The Role of Ecology in Understanding and Modeling Animal and Human Diseases

Muhammad Saqlain¹, Sana Iram^{1,*}, Abdul Rehman¹, Humayun Ali¹, Anam Fatima¹, Sadia Hafeez¹, Zunaira Qamar¹, Muhammad Taimoor¹, Kiran Zahra¹ and Muhammad Ahsan¹

¹Department of Zoology, Wildlife and Fisheries, University of Agriculture, Faisalabad, Pakistan *Corresponding author: <u>sanairam8427@gmail.com</u>

Abstract

Ecology is interaction between organisms in environment that play crucial role in the sustainability of ecosystem by regulates various environmental processes for benefit of global biota. Sometimes these interactions trigger changes that facilitate the circulation of pathogens within ecosystem. Ecology and disease ecology provides better insights into understanding disease dynamics and out-break management. The key reason in increase and expansion of emerging infectious diseases which are directly associated with human-driven factors including, deforestation along with global climate changes and urbanization. Alongside modernization, these worldwide anthropic modification being the cause of the emergence of diseases for wild and livestock animals, and even humans. Emerging pathogens and zoonosis raise pervasive health risks in both animal and human populations. By use of ecological fundamentals with epidemiological modelling approaches provide useful insights in mitigating the exacerbating threats caused by zoonotic spillover. Epidemiological models including meta-population models, compartmental models, agent base models (ABM) together with machine learning models facilitate valuable data like disease prediction, improve both ecosystem and public-health in terms of disease transmission and control. Overall, ecology in combination with epidemiological modelling and disease ecology provide multidisciplinary framework for human and non-humans species health

Keywords: Ecology, Disease ecology, Eco-epidemiological modelling, Zoonosis, Anthropogenic pressures

Cite this Article as: Saqlain M, Iram S, Rehman A, Ali H, Fatima A, Hafeez S, Qamar Z, Taimoor M, Zahra K and Ahsan M, 2025. The role of ecology in understanding and modeling animal and human diseases. In: Abbas RZ, Akhtar T and Arshad J (eds), One Health in a Changing World: Climate, Disease, Policy, and Innovation. Unique Scientific Publishers, Faisalabad, Pakistan, pp: 276-284. https://doi.org/10.47278/book.HH/2025.148



A Publication of Unique Scientific Publishers **Chapter No:** 25-039

Received: 13-Jan-2025 Revised: 19-Apr-2025 Accepted: 12-May-2025

Introduction

Environment of organism comprises of both biotic and abiotic components. Both of these components interact with each other and utilize resources that are available in ecosystem (Friant, 2024). Ecology offers a wide range of environmental services as well constitute life maintenance systems that are foremost in global health (Small et al., 2017). Interaction among animals, human and environment allow the transmission of zoonosis and pathogens from animals to humans. During the previous decades, a prominent rise in the transmission of pathogenic agents was detected. Threats of pandemic become more and more perilous with the circulation of epidemics and zoonosis as well as epizootics (Destoumieux-Garzon et al., 2018). Outbreak of infectious diseases linked with human influences of animal species and their habitats can have substantial effect on human economies, societies and biological diversity conservation (Cunningham et al., 2017).

Increase in the possibility of infectious diseases emergence rise with the alteration in land utilization such as, intensification of agriculture and deforestation (Bernstein et al., 2022). With the utilization of these relationships, aids in numerous challenging and complicated environmental issues (McCallen et al., 2019). As an important application, disease ecology a subfield of ecology deals with environmental and evolutionary factors that impact on transmission, exposure and acquisition dynamics of pathogens between and within human and animal populations (Balasubramaniam et al., 2020). This field is important to improve our capability to predict, understand and mitigate the influence of emerging pathogens diseases and endemics in wild populations. Additionally, outbreak of pathogenic diseases is predicted to be aggravated due to modern problems such as dense human population, climate change and natural ecosystems fragmentation (Valenzuela-Sanchez et al., 2021).

In order to counter these outbreaks, epidemiological modeling drive a key role in public health planning, both in means of general understanding of disease transmission and control also in terms of predictions for specific situations (Hilton & Keeling, 2019). Adapted from ecology species distribution models, joint species distribution models, hierarchical spatial temporal models and mathematical models as well as machine learning interdisciplinary approaches have significant role in public health planning, mapping out disease risk and recognizing zoonotic disease relationships (Hassell et al., 2021).

Ecology and Disease Dynamics

Disease ecology is regarded as crucial for understanding infectious disease dynamics (Johnson et al., 2015). Hosts are commonly affected

by several parasites and these parasites often spread among various hosts as shown in figure 1. Ecology needs to understand and manage emerging diseases which are inherent in natural systems but are frequently aggravated by societal imbalances (Carlson & Mendenhall, 2019). For instance, the effect of degradation of habitat on pathogen spillover are increasing an area of research that can be utilized to inform risk evaluation and environmental strategy (Plowright et al., 2021). It is necessary to develop a strong foundation and expertise for study of infectious disease in their evolutionary and ecological environments to establish an adequate way of living and increase ecosystem and wildlife health; for instance, we continue to confront challenges such as developing pathogens (Andersen et al., 2020).



Fig. 1: How Disease Transmit in Ecosystem.

