disease response in aquaculture. The courses, based on QGIS technologies, will take into account the three aquatic environments (marine, freshwater, and transitional water) and use typical aquatic features and methods. Subsequently, they will also be made available as e-learning modules on

the platform.

- Micro-Projects. This applied research-oriented activity will target specific topics and have appropriate project goals, providing technical expertise according to the actual needs, to achieve final tangible results. These micro-projects will be developed with the GIS technicians of the four beneficiary institutions.
- Feature catalogue. In developing GIS projects, it is recommended to align the data model used to represent spatial objects with the available standardised feature catalogue. This alignment enables developers to take advantage of common concept definitions and recommended attribute bindings, it helps implement methods into geospatial solutions and create geospatial datasets that can be easily understood and are suitable for their intended purposes. The development of the feature catalogue will be based on the identification and analysis of features and methods from recent literature.

The implementation of GIS projects requires both substantial background and skills, in GIS and the scientific domain of application, and project management expertise (Somers R., 2001). Tailored GIS courses and technologies may help develop successful GIS applications.

The Aquae Strength project is financed by the Italian Ministry of Health and supported by the WOAH. The project, led by the Istituto Zooprofilattico Sperimentale delle Venezie (Italy), involves seven other institutes belonging to the network of the Italian Experimental Zooprophylactic Institutes, three external advisors and four beneficiary institutes from North Africa, Middle East, and Far East.

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Modeling the spread of ASF into the US swine industry: the example of Iowa

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Keywords: Agent-based model, swine diseases, stochastic modeling, disease control

Abstract

Recent global spread of African swine fever (ASF) have demonstrated the devastating impact this disease can have on the swine industry, posing a threat to the livelihoods of those who rely on it. While significant progress has been made in understanding the disease's dynamics in the newly infected areas, it has been shown that the effectiveness of interventions varies depending on the environmental and socioeconomic context of the affected population. There is no ASF in the United States (US) yet, but it is likely to be introduced given the global burden of the disease. The state of Iowa is characterized by large-scale operations and intense pig trade. Given the significance and uncertainty surrounding the potential impact of introducing ASF into highly dense areas such as Iowa, we have developed a spatial-explicit agent-based model to assess the overall consequences of the disease and the effectiveness of disease control interventions. Population characteristics were aggregated within a hexagonal grid, where the unit of analysis was each cell with distinctive population attributes such as: number of farms, animal density, movement patterns, among others. The model simulates disease transmission at local and long distance, allowing us to incorporate the spatial heterogeneity of the susceptible population. Local disease dynamics are modeled using ordinary differential equations and the long distance dynamics based on simulated movements between farms. The model uses an agent based approach, where the agents are reactive to the current state of their neighborhood and the interventions implemented for disease control. Some interventions evaluated in the model included: preventive culling, movement restrictions, and improving of biosecurity. These interventions were explored in different combinations under different introduction scenarios. Given the high spatio-temporal resolution of the model, it allows us to present the results using maps and detailed transmission networks, evidencing the key agents in the transmission of the disease. Additionally, a global sensitivity analysis was conducted to identify the most influential parameters affecting our model outcomes. While the model incorporates synthetic population and network dynamics, it remains flexible enough to integrate observed data on precise farm locations and movement records, enabling the evaluation of specific scenarios and providing valuable insights to inform risk mitigation strategies. This

modeling approach is also sensitive to different levels of confidentiality allowing the user to aggregate the population at different spatial scales without significant impacts in the overall epidemic impacts.

Using a spatially-explicit agent-based disease spread model to identify high risk areas and most cost-effective control strategies in the scenario of potential introduction of Chronic Wasting Disease in California

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Keywords: Chronic wasting disease, epidemiology, modelling, cervids, management, risk-based surveillance

Abstract

Chronic wasting disease (CWD) is an always fatal, neurodegenerative prion disease of cervids. In North America, it affects white-tailed deer (*Odocoileus virginianus*), mule deer (*Odocoileus hemionus*), Rocky Mountain elk (*Cervus elaphus nelsoni*), moose (*Alces alces shirasi*), and reindeer/caribou (*Rangifer tarandus*). The disease spreads through direct contact with infected individuals or indirect contact with infectious material (e.g., fluids, feces, and tissues of infected animals). First recognized in Colorado in 1967, CWD has incessantly spread across North America having been detected in captive or free-ranging cervids in at least 30 states of the US, 4 Canadian provinces, Norway, Sweden, Finland, and South Korea. In free-ranging populations, uncontrolled CWD expansion leads to geographical spread, increased prevalence, reduced adult survival rates, and destabilization of population dynamics. While CWD has never been detected in California's cervid populations despite surveillance efforts since 1999, the constant threat remains, as the disease could be introduced at any time through natural or anthropogenic movement of infected animals or materials. This study utilizes an agent-based modeling approach and integrates real mule deer population data, to simulate 5-year epidemiological expansion of hypothetical CWD introductions within the deer conservation units (DCUs) of California. Environmental factors such as wildfires and the presence of various scavenger species were also incorporated. Multiple scenarios were modeled, considering different deer densities and proposed management measures, including surveillance for initial detection, prompt response to the first detection, strategic harvest management, targeted culling, and carcass management. The model assesses the effectiveness of these management strategies, providing estimates of disease transmission probabilities, impacts on deer herds, and population dynamics for each DCU under various

disease introduction scenarios. The model also quantifies the direct and indirect transmission events, as well as the probability of CWD infection across different deer populations. The findings contribute to evidence-based decision-making by providing valuable information to support the design of cost-effective surveillance and management strategies to better prevent and rapidly detect and control CWD in the case of a potential introduction in California.

Combining biosecurity and spatial information to support decision-making in fresh-water fish farms

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Keywords: GIS, Fish farming, Biosecurity

Abstract

According to the new Animal Health Law, the surveillance scheme in fish farms, must consider the health status of the farms and the level of risk of introduction and spread of diseases. The classification of the various risk levels requires heterogeneous information including: spatial location, extent and connection to the hydrological network, and the biosecurity measures implemented. Hereby it is presented a method to rank the farms on the basis of their biosecurity, and integrate this information within the hydrological network, with the ultimate aim of informing the local health authority (LHA) of which farms are exposed to greater risk of transmission, once a disease has been detected.

Sixty-two salmonid farms located in the Autonomous Province of Trento, northeastern Italy, were included in the study. Biosecurity information was collected for each farms through checklists already provided in the National Legislation implementing the EU Directive 2006/88/CE. Although the checklist covered several topics, only information on biosecurity were considered in the study. The resulting 39 biosecurity items were scored via expert elicitation, allowing evaluating the importance of single item, while also accounting for the uncertainty potentially related to each of the 10 experts. Finally, to each farm a score derived by the presence/absence of those 39 items was assigned, permitting to rank the premises accordingly to their biosecurity. Data manipulation and elaborations were performed using the statistical software R. The hydrologic network was implemented, and fully validated, within a geo-database using PostGreSQL with PostGIS and PgRouting extensions. Location of farms and their productive data were acquired from the National Livestock Database. The location of connections between farms and rivers, likely water sources, and other points of interest were georeferenced and validated by veterinarians from the LHA. Biosecurity scores were combined with spatial information of

the farms to produce thematic maps. Finally, a set of specific Geographic Information System (GIS) tools were implemented to support LHA and decision makers, combining spatial operations and biosecurity scores.

Overall the fish farming sector resulted having high biosecurity scores, with only a farms showing suboptimal of poor conditions (N=2/62, 3.23%). In addition, GIS-oriented functionalities were developed for: (i) spatial operations that consider the digital terrain model (e.g. buffers accounting for the slope); (ii) network operations for selecting farm (e.g.: upstream/downstream) and interrogating their biosecurity, (iii) rapid extraction of territorial information near the farms.

The study represent a starting point for creating of a GIS-based risk assessment tool, for identifying farms at risk of disease transmission, increasing the effectiveness of surveillance and disease response measures. Furthermore, the development dedicated GIS features might be exploited to create informative maps to support decision-making.

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Spatial epidemiology and risk factor analysis of bovine brucellosis in Punjab, Pakistan: a population-based study

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Keywords: Bovines, Brucellosis, Spatial distribution, Seroprevalence, Risk-factors, Pakistan

Abstract

Brucellosis is an important zoonotic disease that affects animal and human health worldwide, particularly in developing countries including Pakistan. Punjab is the most populous province having about 50% of the human and animal population of the country. In Punjab, dense animal and human populations, smallholder farming systems, poor husbandry practices, and lack of vaccination and animal movement control are important factors that have increased the risk of transmission of the disease. Hence, the government has launched a brucellosis control program to reduce the spread of bovine brucellosis using an active surveillance approach. This large-scale population-based study under the brucellosis control program aimed to i) estimate the seroprevalence, ii) identify important risk factors and iii) provide the spatial distribution of bovine brucellosis in Punjab province of Pakistan. In this study, 12,406 livestock farms/holdings in 34 districts having 61,084 animals (31,307 cattle and 29,777 buffaloes) were georeferenced and screened for *Brucella* antibodies between July 2020 and June 2021 through an intensive network of laboratories under the directorate of Animal Disease Diagnostic, Reporting and Surveillance, Punjab. The sera were initially tested by Rose Bengal Plate Test and the positive samples were confirmed with Indirect Enzyme-linked Immunosorbent Assay. Data on various farm and animal-level risk factors was also collected and analyzed through multivariable mixed models. The overall animal-level seroprevalence was 0.84% (514/61,084), while the herd-level prevalence was 3.13% (389/12,406). Within-herd prevalence ranged from 0 to 100%. The prevalence was higher in the north-eastern part of the province with the highest in Hafizabad district [herd prevalence: 45.21% (95%CI: 39.88 – 50.64%), animal prevalence: 16.83% (95%CI: 14.49 – 19.38%)], followed by Gujranwala [herd prevalence: 22.17% (95%CI: 16.65 – 28.51%), animal prevalence: 7.47% (95%CI: 5.86 – 9.36%)],

while in 14 districts no seropositive animal was detected. The spatial analysis identified significant clustering in the northeastern part of the province. The chances of *Brucella* infection were 1.70 times higher in females (P=0.029, 95% CI: 1.36-1.92) than in male animals. Every one-year increase in age increased the odds of being *Brucella* positive by 1.26 times (P <0.001, 95% CI: 1.22-1.30). The analysis of herd-level factors revealed that the odds of occurrence of brucellosis were 2.98 times on farms that had an abortion history (P<0.001). Similarly, farms with free stall housing (OR=3.01, P<0.001), animal purchase history during the last year (OR=1.35, P<0.001) and artificial insemination practice (OR=1.35, P<0.001) had also higher odds of occurrence of *Brucella* infection. In conclusion, the study provides a detailed insight into the epidemiology of bovine brucellosis in Punjab that will help to develop more targeted interventions for the control of brucellosis leading to better animal and human health.

