RESEARCH ARTICLE

Archaeology and contemporary emerging zoonosis: A framework for predicting future Rift Valley fever virus outbreaks

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Abstract
Modelling of emerging vector borne diseases serves as an important complement to clinical studies of modern zoonoses. This article presents an archaeo-historic epidemiological modelling study of Rift Valley fever (RVF), using data-driven neural network technology. RVF affects both human and animal populations, can rapidly decimate herds causing catastrophic economic hardship, and is identified as a Category A biodefense pathogen by the US Center for Disease Control. Despite recent origins circa the early 1900s, little is known about the circumstances of its inception nor the relationships between factors that affect transmission. This evidence could be vital as the disease continues to expand from its epicentre in Kenya to other parts of Africa and the Arabian Peninsula. RVF is a relevant case for archaeological/palaeopathological investigations of disease as it intersects between numerous human, animal, spatial, temporal, and sociopolitical dimensions. By integrating landscape archaeology, historical evidence, and climatic data, with evidence of human behaviour gathered through ethnoarchaeological study, this article presents an applied framework for human–animal palaeopathology. This framework aligns with the One Health approach that observes disease to be intrinsically tied to ecological and societal factors. We provide a useable alternative way of thinking about disease modelling in the present and the past, ultimately seeking to support efforts to accurately predict future impacts. Tapping into longitudinal evidence from the last 50–300 years offers a powerful way to respond to the threat zoonoses will pose to human populations around the world as the climate warms.

KEYWORDS
artificial intelligence, Kenya, One Health, Rift Valley fever, slaughter

1 | INTRODUCTION

Rift Valley fever (RVF) is a bunyavirus transmitted by arthropod vectors, such as mosquitoes and blood feeding flies and direct contact with contaminated bodily fluids. It affects humans and their livestock, as well as wild fauna (Hightower et al., 2012).

We present a framework that uses deep learning tools to synthesis evidence from the archaeological, climatic, and historical records to model RVF. The article describes the state of the art for how social sciences and humanities contribute to the study of vector borne disease (VBD), followed by a proposal for future research.
Palaeopathology is increasingly focussed on osteological study, which potentially limits students’ learning, skill sets, and our ability to study disease in the past. Bone is not the only source of evidence on palaeopathology, and we are unlikely to have a complete understanding of the wider disease context, crucial for modelling, without considering the influence of social and ecological dimensions. As Mitchell (2012, p. 320) suggests “historical sources that provide evidence for disease in the past are just as valid a research source as bones, mummies, and latrine soils.”

Palaeopathology risks redundancy if the discipline fails to adopt new approaches (Zuckerman, Harper, & Armelagos, 2016), especially with regards to a rapidly advancing data revolution. Here, we take a multidisciplinary approach entirely devoid of direct evidence from human or faunal bone. Our framework offers palaeopathologists new approaches to data assembly and assessment, adapting these to augment the utility of evidence gathered from archaeological, historical, and climatic records. The main merits of this study lie in the transformative implications for the way we study disease within a broader archaeological framework, how such studies contribute to understanding the contemporary and future challenge posed by zoonotic diseases, and in enhancing our preparedness to deal with these challenges.

Some 60% of human infections caused by pathogens are shared with animals, approximating to 240 of the 400 known zoonotic diseases (Karesh et al., 2012; Morse et al., 2012). This results in a staggering billion cases of human illness each year, millions of deaths, and has accounted for hundreds of millions of dollars in lost economy during the last two decades alone (Jones et al., 2008; Karesh et al., 2012). Over the past 70 years, the majority of emerging infectious diseases have been zoonotic. Endemic zoonoses have also increased. New diseases, combined with ecological and social factors, are exerting a selective pressure leading to some zoonoses becoming increasingly or exclusively dependent on humans as the transmission host (Karesh et al., 2012). Based on review articles (Beard, Wentz, & Scotch, 2018; Gibbs, 2005; Johnson et al., 2015; Weiss & McMichael, 2004), it is especially noteworthy that all recent pandemics, from human immunodeficiency virus to Zika, have been vector borne or zoonotic in nature.