Ecology and Disease Transmission

Transmission is key to disease Ecology and epidemiology as well as transmission emergence of parasites and vectors, which is versatile and complicated (Antonovics et al., 2017). Pathogens spread through a wide variety of pathways and depends on the pathogen's resilience in the environment, temperature, climate, virulence and infectious threshold. Pathogenic microbes are transmitted by contact, air, water, food, contaminated equipment and the environment, more rarely vector-borne by insects or animals. Furthermore, the rate of transmission is rising due to the increased mobility, climate change, overcrowding, war and natural disasters, poor hygiene and inadequate infection management (Anderson and Anderson, 2019). Pathogenic microorganisms come from the environment or an affected host, which may be a human or another animal. Direct or intimate contact with an infected person or animal is the only way to spread many human infections as shown in Table 1.

Table 1: Different modes of transmission that transmit numerous kinds of diseases between animals and humans.

Modes of transmiss	sion Eff	ect														Citatio	on	
Direct contact	An	infected	host	transmi	s a	disease	directly	to	another	host	via	direct	contact	as	AIDS	(Meer	ia	et
	(In	munodefi	ciency	Syndron	e) ca	used by	HIV (Hum	an Ir	nmunod	eficien	cy Vii	rus)				al., 20	19)	
Indirect contact	Oco	cur via fon	nites pr	resent wi	hin t	the imme	ediate envi	ronn	nent of a	n infec	ted p	atient a	and the ob	ojects	s used	(Cai	et	al.,
	on	the infecte	ed pers	on.												2020)	•	
Vector bo	orne Veo	tor-borne	diseas	es are tra	nsmi	tted fron	n person to	per	son via a	compe	tent	vector,	such as m	losqu	iitoes,	(Eder	et	al.,
transmission	mie	lges and fl	ies. Mo	ore than	one r	nillion pe	eople per y	ear o	dying of a	malaria	a, den	igue an	d schistos	somi	asis.	2018)		
Airborne transmission Some (particularly small) droplets can remain airborne for longer periods of time and travel co				nside	erable	(Naza	roff,											
	dist	tances, pro	oviding	path for	dise	ase trans	mission.									2016)		
Water bo	orne Wa	terborne d	lisease	s are trar	smit	ted by th	e fecal ora	l rou	te, from	humar	to h	uman c	or animal	to hu	ıman,	(Gerb	a,	
transmission	so f	hat drinki	ing wat	er is only	one	of sever	al possible	sou	rces of in	fectior	ı.					2015)		
Zoonotic transmiss	sion Dis	eases that	t affect	t human	s ori	ginally o	ame fron	n an	imals ar	id mai	ny of	them	are Ebol	la, h	uman	(Zucca	a et a	al.,
	imı	nunodefic	iency v	rirus (HIV	/AII), aviai	n influenza	and	l Monkey	pox.						2021)		

Animal and Zoonotic Eco-Epidemiology

Emerging zoonotic diseases represent progressively growing risk to world health as well as impact on global health care system specifically developing countries (Shaheen, 2022). Diseases transferred among animals and humans referred to as zoonotic diseases. There are over 200 widespread diseases among animals and humans, a number of which can be transferred through direct contact and several by animal derived products (Nemeth, 2024). Zoonotic diseases might be viral, parasitic, and bacterial or incorporate unconventional substances including fungi

and protozoans (Ferreria et al., 2021). Based on transmission modes zoonotic diseases can be categorized into different types as highlighted in Table 2 (Zhang et al., 2024).

Zoonotic Diseases	Effects on Humans	Citations
Covid-19	Respiratory infections as well as a wide range of metabolic, neurological,	(Lenz et al., 2024)
	pulmonary and cardiac issues.	
Rabies	Central nervous system (CNS) damage	(Bastos et al., 2023)
Influenza	.Upper respiratory tract infections range from mil severe, causing fever, chills,	(Swierczynska et al., 2022)
	muscle soreness, pneumonia, and even death.	
Human Immunodeficiency	HIV weaken the body's defenses against infections and cancers by destroying	(Menza et al., 2024)
Virus (HIV)	specific types of white blood cells.	
Ebola	Multiple organ failure and consequences from hemorrhage	(Hussein et al., 2023)
Zika Virus	Pregnancy-related fetal abnormalities are caused by microcephaly.	(Kadu et al., 2024)
	Encephalomyelitis, hydrocephalus, and mild (headaches, muscle soreness) to	(Javed et al., 2024)
Leptospirosis	severe (jaundice, renal failure).	
Hantavirus Pulmonary	Hemodynamics instability and respiratory failure in kids and teenagers.	(Hall et al., 2024)
Syndrome		
Middle East Respiratory	High death rate, pneumonia and respiratory infections.	(Al-Tawfiq & Memish, 2023)
Syndrome (MERS)		

Table 2: The zoonotic disease transmits from	n animals to humans, these diseases	s significantly affect human a	lot in previous decades.
	/	0	

Social Services Impact on Infectious Disease Dynamics

Anthropogenic pressures including climate change, urbanization and deforestation have progressively altered the integrity of global ecosystem, threatening their ability to deliver vital benefits that supports human well-being (Marcolin et al., 2024). Change in climate significantly facilitate zoonotic and animal diseases globally, destabilizing natural ecosystem providing more viable ecosystem for diseases outbreaks as shown in Figure 2. This assist disease causing viruses, fungi and bacteria to move into new ranges, harming livestock species, humans and wildlife (Abdela & Jilo, 2016). Climatic disruption can have direct or indirect impacts on diseases spillover (Bett et al., 2017).