Being prepared for an avian influenza epidemic with a One Health approach: a cartographic study in Lazio Region to identify animal carcasses burial sites

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Keywords: Avian Influenza, burial sites, cartography, epidemic, GIS, outbreaks

Abstract

According to European and national legislation, in case of avian influenza outbreak or epidemics, carcasses of dead and culled animals should be sent to rendering plants (Ministry of Health, 2014). Competent authorities can authorize burial procedures, if rendering plant cannot dispose on time a large and unexpected number of carcasses (Chowdhury et al., 2019). The burial site should be identified on a specific site study and chosen in a suitable environment (Costa et al., 2019), it must ensure geological stability for several years and the confinement of organic material lasting from a minimum of 2 up to 20 years, to ensure the complete degradation of the organic material and pathogens. The aim of the present study was to create a mapping project to identify suitable sites for the burial of large volumes of avian carcasses in case of avian influenza epidemics. The territory of Lazio Region was classified based on the following factors: presence/absence of environmental constraints and regulations that protect the environment and limit the land use (landscape constraints, protected areas, archaeological sites, drinking water springs), features affecting the susceptibility to pollution (water table depth, hydrogeological vulnerability, hydrographic network) and stability over time (landslides, floods). Official geodata from National and Regional cartography were used: geoportal of the Institute of Environment Research and Protection (Istituto Superiore per la Ricerca e la Protezione Ambientale - ISPRA), geoportal of the Ministry of the Environment (Ministero dell'Ambiente e della Sicurezza energetica), geoportal of Lazio Region (Open Data Lazio), Lazio Region Environment Information System (Sistema Informativo Regionale Ambientale - Sira); geodata archive of the Istituto Zooprofilattico Sperimentale del Lazio e della Toscana (IZSLT). The output is an interactive map that allows to navigate and to choose which different layers apply among the existing 19 layers. The map is available through an ad hoc created website or the exchange of shapefiles/layers of proprietary or open-source geographic information systems. The intended users are regional authorities, Municipalities, veterinarians of Local Health Units, poultry breeders and other stakeholders. The map allows to identify areas not suitable for animal carcasses burial because subject to constraints or

environmental risks. Areas identified as suitable should be further investigated at local level by core samples, soil inspections, existing land-use plans or other resulting constraints not present in this study. In conclusion, overlaying different geographic information levels identified potential areas of suitability for animal carcasses burial in case of infectious diseases epidemics. The use of suitability maps collaborates in preventing impacts on environment, health and animal/human interface.

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An early warning system for mussel aquaculture adapting to climate changes

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Keywords: Mediterranean mussel, aquaculture, hydro-meteorological model, satellite data, fecal bacteria, early warning

Abstract

Nowadays, climate changes are causing severe weather events that are responsible for product losses, structural damages and unsanitary conditions in shellfish farms. During severe rain events, fecal bacteria coming from the river can be accumulated by mollusks farmed along the coasts (Colaiuda et al., 2021). To alert farmers timely, the FORESHELL project (funded by the FLAG Costa Blu trough 2014-20 EMFF program of the Abruzzo Region) developed an early warning system (EWS) able to forecast the main hydro-meteorological-environmental factors that could threaten the production.

The study area encompassed, in the Giulianova Maritime District (Abruzzo, Italy), one Mediterranean mussel (*Mytilus galloprovincialis*) farm and the two rivers facing it: Vibrata and Salinello. The methodology comprised: *a)* the hydrological monitoring of the two rivers through CHyM model (Lombardi et al, 2021) to forecast occurrences of discharge peaks at the river mouth; *b)* sanitary monitoring before and after severe weather events to determine the concentrations of *Escherichia coli* in freshwater at the river mouths and in mussels and seawater at the farming area; *c)* characterization of mussel growth; *d)* environmental parameter monitoring, *in situ* and by remote sensing.

Starting from satellite data, a customized oceanographic model was developed to combine environmental parameters with flow rate data of rivers estimated by CHyM model. The model was integrated into the AquaX platform (ColomboSky®, https://www.aquaexploration.com/). The AquaX platform was provided with an alert system, sending alarms via SMS or email in case of predicted

adverse weather-marine events and anomalous fluctuations of the monitored physical/chemical parameters threatening production, with a predictive capacity of 48 hours. Three flow rate thresholds were defined as an alert system associated with color codes identifying different alert states related to potential *E. coli* contamination of mussels in order to make the whole system easily interpretable by the farmer.

During the project lifetime, *E. coli* concentration in mussels exceeded the legislative limit (230 MPN/100 g) (EU Regulation n. 2019/627) following four severe weather events. The mussels showed a self-purification time ranging from 3 to 6 days and they constantly grew during the investigation period.

In conclusion, the FORESHELL project supplied farmers with easy-to-use tools useful to plan daily activities in order to avoid product losses, structural damages and unsanitary conditions by adapting aquaculture procedures to climate changes.

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Spatial dynamics of mallard ducks (Anas platyrhynchos) and their potential role in the spread of Avian Influenza in Italy

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Keywords: Avian Influenza, GPS, land use, wild birds movements, mallard ducks

Abstract

Between January 2017 and March 2018, Italy experienced a severe H5N8 Highly Pathogenic Avian Influenza epidemic, which was characterized by two waves: the first occurring from January to May 2017, and the second starting in July 2017. Interestingly, the second wave coincided with a period when migratory waterfowl were scarce or absent, indicating the potential involvement of resident wild bird populations. This led to the hypothesis that the virus might have amplified in nestlings and juvenile residential birds in the period between the two waves, and subsequently spread in July and August, when the juveniles left the natal areas following the moulting period.

A study was conducted between July 2019 and May 2021, to assess the extent of the movements of mallard ducks (*Anas platyrhynchos*) in their different phenological periods: breeding (May-June), moulting (July), post-moulting (August-October), and wintering/resting periods (between November and the following February). The study involved the placement of GPS-GSM transmitters on 73 mallards (37 males and 36 females) captured in two coastal and two inland wetlands, in proximity to the Densely Populated Poultry Areas in northeastern Italy. The GPS and satellite-derived data were used to assess the home ranges and land-use in the phenological periods. The results were then used to compute a measure of the probability of finding mallards within the maximum extent of their movements and, consequently, estimating the risk of contact with poultry farms.

The home ranges of mallards and their land-use patterns exhibited marked differences throughout the four periods and accordingly to sex and capture area. During the moulting period, movements resulted very limited, remaining confined within the wetlands of capture and their immediate vicinity. However, during the post-moulting and wintering periods, birds exhibited longer movements, especially those captured in inland wetlands. In the post-moulting/wintering periods the coastal wetlands showed

frequent exchanges of birds, forming a territorial *continuum*. The coastal birds predominantly utilized natural wetlands, with occasional incursions into agricultural areas, while the inland mallards resulted more likely to visit agricultural settings and, to a much lesser extent, urban environments. The probability of encountering mallards was higher in the post-moulting and wintering periods, and for inland birds. For the coastal mallards, the highest presence of birds was confined within the wetlands, with minimal likelihood of encountering birds in the inland areas.

The study of mallard movements provided insights into their behaviour during different phases of their life cycle, highlighting variations in home range and land-use patterns. The measurement of the likelihood of finding mallards accordingly to the land-use might be used in developing risk-based surveillance plans for avian influenza in both wild birds and domestic poultry, aiming at focusing efforts in well-defined areas and temporal periods.

A Spatial Multi Criteria Decision Analysis (MCDA) approach to map the risk of Avian Influenza in Lazio and Toscana (central Italy)

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Keywords: Avian influenza, knowledge-driven models, risk factors, suitability, surveillance, vulnerability

Abstract

Avian Influenza (AI) is an infectious viral disease transmitted by many species of birds. Some wild water birds (Anseriformes and Charadriiformes in particular) have the role of reservoir for domestic birds (poultry) and humans (zoonosis). This causes great concern in terms of high bird mortality rates and economic losses, and as potential source of human pandemic.

AI viruses are globally widespread. In Italy, many outbreaks are notified every year in the north, while sporadic outbreaks occur in other zones. The aim of this study was to map the suitability level (vulnerability maps) for AI, to address risk-based surveillance and control, often poorly supported by data-driven models. A Spatial Multi Criteria Decision Analysis (MCDA) was used. A list of possible risk factors was identified, based on literature research and 3 experts' opinions. 11 risk factors have been considered. They can be grouped into 4 categories:

- Domestic birds farms and related facilities: domestic birds farms, backyard farms, ducks or geese farms, free-range farms, farms belonging to North Italy avian industries, manure treatment plants, poultry slaughterhouses
- Wild birds density
- rivers, lakes and other bodies of water
- roads network

All the risk factors were imported as layers in a GIS project and transformed into raster maps, with a common scale/spatial resolution (3x3 km cells). For each risk factor a weight was calculated, following the Analytical Hierarchy Process (using QGis 2.8.8 plugin “Easy AHP”) based on 3 elicited experts' opinion. Each raster was processed based on a specified fuzzification algorithm (by “Fuzzy membership” in ArcGis® 10.8.1) before their integration in the final map. The range of medium-high risk values (0.49-0.78) covers about the 30% of the total region in Lazio, in particular the inner part of

Viterbo province and the coastal area between Latina and Roma. In Toscana, high risk areas are present on the coast and an inner area between Siena and Arezzo.

MCDA can provide a possible knowledge-based approach to support specific health and surveillance measures in a scenario increasingly oriented to a One-Health perspective.

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A novel approach to estimate the animal movement networks: illustration for the swine industry in Iowa (US) and implications for disease prevention and control using a network-based model

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Keywords: Animal movement, Network analysis, Maximum entropy, Disease transmission, African Swine Fever

Abstract

Animal movement plays a critical role in disease transmission between farms. However, in the United States, the lack of available animal shipment data sometimes coupled with lack also of detailed information about farm demographics and characteristics presents great challenges for epidemic modeling and prediction. In this study, we propose a new method based on maximum entropy to generate "synthetic" animal movement networks that resemble the "real" networks, considering available statistics about the premises operation type, operation size, and the distance between premises. We illustrate our method for the pig movement networks in Iowa, where we had more "real" data to validate our approach. We then performed network analyses to gain insights into the generated pig movement networks and applied the generated networks to a network-based epidemic model to identify potential vulnerabilities of the network in terms of disease transmission. The model was parameterized for African Swine Fever (ASF) as the US swine industry is currently quite concerned about this disease. ASF outbreaks starting from random farms were associated with highly variable outcomes, ranging from no spreading to large outbreaks. However, outbreaks originating from high out-degree farms may lead to large epidemic sizes. This underscores the importance for stakeholders and policymakers to continue improving animal movement records and traceability programs in the US and the value of making that data available to epidemiologists and modelers to better understand risk and more cost-effectively prevent and control disease transmission. Our approach could be easily adapted to any other livestock system or disease. Future work will include sensitivity analysis to evaluate the impact of our assumptions in the "synthetic" swine movement network and validation of our approach with real-world swine movement information obtained from several production systems in the US.

