

Disease Biography Advances and Constraints Using Ecological Niche Modelling**30**

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ABSTRACT

Ecological Niche Modelling (ENM) has emerged as a powerful tool in understanding the dynamics of disease spread and providing valuable insights into disease biographies. This innovative approach integrates ecological and geographical data to model the environmental conditions suitable for the existence and transmission of pathogens. The application of ENM in disease research has yielded significant advances in our comprehension of disease patterns, facilitating better preparedness and response strategies. One notable advance lies in the ability of ENM to predict the geographical distribution of disease vectors and reservoirs, aiding in the identification of high-risk areas for transmission. This predictive capacity is crucial for public health interventions, enabling targeted surveillance, timely resource allocation, and effective preventive measures. Additionally, ENM contributes to our understanding of how environmental factors, such as climate change and land use, influence disease dynamics, allowing for adaptive strategies to mitigate potential outbreaks. However, despite its considerable contributions, ENM faces certain constraints. Limitations arise from the reliance on accurate and comprehensive ecological data, which may be challenging to obtain, especially in resource-limited regions. Model uncertainties, the dynamic nature of ecosystems, and the complex interplay of various factors influencing disease transmission further contribute to the challenges. In conclusion, Disease Biography Advances and Constraints Using Ecological Niche Modelling highlight the pivotal role of ENM in enhancing our understanding of disease ecology. While it provides invaluable insights for disease management and control, addressing data limitations and refining models will be essential to harness the full potential of this approach in combating emerging and re-emerging infectious diseases.

Keywords: Disease biography, Ecology, Environment, Niche, Public health.

CITATION

Ijaz M, Bhatti FE, Liaqat C, Rizvi SBH, Fatima N, Tariq S, Tahira S, Khan R, Rehman A and Jabbar A, 2023. Disease Biography Advances and Constraints Using Ecological Niche Modelling. In: Khan A, Abbas RZ, Hassan MF, Aguilar-Marcelino L, Saeed NM and Mohsin M (eds), Zoonosis, Unique Scientific Publishers, Faisalabad, Pakistan, Vol. I: 400-410. <https://doi.org/10.47278/book.zoon/2023.030>

CHAPTER HISTORY

Received: 07-Jan-2023 Revised: 09-May-2023 Accepted: 15-June-2023

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1. INTRODUCTION

Epidemiology, the study of disease prevalence and its factors in communities, has contributed substantially to improvements in public health. Traditional epidemiological methods, however, could ignore how complex and unique diseases are. A revolutionary approach, called as "disease biography," has recently developed as a new paradigm in epidemiology. Its goal is to revolutionize our understanding of illnesses by evaluating their dynamic and individual trajectories over the time. This chapter examines the fundamental ideas and implications of disease biography, emphasizing how it has the potential to transform an epidemiological study and enhance patient outcomes (Cooter and Stein 2013).

1.1. PRINCIPLES OF DISEASE BIOGRAPHY

1.1.1. LONGITUDINAL PERSPECTIVE

Disease biographies emphasize the value of longitudinal studies that track people over time in order to capture how diseases change over time. Researchers learn a great deal about the complexity of disease dynamics by examining the onset, progression, and outcomes of an illness over the course of a person's life (Burton-Jeangros et al. 2015).

1.1.2. MULTIFACTORIAL APPROACH

The paradigm acknowledges that a wide range of variables, including as genetic predisposition, lifestyle decisions, environmental exposures, and social determinants of health, have an impact on diseases. The intrinsic variety in disease manifestation is accounted for by disease biography by incorporating these various characteristics into analysis.

1.1.3. LIFE COURSE PERSPECTIVE

In disease biography, a life course perspective is essential because it recognizes that experiences and exposures throughout the formative stages of life might affect future health trajectories. Childhood exposures and prenatal variables, for example, can have long-lasting effects on disease risk and prognosis (Colman and Ataullahjan 2010).

