Management of arthropod vector data – Social and ecological dynamics facing the One Health perspective

Giovanni Benelli*a,b,⁎, Mary Frances Dugganc

a Department of Agriculture, Food and Environment, University of Pisa, via del Borghetto 80, 56124, Pisa, Italy
b The BioRobotics Institute, Sant’Anna School of Advanced Studies, viale Rinaldo Piaggio 34, 56025, Pontedera, Pisa, Italy
c Benjamin Franklin Institute of Technology, Boston, MA, United States

A R T I C L E   I N F O

Keywords:
- Dengue
- Emerging infectious diseases
- Filariasis
- Lyme disease
- Malaria
- Mosquitoes
- Ticks
- Vector-borne diseases
- West Nile virus
- Zika virus
- Zoonosis

A B S T R A C T

Emerging infectious diseases (EIDs) are spread by direct and/or indirect contacts between a pathogen or parasite and their hosts. Arthropod vectors have evolved as excellent bloodsuckers, providing an elegant transportation mode for a wide number of infectious agents. The nature of pathogen and parasite transfer and the models used to predict how a disease might spread are magnified in complexity when an arthropod vector is part of the disease cycle. One Health is a worldwide strategy for expanding interdisciplinary collaborations and communications in all aspects of health care for humans, animals, and the environment. It would benefit from a structured analysis to address vectoring of arthropod-borne diseases as a dynamic transactional process. This review focused on how arthropod vector data can be used to better model and predict zoonotic disease outbreaks. With enhanced knowledge to describe arthropod vector disease transfer, researchers will have a better understanding about how to model disease outbreaks. As public health research evolves to include more social-ecological systems, the roles of society, ecology, epidemiology, pathogen/parasite evolution and animal behavior can be better captured in the research design. Overall, because of more collaborative data collection processes on arthropod vectors, disease modeling can better predict conditions where EIDs will occur.

1. Introduction

Arthropod vectors have evolved as excellent bloodsuckers, providing an elegant transportation mode for a rather wide number of infectious agents, covering both parasites and pathogens of great public health importance (Dantas-Torres et al., 2012; Benelli, 2015) (Fig. 1). Besides the widely-known malaria burden, which led to 6.8 million deaths averted globally since 2001 (Malaney et al., 2004; Benelli and Beier, 2017; Benelli et al., 2018a), dengue virus poses at risk 3900 million people in 128 countries (Brady et al., 2012; Bhatt et al., 2013). Mosquito-borne lymphatic filariasis is still ranked among the most important neglected tropical diseases (WHO, 2014; Vadivalagan et al., 2017), while Zika virus outbreaks in the Americas and the Pacific recently attracted high public health attention (Petersen et al., 2015; Benelli and Romano, 2017), mostly due to the Zika virus connection with fetal microcephaly and neurological complications, such as the Guillian–Barré syndrome (Oehler et al., 2014; European Centre for Disease Prevention and Control, 2015; Benelli and Mehlhorn, 2016). Besides mosquitoes, Lyme disease, vectored by ticks transmitting genospecies of the *Borrelia burgdorferi* s.l. complex, is gaining public relevance, with more than 30,000 cases are reported annually only for the United States (CDC, 2017). Therefore, the reliable and eco-friendly management of arthropod vector populations is a timely and important challenge for modern parasitology (Boyce et al., 2013; Bouyer and Lefrançois, 2014; Benelli et al., 2016, 2017; Bourtzis et al., 2016; Hemingway et al., 2016; Khater et al., 2016; Benelli, 2018a, 2018b).

This review focused on how biting arthropods confound public health strategies by amplifying and transporting pathogens and parasites from one host to another. The discussion involves a critical analysis of multi-disciplined research that crosses human, animal, and environmental health fields and the strategy to integrate this research into a collaborative framework. It addresses the challenges found in health research data collection that has grown in isolation and now must collaborate to address the challenges in global human health. Blending the social and ecological practices into one system of study is referred to as the social-ecological system (SES) theory. SES theory is used to describe an interaction where human social and environmental dynamics are embedded in complex ways (Ostrom, 2009). Here, it will be applied to public health systems specifically addressing human disease surveillance data and modeling.
Common practices in early public health, when the relationship of humans, animals, and environment was more commonly looked at as an integrated system, are reemerging. One Health (OH) is an initiative that aggregates these concepts and is being used as a framework to describe public health research efforts in contemporary literature (Atlas, 2012). OH, as seen in the SES theory perspective, seeks to integrate and embed the complex influences of animals, humans, and the environment in public health (Fig. 2a). Public health concerns in this discussion are global health issues with a major focus on infectious diseases. The ability of a pathogen or a parasite to move from host to host and country to country creates a global disease threat that drives organizational thinking and policy cooperation across traditional national and scientific divides (Brown et al., 2006).