The modern context summarized above provides sobering reading. A chronologically contextualized study of zoonoses offers palaeopathologists a route to help tackle this global challenge, simultaneously responding to the mandate to make archaeology relevant.

2 | DIMENSIONS OF ZOONOSES AND TIME DEPTH

Epidemiological modelling of zoonoses helps to establish emergence and transmission of a given disease and refine the connection between climate and vectors (Mordecai et al., 2013). Given the complexity of interactions between a host, the pathogen, vector, and the environment, contemporary models tend to focus on single parameters; considering the time, cost, and effort to collate modern data, studies typically have a conservative longitudinal range. These two factors limit our ability to understand disease over time.

The climatic influence on disease is complex (Daszak, Cunningham, & Hyatt, 2000; Mordecai et al., 2013; Morens, Folkers, & Fauci, 2004; Pajamans et al., 2010), and remains poorly understood, even for well-studied diseases such as malaria (Shah et al., 2019; Zhou, Minakawa, Githeko, & Yan, 2004). It is now recognized that we will observe changes in various directions as a consequence of global warming, rather than a linear relationship, that is, higher temperatures leading to increased prevalence (Lafferty, 2009; Lafferty & Mordecai, 2016; Rogers & Randolph, 2006; Ryan, Carlson, Mordecai, & Johnson, 2019).

Intensified food production, escalating land-cover change and mass travel affect how zoonoses “act” in the environment, leading to detrimental impacts on well-being (Gibbs, 2005; Jones et al., 2008). The unintentional introduction of vectors has also served to facilitate the spread of new diseases (Kilpatrick & Randolph, 2012). The current situation is conditioned by social and behavioural factors (Janes, Corbett, Jones, & Trostle, 2012) and predicated on centuries of direct and indirect ecological and social engineering tied to major cultural developments in antiquity: domestication, the advent of agriculture, insipient urbanization, and long-distance migration (Daszak, 2012).

In our research, we conceptualize time depth as critical to a better assessment of disease and ways to mitigate future impacts. This approach is not without precedence. Archaeological research from South East Asia (King, Halcrow, Tayles, & Shkum, 2017) and Greece (Papathanasiou, 2011), as well as studies focussed on specific diseases such as plague and tuberculosis (DeWitte, 2016), or on particularly important moments in antiquity, for example, the advent of farming (Fournié, Pfeiffer, & Bendrey, 2017), have attempted to create palaeoepidemiological frameworks for zoonoses. Historians (Spielman, 2001) and climate scientists (Rohr et al., 2011), as well as vets (Gibbs, 2005), clinicians, global health specialists, and disease ecologists all recognize the utility of chronological context (Janes et al., 2012; Pulliam et al., 2012). Our approach is distinctive from these efforts as it operates with a significantly broader range of sources and integration of data. We introduce the term “Data Rich Time Depth Repositories” (DRTDR) to describe data with a chronological dimension, marshalled under one umbrella with the aim of utilizing these resources within an integrative, transdisciplinary framework, working to mitigate the limitations outlined above.

Challenges exist with our approach, namely, how to integrate data derived from different sources, which platform to use, and how to overcome jargon that can be institutionalized within disciplines. As this approach is a new one, there are few guiding principles to draw on.

However, the potential benefits of incorporating greater time depth into disease research are considerable. Archaeology provides much-needed context on the emergence of ancient pathogens and parasites (Wolfe, Dunavan, & Diamond, 2007; Dittmar, Araújo, & Reinhard, 2012, pp. 180–182) and the escalating impact on human health and well-being (Horwitz & Smith, 2000). Beyond providing chronological context, archaeology contributes data on ecology,
climate, human behaviour, and socioeconomic parameters that influence disease, and provides an approach that can assemble data from various sources over time, and help forecast likely future impacts based on multiscalar evidence.