1.2. PERSONALIZED MEDICINE AND PREVENTION

1.2.1. PRECISION MEDICINE

The concept of personalized medicine, in which treatments and interventions are adapted to the unique characteristics of each patient, is consistent with disease biography. Clinicians can design targeted medicines with increased efficacy and fewer side effects by taking into account each patient's particular disease biography (Kulkova et al. 2023).

1.2.2. PREVENTIVE STRATEGIES

Personalized preventive measures can also be influenced by knowing a person's disease biography. Public health interventions can be created to successfully slow the onset or course of disease by identifying early risk factors and high-risk times (Kulkova et al. 2023).

1.3. CHALLENGES AND FUTURE DIRECTIONS

1.3.1. DATA INTEGRATION

Implementing disease biography necessitates combining several data sources, including genetic data, socioeconomic characteristics, environmental data, and electronic health records. Realizing the full potential of this paradigm presents problems to create comprehensive data infrastructure and safe sharing platforms (Gligorijević and Pržulj 2015).

1.3.2. ETHICAL CONSIDERATIONS

In particular, data privacy and informed consent require careful consideration in longitudinal investigations. In disease biography research, balancing the advantages of individualized insights with potential hazards is crucial.

1.3.3. INTERDISCIPLINARY COLLABORATION

Collaboration between epidemiologists, doctors, geneticists, bio-statisticians, and social scientists are essential to the success of disease biographies. Innovative approaches and holistic viewpoints can result from an interdisciplinary approach (Bendowska and Baum 2023).

2. ECOLOGICAL NICHE OF PARASITES FROM DISEASE REPORTS TO DISEASE MAPS

The term "ecological niche" describes a species' place and function in its environment, including its interactions with other creatures and the physical conditions needed for it to thrive and procreate. Because they depend on their host for food and dwell inside or on them, parasites have distinct ecological niches (Poulin and Morand 2000).

2.1. PARASITIC DISEASE REPORTS

In order to estimate the number of illnesses, complications, and deaths for ten helminth diseases and toxoplasmosis, the researchers combined data from national estimates of foodborne diseases, systematic reviews (studies that identify all the research on a topic using predefined criteria), national surveillance programs, and other sources. They also calculated the total and regional disability adjusted life years (DALYs) for each condition. A disease's burden is measured by DALYs, which are the disease-related losses of one year of full health due to premature death or disability. In 2010, these illnesses collectively resulted in 48.4 million cases of sickness, 59,724 fatalities, and 8.78 million DALYs. According to the study, contaminated food was responsible for 48% of these parasitic illness cases, which resulted in 6.64 million DALYs. Ascaris infection and toxoplasmosis (12.3 million and 10.3 million cases, respectively) were the most widespread parasite infections transmitted by food. The biggest disease loads were caused by

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foodborne cysticercosis, trematodes infection, and toxoplasmosis, and the Western Pacific and African regions had the highest burdens of foodborne parasite disease (Torgerson et al. 2015).

2.2. IDENTIFY PARASITIC DISEASES

The history of parasitic disorders today primarily focuses on attempting to comprehend the circumstances that led to the discovery of parasites and their subsequent accusation in the etiology of the disease. Only a few of the most significant parasites, those that cause disease and produce recognizable signs and symptoms, can be discussed in this article (Table 1) diseases and their parasites, while other parasitic infections are briefly described in the chapter (Cox 2004).

2.3. EVOLUTIONARY ECOLOGY OF PARASITES

In many animal lineages, parasites have independently evolved, and they currently make up a sizeable fraction of the diversity of life. In addition to having a profound influence on people and other creatures, they have recently emerged as a potent model system for the study of ecology and evolution,

Table 1: DISEASES AND THEIR PARASITES.