Fig. 2: How Climate Change Fcilitates Pathogens.

Deforestation is another significant issue has been associated with increased risk of zoonotic diseases as shown in Figure 3 (MacDonald & Mordecai, 2019). Human explorations into new areas and formation for recreational activities that elevates the interaction between animal and humans. Additionally, zoonosis risk increases significantly with frequent contact with livestock species, domestic pets, birds and rodents as well as interaction with exotic species (Green et al., 2020). The recent pandemic, the covid-19 has many effects on food supply domain and global health (Attia et al., 2022). The increase in cities and peri-urban zones has directed to expansion of numerous infectious endemics by several means. Urbanization increases the proportion of paved areas that limits the species diversity, change species composition, reduce availability of natural habitat and warms the climate, increases human density leads to changes in social structure, inequality and behavior (Bharti et al., 2015).

The diseases caused by mosquito borne viruses, included Zika, chikungunya, dengue facilitated by *Aedes aegypti* are the canonical diseases linked to urbanization (Nova et al., 2022). Change in land use is process in which unmodified wildlife habitats are altered by human actions, whereby this anthropic modified land serves for economic activities (Winkler et al., 2021). These activities create habitat fringes at the

intersection between human and wildlife, elevating the potential for facilitation of infections within human, domestic animals and wildlife (Glidden et al., 2021). Likewise, severe weather processes such as heat waves, droughts, dryness or water scarcity, heavy rainfall and flooding, melting snow and wildfires highly contribute to the outbreaks of pathogenic diseases (El Sayed et al., 2020).



Contemporary Fig. 3: anthropic pressures such as climate alteration, deforestation and urbanization and agricultural intensification leads many negative impacts on ecosystem that facilitate zoonosis emergence that create problems for global health.

Eco-Epidemics Modeling

A number of models and functional categories have been developed to gain a better understanding of ecological systems and the diseases they regulate (Machado & Oliveira, 2024). In ecological fields, models are simplified representations of complicated systems. Depending on the study's goal, models might be anything from extremely comprehensive to more generic. Their classification is based on their prediction skills, which impacts their use in research by either extrapolating beyond observed conditions or interpolating within known data ranges (Escobar, 2020). In the study of ecological systems, modeling has emerged as a key instrument. Ecological modeling can assist implement sustainable development, mathematical models and system analysis that illustrate how ecological processes might support sustainable resource management (Abbasi et al., 2024). For a number of infectious diseases, reports of the geographic locations of pathogens, disease vectors or reservoirs are growing in quantity, high quality and easily accessible. These factors can be coupled with disease data to rebuild or forecasting the geographic distribution of vector-borne (e.g., Bluetongue), environmentally (e.g., Anthrax) and directly transmitted diseases (e.g., Rabies), that are significant to veterinary medicine (Hengl et al., 2017).

Two significant areas of study in mathematical biology are ecology and epidemiology. Eco-epidemiology is the field that coupling epidemiology and ecology. Eco-epidemiology incorporates epidemiology and ecological approaches to examine how infectious diseases affects ecological communities and how interspecific interactions can change disease dynamics (Gomez-Hemandez et al., 2024). Mathematical modeling of ecological interaction is an important tool to predict population growth, predator-prey relationships, and disease transmission patterns (Berg et al., 2018). Compartmental models, agent-based models (ABM), and machine learning models are the three primary types of mathematical models that are used to shed light on the overall course of an epidemics, capture the intricacy of individual interactions and behaviors, detect patterns and forecast future trends as well as meta population, spatial and contact models are utilized to address diseases that transmit throughout fragmented wildlife populations (Gomez-Hemandez et al., 2024).

Compartmental Models

Compartmental modeling is one of the main methods for tracking the spread of an epidemic. The study of infectious disease transmission frequently makes the use of compartmental models, such as the SIR and SEIR models. Differential equations are used in these models to represent how individuals migrate between the distinct compartments into which population is divided. However, recent studies have been modeling the spread of disease in real-world environment using stochastic techniques (Ward et al., 2023).

1. SIR Model

The hypothesis of homogeneous mixing underlies the SIR model's action, it's frequently an erroneous presumption because people can communicate in different ways depending on their surroundings. In epidemiology, in spite of its clarity this model is intrinsic and prime approach that give the perception about fundamental processes of illness (Mendes et al., 2024). In its standard version, the SIR-model exhibit

in following shapes S(t) for susceptible, I(t) for infectives and R(t) for recovered (including deceased) individuals. A precise set of equations link the constraints of this model for the spread of illness (contact rate α) and rehabilitation (and death) (factor β) (Kudryashov et al., 2021). Regarding a microbe, granting immunity from upcoming infections, a subsequent group of equations emerges from this segmentation that illustrate how people move from one disease to another.