Introduction and exposure of wild boar to African swine fever virus by contaminated pork products in Spain via seaports

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Keywords: African swine fever, disease introduction, pork products, seaports, spatial analysis, wild boar

Abstract

African swine fever (ASF) is a severe hemorrhagic disease that affects domestic and wild suids. Since its introduction nine years ago in the European Union, the wild boar population is one of the main drivers of the disease's local spread and its maintenance there. Spain is currently free of ASF, although the risk of introduction is non-negligible. Due to the worldwide distribution of the disease, contaminated pork products with ASF virus (ASFV) pose a major threat to ASF-free regions. Thus, the aim of the study was to identify areas in mainland Spain with a higher risk of indirect exposure of wild boar to ASFV-contaminated pork products illegally introduced via seaports in the event that the scenario ever occurs.

First, the Spanish seaports that receive traffic from ASF-affected countries were detected. A risk score was assigned to each seaport based on several parameters, related to the intensity of connections between each at-risk seaport and the origin countries, the number of connections, as well as the level of ASF affectation of the origin countries. Places where the indirect exposure of wild boar to potential ASFV-contaminated products was identified: gas stations, rest areas, and near roads in protected natural spaces. Then, we used a weighted linear combination analysis accounting for the Kernel density of the inverse distance of gas stations, rest areas, and protected natural spaces to seaports, as well as the first two contact areas to the suitability of wild boars.

Our findings highlighted relatively small at-risk areas where wild boar exposure to ASFV-contaminated products could occur. Two seaports, namely Barcelona and Valencia, presented a higher relative risk of wild boar exposure and higher risk score. This early warning system tool can aid with the implementation of cost-effective active surveillance and preventive measures in the framework of the Spanish wildlife health surveillance program for ASF.

Eco-Epi cartographic tool for managing ASF in Africa: mapping African wild suids distribution based on the quality of available habitat

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Keywords: African swine fever, African wild suids distribution, habitat quality, spatial analysis, ASF sylvatic virus cycle, eco-epi-tool, disease management

Abstract

African Swine Fever (ASF) is a contagious viral disease that affects all members of the family Suidae and represents a threat to the swine industry due to its potentially devastating socio-economic and political consequences. The disease is currently distributed on five continents, affecting 66 countries with different epidemiological scenarios, a range of hosts (domestic pigs and wild suids), and vectors. The lack of effective vaccine and treatment options makes it difficult to control of the disease. Therefore, knowledge of the distribution of wild suids is essential to understanding and helping predict disease infection dynamics and designing effective prevention and control strategies. In this work, we focus on the African scenario, where the ASF virus originated, it is a reservoir network with complex

eco-epidemiology, and high viral diversity. In this scenario, the main host actors and vectors involved in this disease are: the common warthog (*Phacochoerus africanus*), considered the original vertebrate host of the ASF virus; other African wild suids (primarily bushpigs, *Potamochoerus larvatus*), domestic pigs and the *Ornithodoros* spp., the soft tick vector. To date, three cycles have been described in the endemic African setting. One is the ancient sylvatic virus cycle (where *Ornithodoros* ticks play a role in the maintenance of the virus, and warthogs act as seasonal amplification hosts). Another is the domestic pig-tick cycle (where the virus circulates between soft ticks associated with domestic pig sties and pigs, to the exclusion of wild suids). Lastly, the pig cycle involves a single host, the domestic pig (without the involvement of vertebrate or invertebrate sylvatic hosts). In this study, we developed a standardized distribution map based on global land cover and vegetation (GlobCover) that quantifies the quality of available habitats (QAH) for African wild suids (warthog, bushpig). Both wild suid species participate in the sylvatic cycle, contributing to the endemicity and maintenance of ASF in many countries in Africa. QAHs were estimated using a quantitative method based on expert opinion integrating spatial environmental information and epidemiological data. There was a high correlation between the QAH levels and the georeferenced presence of wild suids (n=981), the ticks' presence (n=885), and the ASF notifications in wild suids and domestic pigs between July 2005 and June 2023 (n=517). These results suggest that the QAH map is a useful epi-tool to help predict and understand the patterns of the sylvatic cycle of ASF in the African scenario. Also, this tool could improve the management of the disease, defining risk scenarios for ASF in wild-tick-domestic pig interface, as well as for improving the prevention, control, and surveillance of ASF and other diseases that potentially affect swine and wild suids in Africa.

Real-time monitoring and forecasting of Rift Valley fever in Africa to drive preparedness and anticipatory actions

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Keywords: Rift Valley fever, early warning, real-time risk modelling, forecasting, preparedness, decision support tool

Abstract

Rift Valley fever (RVF) is a vector-borne disease that has severe impacts on livelihoods, national and international markets, and human health. RVF is currently limited to Africa and parts of the Near East with the potential to expand globally. In livestock, the disease affects sheep, goats, cattle, buffaloes, and camels. Outbreaks are closely associated with climate anomalies (e.g., periods of heavy rains and prolonged flooding), which increase habitat suitability for vector populations, influencing the risk of disease emergence, transmission and spread. Early warning systems represent an essential tool to enable national authorities to implement measures preventing outbreaks. In this context, the Food and Agriculture Organization of the United Nations (FAO) has developed a web-based RVF Early Warning Decision Support Tool (RVF DST), which integrates near real-time RVF risk maps with geospatial data, RVF historical and current disease events from EMPRES Global Animal Disease Information System (EMPRES-i) and expert knowledge on eco-epidemiology. This tool has been crucial in successfully forecasting hotspots for RVF vector amplification, as it provides recommendations and early warning messages for countries at risk of RVF outbreaks. The tool is used to build capacity for early warning and forecasting at country level, and demonstrates how near real-time modelling, risk forecasting and digital innovation can enhance preparedness and anticipatory actions.

Improving the efficacy of surveillance in wild boars of South Korea

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Keywords: African swine fever, Asia, South Korea, Surveillance, Wild life

Abstract

Since African swine fever (ASF) was confirmed in South Korea in September 2019, the disease keeps spreading primarily in wild boars. The key element contributing to this situation is the lack of identification of risk factors lead by surveillance bias. The high-elevation mountainous terrain covering 70% of the country makes search challenging. Inadequate application of surveillance programs to this unique orography results in missed cases and also poses a threat to the swine industry. Identifying potential under-surveillance areas would contribute to early detection of disease and improve the current surveillance system.

The directional distribution analysis was first performed to characterize the spatiotemporal distribution trends of ASF-positive wild boars. Then combinations of geospatial analysis and statistical approaches were applied to estimating potential under-surveillance areas. For South Korea, another important surveillance subject is the river shared with North Korea in terms of the continuous source of the virus introduction. While these countries are separated by the demilitarized zone serving as a physical barrier to the wild boar's movement, several rivers spanning both countries allow for the influx of infectious agents. The statistical analysis was performed to determine the relationship between ASF-positive wild boars and water, and then hydrologic analysis was applied to identify points for monitoring the risk of ASF spread.

The directional distribution analysis indicated a gradual shift in the center of ASF occurrence to the southeast, most likely due to the wild boar's movement. At the same time, several groups possibly infected by other routes were observed in distant areas.
Pearson's rho test indicated that elevation (rho= -0.908, p-value < 0.001) and distance from roads (rho= -0.979, p-value < 0.001) may have a significant impact on limiting surveillance activities, while the quality of available habitat for wild boar (QAH) map was shown to be useful in South Korea to indicate the probability of wild boar presence (rho = 0.786, p-value = 0.036).
The map of potential under-surveillance areas was created considering these results, and was validated by a

chi-square goodness-of-fit test (X-squared = 208.03, df = 1, p-value < 0.001).

The strong negative correlation between ASF-positive wild boars and distance from water sources (rho= -0.997, p-value <0.001) suggests that areas around rivers are one of the priority areas for monitoring. Furthermore, the hydrological analysis provided strategic surveillance points to monitor the risk of ASF spreading through the water inside South Korea as well as the continuous risk of ASF entry from North Korea.

In this study, we have developed tools to improve surveillance activities for the early detection and warming system of ASF. The identification of potential under-surveillance areas as well as missed risk factors can greatly improve monitoring systems. Thus, more effective and efficient countermeasures can be implemented.

Analyzing the movement network of swine within and between states in the United States

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Keywords: network analysis, swine diseases, Spatial Epidemiology, Animal movement

Abstract

Most preventative and countermeasure tactics aimed at controlling between-premises disease spread in livestock systems rely on identifying and restricting animal movement. Therefore, it is essential to uncover between-premise movement dynamics, including nationwide network profiles and distances to which animals are transported, to develop network-based control strategies. Currently, within-state animal movements in the U.S. are not regulated, making it difficult to acquire accurate data necessary to describe animal movement patters at large-scale. Here, we present an approach which combines network and spatial analysis using large-scale data of six swine production companies is the US. We analyzed three years of between-premises pig movements, which include 197,022 unique animal shipments, 3,973 premises, and 391,625,374 pigs transported across 22 U.S. states. We calculated premises-to-premises movement distances and identified the main transportation routes used by each company by considering origin and destination geolocations. Furthermore, we constructed an unweighted directed temporal farm contact network at 180-day intervals to calculate farm degree loyalty. With this information, we developed an out-going farm, temporal contact chains model to obtain infection chain distributions. Model outputs were used to identify hubs in the network which can aid in developing targeted control actions via node removal over the network, and compare multiple scenarios (e.g., 5%, 10%, 15%, 20%, 25% of the farms are removed). Node removal is carried out by considering the network metrics degree, betweenness, and cluster coefficient. Our results showed that the median distance between pig premises movements was 74.37 km, with a median of 52.71 km and 328.76 km for interstate movements. On average, 2,842 premises were connected via 6,705 edges. The premises-level network exhibited a loyalty, with a median of 0.65 (IQR: 0.45 – 0.77). When targeting 25% of the premises based on degree and betweenness, we reduced the spread to 1.23% and 1.7% of infected premises, respectively. While a complete shipment movement record for the entire U.S. does not exist, our results demonstrated the value of multi-state movement data to enhance the development of outbreak mitigation tactics.

Spatio-temporal patterns of Pelvic Organ Prolapse in the swine industry in the Midwest region of the United States

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Keywords: cluster analysis, Scan statistics, Swine diseases, Sow mortality

Abstract

Swine pelvic organ prolapse (POP) is a significant concern in the swine industry, adversely affecting sow welfare and reproductive performance. Despite being one of the leading non-infectious causes of mortality in recent years, the underlying causes of POP remain poorly understood, and there is limited information regarding its baseline prevalence in the swine industry. POP has been hypothesized to be influenced by multiple factors, including genetics, age, parity (number of previous pregnancies), body condition, and prolonged or difficult farrowing. The Midwest region in the United States is the main swine production region in the US, offering a unique setting to study the dynamics of POP. In this study, we investigated the spatio-temporal evolution of POP over the past five years across 25 different states in the Midwest region of the US and parts of Canada. Our dataset comprised reports from 106 farms within a large-scale operation system, covering the period from 2018 to 2023.

We used descriptive statistics to provide regional estimates of the POP prevalence, and assessed the spatial and temporal autocorrelation of POP incidence using correlation analysis and Moran's I. Additionally, space-time scan statistics were used to identify clusters of high POP incidence during the study period. The percentage of farms with an incidence greater than 0 increased from 43.44% in 2018 to 72.41% in 2023. The average incidence per farm also increased from 1.02 in 2018 to 4.54 in 2023. Notably, we identified seven significant clusters during the study period, with relative risk estimates ranging from 2.09 to 12.67.