Disease	Parasite
Malaria	Plasmodium spp.
Amoebiasis	Entamoeba histolytica
Sleeping sickness	Trypanosoma brucei gambiense and T.b.rhodesiense
Chagas' disease	Trypanosoma cruzi
Schistosomiasis	Schistosoma spp.
Hookworm	Ancylostoma duodenale and Necator americanus
Lymphatic filariasis	Wuchereria spp, Brugia spp
Loiasis	Loa loa
Onchocerciasis	Onchocerca volvulus
Guinea worm disease	Dracunculus medinensis
Larval cestodiasis	Taenia spp, Echinococcus granulosus

with applications in the field of disease prevention. Robert Poulin offers an evolutionary ecologist's perspective on the biology of parasites in this edition of his influential earlier work, which has been extensively edited and updated. With information from scales ranging from the characteristics of individual parasites to the dynamics of parasite populations and the structure of parasite communities, he presents a thorough synthesis of parasite evolutionary ecology. In order to gain a deeper knowledge of why parasites behave the way they do and give an evolutionary framework for the study of parasite biology, Evolutionary Ecology of Parasites combines theory with practical evidence. The book is a perfect teaching resource for advanced courses on the topic because it provides an up-to-date synthesis of the field. It will also be a priceless resource for researchers looking to advance our understanding of parasite ecology and evolution because it points towards promising directions and establishes a research agenda (Poulin 2011).

3. CURRENT METHODS FOR DISEASE MAPPING

3.1. DISEASE MAPPING

A disease map illustrates and analyzes patterns and risk factors associated with disease distribution. It aids in prevention and management by providing insight into strategies, resource allocation, and interventions.

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It enhances public health research and surveillance by detecting outbreaks, monitoring trends, and assessing disparities. Providing insights to make effective decisions is one of the most important functions of disease mapping in policy-making, which facilitates targeted interventions in areas with a high disease burden by allocating resources to those areas. It helps to control and prevent diseases by understanding the geographic distribution of diseases. Disease mapping is an essential tool in public health, aiding in understanding, managing, and mitigating the impact of diseases (Andrew and Lawson 2001).

In this chapter, we will look at the most popular methods of current disease mapping, along with their applications in public health research and interventions. In the area of veterinary epidemiology, model-based geo-statistics and Bayesian techniques are helpful when point data have been acquired using the right study design. In order to examine the risk of dog parasite infection in the city of Naples, 2004–2005, we make use of an example of epidemiological surveillance on urban settings where a two-stage sampling strategy with first stage transects is implemented. To forecast the continuous risk surface of parasite infection on the research region, we did Bayesian kriging and specified Bayesian Gaussian spatial exponential models. We contrasted the findings with the proportion of positive specimens by transect obtained by using hierarchical Bayesian models to areal data. The models' findings agreed with one another, and the Bayesian geostatistical method worked better at spotting places where zoonotic parasitic illnesses can spread. Larger danger areas were generally found along city borders where domestic dogs and wild dogs coexisted and there were less human or municipal barriers (Biggeri et al. 2006).

3.2. METHODS OF DISEASE MAPPING

3.2.1. SPATIAL AGGREGATION

In disease mapping, spatial aggregation is a technique that groups cases or health-related occurrences into geographical units like counties, states, or postal codes in order to analyse disease occurrence. Spatial aggregation enables comparisons and the discovery of disease trends by compiling disease data at various geographical scales (Wakefield 2007; Jeffery et al. 2014). For example, suppose a study aims to understand the prevalence of infectious disease across various states of a country. Researchers can visualize and compare disease burden by averaging the number of cases reported in each state, highlighting areas with a greater incidence or prevalence.

3.2.2. KERNEL DENSITY ESTIMATION

The effective disease mapping methodology known as kernel density estimation makes use of statistical methods to calculate the spatial distribution of disease cases based on their geographic coordinates. It produces a continuous surface that depicts the density of disease occurrences, enabling the detection of regions with dense populations of cases, often known as disease hotspots (Cai et al. 2012). For example, think of a study that looks at the prevalence of a disease spread by mosquitoes in a particular area. By compiling the geographic coordinates of disease cases, kernel density estimation can create a smooth density surface that depicts regions with a high density of cases, indicating probable hotspots where the disease is more frequent.