Susceptible(S)

Infected (I)

$$\frac{dS}{dt} = \vartheta - \beta SI - \mu S$$
$$\frac{dI}{dt} = \beta SI - \gamma - \mu I$$

 $\frac{dR}{dt} = \gamma I - \mu R$

Recovered (R)

2. SEIR Model

The SIR framework is expanded upon by the SEIR model (Susceptible-Exposed-Infected-Recovered), which includes an "exposed (E)" compartment for infected but non-infectious people. The illnesses with symptoms that are not visible, such as tuberculosis and chickenpox, isolation states have been added to the SEIR model (SA et al., 2023). During the COVID-19 pandemic, this modification was essential for improving the resource distribution and forecasting infection trends (Kamrujjaman et al., 2022) The SEIR model utilized for concentrating on the part infected *Aedes albopictus* mosquito eggs play in transmission dynamics and in investigating dengue hemorrhagic fever. Functional programming is utilized for imitation and stability assessment. By utilizing mass-action law, most of these models depict the changes between different demographic groups. This makes it impossible to replicate the observable aspects of an infection, such as the development of illness symptoms and gestation time. Nevertheless, these models failed to consider the non-testing subpopulations, asymptomatic carriers and severity of the illness's course (Kiselev et al., 2023).

Agent-Based Models (ABMs)

Agent-based models have demonstrated themselves to be an influential tool, predicting future impacts for varied situations and provides insights into disease dynamics, which direct populations at the individual level, resulting in combined system evolution and are particularly well suited to capture the complex individual behavior, making these models suitable tools for analyzing disease expansion within highly diverse populations (Suer et al., 2023). A valuable framework for the analysis of complex systems, provided by ABM, models individual components, their interactions and actions within an environment. It also evaluates the evolution of virus infections in a society and provides a beneficial tool for examining social aspects (Khodabandelu & Park, 2021).

Various cases, like social interplay and incorporating mobility limitations, can be modified by ABMs, which are key to understanding epidemic dynamics. Disease dynamics efficiently represent via agent-based models by expressing artificial populations and their interactions, which are significant for informing epidemiological approaches and the spread of infection. In contrast, ABMs may introduce biases due to presumptions about different populations' baseline risks and causal structures, influencing the precision of extensibility of observations and disease expansion hypothesis (Keyes et al., 2017). Agent-Based Models (ABMs) provide resilience for real-world modeling but are frequently unappreciated by statisticians due to challenging probability functions, which are difficult for variance determination and parameter estimation. Yet, this approach faces limitations in parameter recognizability and statistical efficiency (Um & Adhikari, 2024).

Machine Learning Models

For example, it becomes possible to expand further the current understanding of these processes by applying the currently developed analytical techniques such as machine learning (ML) to data growing in dimension. This might give new insight into subtle ecological phenomena, such as disease spread in isolated populations (Han et al., 2020). They are better in terms of measuring the relationship between the variable and non-linear inter-variables and results compared to the basic statistical models (Alaa et al., 2019). Logistic regression worked better, instead of this, the novel analytics tools ML centering enhance their understanding of ecological processes and pathogen transmission processes (Han et al., 2020). However, complex non-linear machine learning models may limit the biological interpretability of differential expression, which has not been an issue up to this point. This might lead to inadequate downstream analysis, validation, and overall biological characterization (Choi et al., 2020). Due to this reason, deep learning models can be suitable where such a system can handle complex and large pictures; they are perfectly designed for high-resolution photographs (Ullah et al., 2019). However, these methods can't be very effective for invisible conditions because large amounts of labeled training data are needed. Furthermore, some applications are constrained by the computing costs of machine learning models (Ali et al., 2023).

Meta-Population Model

Population structure significantly affects the demography of social species as well as the spread of infectious diseases in their populations

(Brandell et al., 2021). Infectious diseases mainly spread locally between individuals in physical contact, but group-to-group movement can facilitate geographical spread. Metapopulational models originally devised for ecological purposes have been very successful in describing spatially the dynamics by dividing populations into subpopulations. This theory suggests that transmission rates are higher in a group than between groups, thus leaving it possible for every subpopulation to have characteristics that are mainly isolated (Berg et al., 2018).

Mathematical models play an important role in epidemiology, as seen during the COVID-19 pandemic, making it important for researchers to re-examine the essential metapopulation model applied early during this crisis. Through self-critical data analysis, they conclude that the lockdown initiated in China, 2020, was more effective than assessments earlier claimed (Li et al., 2024). Two critical parameters of a species' social structure are the total number of individuals and the number of populations in a community, which scientists keep track of through a meta-population model. We apply a global model to fit this model and simulate the evolutionary trajectory of the Yellowstone population of wolves and two associated diseases, eczema and feline malnutrition (Brandell et al., 2021).

Network Models

Network models focus on connections that exist between individuals or groups, outlining the roles of interactions in disease spread. In wildlife disease ecology, contact network models are more commonly used to describe how infections spread within social groups wherein contacts between animals are not random but structured (Berg et al., 2018). Ecological Interaction Networks are graphs that represent species interaction and illustrate the structure and dynamics of ecosystems. Social Interaction networks analyze relational data and communications patterns, using Bayesian frameworks to model interactions effectively; therefore, effective disease preparedness is required to mitigate the possibly devastating impact of disease on the aquaculture industry. This paper describes the stochastic, data-driven Aquaculture Disease Network Model, AquaNet-Mod, for disease epidemic and control measure assessment in aquaculture and is coupled with a case study of Viral Hemorrhagic Septicemia in the salmonid industry, work still in progress (Khodabandelu & Park, 2021).