Practical benefits include better contextualized climate data through the inclusion of anthropological insight, the ability to identify cryptic drivers of transmission based on historical contextualization, a more nuanced assessment of the influence of landscape to identify risk factors, and improved predictive capacity. One conceptual benefit serves as a bridge between specialist focussed on ancient and modern disease. The One Health approach (Fig. 1), developed in the veterinary field and widely adopted as a collaborative enterprise to tackle human, animal, and environmental health (Gibbs, 2014), seeks to deepen our understanding of disease by situating and crystalizing climatic and social influences. To this, we simply emphasize one more dimension: time.

3 | THE CASE STUDY

The RVF case is based on another interdisciplinary VBD project seeking to better assess the impacts of malaria on Mauritius (Seetah, 2018; Seetah, in prep). First documented by Daubney et al. (1931), RVF offers an opportunity to identify the inception, transmission, and escalation to epidemic proportions of a zoonotic disease. RVF is an ideal candidate for a longitudinal modelling study. Its emergence coincided with British Imperialism in this region of Eastern Africa and sits at the nexus of food production, human–animal relationships (Cook et al., 2017; Grossi-Soyster, Lee, King, & LaBeaud, 2019), local cultural agency, and European hegemony. Colonial interventions were characterized by massive landscape modifications, wide-spread demographic transitions, and new practices governing animal husbandry and trading, all driven by major political and infrastructural upheaval. RVF has been well studied from a contemporary epidemiological perspective (Cook et al., 2017; Grossi-Soyster et al., 2017, 2019; LaBeaud et al., 2015; LaBeaud, Ochiai, Peters, Muchiri, & King, 2007); thus, new research is easily situated within an established framework.

The disease is highly contagious and infects both animals and humans. Human cases arise from exposure to diseased animal products or directly as a consequence of slaughter (Anyangu et al., 2010; Cook et al., 2017). The disease in general has relatively mild symptoms, presenting as fever (Bosshra, Lorenzo, Busquets, & Brun, 2011). A small percentage of individuals (<1%) manifest acute symptoms, including ocular lesions, meningoencephalitis, and fatal hemorrhagic fever (Muga, Onyango-Ouma, Sang, & Affognon, 2015; WHO, 2019). When transmitted via the Aedes mosquitoes to livestock, it can decimate entire herds mainly through spontaneous abortion (Khan & Smith, 2016). During the 1950–1951 epizootic in Kenya, 5 million sheep aborted, and 100,000 adult animal deaths were recorded (Woods et al., 2002). Considering that the disease affects the poorest pastoralist communities, the broader impact on human health, well-being, and poverty resulting from livestock mortality is highly damaging and far reaching.

The epicentre of the disease appears to be the Rift Valley region in Kenya. By 1950, a major outbreak had resulted in 200,000 human cases in South Africa. Outbreaks have since occurred in Egypt (1971–1978, 1999), Senegal (1993), Somalia, and Tanzania (1987 and 1998). In 2000–2001, the first outbreaks outside of continental Africa occurred in Saudi Arabia and Yemen in the Arabian Peninsula, with the Indian Ocean islands of Mayotte, Comoros, and Madagascar affected in the latter 2000s (Davies, 2010; Murithi et al., 2011; Muga et al., 2015). This expanding trend has heightened fears of the disease spreading to Europe and the United States, where all the necessary vectors and hosts to allow transmission are present (Rolin, Berrang-Ford, & Kulkarni, 2013), leading to the US Center for Disease Control listing RVF as one of the top three threats to the livestock industry (Dar, Hogarth, & McIntyre, 2013).