3.2.3. CLUSTER DETECTION

Cluster detection is a disease mapping technique that locates statistically significant clusters of disease cases. In order to locate regional clusters and identify epidemics, it analyses observed and anticipated case counts in a specified geographic area (Aamodt et al. 2006). For instance, take a study on the

prevalence of cancer in a specific area. With the use of cluster identification, scientists may pinpoint regions where the observed number of cancer cases is noticeably greater than predicted. To learn about probable risk factors or environmental exposures causing the greater disease incidence, more research can be done on these identified clusters. In order to address the heightened cancer risk in those particular places, this knowledge supports targeted public health interventions, resource allocation, and surveillance efforts.

3.2.4. GEOGRAPHICAL INFORMATION SYSTEMS (GIS)

Geographical information systems (GIS) combine spatial data with information about diseases to allow for sophisticated analysis and visualisation. GIS investigates relationships and risk variables by superimposing disease data on spatial layers like demographics, environment, or medical facilities. For example, in a study on the distribution of a vector-borne disease, GIS can overlay disease cases onto a map showing the locations of mosquito breeding sites, climate data, and human population density. By visually analyzing this spatial context, researchers can identify areas where high disease prevalence coincides with specific environmental conditions or population characteristics. This information helps in understanding the underlying determinants of disease patterns (Murad and Khashoggi 2020).

3.2.5. BAYESIAN DISEASE MAPPING

Bayesian Disease Mapping is an advanced method in disease mapping that employs Bayesian statistical techniques to estimate disease rates or prevalence at unobserved locations. This method produces more reliable estimates, particularly when data are scarce, by combining disease data with prior knowledge and assumptions (MacNab 2022). For example, it can be used in a study on the prevalence of a rare disease to estimate disease rates in areas with sparse data by combining existing data from nearby regions with previous knowledge of disease patterns. Bayesian approaches produce detailed disease risk maps that show regions with a higher or lower disease burden by taking spatial interdependence and the estimation process' uncertainty into account.

3.2.6. CHOROPLETH MAPPING

Using colour shading or patterns over different geographic areas, choropleth mapping visually depicts disease rates or prevalence. It helps to identify high-risk regions and trends. For example, a choropleth map can employ colour gradients to depict differing rates in different regions of a cancer incidence research. Lighter colours signify lower disease rates, while darker shades imply greater rates. This makes it easier to identify regions in need of targeted interventions (Andrienko et al. 2001).

3.2.7. SPATIO-TEMPORAL MAPPING

Spatio-temporal mapping techniques, such as spatio-temporal clustering or spatio-temporal regression models, are used to analyze disease patterns over both space and time (Coly et al. 2015). The analysis of influenza epidemics across various regions and seasons is an example of spatio-temporal mapping. Researchers can locate regions with shifting sickness rates, spot persistent clusters, and monitor the spread and development of the illness by analysing data on influenza cases over a number of years. Table 2 shows the summary of disease mapping methods with examples.

4. ENVIRONMENTAL VARIABLES USED IN ECOLOGICAL NICHE MODELING

Ecological niche modeling (ENM) is a crucial tool for understanding zoonotic diseases and forecasting species distribution. Researchers can discover disease hotspots and evaluate disease dynamics by using ENM to map potential habitats for species. The increasing number of interactions at the animal-human interface is affecting the emergence and spread of zoonoses worldwide. Protecting human health requires an understanding of zoonotic illnesses in relation to environmental changes. ENM improves our capacity to foresee and control zoonotic outbreaks by examining the interdependence of ecosystems and human-animal interactions.