The model simulates transmission through several pathways, namely live fish movement and river spread. Network models often rely on the assumption of random mixing in populations. This neglects social network structures, which can lead to misleading estimations of important epidemiological parameters, such as herd immunity thresholds and the basic reproduction number. A study reveals that superspreading events are scale-free or extremely heterogeneous; in other words, applying the random-mixing assumption might be highly overestimating predictions of infectiousness. Heterogeneous and dynamic networks may also contribute to having more than one wave of infections, which is not predictable by random mixing (Rosenkrantz et al., 2022).

Conclusion

The Interdependence among humans, animals and the environment facilitate the transmission of pathogens in animals to humans, become cosmopolitan health problem. These novel pathogen and diseases create new challenges for wildlife and public health. By utilization of epidemics ecology provides better understanding of disease dynamics and essential approaches against epidemics. In rapidly changing world where social pressures such as climate change, urbanization, deforestation and agricultural intensification have large contribution in the emergence and transmission of disease outbreaks. To mitigate these problems, ecological and epidemiological modeling proves as interdisciplinary approach that helps in the prediction and map-out high-risk areas as well as preventive measures to minimize the zoonosis spread. Further epidemiological models including mathematical models, agent-base models (ABM) and machine learning disease models are modern tools provide data about complex species interaction and important measures in improvement of environmental and public health. With certain advantages, epidemiological modeling still faces limitations that requires an improved framework for real time disease predictions as well as further utilization of ecological disease modeling at genetic level can be a holistic approach in global health. In addition to this, direct human intervention in ecosystem health alteration should be minimized by conservation efforts.

References

- Abbasi, M. A., Din, Q., Albalawi, O., Niaz, R., Alomair, M. A., & Alomair, A. M. (2024). Analysis of the stability and chaotic dynamics of an ecological model. *Complexity*, 2024(1), 1681557. https://doi.org/10.1155/2024/1681557
- Abdela, N., & Jilo, K. (2016). Impact of climate change on livestock health: A review. *Global Veterinaria*, *16*(5), 419-424. http://dx.doi.org/10.4314/ovj.v10i2.7
- Alaa, A. M., Bolton, T., Di Angelantonio, E., Rudd, J. H., & Van der Schaar, M. (2019). Cardiovascular disease risk prediction using automated machine learning: A prospective study of 423,604 UK Biobank participants. *PloS One*, 14(5), e0213653. <u>https://doi.org/10.1371/journal.pone.0213653</u>
- Ali, F., Kumar, H., Alghamdi, W., Kateb, F. A., & Alarfaj, F. K. (2023). Recent advances in machine learning-based models for prediction of antiviral peptides. Archives of Computational Methods in Engineering, 30(7), 4033-4044. <u>https://doi.org/10.1007/s11831-023-09933-w</u>.
- Al-Tawfiq, J. A., & Memish, Z. A. (2023). Middle East Respiratory Syndrome Coronavirus (MERS-CoV) is not circulating among Hajj pilgrims. Journal of Epidemiology and Global Health, 13(3), 387-390. <u>https://doi.org/10.1097/mcp.000000000001051</u>
- Andersen, K. G., Rambaut, A., Lipkin, W. I., Holmes, E. C., & Garry, R. F. (2020). The proximal origin of SARS-CoV-2. *Nature Medicine*, 26(4), 450-452. <u>https://doi.org/10.1038/s41591-020-0820-9</u>
- Antonovics, J., Wilson, A. J., Forbes, M. R., Hauffe, H. C., Kallio, E. R., Leggett, H. C., ... & Webster, J. P. (2017). The evolution of transmission mode. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 372(1719), 20160083. <u>https://doi.org/10.1098/rstb.2016.0083</u>
- Attia, Y. A., Rahman, M. T., Hossain, M. J., Basiouni, S., Khafaga, A. F., Shehata, A. A., & Hafez, H. M. (2022). Poultry production and sustainability in developing countries under the COVID-19 crisis: Lessons learned. *Animals*, 12(5), 644. <u>https://doi.org/10.3390/ani12050644</u>