To facilitate data visualization and ongoing monitoring, we developed an interactive dashboard to present the results and incorporate new reports. To the best of our knowledge, this analysis represents the first comprehensive evaluation of POP's temporal evolution and includes a spatial description of the at-risk population.

The role of GeoCetus Geographic Information System in monitoring the impact of fishing on cetaceans and sea turtles along the Abruzzo and Molise coasts over three years (2020-2022)

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Keywords: anthropic interactions, bycatch, cetaceans, sea turtles, stranding events, web-GIS

Abstract

The pressure of fishing activity has intensified dramatically during the last decades, resulting in increasing impacts on marine fauna (Carlucci et al., 2021; Lucchetti et al., 2019). Several are the reports of alive/dead stranded and/or bycaught sea turtles and cetaceans along the Italian coasts, underling a remarkable interaction of these animals with fishing activity. Although these reports are significant in number on a national basis, the only open-access database that collects the most important data on stranding and capture events is GeoCetus. The information can be used through the different tools made accessible on the web portal: a web-GIS application, an API, and a repository on GitHub. GeoCetus is a georeferenced database developed in 2012 by Centro Studi Cetacei, and improved over the years for the collection of usable data on cetacean and sea turtle stranding and capture events. The system is based on a completely open-source technology stack composed of a PostgreSQL Relational Database Management System (RDBMS) with PostGIS extension, a PHP business logic that exposes data via API, and a public presentation layer - the Web GIS - providing users with a user-friendly exploration and consultation tool. The data collected in the field are imported into the database via the management application, available for authorized users only. A unique code is automatically generated for each record. Data about the taxonomy, biometry, fishery interactions, location and other details - that have become more specific over the years - are entered along with photos (jpg/png) and necropsy sheet (pdf). The data are made available according to a Creative Commons license (CC BY-NC-SA 3.0 EN). Furthermore, using the web-GIS application or the public API, it is possible to query the contents of the database and return a customized dataset ready to be explored and exported (Di Lorenzo et al., 2013). To date, 4168 reports (607 cetaceans - 3561 sea turtles) have been listed and displayed in GeoCetus. Among them, 446 sea turtles (115 alive, 331 dead) and 48 cetaceans (2 alive) have been

registered from 2020 to 2022 along the coasts of Abruzzo and Molise. Interactions with human activities were reported in 137 cases of sea turtles: 73% in alive individuals, and 16% in carcasses. Concerning cetaceans, interactions were observed in 12 cases (26%). Thanks to the data gathered into the system, we observed there could be an underestimation of the data due to cadaveric alteration which precludes the necropsy insights in approximately 80% of sea turtles and 60% of cetacean carcasses. GeoCetus allows us to investigate several useful ecological data, also linked to human activities interaction mainly related to fishing, and to collect and freely share with the scientific community useful data aimed at conservation.

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Data and Other Considerations When Using GIS to Support Animal Emergency Preparedness and Response in Appalachia

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Keywords: Appalachia, companion animal, livestock, preparedness, GIS

Abstract

The Appalachian Region in Eastern United States is a socioeconomically challenged area that spans 206,000 square miles across 13 states. Over 26 million people live in the 423 counties and 8 independent cities included in this region. The Appalachian Region is often classified as 'rural', but the United States Department of Agriculture (USDA) Economic Research Service only classifies about 25% of the localities as truly rural with the others falling along the urban spectrum. This indicates that the Appalachian Region is not homogeneous in nature and should not be treated as such when it comes to planning for animal emergencies.

Animal population estimates for this project were obtained from multiple sources. Livestock and poultry numbers were downloaded from the USDA 2017 Census of Agriculture. County-level dog and feline numbers were calculated based on United States Census Bureau household numbers and American Veterinary Medical Association state level multipliers. State veterinary licensure data for the 13 Appalachian states was aggregated at county level for those who listed an in-state address only. AVMA veterinary clinic data was accessed through ESRI ArcGIS Online. Other data layers, ecoregions and internet distribution, were also added to the project in ESRI ArcMap 10.8.2.

Cattle, equine, and small ruminants are distributed throughout most of Appalachia with an exception being some of the counties located within the Appalachian Mountain ecoregion. Swine and poultry are heavily concentrated in the southern part of Appalachia with pockets found in several other areas. The distribution of dogs and cats align with the human population distribution since the calculations involve household numbers. More than 27% of the localities in Appalachia either have '0' or '1' veterinary clinic located in their vicinity. Finally, multiple jurisdictions report less than 70% of households have internet subscription which doesn't necessarily reflect access to broadband internet.

While planning is usually done locally, a regional exploration of data might be helpful in locating other

jurisdictions that might have a similar distribution of animals enabling localities to share best practice or plans. For instance, 45 counties report more than 2.5 million broilers. Additionally, a regional approach might be needed if an area is a 'veterinary desert' and there are not many options to house or treat animals in certain situations. One issue with large datasets is the accuracy of the data. For instance, another equine population estimate reports that are over twice the total number of equine in the US compared to the USDA data meaning methodology and limitations must be explored to determine which number to include as this could affect the ability and capacity to respond to animal emergencies. Finally, GIS can be used to identify impediments such as geography or inability to communicate which may affect planning.

Cluster analysis of Bovine TB using multiple methods, and considerations when constructing a Composite Index

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Keywords: Anselin Local Moran's I, Bovine Tuberculosis, Composite Index, Getis Ord-Gi*, Incidence, Space-Time

Abstract

Multiple methods were employed to analyze spatial clustering of Bovine Tuberculosis (TB) breakdowns in cattle across the High Risk Area (HRA) of England using data from 2013-2021. Located in South-West England and the West Midlands region, the HRA is one of three TB Risk Areas in England, and is often associated with the majority of TB incidents in the country (APHA, 2022). These methods employed Spatial Statistics tools and Space Time Pattern Mining tools in ArcGIS Pro, use of SaTScan^{tm}, and ETL processing using FME and Model Builder.

The first method built on techniques applied to data from the Edge Area of England by Downs et al. (2021), utilizing circular 25km^2 spatial units and set cut-off criteria for three rolling 7-year periods to determine the strength of evidence for a local reservoir. The circular spatial units aligned to a grid of centroids 2km apart, creating overlap between the spatial units, and addressing potential uncertainty as to the boundary of any reservoir found with contiguous spatial units.

The second method utilized the same circular 25km^2 spatial units but this time estimated TB infection using herd incidence per 100 herd-years at risk. Initially this was calculated per circle, and later applied the nearest 100 herds to each circle.

The third method used Hot Spot Analysis via the Getis-Ord Gi* statistic to identify statistically significant hot and cold spots of TB per year across contiguous hexagonal 25km^2 spatial units. These same spatial and temporal units were used in Cluster and Outlier Analysis using the Anselin Local Moran's I statistic as the fourth method. TB breakdown hot spots and cold spots were identified, as well as statistically significant spatial outliers. For both the Getis-Ord Gi* and Anselin Local Moran's I

statistics, parameters were tested using ArcGIS's Conceptualization of Spatial Relationships to optimize cluster identification.

The fifth method involved Space Time Pattern Mining and implemented the Getis-Ord Gi* and Anselin Local Moran's I statistics across a space-time cube of comparable spatial and temporal extent.

The sixth method utilized SaTScan^{tm} to analyze the space-time clustering of TB breakdowns for five biennial periods within the time of the study. Clusters were identified and then ranked by their statistical significance for each period.

Spatial and spatio-temporal correlation and difference were noted across the different methods, and Composite Indexing was investigated for its viability in combining the multiple methods into a single index. The methodology for integration of spatial and temporal units and extents is described, noting the importance of expert opinion and degree of subjectivity in parameter selection when creating an index.

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Spatial risk maps for African Swine Fever transmission in the Latvian wild boar population

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Keywords: Spatial transmission kernel, vaccination strategies, ASF, transmission risks, modelling disease, African Swine Fever, spatial transmission risk, wild boar, attenuated-acute ASF virus strains, vaccination coverage, Latvia

Abstract

Spatial transmission kernel modelling is a powerful approach for modelling disease transmission risks between localized population units, such as livestock farms. In this study, we applied this modelling approach to African Swine Fever (ASF) transmission in Latvian wild boars, using spatial grid cells representing local wild boar habitat areas as population units. In particular, we consider the context of designing wild boar vaccination programs and use the risk maps to investigate the influence of vaccination coverage on transmission risk. Using transmission kernel estimates obtained from outbreak data in Estonia and wild boar hunting bag information from Latvia, we first calculated spatial transmission risk maps for ASF in Latvian wild boars. We expect comparing close-by countries the transmission kernel estimated for ASF transmission in Estonian wild boar will also be representative of the Latvian context. However, considering the occurrence of attenuated ASF virus in Latvia since 2017, we also expect that the Latvian outbreak data could as well be different from the one used for Estonia, particularly since the infection might have evolved and epidemic dynamics could be different from those observed 5 years ago. We used these risk maps to identify predicted high-risk areas of transmission and compared, retrospectively these to actual ASF transmission patterns observed in Latvia. Subsequently, we investigated how predicted transmission risks scale down for different wild boar vaccination coverage scenarios. We discuss the possible implications for the effectiveness of vaccination strategies in the Latvian wild boar population, considering both attenuated and acute ASF virus strains.

Avian Influenza at the Wild Waterfowl – Domestic Poultry Interface

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Keywords: Avian Influenza, Modelling, Poultry, wild birds, wild-domestic interface

Abstract

Highly pathogenic avian influenza (HPAI) is a growing risk for both wild birds and the poultry industry. The 2022–2023 HPAI H5N1 outbreak in the United States is the largest and most costly animal health event in U.S. history. Based on the results of full genome sequencing, wild bird introductions have been the primary mechanism of introduction of virus into poultry operations. As prevalence increases in North America, better tools are needed to assess changing risks associated with HPAI spillover from wild animal populations into poultry operations. Through an interagency partnership, we have created a series of spatially explicit models for the United States to assess the prevalence of avian influenza in various waterfowl host species and the relative risk of spillover events at poultry operations across different times of year. These models account for not only the number of waterfowl in an area, but also species-specific prevalence rates to determine the effective waterfowl population or presented disease risk. When paired with information on the distribution of poultry farms, we can identify an area's risk of spillover. Preliminary models have been validated using genetically identified wild bird introduction events from the current outbreak and have performed well at predicting spillover events during the 2022 HPAI outbreak. Over 90 percent of wild bird introductions occurred in areas with predicted moderately high and high spillover risks. Next steps will include incorporating climate, landcover, and anthropogenic inputs and using phylogenetic analyses of the current H5N1 outbreak.

Preliminary results are publicly available in an interactive model data visualization tool and allow for investigation across spatial scales at specific locations, for more informed decisions regarding overall risk, monitoring, and prevention.