At present, we have an incomplete understanding of the influence of climate on RVF spread; the drivers of RVF outbreaks are typically sporadic, although there are clear associations with flooding events (Anyamba et al., 2009). With notable exceptions (Muga et al., 2015), the historic and social contexts remain poorly understood. Archival research undertaken by AA in Kenya’s National Archive, Nairobi, point to potential gaps in current understanding of the social and environmental dimensions. For example, although RVF was noted clinically in 1930/1931, only white settler farms had access to designated vet services. African pastoral zones were never assessed for the disease. RVF may not have actually originated in the Rift Valley district. This and other highland areas were favoured by colonial settlers because of the cooler climate at altitude and reduced risk of malaria (Morgan, 1963). Thus, lacuna in our historical assessment, as well as the socioeconomic costs and increasing geographic expansion, serve as

Figure 1 The One Health concept represented schematically (credit: Image created by Thddbfk—own work, CC BY-SA 4.0. License https://commons.wikimedia.org/w/index.php?curid=81872126). [Colour figure can be viewed at wileyonlinelibrary.com]
impetus to galvanize efforts to better understand the triggers of the disease.

4 | THE APPROACH

Epidemiological research focussed on mosquito vectors for dengue illustrate that prevalence and spread of disease are linked to numerous factors, encompassing sociological changes, habitat, and climate (Thongsripong et al., 2013). This reinforces why an approach combining data from DRTDR on climate, with evidence from the archaeological record and anthropological research that can describe human behaviour, is particularly relevant. The impact of bridging such diverse data sets through computation is exemplified by studies that provide novel insight on population distributions in human history (Pagani et al., 2016; Timmermann & Friedrich, 2016).

4.1 | Modelling multidisciplinary data

4.1.1 | Archaeology/ethnoarchaeology

Archaeology aligns climatic, textual, and material evidence into a cohesive whole to support chronological contextualization. More directly, a landscape archaeological approach is adopted to help better understand animal husbandry and pastoralism in the region, that is, how domestic fauna are transported and patterns of trade, to identify relationships between mobility and risk. Mapping a range of spatial variables, for example, density of slaughter facilities and parameters dictating herd mobility, provides a way to identify and situate potential hazards within the context of expanding urbanization. For example, as Figure 2 illustrates, small-scale slaughter takes place in close juxtaposition to settlements, which could lead to exposure to disease. Archaeology will also provide climate proxy data derived from terrestrial soil cores extracted as part of excavations in the region. Cores provide evidence of changes in geomorphology (soil structure) and vegetation (pollen and phytoliths). These data have already shown the extensive consequences of anthropogenic land-cover change on soil erosion (Fleitmann et al., 2007; Lane, 2009; Mworia-Maitima, 1997) and illustrate changes in habitat that influences vector activity and wild and domestic herbivore feeding and mobility.

The human–animal relationship is a critical component of RVF. Research shows that the diversification of professions associated with animal husbandry and slaughter has implications for understanding disease transmission. Humans are exposed via animal husbandry, slaughter and butchery, and ingesting diseased meat, milk, and blood (Mohamed et al 2010; Cook et al., 2017; Grossi-Soyster et al., 2019). Ethnoarchaeological research provides important evidence of human behaviour, in particular, as it relates to changing slaughtering practices over time. Slaughtering practice data are based on work ongoing since 2010 assessing the division of labour as part of animal husbandry and provisioning of meat. Similar research has shown the extensive social stratification, and gendered nature, characteristic of butchery (Mooketsi 2001). Through ethnoarchaeology, we assess contemporary attitudes of those involved in animal husbandry, for example, in terms of adherence to best practice in slaughterhouses (e.g., Figure 3: inspecting sheep livers for parasites) and surveillance and monitoring of uninspected meat (Rich & Perry 2011). Changing practices from traditional slaughter of pastoral groups, such as the Maasai, to larger scale commercial slaughter (Seetah., 2019: p. 30, pp. 101–103) could pose a significant escalation in risk. This arises as a consequence of numerous factors. In the commercial setting, there is greater mixing of animals from various locations; thus, monitoring of animal populations for disease is harder; there are many more animals slaughtered in a...
relatively shorter span of time, reducing the capacity for surveillance of sick individuals as animals may be processed before infections are noted; and waste, in the form of blood and faeces, are accumulated close to urban settlements (Figures 4 and 5: smallest scale commercial slaughter in a "slab").