- Balasubramaniam, K. N., Sueur, C., Huffman, M. A., & MacIntosh, A. J. (2020). Primate infectious disease ecology: insights and future directions at the human-macaque interface. *The Behavioral Ecology of the Tibetan Macaque*, *7*, 249-284. <u>https://doi.org/10.1007/978-3-030-27920-2_13</u>
- Bastos, V., Pacheco, V., Rodrigues, E. D., Moraes, C. N., Nobile, A. L., Fonseca, D. L. M., ... & Cabral-Marques, O. (2023). Neuroimmunology of rabies: New insights into an ancient disease. *Journal of Medical Virology*, *95*(10), e29042. <u>https://doi.org/10.1002/jmv.29042</u>
- Berg, S. S., Forester, J. D., & Craft, M. E. (2018). Infectious disease in wild animal populations: Examining transmission and control with mathematical models. In *The Connections Between Ecology and Infectious Disease* (pp. 239-266). Cham: Springer International Publishing. <u>https://doi.org/10.1007/978-3-319-92373-4_7</u>
- Bernstein, A. S., Ando, A. W., Loch-Temzelides, T., Vale, M. M., Li, B. V., Li, H., & Dobson, A. P. (2022). The costs and benefits of primary prevention of zoonotic pandemics. *Science Advances*, *8*(5), eabl4183. <u>https://doi.org/10.1126/sciadv.abl4183</u>
- Bett, B., Kiunga, P., Gachohi, J., Sindato, C., Mbotha, D., Robinson, T., & Grace, D. (2017). Effects of climate change on the occurrence and distribution of livestock diseases. *Preventive Veterinary Medicine*, 137, 119-129. <u>https://doi.org/10.1016/j.prevetmed.2016.11.019</u>
- Bharti, N., Lu, X., Bengtsson, L., Wetter, E., & Tatem, A. J. (2015). Remotely measuring populations during a crisis by overlaying two data sources. *International Health*, 7(2), 90-98. <u>https://doi.org/10.1093/inthealth/ihv003</u>
- Brandell, E. E., Dobson, A. P., Hudson, P. J., Cross, P. C., & Smith, D. W. (2021). A metapopulational model of social group dynamics and disease applied to Yellowstone wolves. *Proceedings of the National Academy of Sciences*, 118(10), e2020023118. <u>https://doi.org/10.1073/pnas.2020023118</u>
- Cai, J., Sun, W., Huang, J., Gamber, M., Wu, J., & He, G. (2020). Indirect virus transmission in cluster of COVID-19 cases, Wenzhou, China, 2020. *Emerging Infectious Diseases*, 26(6), 1343. <u>https://doi.org/10.3201/eid2606.200412</u>
- Carlson, C. J., & Mendenhall, E. (2019). Preparing for emerging infections means expecting new syndemics. *The Lancet*, 394(10195), 297-312. https://doi.org/10.1016/S0140-6736(19)31237-1
- Choi, Y., Qu, J., Wu, S., Hao, Y., Zhang, J., Ning, J., & Huang, J. (2020). Improving lung cancer risk stratification leveraging whole transcriptome RNA sequencing and machine learning across multiple cohorts. *BMC Medical Genomics*, 13, 1-15. https://doi.org/10.1186/s12920-020-00782-1
- Cunningham, A. A., Daszak, P., & Wood, J. L. (2017). One Health, emerging infectious diseases and wildlife: two decades of progress? *Biological Sciences*, 372(1725), 20160167. https://doi.org/10.1098/rstb.2016.0167
- Destoumieux-Garzon, D., Mavingui, P., Boetsch, G., Boissier, J., Darriet, F., Duboz, P., & Voituron, Y. (2018). The one health concept: 10 years old and a long road ahead. *Frontiers in Veterinary Science*, *5*, 14-23. <u>https://doi.org/10.3389/fvets.2018.00014</u>
- Eder, M., Cortes, F., Teixeira de Siqueira Filha, N., Araujo de Franca, G. V., Degroote, S., Braga, C., & Turchi Martelli, C. M. (2018). Scoping review on vector-borne diseases in urban areas: transmission dynamics, vectorial capacity and co-infection. *Infectious Diseases of Poverty*, 7, 1-24. <u>https://doi.org/10.1186/s40249-018-0475-7</u>
- El-Sayed, A., & Kamel, M. (2020). Climatic changes and their role in emergence and re-emergence of diseases. *Environmental Science and Pollution Research International*, 27(18), 22336-22352. <u>https://doi.org/10.1007/s11356-020-08896-w</u>
- Escobar, L. E. (2020). Ecological niche modeling: an introduction for veterinarians and epidemiologists. *Frontiers in Veterinary Science*, *7*, 519059. <u>https://doi.org/10.3389/fvets.2020.519059</u>
- Friant, S. (2024). Human behaviors driving disease emergence. *Evolutionary Anthropology: Issues, News, and Reviews*, 33(2), e22015. https://doi.org/10.1002/evan.22015
- Gerba, C. P. (2015). Environmentally Transmitted Pathogens. Environmental Microbiology, 8, 509-550. https://doi.org/10.1016/B978-0-12-394626-3.00022-3
- Glidden, C. K., Nova, N., Kain, M. P., Lagerstrom, K. M., Skinner, E. B., Mandle, L., & Mordecai, E. A. (2021). Human-mediated impacts on biodiversity and the consequences for zoonotic disease spillover. *Current Biology*, 31(19), 1342-1361. <u>https://doi.org/10.1016/j.cub.2021.08.070</u>
- Gomez-Hernandez, E. A., Moreno-Gomez, F. N., Cordova-Lepe, F., Bravo-Gaete, M., Velasquez, N. A., & Benitez, H. A. (2024). Ecoepidemiological predator-prey models: A review of models in ordinary differential equations. *Ecological Complexity*, 57, 101071. <u>https://doi.org/10.1016/j.ecocom.2023.101071</u>
- Green, J., Jakins, C., Asfaw, E., Bruschi, N., Parker, A., de Waal, L., & D'Cruze, N. (2020). African lions and zoonotic diseases: implications for commercial lion farms in South Africa. *Animals*, *10*(9), 1692. <u>https://doi.org/10.3390/ani10091692</u>
- Hall, A. D., Fayad, D., & Staat, M. A. (2024). Hantavirus Pulmonary Syndrome in an Adolescent from North Dakota. *The Pediatric Infectious Disease Journal*, 43(6), e212-e214. https://doi.org/10.1097/inf.00000000004284
- Han, B. A., O'Regan, S. M., Paul Schmidt, J., & Drake, J. M. (2020). Integrating data mining and transmission theory in the ecology of infectious diseases. *Ecology Letters*, 23(8), 1178-1188. <u>https://doi.org/10.1111/ele.13520</u>
- Hassell, J. M., Newbold, T., Dobson, A. P., Linton, Y. M., Franklinos, L. H., Zimmerman, D., & Pagenkopp Lohan, K. M. (2021). Towards an ecosystem model of infectious disease. *Nature Ecology & Evolution*, *5*(7), 907-918. <u>https://doi.org/10.1038/s41559-021-01454-8</u>
- Hengl, T., Mendes de Jesus, J., Heuvelink, G. B., Ruiperez Gonzalez, M., Kilibarda, M., Blagotic, A., & Kempen, B. (2017). SoilGrids250m: Global gridded soil information based on machine learning. *PLoS One*, *12*(2), e0169748. <u>https://doi.org/10.1371/journal.pone.0169748</u>
- Hilton, J., & Keeling, M. J. (2019). Incorporating household structure and demography into models of endemic disease. *Journal of the Royal Society Interface*, 16(157), 20190317. https://doi.org/10.1098/rsif.2019.0317
- Hussein, H. A. (2023). Brief review on Ebola virus disease and one health approach. *Heliyon*, *9* e19036. https://doi.org/10.1016/j.heliyon.2023.e19036
- Javed, N., Kelly, P., & Khaja, M. (2024). An Unusual Presentation of Leptospirosis: A Case of Septic Shock and Proteinuria. Cureus, 16(7), 1-13.