Early warning of bovine tuberculosis for veterinarians using spatio-temporal models

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Keywords: bovine tuberculosis, disease mapping, spatial statistics, spatio-temporal, standardised incidence ratio

Abstract

Bovine tuberculosis (bTB), caused by infection with *Mycobacterium bovis* is endemic in cattle in many countries worldwide including Ireland. The incidence rate in Ireland varies by herd and location and it is hoped that statistical disease-mapping models accounting for both spatio-temporal correlation and covariates might contribute towards explaining this variation. The final goal of this work is to produce a user-friendly, near real-time application that incorporates predictions from these models along with other metrics to serve as an early warning system to aid veterinarians in the field. Implementing different spatio-temporal random-effects models (e.g., negative binomial Besag-York-Mollié), we explored the association between covariates and the number of bTB cattle at an areal level by dividing Ireland into equally sized hexagons and determining the best fitting model. Data from the national bTB eradication programme was utilised. Models were fitted in a Bayesian framework and estimates were obtained using the integrated nested Laplace approximation (INLA) approach. We found that spatial models that accounted for spatial dependency offered a statistically significantly better fit in comparison to non-spatial versions where independence between hexagons was assumed. As an epidemiological tool, we have developed and improved on previous iterations, an interactive online dashboard to explore results. By developing a user-friendly, interactive dashboard, it allows the results from complex models to be presented in an accessible manner for veterinarians. The outstanding challenge is to fully automate the dashboard so that near real-time data is being used so that it is most beneficial for the bTB eradication programme.

Incidence rates of tumors in dogs (Campania Region – 2018/2022)

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Keywords: Tumors, Dogs, Incidence rate, Human Health, Standardization

Abstract

Knowing the health state of synanthropic animals has a high sanitary importance: it acts as a mirror for human health state as dogs share the same enviroment. Animal populations spontaneously exposed to contaminants and mutagens can represent sentinel of environmental risk factors, recognizing in them a sentinel role. The Animal Cancer Registry (RTA) is essential for the collection and comparison of data related to human/animal neoplastic pathology. Animal sentinels develope cancer erlier than man Kind: this allows the development of risk maps, reducing the time for preventive action.

The aim of the work is to evaluate if there is a difference between the incidence rates of tumors in dogs of Salerno province and in dogs of Naples province ; this evaluation could be use for in order to focus activities to safeguard Human Health.

Data of Campania RTA (provinces of Salerno and Naples in the years 2018-2022) for the canine species have been analysed. Data were extracted from the BDU (regional database) and from the Laboratory Management System of the Experimental Zooprophylactic Institute of Southern Italy. The statistical analysis was carried out through the software R version 4.1.0.

The dataset consists of 493 cases in dogs. For the provinces analysed, four age groups were identified; subsequently, a direct standardization was performed to compare the two incidence rates by eliminating the effect of age as a confounder.

The crude incidence rate for the province of Naples is 6.20 while for the province of Salerno it is 5.82: Naples shows a higher incidence rate than Salerno. Therefore with direct standardization we obtain that for the two provinces the rates are similar: the incidence rate of tumors in dogs in Salerno is 0.26 while in Naples it is 0.24.

Spatial Analysis of A Viral Agent First Time Appeared In Turkey By Geographic Information System: Cattle Noduler Exhantem (Lumpy Skin Disease-LSD)

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Keywords: Cluster analysis, Geographic Information System (GIS), lumpy skin diseases, spatial epidemiology

Abstract

Spatial analysis are of increasing importance in health researches in terms of the distribution of health incidents, collecting data about the regions where they are clustered. The aim of our study is to investigate spatially notifiable Lumpy Skin Disease (LSD), causes noduls on the skin, outbreaks first seen in August 2013 in Turkey and turned into endemic outbreak between 2013 and 2017, to determine the regions where they are clustered, to assess the patterns during the years. Geographic information system (GIS) software QGIS™ was used for data analysis and SaTScan™ was used for cluster analysis. Clusters were determined by the space-time permutation model. 1552 LSD outbreaks data obtained from OIE and Turkish Ministry of Agriculture and Forestry were used. During the 5-year period, outbreaks were observed in 68 provinces, 340, districts and 1289 villages. The most outbreaks were in 2014 (n=784), the least outbreaks were in 2017 (n=17), the most cases were in 2016 (n=3258) and the least cases were in 2017 (n=130). The most outbreaks were reported in Sivas province (n=164) and the most outbreaks were reported in August (n=249). The clustering analysis showed that cases were clustered in different regions by years. Statistically significant clusters were detected in provinces where the population of dairy cattle is high, with a humid, warm climate and close to countries such as Syria, Iran, Iraq and Georgia. Outbreaks is observed to be concentrated around Asi, Kizilirmak, Murat and Ceyhan rivers on the created outbreak maps. Total of 4524 animals were culled for five years and the highest culling occurred in 2016 (n = 2717). After the least outbreak occurred in 2017, LSD outbreaks started to rise again in 2018 (n = 53). Culling is seen succesful way against to LSD. It is recommended that the protection provided by the sheep-goat pox vaccine against LSD needs to be revised. This is the first published study conducted cluster analysis with LSD outbreaks seen in Turkey.

First attempt to develop risk indicators for earthquake impact assessment on animal health and welfare for the preparation of contingency plans and implementation of the Information System for the Management of non epidemic veterinary emergencies

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Keywords: Animal Welfare, animal health, mitigation, prevention, risk indicators, seismic risk

Abstract

Non-epidemic emergencies caused by major adverse events, like earthquakes, can have immediate and long-term impacts on human as well as on animal health and welfare. Estimating possible impacts induced by seismic events is a crucial point for planning and preparing mitigating actions. Literature is scarce regarding the existence of indicators aimed at estimating the allocation of resources for preserving animal health and welfare in a seismic risk scenario. The aims of this pilot study were: to estimate the impact of an earthquake on animal health and welfare through the identification of all hazards related to, as prerequisite for targeting interventions and quantifying human, instrumental and financial resources and to build relevant indicators for risk mitigation as relevant tools for Veterinary

Authorities involved in the management of non-epidemic veterinary emergencies, especially in the seismic one. 31 experts from research, Veterinary Public Health fields and Civil Protection were enrolled in a first Expert Knowledge Elicitation that was carried out according to the rules of the Appreciative Inquiry Summit, a model built on 4 phases - discovery, dream, design and destiny that was applied in plenary elicitation sessions alternating with 4 subgroups elicitation sessions guided by 7 facilitators. The 4 subgroups were composed on average of 8 experts, suitably balanced with respect to professional profiles and respective affiliations were guided in the discussions by one or two facilitators. The results achieved by each of the 4 subgroups were presented in plenary, they were extensively compared and debated. A list of hazards with related causes, interventions and resources needed was drafted. At the end of the Expert Knowledge Elicitation phase, each of the 4 subgroups was tasked to build relevant indicators according to the hazards identified. Overall, 23 risk indicators were identified. Of these, 14 were classified as belonging to mitigation, prevention and preparedness phases, that is in peacetime or defined as *pre-earthquake indicators*, 9 indicators were attributed to the response and recovery phases or defined as *post-earthquake indicators*. To the best of our knowledge this is the first study aimed at identifying useful indicators for the management of earthquakes in the veterinary field to be included in the national contingency plan in accordance with the WOAH *"guidelines on disaster management and risk reduction in relation to animal health and welfare and veterinary public health*". The risk indicators represent a tool needed for the implementation of the National Information System for non-epidemic veterinary emergencies (SIVENE) web GIS, namely for emergency planning, response and recovery to facilitate decision-making process at local, regional and national level; they could have potential applicability at national level being derived from a representative group of experts and the majority of them could be also extended to other type of disasters.

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Genomic surveillance and phylogeographic analysis of vampire bat rabies across Central America using FTA cards and Nanopore sequencing

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Keywords: Genomic surveillance, Phylogeographic analysis, Vampire bat rabies

Abstract

Vampire bat rabies (VBR) poses a major threat to animal and human health and is a chronic economic burden across Central America. Current efforts to reduce the burden, including vaccinating humans and livestock, and bat population control, would benefit from deeper understanding of viral circulation in the bat reservoir. However, long term viral maintenance of VBR arises through complex spatial processes, including co-circulation of viral lineages and transboundary viral invasions. We hypothesise that the highly heterogeneous, narrow, landscape of Central America could favour viral diffusion along ‘transmission corridors’, which may be strategic points to target interventions. To understand epidemiological linkages within and across countries, international scale molecular level monitoring is required, but existing national surveillance systems are largely disjoined and most lack capacity for virus molecular characterisation.

We present viral genomic data from 7 countries derived from a new cooperation involving the 9 member countries (Belize, Costa Rica, Dominican Republic, El Salvador, Guatemala, Honduras, Mexico, Nicaragua and Panama) of the International Regional Organisation for Agricultural Health (OIRSA). Rabies positive brain samples are preserved in duplicate on Whatman or Qiagen FTA cards for robust sample banking in the country of origin, and room temperature shipping to regional reference laboratories. Rabies genomes are enriched by amplification of 400bp overlapping regions, prior to WGS using Oxford Nanopore Technologies MinION. Regionally derived sequences and spatiotemporal metadata are analysed using IQTREE for phylogenetic tree generation and MADDOG for high-resolution lineage assignment with results updated on a map for internal reporting.

Initially, 126 FTA cards were obtained from 7 countries from wild and domestic animals, spanning 8 years. Whole genome sequencing (WGS) coverage of >90% was obtained for 65% of the first 58 samples processed using two initial primer schemes (broadly representing 'North' and 'South' viral circulation). We found strong amplification bias towards lineages most closely related with the reference sequences, but only 7% of samples were undetectable. Our analysis designated 3 new rabies lineages, for which we observed within-country co-circulation, and revealed high levels of viral sharing between neighbouring countries according to the clustering of the phylogenetic tree.

Our regional rabies sequencing network has built laboratory and data analysis capacity in a region where few full rabies genomes were previously available. Future work will apply evolutionary landscape resistance models to our growing VBR dataset to reveal the spatial-temporal dynamics of VBR dispersal and transmission corridors, ultimately supporting more efficient rabies prevention strategies.

Preliminary analyses of two floodwater mosquito populations and Earth Observation data (Sentinel2 spectral bands) in collection sites in Central Italy

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Keywords: Floodwater mosquitoes, Earth Observation data, Normalized Difference Water Index

Abstract

Vector presence and population dynamics are strongly linked to climatic factors (Chevalier et al., 2004), which consequently can have an impact on the transmission of vector borne diseases. In particular, the abundance of floodwater mosquitoes results from the successive waves of adult emergences due to different flooding of the breeding sites (Becker et al., 2010). Floodwater mosquitoes (e.g. *Aedes vexans* and *Aedes caspius*) commonly reach high abundance levels, causing tremendous nuisance in the near and far surroundings, and possibly acting as vectors of arboviruses (e.g. Rift Valley Fever and West Nile viruses). In this preliminary analysis, the abundance of floodwater mosquitoes, determined by field data collections, was compared with Earth Observation data of the same area.