4.1.2 | History

The historical human–animal context is key and the Kenyan National Archives, Nairobi, contains several hundred records that provide evidence on colonial impacts in the region. Britain established the East African Protectorate in 1895, naming the region the Kenya Colony in 1920. Our research taps into troves spanning from circa 1916 to 1988, some 20 years after independence in 1964. Annual colonial reports detail developments such as long-distance transportation of domestic animals (PC/RVP/2/3/1 Rift Valley Province Annual Reports [late 1920s]), the introduction of new breeds (that were less resistant to RVF, Evans et al 2008), the development of a meat trade and subsequent industrialization of meat production, working conditions of those involved in the profession, the centralization and institutionalization of new systems for slaughter, that is, the abattoir, and the establishment and influence of the Kenyan Meat Commission, providing vital clues as to the apparent sudden emergence of RVF in Kenya. Records also include evidence of land-cover change and impacts on provisioning as they relate to colonial expansion in the area, military interventions by European imperial powers, and the provisioning of military personal. In all cases, there was a need for new animal trading regimes to accommodate these changes, potentially holding the key to revealing why the first outbreak occurred. In addition to these qualitative accounts detailing changes in the human–animal relationship, extensive climate data are also available from the historical archives. For example, comprehensive rainfall and temperature records have been maintained as part of colonial efforts to introduce crops such as sugar, alongside meteorological data maintained as part of the introduction of western ideas of "science" to monitor the local environment. At a more specified level, there is also considerable evidence of disease outbreaks in the archival data, mainly on diseases such as rinderpest (PC/RVP/6A/23/5: veterinary, livestock diseases, quarantine and movement of livestock, and quarantine for Masai) and foot and mouth (DC/FH/3/18/5 Colony and Protectorate of Kenya—Department of Veterinary Services 1956), which could prove useful for comparative purposes. There are also specific references to RVF in the decades that followed its emergence (K962-3 KEN Department of Agriculture Annual Report [1932]; Colony and Protectorate of Kenya [1938]; Department of Veterinary Services Annual Report [1937]).

4.1.3 | Climate science

Understanding the ecological and climatic context of RVF outbreaks is critical given the dependence of the vector on specific conditions. The disease is closely linked to heavy rainfall following periods of drought (Anyamba et al., 2009; Anyamba, Linthicum, & Tucker, 2001). In this regard, both large-scale global weather systems such as El Niño, and local conditions, have an impact on transmission and ultimately, epidemics. Understanding the role of climate and ecology is complicated; for example, local topography can serve to mask large-scale weather patterns. For this reason, climatic evidence is gathered from a range of sources to produce as comprehensive a climatic profile as currently
possible, spanning the historic to modern periods. Directly recorded evidence of climate is available from historical instrumental records on rainfall and temperature, available from the National Archive, Kew, the British Library, London, and the Kenyan National Archives, Nairobi (e.g., Colony of Kenya and the East African Protectorate [1920] Meteorological records 1914–1919, Bulletin No. 4, Nairobi: Department of Agriculture). Archival temperature data will be calibrated using modern satellite evidence, which provides precise data for the last two decades and which will then serve as the basis for fine-tuning data from previous decades. Data on precipitation also derive from historical sources overlaid with modern data, for example, from the Global Network of Isotopes in Precipitation.

4.1.4 | Data science

Traditional statistics focus on understanding the relative importance of specific factors for a single outbreak, effectively seeking significant triggers. This methodology is well developed and offers a rich toolset applicable for predicting another epidemic with similar triggers. Statistical modelling is less useful when we know that multiple configurations of triggers can result in epidemics. What was observed previously may not reoccur, although new epidemics may arise from combinations of the same or related factors.