Understanding the environmental variables is crucial for ecological niche modelling. Environmental variables are factors in the environment that impact the presence and distribution of species. They can be abiotic, such as temperature and precipitation, which affect the physical conditions of an area. Biotic variables, like vegetation and soil, are influenced by living organisms. Evaluating these variables are the main key in predicting the distribution of zoonotic diseases.

4.1. KEY ENVIRONMENTAL VARIABLES IN ECOLOGICAL NICHE MODELING

Key Environmental Variables in ecological niche modeling play a vital role in understanding zoonotic diseases. Temperature, a primary variable, influences species distribution by shaping their physiological tolerances.

Table 2: Summary of Disease Mapping Methods.

Method	Description	Example
Spatial Aggregation	Grouping disease cases into geographical units (counties, states, etc.) to analyze disease occurrence across different states in a country (Wakefield trends (Wakefield 2007; Jeffery et al. 2014).	Understanding infectious disease prevalence across different states in a country (Wakefield 2007; Jeffery et al. 2014).
Kernel Density Estimation	Statistical method estimating the spatial distribution of disease cases based on geographic coordinates (Cai et al. 2012).	Identifying hotspots of a mosquito-borne disease in a specific area (Cai et al. 2012).
Cluster Detection	Technique identifying statistically significant clusters of disease cases (Aamodt et al. 2006).	Identifying regions with significantly higher cancer cases than expected in a specific area (Aamodt et al. 2006).
Geographical Information Systems (GIS)	Integration of spatial data with disease information for analysis and visualization (Murad and Khashoggi 2020).	Overlaying disease cases on a map with mosquito breeding sites and population density (Murad and Khashoggi 2020).
Bayesian Disease Mapping	Bayesian statistical method estimating disease rates or prevalence at unobserved locations (MacNab 2022).	Estimating disease rates in areas with sparse data for a rare disease (MacNab 2022).
Choropleth Mapping	Visual representation of disease rates or prevalence using color shading or patterns (Andrienko et al. 2001).	Depicting varying cancer incidence rates in different regions through color gradients (Andrienko et al. 2001).
Spatio-temporal Mapping	Analyzing disease patterns over space and time using clustering or regression models (Coly et al. 2015).	Studying influenza outbreaks across regions and seasons to monitor spread and progression of the disease (Coly et al. 2015).

Seasonal changes affect migration patterns of disease vectors, impacting disease spread. For example, rising temperatures due to climate change may expand the range of disease-carrying mosquitoes, leading to the spread of vector-borne diseases like malaria and dengue fever (Rupasinghe et al. 2022).

Precipitation affects water availability, influencing habitats and subsequently the occurrence of zoonotic pathogens. For instance, heavy rainfall can create breeding sites for disease vectors, increasing the risk of

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outbreaks. Land Cover/Land Use types determine the availability of suitable habitats for both disease reservoirs and vectors. Deforestation can alter the ecosystem, bringing humans into closer contact with wild animals, potentially leading to spillover events. For instance, the destruction of forests in Southeast Asia has been linked to the emergence of zoonotic diseases like Nipah virus (Chua et al. 2002).

Altitude affects temperature, thereby influencing zoonotic disease patterns. For example, high-altitude regions may have a reduced prevalence of certain diseases due to lower temperatures and altered ecological conditions.

Soil Type impacts the survival and transmission of zoonotic agents. Certain pathogens thrive in specific soil environments. For instance, soil-transmitted helminths find suitable conditions in moist and warm soils, leading to human infection through contact or ingestion.

Human Disturbance, such as urbanization and agricultural expansion, can modify environments, increasing disease exposure and transmission. For example, encroachment of human settlements into wildlife habitats can lead to increased contact with disease reservoirs, as observed with the spread of Ebola in Africa (Pigott et al. 2016).

Understanding and incorporating these key environmental variables into ecological niche modeling allows researchers to predict disease hotspots, identify high-risk areas, and implement targeted interventions to prevent and control zoonotic diseases.