The field data were collected during an intensive and systematic entomological surveillance, carried out in Abruzzo and Molise Regions, as part of the National Plan for prevention, surveillance and response to West Nile and Usutu viruses, and other research projects. The field activity was carried out in four mosquito seasons (2019 – 2022) from May to November; the insect collections were performed weekly or biweekly, using CDC-light traps baited with CO_2. Overall, 2,145 collections were made in 60 collection sites and almost 45,000 mosquitoes were morphologically identified, belonging to the 7 genera present in Italy and to 20 different species. Basing on the abundance of floodwater mosquitoes, two collection sites were selected to for this study: Campomarino (Molise Region), where 87.1% of collected mosquitoes belongs to *Aedes caspius*, and Altino (Abruzzo Region), where *Aedes vexans* shows its highest abundance. The two sites are close to a marshy area and a river, respectively.

To catch the local characteristics of the possible mosquito breeding sites, the field data collected in two sites were compared with high resolution images by means of the Normalized Difference Water Index (NDWI) trend, using the free web application EO browser (https://www.sentinel-hub.com/explore/eobrowser/) and selecting the time range relevant for mosquito

emergence. NDWI index is used to monitor changes related to water content in water bodies, using green and near infrared bands of the electromagnetic spectrum (McFeeters, 1996). Abundance peaks of the two mosquito populations were detected approximately 3 weeks after the increase in water surface, following periods of drought.

This work is a preliminary attempt to use Sentinel-2 data to explain trend/abundance in two mosquito species in central Italy. Limitations due to differences in timing among mosquito collections, satellite passages, cloud coverage, should be considered in further analyses, as well as integration of other data and sources.

Understanding the main drivers leading to abundance peaks of mosquito population would be helpful to focus vector control programs. In this perspective, new insights could derive using new satellite imagery.

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Exploring the effects of outdoor access and farm size on highly pathogenic avian influenza virus diffusion among poultry farms in southwest France

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Keywords: Modeling, Mechanistic, Transmission, Spatial, Avian flu, Biosecurity

Abstract

Highly pathogenic avian influenza (HPAI) continues to be a severe on-going threat to domestic and wild birds, with the French poultry sector experiencing both animal health and economic impacts every year. Current between-farm transmission dynamics have been mechanistically explained through farm populations having species-dependent infectivity and susceptibility. During the 2016-2017 French epidemic, dynamic models have shown that duck farms were both more infective and susceptible to HPAI than poultry farms. However, aviculture farms differ across more qualities than only species presence, including rearing practices and environmental exposure, flock sizes, and temporal activity periods. Differences in infectivity and susceptibility among duck farms are hypothesized to be related to indoor and outdoor farming practices, as different stages in the production cycle occur in different environments. Further, differences in individual farm contribution to epidemic propagation is hypothesized to be explained through farm size. To test these hypotheses, we developed an individual-based, spatially-explicit, deterministic model of HPAI transmission that accounts for the varying periods of activity and inactivity among farms, and also considers the dynamic nature of outdoor raising restrictions. This model is currently being parameterized to 2021–22 historical epidemic data of southwest France, and will be used to elucidate transmission rates, relative susceptibility, and relative infectivity of the different types of duck farms. The discovered parameters will then be fed into stochastic models to explore alternative epidemic outcomes across different biosecurity scenarios, such moving the pre-fattening stage of foie gras duck raising exclusively indoors, or instituting various poultry vaccination strategies.

Investigation on the presence of Hepatitis E virus in different animal species populations in Abruzzo and Molise Regions during the 2015-2021 period, Italy

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Keywords: wild boar, pig, epidemiology, hepatitis E virus (HEV), public health, wildlife, zoonoses

Abstract

Hepatitis E virus (HEV) is a zoonotic pathogen, causing infectious hepatitis in man. Pigs and wild boars are the natural asymptomatic reservoirs, while the disease in humans could be either asymptomatic or evolve in hepatitis. In Europe, an increasing number of human infections from HEV has been reported over the last years. Up to now, HEV prevalence in Italian northern Regions has been extensively determined in wild boars and pigs, while less data have been collected from the central-southern ones, especially in wild animals. Moreover, the Abruzzo Region located in central Italy is considered a hot spot for HEV human infections and Molise Region, located in southern Italy and close to Abruzzo, should be also taken in consideration. The aim of this study was to investigate the circulation of HEV in different animal species from Abruzzo and Molise Regions, central-southern Italy. Liver, gallbladder and faeces samples were collected from pigs coming from closed farms or kept free-ranging and from hunted wild boars. Liver samples from other wild species were also considered. Overall, RNA from HEV virus was detected in 336 samples out of the 4,486 collected during the 2015-2021 period (7.5%, CI 6.8% - 8.3%). Animal species in which HEV genome was detected were wild boars (10.3%, CI 9.2% - 11.6%), domestic swine (5.6%, CI 4.6% - 6.9%), roe deer (2.2%, CI 1.0% - 4.8%), deer (2.4%, CI 0.7% - 8.3%), and badger (1.7%, CI 0.4 – 9.1). The positivity in liver samples was higher than in faeces, which was higher than in gallbladder. The higher number of positive samples was found in wild boars, and especially in liver. The results of this study suggest that HEV infection seems to be endemic in the wild boars living the two Regions under study. The detection of HEV RNA in other non-target species, such as roe deer, deer, and badgers also warrant consideration in surveillance programs and in estimating the risk for HEV human infections.

Network Analysis and Modelling for Prevention and Control of Equine Infectious Diseases in Italy: A Data-Driven Approach

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Keywords: Spatio-Temporal analysis, network analysis, Equine Infectious Diseases, Data-Driven approach, ML, Tracing

Abstract

The equine sector in Italy is of great importance and contributes significantly to the country's economy. However, it faces numerous challenges in preventing and controlling infectious diseases, which can have devastating effects on horse health, welfare, and the equine industry as a whole. The Italian Ministry of Health-funded research project (2021-2022) aimed to assess the vulnerability of the equine sector to disease incursions such as the African Horse Sickness Virus (AHSV) or the spread of Equine Infectious Anaemia Virus (EIAV), and others (Dominguez et al., 2016; Fairbanks et al., 2022).

Through network analysis, spatial-temporal analysis, and machine learning techniques, we identified high-risk areas, periods, and strategic nodes within the Italian equine network to be targeted for preventing and controlling the risk of incursions from abroad and the internal spread of diseases.

Machine learning approaches combined national entomological surveillance data with satellite-derived temperature time series to determine if establishments introducing animals from abroad were suitable for AHSV vectors. The Random Forest algorithm achieved an 84% accuracy in this task.

Spatio-temporal clustering identified significant clusters of importing establishments, primarily in northern Italy, central Italy, and the Lazio Region, with equestrian sport, recreational equestrian, and riding schools being the most at-risk sectors (comprising 76% of high-risk activities). Spring and summer were identified as the most at-risk seasons (Martínez-López et al., 2011). To assess the size and speed of a possible epidemic's spread on the internal movement network, we calculated the Giant Strongly Connected Component (GSCC). This encompassed 33% of the network's nodes, evenly distributed throughout the country. Within the GSCC, approximately 2.5% of the nodes were identified

as super hubs, i.e. nodes exhibiting high values of both degree and betweenness. These establishments play a crucial role, as they can infect many nodes directly connected or act as bridges between groups of nodes, thus facilitating rapid and vast hypothetical epidemics. Moreover, 1% of all establishments proved to be spatial super-spreaders and or super-susceptibles, that is to say, they can spread the infection over long distances.

The analysis conducted to prevent the spread and introduction of equine diseases in Italy has been complemented by EquiTracing, a disease control web tool. This integration significantly enhances efforts to contain the spread of equine diseases. By utilizing cutting-edge technology, it enables real-time access to data from the National Animal Disease Reporting System (SIMAN) and the Equine Movement Database (BDN-E).

EquiTracing empowers authorities to trace equine movements, identifying infection sources and contact chains. It offers interactive tables, maps, graphs, querying and analyzing tools, tracing animals or batches, and generating dynamic reports.

In conclusion, these results start an ongoing research journey. The data-driven approach and knowledge aid informed decisions and efficient prevention plans for equine diseases.

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The role of multi-species bird migration network in West Nile disease dynamics in Italy

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Keywords: Bird migration, West Nile Virus, spatial clustering, network analysis, One Health, vector-borne diseases

Abstract

Avian migration plays a critical role in the transmission of vector-borne diseases, including West Nile Virus (WNV). WNV has become endemic in Northern Italy's Po Valley since 2008, affecting many resident bird species, and in Sardinia, where WNV circulation has been mainly reported in migratory birds. Sporadic cases have also been reported in southern Italy, and some northern regions along the Tyrrhenian coast. A comprehensive One Health approach, integrating human, terrestrial vertebrate, and entomological surveillance, is vital for the timely detection of the seasonal virus spread to applying preventive measures (Candeloro et al., 2020).

This study investigates avian migration's role in shaping the dynamics of WNV in Italy, enhancing understanding of transmission patterns. Ringing and recovery data of birds ringed in Italy (from 2008 to 2017) were retrieved from ISPRA's Italian Ringing Center.

Spatial clustering and network analysis were employed to generate and characterize the bird migration network (Lamb et al., 2019). The network included 31 spatial clusters and 71 links. Strong agreement between network metrics (In-degree, Out-degree, In-strength, Out-strength, and Betweenness) and WNV cases was observed. Clusters encompassing regions featured by the presence of endemic areas were found to be highly vulnerable or able to spread the infection. Tuscany and Lazio Regions emerged as network hubs, underlining their significant role in WNV circulation.

The Giant Strongly Connected Component (GSCC) linked the endemic area to other WNV-affected Regions. Community detection analysis highlighted connections during the spring season between northern Sardinia, Tuscany, and Abruzzi Regions, accordingly with GSCC. During summer, GSCC extended to southern Sardinia. Except for Campania, low northern-southern Italy connections correlated with fewer outbreaks observed in the latter. Dynamic measures, like Forward/Backward

Reachable Set (FRS/BRS), accounted for time/direction and confirmed the previous results. BRS, during the epidemic season, showed a limited connection from the endemic area to central-southern Italy.

To explain the disease's spatial-temporal distribution, we developed a network-based stochastic SEI model, accounting for the suitability of WNV circulation, uncertainty in the timing of movements, and disease incubation period. Evaluated scenarios: 1) Disease spread within Italy from endemic areas, 2) Introduction from Africa.

Results confirmed and expanded on network analysis. In scenario 1, infection reached clusters including Sardinia, Campania, and Basilicata (30-35% simulations), despite unfavorable seasonal conditions for viral circulation at the time of exposure. Liguria showed infection during favorable conditions. In scenario 2, southern Italy (e.g., Puglia) had foreign-origin infections. Notably, northern Sardinia, in Scenario 1, showed autumn exposure pick in this scenario.

The study analysed selected bird species' migration in Italy using static, seasonal, and dynamic network analysis. Viral circulation was detected and supported by the SEI model. Concerns about data representativeness, particularly in Sicily and Sardinia, highlighting the need for broader migration data, including telemetry data.