Artificial intelligence (AI) has found application where large amounts of interconnected data carry information. This clearly characterizes the types of data archaeologists generate, and as such, AI is likely to have major implications for the subject, as well as for the humanities and social sciences more generally. For example, AI and machine learning are transforming how archival sources are utilized through large-scale digitization programs that facilitate search and analytical capabilities. To date, the limited use of AI in archaeology has focussed on locating sites (Barceló, 2007). However, as a methodology, AI is well suited to integrate archaeo-historic data into disease modelling. We use deep learning, a form of machine learning based on neural networks. Although early forms of neural networks and deep learning trace back to the 1960s, fast implementations of these algorithms using accelerated hardware led to rapid adoption in many fields (Ciresan, Meier, Gambardella, & Schmidhuber, 2010; Oh & Jung, 2004; Raina, Madhavan, & Ng, 2009). Deep learning architectures have been applied to speech recognition, natural language processing, audio recognition, social network filtering, drug design, and medical image analysis, where they have produced results comparable with or superior to human experts (Krizhevsky, Sutskever, & Hinton, 2012; Ciresan, Meier, & Schmidhuber, 2012). Increases in computational power, advances in the architecture and support for neural networks, and the availability of large data sets have transformed the field and its applications (Cao, Wang, Ming, & Gao, 2018; Singh, Mittal, & Bhatia, 2019). Deep learning is well suited to discern patterns in complex data sets where unknown interactions, that is, context, affect outcome. Originally used to classify data, it is increasingly used to generate data that conform to complex patterns (Basu, Bhattacharyya, & Kim, 2010; Yun, Huyen, & Lu, 2018). In the current research, deep learning is utilized to learn patterns related to outbreaks at a given time and place. The complexity of the factors contributing to outbreaks has prevented statistical methods that do not consider the context of data from discovering reliable predictive patterns. Our work and that of others in generative and predictive AI show that neural networks can succeed across multiple time scales and have produced working solutions using diverse data (Hannun et al., 2019; Kim & Shin, 2007).

Our preliminary research utilized publicly available data covering East Africa were added to the localized data collected from three communities in Kenya by D. L. and E. G-S. Historical census data, along with climate data from archives and satellite data, provided evidence on temperature and precipitation from locations across Kenya. These were labelled by latitude, longitude, and date to create a three-dimensional data block compatible with localized data and well suited for submission to neural networks for deep learning. We used a dual channel approach pioneered in facial recognition where incomplete data are supported by a “backdrop” of general facial scans (Elmahmudi & Ugail, 2019), essentially, using the regional backdrop to examine the localized data in context.

5 | ANTICIPATED OUTCOMES AND CONCLUSIONS

At this early stage in our research, we are limited to presenting preliminary findings, but we are able to discuss anticipated outcomes and specific challenges in greater detail.

Our initial findings suggest that the recurrence of outbreaks of zoonotic disease under specific conditions (exemplified by repeated RVF and Ebola epidemics in Africa in the last decades) supports the ideas put forth in this paper, namely, that although each outbreak occurs only once, historical, ecological, demographic, economic, and climatic factors interact in ways that predispose an environment to zoonosis or epidemics. On a practical level, we are encouraged by our own findings where the inclusion of census and climate data spanning a century or more increase prediction accuracy of our technology from 60% to nearly 80% (Kumm, Seetah, Grossi-Soyster, & LaBeaud, in prep.). Further validation of the approach will involve archival data and trade data from East Africa.