https://doi.org/10.7759/cureus.64982

- Johnson, P. T. J., de Roode, J. C. & Fenton, A. (2015). Why infectious disease research needs community ecology. *Science*, 349, 1259504. https://doi.org/10.1126/science.1259504
- Kadu, B., Maldhure, S., & Babhulkar, L. (2024). A short review on Zika virus. *Research Journal of Pharmacology and Pharmacodynamics*, 16(3), 181-184. <u>https://doi.org/10.52711/2321-5836.2024.00031</u>
- Kamrujjaman, M., Saha, P., Islam, M. S., & Ghosh, U. (2022). Dynamics of SEIR model: A case study of COVID-19 in Italy. *Results in Control and Optimization*, 7, 100119. <u>https://doi.org/10.1016/j.rico.2022.100119</u>
- Keyes, K. M., Tracy, M., Mooney, S. J., Shev, A., & Cerda, M. (2017). Invited commentary: agent-based models—bias in the face of discovery. American Journal of Epidemiology, 186(2), 146-148. <u>https://doi.org/10.1093/aje/kwx090</u>
- Kiselev, I. N., Akberdin, I. R., & Kolpakov, F. A. (2023). Delay-differential SEIR modeling for improved modelling of infection dynamics. *Scientific Reports*, 13(1), 13439. <u>https://doi.org/10.1038/s41598-023-40008-9</u>
- Kudryashov, N. A., Chmykhov, M. A., & Vigdorowitsch, M. (2021). Analytical features of the SIR model and their applications to COVID-19. *Applied Mathematical Modelling*, 90, 466-473. https://doi.org/10.1016/j.apm.2020.08.057
- Khodabandelu, A., & Park, J. (2021). Agent-based modeling and simulation in construction. Automation in Construction, 131, 103882.
- Lenz, C., Slack, M. P., Shea, K. M., Reinert, R. R., Taysi, B. N., & Swerdlow, D. L. (2024). Long-Term effects of COVID-19: A review of current perspectives and mechanistic insights. *Critical Reviews in Microbiology*, 50(3), 315-328. <u>https://doi.org/10.1080/1040841X.2023.2190405</u>
- Li, J., Ionides, E. L., King, A. A., Pascual, M., & Ning, N. (2024). Inference on spatiotemporal dynamics for coupled biological populations. *Journal* of the Royal Society Interface, 21(216), 20240217. https://doi.org/10.1098/rsif.2024.0217
- MacDonald, A. J., & Mordecai, E. A. (2019). Amazon deforestation drives malaria transmission, and malaria burden reduces forest clearing. Proceedings of the National Academy of Sciences, 116(44), 22212-22218. <u>https://doi.org/10.1073/pnas.1905315116</u>
- Machado, J. P., & Oliveira, V. P. (2024). Seaweed functional ecology models: a comprehensive review of theory and applications. *Journal of Applied Phycology*, 8, 1-16. <u>https://doi.org/10.1007/s10811-024-03293-z</u>
- Marcolin, L., Tonelli, A., & Di Marco, M. (2024). Early-stage loss of ecological integrity drives the risk of zoonotic disease emergence. *Journal of the Royal Society Interface*, *21*(215), 20230733. <u>https://doi.org/10.1098/rsif.2023.0733</u>
- McCallen, E., Knott, J., Nunez-Mir, G., Taylor, B., Jo, I., & Fei, S. (2019). Trends in ecology: shifts in ecological research themes over the past four decades. *Frontiers in Ecology and the Environment*, *17*(2), 109-116. <u>https://doi.org/10.1002/fee.1993</u>
- Meena, M., Swapnil, P., Barupal, T., & Sharma, K. (2019). A review on infectious pathogens and mode of transmission. *Journal of Plant Pathology Microbiology*, 10, 472. <u>https://doi.org/10.1002/fee.1993</u>
- Mendes, J. M., Baptista, H., & MacNab, Y. C. (2024). Bridging Compartmental Models and Network Analysis in Epidemiological Modelling. *Epidemiology Public Health*, 2(2), 1036.
- Menza, T. W., Berry, S. A., Dombrowski, J. C., Cachay, E., Crane, H. M., & Mayer, K. H. (2024). Estimating the Proportion of People Living with HIV Who May Benefit from the Reverse Algorithm for the Diagnosis of Incident Syphilis. *Sexually Transmitted Diseases*, 51(6), e26-e29. <u>https://doi.org/10.1097/olq.0000000000001955</u>
- Nazaroff, W. W. (2016). Indoor bioaerosol dynamics. Indoor Air, 26(1), 61-78. https://doi.org/10.1111/ina.12174