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The "Land of Fires" Platform for emergency management, data sharing and dissemination

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Keywords: Campania Region, environmental emergency, geoportal, land of fires, web-GIS

Abstract

During the past years, Campania Region experienced an environmental emergency due to illegal dumping of industrial and domestic waste, often set on fire so the involved area was dubbed “Terra dei Fuochi” (Land of Fires-TdF). This led to deep concerns over population health and over potentially devastating impact on the agricultural market, one of the pillars of the region’s economy (Comba et al., 2006). In such a context, a timely, accurate, and reliable flow of information, aimed both at the population and at stakeholders, is crucial for establishing a proper dialogue between institutions and people, driving the empowerment of citizens.

In response to the emergency, the Italian Government issued the Law n. 6 of 2014, converting the Decree 136 of 2013 (D.L. 2013), and set up an ad hoc multidisciplinary Working Group (WG) to identify the sites affected by spills and illegal disposal on the territory. Moreover, WG defined a process to classify those sites in terms of ban production rather than a limitation to specific crops, consequently, allowing appropriate measures to restore the affected sites.

An adequate infrastructure to support knowledge sharing is a strategic component for efficient and effective emergency management. For this purpose, the Italian Government commissioned the IZS Abruzzo e Molise “G. Caporale” (IZS-Teramo), the development of an IT platform (D.L. 2016) to gather and disseminate standardized data, knowledge, and technologies.

The Land of Fires Platform collects a variety of geographical and non-geographical datasets, in ESRI Shapefile and Excel spreadsheets, which have been processed, and normalized to fit the Oracle 12g database structure. The database was connected to an ArcGIS Server 10.8.1 sharing a ReST and a WMS interface to the underlying data.

The platform front-end is a GeoPortal providing users with various applications and services such as a

web application for documents management and a GIS Dashboard allowing viewing results through graphs, tables, and an interactive thematic map. Lands belonging to the municipalities under investigation are also available as OGC WMS and ReST web services in order to maximize opportunities for information reuse. Furthermore, a weekly scheduled procedure publishes updated data on a public repository hosted on the GitHub platform.

In particular, the TdF GIS Dashboard has been realized through the ArcGIS Online Operations Dashboards cloud platform in conjunction with a custom application developed using JavaScript open source libraries.

Despite the technical challenges of fusing data from mixed sources and the potential concerns on data ownership, the platform represents an excellent result of collaboration and cooperation for emergency management and data dissemination and a valid point of reference for the definition of a model of communication between stakeholders and community engagement, that can be reproduced and reused in different areas, at national and international level.

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Evaluation of Sea Surface Temperature trend across aquaculture sites in Central Adriatic Sea

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Keywords: Sea Surface Temperature, Time Series, trend, Abruzzo Region, Adriatic Sea, Aquaculture

Abstract

Water temperature is an important variable in aquaculture as growth and survival of aquatic animals and molluscs strongly depend on it. Water temperature can be measured through satellites by using the infrared part of the electromagnetic spectrum and capturing the thermal emission. Satellites dedicated to Earth Observation (SEO) regularly acquire information both on land and at sea.

The aim of this study was to collect analysis ready data derived from Earth Observation to investigate the trend of Sea Surface Temperature (SST), over the last 15 years of the coastal waters facing Abruzzo Region. Knowing the trend of sea temperature could help shellfish farming management, as temperature is a key factor for the growth and survival of all organism. To provide aquaculture with useful information, the SST values were extracted at the central point of the farms, for both existing and potential sites.

Among the available satellite-derived products, the “Mediterranean Sea High Resolution and Ultra High Resolution Sea Surface Temperature Analysis" was chosen from the CMEMS repository of European Copernicus programme as a good compromise among spatial accuracy, temporal frequency and temporal coverage (Buongiorno Nardelli et al., 2013), besides undergoing gap-filling procedure.

The data spanning from 2008 to 2022 was acquired and processed using customized procedures developed within the framework of open-source software, specifically R and QGIS.

A time series analysis method was applied to the average daily values of the SST identifying the components of the additive model: trend, seasonality and random effects. The significance of the trend was evaluated through the Mann-Kendall statistical test for all farms, most of which showed a statistically significant increasing trend. A linear regression analysis applied on trend data (excluding seasonality and background noise), estimated an annual average temperature increase of 0.010

degrees Celsius over the given period (Filipponi et al., 2017).

The SST seasonality follows the atmospheric temperature one, with colder winters and hot summers in the study area.

Climate change represents a potential limiting factor for the breeding of bivalve molluscs by directly interfering with their survival and their behaviour. It has been demonstrated that the increase in temperature is also one of the main factors triggering events that lead to the accumulation of some biotoxins in European bivalves (Dhanji-Rapkova et al., 2023).

Continue monitoring the surface temperature of the seas is of fundamental importance for assessing the ecosystem health and evaluate the resilience of marine ecosystems. Satellite Earth Observation could greatly help in this objective, providing free data of sea surface waters, remotely detected, with high frequency and high accuracy.

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Tibaldi Alberto
Tironi Marco
Tizzani Paolo
Toccaceli Barbara
Tocchio Antonio
Toffan Anna
Tomassetti Barbara
Tomassone Laura
Tonazzini Sara
Tora Susanna
Toro Michela
Toson Marica
Tran Annelise
Tratalos Jamie
Triguero-Ocaña Roxana
Upton Paul
Valbonetti Luca
Valencio Artur
Valls-Fox Hugo
Van Boeckel Thomas P.
Van Bortel Wim
van Klink Ed G.M.
Vanwambeke Sophie O.
Venegas Cureno Emilio
Vergne Timotheé
Viani Annalisa
Vicente Joaquín
Villaudy Sylvain
Viltrop Arvo
Vincenti Gonzalez Maria Fernanda
Visée Corentin
Vogels Chantal B.F.
Vroegindewey Gary
Wang Yu
Ward Michael P.
Wells Konstans
Widgren Stefan
Wint William
Wiratsudakul Anuwat
Wisnieski Lauren
Wisser Dominik
Yah Donaldo
Yang Qihui
Zenobio Valentina
Zhao Cheng
Zoppi Giacomo
Zurno Jacob

GEOVET 2023

Expanding boundaries: Interdisciplinary geospatial research for the One Health Era

Program

September 19th - 21st 2023

Silvi Marina, Teramo, Italy

IZS
TERAMO

Tuesday, 19th September

8:30am - 9:00am

Opening Ceremony
Chair: **Annamaria Conte**

SESSION 1

From Science to Policy: GIS and One Health integration
Chair: **Michael Ward**

9:00am Keynote Talk: **“The challenges of real-time science communication and decision support in a pandemic context: building the plane instruments after take-off”**
Speaker: **Marius Gilbert,** *Vice-rector of research and Head of the Spatial Epidemiology Lab (SpELL), Université Libre de Bruxelles, Belgium*

9:40am Senior Oral Talk: **“Communication Breakdown – Of disease clusters, a trillium and One Health”**
Speaker: **Olaf Berke,** *Department of Population Medicine, OVC, University of Guelph, Canada*

10:05am **“The use of spatial metrics to select regions for enhanced bovine tuberculosis control measures in Ireland”**
Speaker: **Jamie Tratalos,** *Centre for Veterinary Epidemiology and Risk Analysis. University College Dublin, Ireland*

10:20am **“Poultry intensification and emergence of Highly Pathogenic Avian Influenza”**
Speaker: **Maria Fernanda Vincenti Gonzalez,** *Universite Libre de Bruxelles, Belgium*

10:35am **“Precision epidemiology in practice: applications to better prevent and control endemic diseases in the US swine industry”**
Speaker: **Beatriz Martínez-López,** *CADMS, Department of Medicine & Epidemiology, School of Veterinary Medicine, University of California, Davis, USA*

10:50am **“How to combine spatio-temporal information and Danger theory for animal disease surveillance?”**
Speaker: **Bahdja Boudoua**, *INRAE, France*

11:00am – 11:30am coffee break

SESSION 2

Exploring Novel Data Sources and Operational Tools
Chair: **Guy McGrath**

11:30am Senior Oral Talk: **“Mapping global coldspots of veterinary capacity”**
Speaker: **Nicola G. Criscuolo,** *ETH Zürich, Switzerland*

11:55am **“Anthropogenic and environmental factors associated with koala deaths occurring through vehicle collisions and dog attacks in South East Queensland, Australia”**
Speaker: **Mark Stevenson,** *Melbourne Veterinary School, Faculty of Science, The University of Melbourne, Australia*

12:10am **“Epidemic intelligence data and disease risk mapping: the case of Crimean-Congo haemorrhagic fever (CCHF)”**
Speaker: **Angela Fanelli,** *Department of Veterinary Medicine, University of Bari, Italy*

12:25am **“Geospatial Methods for Reporting During the United States 2022-2023 Highly Pathogenic Avian Influenza (HPAI) Outbreak and Ongoing Emergency Response Preparedness“**
Speaker: **Andrew Fox,** *U.S. Department of Agriculture (USDA) Center for Epidemiology and Animal Health (CEAH), USA*

1:00pm – 2:00pm lunch

Tuesday, 19th September

SESSION 3

Climate, human and enviromental impact on animal health

Chair: **Annalise Tran**

2:00pm Keynote Talk: **"Decision-support tools to track and predict climate-sensitive infectious diseases at cascading spatial scales"**
Speaker: **Rachel Lowe,** *ICREA Research Professor at Barcelona Supercomputing Center – Centro Nacional de Supercomputación (BSC-CNS), Spain*

2:40pm Senior Oral Talk: **"Impact of climate change on soil-borne and vector-borne diseases"**
Speaker: **Cyril Caminade,** *Abdus Salam International Centre for Theoretical Physics, Italy*

3:05pm **"Contribution of climate change to the emergence of West Nile virus in Europe"**
Speaker: **Diana Erazo,** *Université Libre de Bruxelles (ULB), Belgium*

3:20pm **"Reducing data collection costs through sensitivity analysis of spatial data in GLEAM"**
Speaker: **Armando Rivera Moncada,** *Université Libre de Bruxelles (ULB), Belgium*

3:35pm **"Predicting socioeconomic and intervention-related factors influencing the risk of vector-borne diseases using Demographic and Health Surveys; a case study of malaria"**
Speaker: **Camille Morlighem,** *Department of Geography, University of Namur, Belgium; ILEE, University of Namur, Belgium*

3:50pm – 4:15pm coffee break

SESSION 4

Spatial methods in ecology and epidemiology

Chair: **Marius Gilbert**

4:15pm **"Using joint species distribution models to improve predictions of co-infection in veterinary epidemiology"**
Speaker: **Francisca Powell-Romero,** *School of Veterinary Science, The University of Queensland, Gatton, Qld, Australia*

4:30pm **"Combining key hazard-and exposure-related drivers to model the probability of occurrence of TBE human cases in Europe"**
Speaker: **Francesca Dagostin,** *Fondazione Edmund Mach, Italy*

4:45pm **"Reducing uncertainty in spatial analysis involving fragmentated farms"**
Speaker: **Guy McGrath,** *University College Dublin, Ireland*