The call for multidisciplinarity in the study of zoonoses has been made repeatedly in the literature (e.g., Janes et al., 2012). However, this is not with disciplines like archaeology, anthropology, or history in mind. Thus, one important outcome has been the demonstrable benefit of working across disciplines that do not traditionally collaborate, leading to innovative strategies for research. Integrating the social sciences and humanities (Janes et al., 2012) with clinical and computational expertise affords an opportunity to bring new lines of evidence and approaches to bear and deepens our understanding of how social and ecological factors interrelate to influence disease (Weiss & McMichael, 2004). However, this particular assembly of disciplines faces specific challenges. A longitudinal approach will require clinicians to reconsider the cyclical nature of disease and how this might
help understand disease emergence and re-emergence, to seek new data sets from nontraditional, or unconventional, sources, and to integrate longevity as a concept within the context of interventions and remedies, shifting expectations of what is meant by “long-term solutions.” Specific challenges also face archaeology, not least that the subject has little visibility in the areas of the world and habitats that zoonoses are proposed to emerge in. This could serve as an impetus for research in the Global South. This need not necessarily mean more archaeological excavation, although that would be welcome, but rather to apply material and longitudinal contextualization, as well as the inherent multidisciplinarity, that lies at the core of the subject.

Although the findings of this project are relevant to present day knowledge and prediction of VBD, the approach is equally relevant to studies focussed on archaeological interpretation. For example, researchers may be able to define or anticipate points in history when an epidemic would be expected, based on multifactorial data, and from this, build models describing demographic, social, and economic change and adaptation. Our approach could also be critical for more accurate modelling of human mortality profiles as a consequence of globally significant events such as slavery, which had major impact on disease ecologies in colonial enclaves (Arnold, 1991) or over protracted events, such as the transition to agriculture and accompanying sedentarism (refer to chapters in Pinhasi & Stock, 2011), which are closely tied to ecological changes both natural and anthropogenic.

Ultimately, the tangible project output will include a generalizable framework and shared resource approach to develop collaborations with funders, national and regional epidemiological monitoring efforts, and academic research endeavours.

By integrating climatic, demographic, archaeo-historic, and human behaviour data into one model, we propose to produce a predictive model for RVF outbreaks. Interdisciplinary and synthetic, this tool will link measurable data between retrospective and future epidemics. The objective is to identify regions, time periods, and populations at risk from RVF disease outbreaks and to suggest effective mitigation strategies. This will provide a substantial step forward in preparedness in low-resource settings.

5.1 | What can archaeology contribute to contemporary zoonotic disease modelling?

As archaeology has traditionally been concerned with the origins of ancient diseases, it is well placed to help understand inception events of modern zoonoses. Although only two epidemic diseases, smallpox and rinderpest, have been eradicated on a global scale, over the last few decades, important strides have been made in tackling a suite of diseases that have affected humanity for centuries, if not millennia. Emerging zoonoses, therefore, are now likely to pose an ever-greater challenge to public health. Understanding and assessing disease emergence will become more important for mitigation and control.

A chronologically contextualized approach also has utility in considering the longer term dimensions of a given disease. In the case of RVF, but also many other VBDs, contemporary epidemiological and clinical studies tend to focus on periods of major outbreaks. This effort is critical but potentially leads to an overemphasis on specific ecological or social dimensions that bias understanding of inter-epidemic periods and could mask impacts that occur outside of the epidemic phase. For RVF, periods of heavy rain lead to explosions in mosquito populations that then catalyse outbreaks. However, the ecological condition of Kenya’s Rift Valley and the surrounding area are characterized by drought. Local communities have adapted to this state. The Maasai maintain stricter control over grazing herds and make efforts to segregate their livestock from wild ungulates during drought. This reduces the risk of transmitting disease when wild and domestic animals congregate around diminishing water holes. Maasai also practice mix-herding strategies to mitigate risk from diseases that could disproportionately affect their stock if it comprised a single domesticate. Animals will also be sequestered and migrated to other communities, tied by personal relationships, in areas that are less affected by drought and the accompanying risk of infection. We do have some insight on how the disease persists during drought but need to place greater research effort on interepidemic/postepidemic periods, as exemplified by LaBeaud et al. (2008, 2011), to complement the epidemiological research. New models would benefit from observing RVF as systematic and predictable, noting the importance of the phase of perseverance through periods of drought.