Scientists utilize Geographic Information Systems (GIS) and remote sensing technologies to acquire spatial information, such as temperature, precipitation, land cover, and altitude. Statistical algorithms are then employed to analyze the data, identifying correlations between environmental variables and zoonotic disease occurrences, aiding in disease prediction and prevention strategies.

4.2. CASE STUDIES

In a study titled "Ecological Niche Modeling of Hantavirus Pulmonary Syndrome in the Southwestern United States," researchers utilized ecological niche modeling to understand the dynamics of hantavirus pulmonary syndrome (HPS) transmission. They found that variables like temperature, precipitation, and vegetation type were critical in predicting disease hotspots. By analyzing these factors, they identified specific regions with a high likelihood of HPS occurrence, aiding in targeted surveillance and preventive measures (Gongóra-Biachi et al. 1999).

In another article "Predicting the Geographical Distribution of Lassa Fever Virus," researchers applied ecological niche modeling to understand Lassa fever dynamics. They identified variables such as temperature, land cover, and proximity to water bodies as critical factors for disease transmission. The study highlighted specific regions in West Africa with suitable environmental conditions for the virus, helping public health authorities focus on prevention and control strategies (Vieth et al. 2007).

Ecological niche modeling has significant implications for zoonotic disease research and control. It allows predicting disease emergence and implementing preventive measures. Future research should focus on integrating climate change scenarios and enhancing data collection methods to improve modeling accuracy and enhance disease preparedness.

5. PARASITE, VECTOR, RESERVOIR: WHAT TO MODEL IN THE DISEASE SYSTEM?

The nature of diseases brought on by unknown or inadequately figured out parasites, such as the Marburg and Ebola viruses, can be better understood through ecological niche modelling (Peterson et al. 2004). The most qualified species to serve as a parasite's repository may need to be identified (e.g., competitor repositories for Tanapox infection in tropical Africa; Monroe et al. 2014), or researchers may need to provide potential vector species within a framework for the disease with obscure vectors (e.g., up-and-

comer vectors for Chagas illness in Brazil) (Gurgel-Gonçalves et al. 2012). Thus, the use of parasites, vectors, or reservoir occurrences can be used to calibrate ecological niche models. As they provide a comprehensive overview of the illness system (referred to as "black-box models" in ecological niche modelling), reports of human or animal diseases could also be used for modelling (Peterson 2007).

Once the ecological niche of a parasite has been identified, this knowledge can be used to predict potential habitats for the parasite in the future or outside of its current distribution. Today, spatial epidemiology is using this method, which Peterson and Vieglais first outlined and patent-protected in 2001, to pinpoint possible epidemic hotspots (Peterson et al. 2004). The idea that a parasite's ecological niche will remain stable throughout time underlies the use of it to locate new potential locations for expansion. Simply put, the ecological niche will not change. According to empirical data the ecological niche will remain constant. As a matter of fact, it is accepted that a parasite's specialty does not vary despite virulence variations among strains. For instance, *Toxoplasma gondii* strains may become more virulent after encountering animals, but the abiotic niche still exists. At large scales, abiotic alterations to ecological niches are uncommon (Soberón and Peterson 2011).