5:00pm **"Mapping bioclimatic suitability for cattle ticks in Ecuador"**
Speaker: **Ximena Pérez-Otáñez,** *Université Catholique de Louvain, Belgium*

5:15pm **"Remote sensing as an additional tool for modelling spatiotemporal dynamics of questing *Ixodes ricinus* on Italian northwestern Alps"**
Speaker: **Alessandro Bellato,** *Università di Torino, Dipartimento di Scienze Veterinarie, Italy*

5:30pm *Poster Session*

6:30pm **Closure of the day**

7:00pm **Free time: Shuttle bus to Pescara**

SESSION 5

Expanding boundaries of Remote Sensing

Chair: **Cyril Caminade**

8:30am Keynote Talk: **“Infectious water-associated diseases: the role of the environment”**
Speaker: **Shubha Sathyendranath,** *Merit Remote Sensing Scientist, Plymouth Marine Laboratory, UK*

9:10am Senior Oral Talk: **“Mapping Global Bushmeat Activities to Improve Zoonotic Spillover Surveillance”**
Speaker: **Cheng Zhao / Thomas Van Boeckel,** *ETH Zürich, Zurich, Switzerland*

9:35am **“How to integrate satellite-derived indicators into models of animal mobility?”**
Speaker: **Annelise Tran**, *CIRAD – Center for International Cooperation in Agricultural Research for Development, France*

9:50am **“Use of Satellite Earth Observation to monitor aquaculture sites in coastal Abruzzo region, Adriatic Sea”**
Speaker: **Carla Ippoliti,** *IZS-Teramo, Italy*

10:05am **“How the scale of temperature measures affects the estimate of transmission of mosquito-borne diseases”**
Speaker: **Sebastian Napp,** *Centre de Recerca en Sanitat Animal (CReSA)-Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Barcelona, Spain*

10:20am **“Tick’s suitability habitat maps and tick-host relationships in wildlife. A One Health approach based on multitemporal remote sensed data, entropy and Meta® population dataset in Aosta Valley, NW Italy.”**
Speaker: **Annalisa Viani / Tommaso Orusa,** *IZS PLV S.C. Valle d’Aosta—CeRMAS (National Reference Center for Wildlife Diseases), Quart, Italy*

10:35am

Senior Oral Talk: **“Landscape phylogeography — using viral gene sequences to compare and explain the heterogeneous spatial dynamics of virus epidemics”**

11:00am – 11:30am coffee break

SESSION 6

Modelling for ASF emergency

Chair: **Paolo Calistri**

11:30am Senior Oral Talk: **“Choice of Landscape Discretisation Affects the Rate of Spread in Wildlife Disease Models”**
Speaker: **Mossa Merhi Reimert,** *University Of Copenhagen, Denmark*

11:55am **“Examining the Impact of Fencing on the Front Wave of African Swine Fever in the Korean Wild Boar Population”**
Speaker: **Jun-Sik Lim,** *Ecole Nationale Vétérinaire de Toulouse, France*

12:10am **“Elucidating African swine fever transmission cycle dynamics at the domestic-wildlife interface: Multihost epidemic modeling in Romania”**
Speaker: **Brandon Hayes**, *IHAP, University of Toulouse, INRAE, ENVT, Toulouse, France*

12:25am **“Spatially explicit agent-based modeling as a tool in aiding African swine fever mitigation and eradication in Thailand”**
Speaker: **Peerawat Chintrakulchai / Beatriz Martínez-López,** *CADMS, School of Veterinary Medicine, University of California, Davis, USA*

12:40am **“Spatial analysis to inform African Swine Fever spread modelling in Laos”**
Speaker: **Michael Ward,** *Sydney School of Veterinary Science, The University of Sydney, Australia*

1:00pm – 2:00pm lunch

Wednesday, 20th September

SESSION 7

Artificial intelligence for One Health

Chair: **Rowland Kao**

2:00pm Keynote Talk: **"Issues and challenges in fair and robust AI models"**
Speaker: **Elisa Ficarra,** *Department of Engineering "Enzo Ferrari" University of Modena and Reggio Emilia, Italy*

2:40pm Senior Oral Talk: **"Shade from Space: Utilizing Satellite Imagery to Assess Shade Provision on New Zealand Dairy Farms"**
Speaker: **Matthew Edwards,** *EpiVet, New Zealand*

3:05pm **"Earth Observation-based Self Organizing Map for Northern Africa regions"**
Speaker: **Annamaria Conte,** IZS-Teramo, Italy

3:20pm **"Predicting spatially explicit swine premises using deep learning and aerial imagery to improve disease monitoring and surveillance"**
Speaker: **Felipe Sanchez,** *Center for Geospatial Analytics, Department of Population Health and Pathobiology, College of Veterinary Medicine, North Carolina State University, USA*

3:35pm **"Forecasting West Nile Virus Circulation through Sentinel and Landsat Imagery and Graph Neural Networks"**
Speaker: **Lorenzo Bonicelli,** *Department of Engineering "Enzo Ferrari" University of Modena and Reggio Emilia, Italy*

3:50pm – 4:15pm coffee break

4:15pm *Roundtable*
"GeoVet science into practice for One Health"
Moderator: **Barbara Alessandrini**

5:30pm *Poster Session*

6:30pm - 6:45pm **Closure of the day and group photo**

8:00pm **social dinner**

SESSION 8

Network analysis for transmission pathways
Chair: **Beatriz Martínez-López**

8:30am Keynote Talk: **"Emergent infection disease problems under environmental land management"**
Speaker: **Rowland Kao,** *Professor of Veterinary Epidemiology and Data Science Roslin Institute & School of Physics and Astronomy, University of Edinburgh, UK*

9:10am Senior Oral Talk: **"Landscape Connectivity and travel corridors routes for predicting the spread of ASF in European wild boar"**
Speaker: **Jaime Bosch,** *VISAVET Health Surveillance Centre and Animal Health Department, Complutense University of Madrid, Spain*

9:35am **"Multihost foot-and-mouth disease dissemination model: why using just cattle data neglects the disease spread potential and covered transmission routes"**
Speaker: **Nicolas Cespedes Cardenas,** *North Carolina State University, USA*

9:50am **"Integration of spatial and network analysis to undercover community exposure to zoonotic vector-borne diseases: the example of Ross River Virus during the COVID19 lockdown in Brisbane Australia"**
Speaker: **Tatiana Proboste,** *University of Queensland, Australia*

10:05am **"On the interaction between bovine and bubaline trade network in epidemic spreading"**
Speaker: **Giacomo Zoppi,** *Data Analysis and Modeling Unit, Department of Veterinary Sciences, University of Torino, Italy*

10:20am **"Development and application of a network model to understand the epidemiological and economic burden of an aquaculture disease outbreak under different control strategies"**
Speaker: **Sarah Alewijnse,** *Centre for Environment Fisheries and Aquaculture Science, UK*

10:35am **"Movenet: a toolkit facilitating the use of livestock movement networks in veterinary public health"**
Speaker: **Carlijn Bogaardt,** *School of Computing Science, University of Glasgow, UK*

10:50am – 11:30am coffee break

SESSION 9

Genetics and Bioinformatics
Chair: **Olaf Berke**

11:30am **"Development of an operational tool for genomic and phenotypic surveillance of antimicrobial resistance: applications for swine pathogens in the United States"**
Speaker: **Ruwini Rupasinghe,** *CADMS, Department of Medicine & Epidemiology, School of Veterinary Medicine, University of California, Davis, USA*

11:45am **"Geographical isolation in an interconnected world: application of phylodynamic and phylogeographic methods for the investigation of Porcine circovirus type 4 history"**
Speaker: **Giulia Faustini,** *Department of Animal Medicine, Production and Health (MAPS), University of Padua, Italy*

12:00am **"Unravelling the epidemiology of *Mycobacterium bovis* in North Cameroon using genomic, environmental and demographic data"**
Speaker: **Gianluigi Rossi,** *University of Edinburgh, UK*

12:15am “West Nile Virus in Europe: a return ticket to Africa”
Speaker: **Giulia Mencattelli,** *IZS-Teramo, Fondazione Edmund Mach, University of Trento, Italy*

12:30am “Antimicrobial resistance in food animals: priority drugs maps to guide global surveillance”
Speaker: **Cheng Zhao,** *ETH Zürich, Zurich, Switzerland*

1:00pm – 2:00pm lunch

SESSION 10

Spatio-temporal surveillance and modelling

Chair: **Mark Stevenson**

2:00pm “Disentangling the role of wild bird species in Avian Influenza transmission to domestic poultry”
Speaker: **Diletta Fornasiero,** *IZSVe, Italy*

2:15pm “Estimating the coverage of slaughterhouse surveillance for bovine tuberculosis”
Speaker: **Jose HH Grisi-Filho,** *Universidade de São Paulo, Brazil*

2:30pm “Modelling transmission of avian influenza in wild birds using a spatiotemporal cellular automata model”
Speaker: **Yangfan Liu,** *Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark*

2:45am “Spatial distribution of poultry farms using point pattern modelling: a methodology to address disease transmission risks.”
Speaker: **Marie-Cécile Dupas,** *University of Brussels (ULB), Belgium*

3:00am “Assessing the risk of arbovirus outbreaks in non-endemic regions”
Speaker: **Bruno Valdemar Guerrero Borges,** *Basque Center for Applied Mathematics, Spain*

3:15am “Surveillance data and early warning models of highly pathogenic avian influenza in East Asia, 2020-2022”
Speaker: **Lene Jung Kjær,** *University of Copenhagen, Denmark*

3:30am “A raster-based compartmental model combining the host's density and movements, driven by vector suitability”
Speaker: **Luca Candeloro,** *IZS-Teramo, Italy*

4:00pm – 5:00pm **Closure of the conference – Awards – Next GeoVet**

Thanks to all GeoVet2023 participants

Dear GeoVet 2023 participants,

I would like to thank you all for your active participation and enthusiasm in making GeoVet 2023 a resounding success. It has been an incredible journey.

I am immensely proud of what we have achieved together. GeoVet 2023 featured an impressive program, consisting of 5 enlightening keynote talks, 8 senior talks, 43 captivating presentations, and 50 insightful posters. The roundtable dialogue with International Organizations and Scientists showcased the potential collaborations and solutions to explore the symbiotic relationship between science and policy-making. This dialogue has opened doors to constructive engagement between scientists and international organizations, paving the way for impactful change.

I am confident that the relationships forged and the knowledge shared during this conference will continue to shape the future of interdisciplinary geospatial research for the One Health era.

The next GeoVet in 2026 will be hosted in Brussels, organized by Université Libre de Bruxelles, Université de Namur, and AviaGIS. With the handing over of the torch, another monumental event for our community is going to happen.

Again, I thank you for your unwavering support and active participation. Let's carry the spirit of GeoVet 2023 forward as we work together to address the most pressing health challenges of our time.

Annamaria Conte
Chair of the GeoVet 2023 Conference
Head of Statistics and GIS Unit of the National Reference Centre for Epidemiology
IZS-Teramo, Italy

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