- Nemeth, K. (2024). A review of canine-related zoonotic dermatologic diseases. *International Journal of Dermatology*, 63(10), 1289-1290. https://doi.org/10.1111/ijd.17457
- Nova, N., Athni, T. S., Childs, M. L., Mandle, L., & Mordecai, E. A. (2022). Global change and emerging infectious diseases. *Annual Review of Resource Economics*, *14(1)*, 333-354. https://doi.org/10.1146/annurev-resource-111820-024214
- Plowright, R. K., Reaser, J. K., Locke, H., Woodley, S. J., Patz, J. A., Becker, D. J., Oppler, G., Hudson, P. J., & Tabor, G. M. (2021). Land useinduced spillover: a call to action to safeguard environmental, animal, and human health. *The Lancet Planetary Health*, 5(4), e237-e245. https://doi.org/10.1111/rec.13357
- Rosenkrantz, D. J., Vullikanti, A., Ravi, S. S., Stearns, R. E., Levin, S., Poor, H. V., & Marathe, M. V. (2022). Fundamental limitations on efficiently forecasting certain epidemic measures in network models. *Proceedings of the National Academy of Sciences*, 119(4), e2109228119. <u>https://doi.org/10.1073/pnas.2109228119</u>
- SA, L. S., Patel, B., Banavar, M. K., Tepedelenlioglu, C., Spanias, A., & Schuckers, S. (2023, October). Analysis of a Modified SEIRS Compartmental Model for COVID-19. In 2023 57th Asilomar Conference on Signals, Systems, and Computers (pp. 965-969). IEEE. https://doi.org/10.1109/IEEECONF59524.2023.10477067
- Shaheen, M. N. (2022). The concept of one health applied to the problem of zoonotic diseases. *Reviews in Medical Virology*, 32(4), e2326. https://doi.org/10.1002/rmv.2326
- Small, N., Munday, M., & Durance, I. (2017). The challenge of valuing ecosystem services that have no material benefits. *Global Environmental Change*, 44, 57-67. https://doi.org/10.1016/j.gloenvcha.2017.03.005
- Suer, J., Ponge, J., & Hellingrath, B. (2023). EpiPredict: agent-based modeling of infectious diseases. *KI-Kunstliche Intelligenz*, *6*, 1-5. https://doi.org/10.1007/s13218-023-00819-4
- Swierczynska, M., Mirowska-Guzel, D. M., & Pindelska, E. (2022). Antiviral drugs in influenza. International Journal of Environmental Research and Public Health, 19(5), 3018. <u>https://doi.org/10.3390/ijerph19053018</u>
- Ullah, A., Muhammad, K., Haq, I. U., & Baik, S. W. (2019). Action recognition using optimized deep autoencoder and CNN for surveillance data streams of non-stationary environments. *Future Generation Computer Systems*, 96, 386-397. https://doi.org/10.1016/j.future.2019.01.029
- Um, S., & Adhikari, S. (2024). Considerations in Bayesian agent-based modeling for the analysis of COVID-19 data. Statistical Analysis and Data Mining: The ASA Data Science Journal, 17(1), e11655. https://doi.org/10.1002/sam.11655
- Valenzuela-Sánchez, A., Wilber, M. Q., Canessa, S., Bacigalupe, L. D., Muths, E., Schmidt, B. R., & Cayuela, H. (2021). Why disease ecology needs

life-history theory: a host perspective. Ecology Letters, 24(4), 876-890. https://doi.org/10.1111/ele.13681

- Ward, C., Brown, G. D., & Oleson, J. J. (2023). Incorporating infectious duration-dependent transmission into Bayesian epidemic models. *Biometrical Journal*, 65(3), 2100401. <u>https://doi.org/10.1002/bimj.202100401</u>
- Winkler, K., Fuchs, R., Rounsevell, M., & Herold, M. (2021). Global land use changes are four times greater than previously estimated. *Nature Communications*, *12*(1), 2501.
- Zhang, L., Lv, C., Guo, W., & Li, Z. (2024). Temperature and humidity as drivers for the transmission of zoonotic diseases. *Animal Research and One Health*, 2(3), 323-336. <u>https://doi.org/10.1002/ar02.75</u>
- Zucca, P., Rossmann, M. C., Dodic, M., Ramma, Y., Matsushima, T., Seet, S., & Zamaro, G. (2021). What do adolescents know about one-health and zoonotic risks? A school-based survey in Italy, Austria, Germany, Slovenia, Mauritius, and Japan. *Frontiers in Public Health*, *9*, 658876. https://doi.org/10.3389/fpubh.2021.658876