The anthropological context is crucial as a means of integrating knowledge from local pastoral groups on how the disease is recognized and managed. It also serves to counteract the colonial bias of historical records. Recent ethnographic research conducted by K. S. with Maasai herders in Kimana, Kenya, revealed that the local historical background of the disease is well known. Diseases like RVF were and continue to be dealt with in a range of ways, including quarantining of diseased animals. RVF is known as Sadik by Somali pastoralists in northern Kenya; the disease aetiology is distinct and as such, should be identifiable from oral accounts. This could have important implications for harnessing evidence that is deeply contextualized both ecologically and culturally (Muga et al., 2015). Given the historical context, suggestions that the disease is recent could be a construct of a reliance on written history and an underrepresentation of oral traditions, indigenous and local knowledge, and ethnoveterinary medicine (Martin, Mathias, & McCorkle, 2001).

An archaeo-historic lens pushes us to more carefully consider the colonial dimension. RVF seems to have emerged as a direct consequence of colonial interventions on land use and animal husbandry, factors that also facilitated transmission. To better assess this theory, we need more evidence on the origin, and reservoir, of RVF.

It has been important to illustrate the utility of a longitudinal, applied archaeological framework, to a case that does not have a strong archaeological context. Ultimately, the approach needs to be applicable to other emerging VBDs to elevate the research beyond an archaeo-historic narrative, serving as an impetus for institutions and researchers to focus on other ancient, historic, and emerging VBDs.

Looking to the future, although a palaeopathological approach to disease has traditionally been concerned with antiquity, advances
in both archaeological and data science should stimulate new research focused on tackling contemporary contexts. Archaeologists are ideally positioned to facilitate the integration of time depth into the One Health concept to support a better understanding of the varied dimensions of disease. Indeed, the biocultural approach in bioarchaeology specifically emphasizes the holistic relationship that humans have with their sociocultural and ecological environments (Zuckerman & Armelagos, 2011; Zuckerman & Armelagos, 2012). Although the biocultural stance is not specifically focused on disease but human health more broadly, one of the defining studies that galvanized development of this approach in the 1950s centred on the way malaria, humans, and ecosystems were intrinsically intertwined (Dufour, 2006). Both the One Health and biocultural approaches share a conceptualization of disease as influencing and influenced by society, seeking to understand how ecology, climate, human behaviour, and sociopolitical attitudes impact on disease; chronology is a critical component of these varied dimensions within a global health framework. An explicit effort by archaeologists to study and tackle zoonoses is extremely important and timely. The extensive multifocal research on human–animal interactions over time situates us well to respond to one of the concerns identified by the One Health Initiative Task Force, indicating “Our increasing interdependence with animals and their products may well be the single most critical risk factor to our health and well-being with regard to infectious diseases” (American Veterinary Medical Association, 2008).

Ultimately, one fact should galvanize our efforts: Despite increasing sophistication in surveillance and recognition of the impacts of zoonoses on human health and economy, no pandemic has so far been predicted (Morse et al., 2012). An approach harnessing evidence from the last 50–300 years is precisely what is needed to predict the pattern of disease transmission over the next 50–100 years, as the climate warms, and populations rise.

5.2 Final comments

Underpinning this project is an endeavour to collect a robust and diverse data set and develop, refine, and validate a deep learning analytical framework—effectively, to quantitatively examine RVF disease outbreaks using neural networks. This is a first step towards a prediction of specific outbreaks rather than estimating general risk, going beyond the identification of single important factors that contribute to, but do not determine, outbreak occurrence. Ultimately, the long-term goal is for real-world outbreak prediction that directly benefits the poorest members of our international community.

CONFLICT OF INTEREST

The authors register no conflict of interest in preparing and submitting this article.

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