Ecological niche models typically predict that illnesses including cholera (Escobar et al. 2015), leishmaniasis, and malaria would spread more widely under the current trends in climate change. Future study should focus on how parasites conform to novel ecological circumstances and changes in virulence. Experimental investigations spanning a lengthy parasite generational period, greater than "human" time, are required to comprehend Evolution of the parasite niche and modifications to environmental tolerance. Given some taxa's rapid generation times, such investigations might be possible (e.g., bacteria). Risk regions in simulations of ecological niches can be thought of as places with environmental factors that favor the existence of the parasite either its reservoirs or its vectors. When defining risk in terms of the environment, local scale factors might be added as a supplement. Since the "disease-transmission risk" or "parasite-exposure risk" theories are strongly encouraged, even in communities where the parasite is common, disease per se may not exist (i.e., asymptomatic hosts), while the word "disease risk" implies exposure, infection, and symptomatology. For the simple reason that recently discovered parasites might not be harmful, recent parasite discoveries should not be interpreted as a pathogen report. (e.g., Bai et al. 2011). In the same way, the presence of a parasite inside an arthropod does not necessarily mean that the arthropod acts as a vector for the spread of the illness. However, due to similarities (i.e., taxonomical, morphological, behavioral) with known pathogens or vectors in both circumstances, risk may be "assumed" in terms of the probability that the parasite or arthropod may participate in a disease system. Reports on the risk of developing diseases also contain noise. Emergent infections may have gone unnoticed in the past but may now surface because of social factors such as increased monitoring efforts, improved diagnostic techniques, or the introduction influx of a fresh, weak population into the parasite's habitat. In such case, danger was not considered even though the population was always at risk of infection. In conclusion, the term risk needs to be defined in every study because it depends on the context and because its presumptions and characteristics vary depending on the population of interest (Monroe et al. 2014).

Risk may be generalized to mean "No people, no risk" in the context of public health, for instance. Environmental conditions that support the existence of the parasite, either its reservoirs or its vectors are referred to as risk zones in ecological niche models. When defining risk in terms of the environment, local scale factors might be added as a supplement. Since disease per se may not exist in populations where the parasite is abundant (i.e., asymptomatic hosts), we highly recommend the use of the "disease-transmission risk" or "parasite-exposure risk" notions. The term "disease risk" implies exposure, infection, and symptomatology. For the simple reason that recently discovered parasites might not be harmful, recently discovered parasites should not be regarded as a reliable report of a pathogen (Bai et al. 2011). In the same way, arthropod does not necessarily act as a vector for the disease when a parasite is present

inside of it. However, in both cases, risk may be "assumed" in terms of the possibility that the parasite or arthropod may take part in a disease system because of similarity (i.e., taxonomical, morphological, behavioural) with identified pathogens or carriers.

Reports on the risk of developing diseases also contain noise. Emergent infections may have gone unnoticed in the past but may now surface because of social factors such as increased monitoring efforts, improved diagnostic techniques, or the introduction influx of a fresh, weak population into the parasite's habitat. In this case, danger was not considered even though the population was always at risk of infection. (Gurgel-Gonçalves et al. 2012).

6. CONCLUSION

Disease biography represents a revolutionary shift in epidemiology, emphasizing the unique, changing, and complex nature of diseases over time. By adopting a longitudinal, multivariate, and life course approach, this paradigm has the potential to transform healthcare practices and public health regulations. Embracing personalized medicine and prevention, disease biography can lead to more effective therapies, improved patient outcomes, and a healthier global community. However, challenges like data integration, ethical considerations, and interdisciplinary collaboration must be addressed for widespread adoption. With continuous research and dedication, disease biography can advance epidemiology towards a more patient-focused and impactful future.

Disease mapping methods like spatial aggregation, kernel density estimation, cluster detection, GIS, Bayesian disease mapping, and choropleth mapping enhance our understanding of disease distribution and inform targeted interventions. They reveal patterns, hotspots, and risk factors, guiding resource allocation and public health strategies. Disease mapping plays a vital role in evidence-based decision-making and improving our understanding of disease dynamics.

In conclusion, ecological niche modeling (ENM) is a powerful tool for understanding and combating zoonotic diseases. It helps predict disease hotspots and identify potential reservoirs, crucial for safeguarding human health amidst increasing human-animal interactions. By integrating climate change scenarios and enhancing data collection, ENM enhances disease preparedness and guides proactive measures. This research provides valuable insights into disease ecology, enabling effective protection of human and animal populations in a changing world. In conclusion, every study must define risk since it varies depending on the setting and because of its presumptions and characteristics vary depending on the population of interest. Risk may be generalized to mean "No people, no risk" in the context of public health.

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