A disease is an issue that impacts both the single individual and the community. The individual must deal with the effects of bad health, while the community may need to address environmental issues leading to less healthy environments for the whole community (Stokols, 1992). From a human health research standpoint, it is the field of epidemiology that studies the distribution and determinants of health risks in populations (Dicker et al., 2011). This research effort produces data used to map and model a disease process with the goal to manage better health outcomes (Heesterbeek et al., 2015). Disease models evolve as new data and variables are discovered. A major concern in disease management is the outbreak of a new disease that has not been modeled or assessed in the past. This recently occurred — for example — with Zika virus in the Americas (Petersen et al., 2015; Benelli and Mehlhorn, 2016). An emerging infectious disease (EID) is a disease caused by a new or previously unrecognized pathogen or parasite (Racaniello, 2004). Pathogens and parasites can adapt and evolve in ways that allow them to infect new hosts. Zoonotic pathogens or parasites (animal to human transmission) cause more than 60% of EIDs (see also Fig. 1). In the decade that preceded 2008, 28.8% of the reported EIDs were vector-borne diseases (Jones et al., 2008). The transmission of EIDs via arthropod vectors requires a concentrated focus on vectors of selected pathogens/parasites to map and model the relationships that occur in the human environments. Using a OH approach to develop models that anticipate and manage zoonotic disease emergences also requires an accurate understanding of the role of arthropod vectors in disease transfer.

In this scenario, a major research question is: can SES-specific arthropod vector data be better utilized to improve OH initiatives? Moreover, concerning potentially at-risk host populations, is this approach helpful to provide more accurate predictive indicators of human disease vulnerability in advance of an emerging zoonotic outbreak? In the paragraphs below, we critically discussed current knowledge to reply to these major questions in a multidisciplinary perspective.

2. Social-ecological systems theory

The health of humans, animals, and the environment are linked (Grzywacz and Fuqua, 2000). However, the strategy to research and study across many specializations is not a standardized process. With increased knowledge about health, higher capacities for data analysis, and a tendency to silo around one area of academic specialization, promoting transdisciplinary efforts has been challenging to implement. One way to address this diversity is to advocate a systems approach (Holling, 2001). Here, defining a system provides the foundation for exploring how arthropod vector data can enhance the research outcomes in disease transfer studies. Linking vector and pathogen/parasite evolution to disease management is a critical step for building prevention strategies in public health. Understand the opportunity for pathogens and parasites to move in the environment includes their direct contact with hosts as well as — most importantly — arthropod vector-mediated contact, resulting in a host-vector-host infection route. Social-ecological systems describe the relationships interconnected in a disease cycle and have the flexibility to add the impacts of individual processes on the system as a whole.

Describing a disease transfer system requires descriptions of many dynamic and interrelated relationships. A review of SES theory provides a framework to describe strategies used in research to link humans, animals, and the environment. SES links changes taking place across scales and hierarchies that illustrate how a system can function and adapt to change (Holling, 2001). At the SES level of analysis, individual actions of each element of the system are separable but also can produce interactions that feedback into the system and can impact outcomes (Ostrom, 2009).
Fig. 2. (a) The One Health concept is a worldwide strategy for expanding interdisciplinary collaborations and communications in all aspects of health care for humans, animals and the environment (courtesy of B. Kaplan, One Health Initiative). (b) Zoonotic diseases and arthropod vector activity in social-ecological systems represented within the One Health perspective.
A dynamic and flexible equilibrium between social and ecological considerations are the boundaries a successful SES analysis. Resilience and sustainability research in environmental systems are early adopters of the SES strategy (Walker et al., 2002). The future success of an established system during a period of change lies in its capacity to withstand shocks and disruptions imposed on it by any of the individual components of the system. Therefore, the linkage of sustainability by resilient action in the face of changes defines the SES (Campbell and Almás, 2012). To model a SES, a researcher must have a perspective on scale and complexity, as well as stability and resilience. The system also needs well-defined subsystems, and when the model design is complete, it is often an idealized model. Subsequent models based on more observation would include multiple resources used by many participants and employ various technologies. These complex systems in a SES must also have stability to define the system as a system. A resilient SES is one that can be maintained within the stated limits for the environment over a period of time (de Albuquerque Possas, 2001).

The adaptability of SES boundaries provides an opportunity for the theory to work in diverse research areas. In the case of health, several frameworks have been used for research purposes. Major ones are discussed here. All have roots in the SES approach and most overlap in some areas of interest. Examples of initiatives emerging as health-focused systems that promote transdisciplinary cooperation include One Medicine, Ecohealth, and OH approaches.

3. Ecohealth

Ecohealth is a multidisciplinary systems approach to health where ecosystems act in health dynamics as a set of interdependent services, each with intrinsic value. The analysis focus is on the interaction between the ecological and social-economic processes and their influence on human health, ecosystem health, and ecosystem quality of services (Charron, 2012). In 2003, the International Forum on Ecosystem Approaches to Human Health developed vital principles of linking health, ecosystems, and sustainable development that resulted in an Ecohealth framework. The International Development Research Center (IDRC) has been built upon that framework to foster a Community of Practice on EcoHealth (COPEH). By expanding the interests of health to include ecosystems, this effort added context to biomedical approaches to health that primarily focused on pathogens, parasites, infectious diseases, and human health. Ecohealth is designed to be active and participatory research that depends on transdisciplinary interactions, social justice, gender equality, and stakeholder participation (De Plaen and Kilelu, 2004). The goal is active community implementation of solutions developed with health resource management practices that will work within the capacity of current community resources (Bopp and Bopp, 2004).

Ecohealth encourages policy outcomes combining itself with good governance. To join research and community action, it works to synthesize knowledge, accommodate stakeholders, and reconcile differences. One example of desired outcomes would be to innovate solutions and elicit participation in health awareness programs (Lebel, 2004). In 2006, the first conference of the International Ecohealth Association was organized to further promote the understanding of the linkage between ecology and health (Patz, 2006). Ecohealth was one of the holistic approaches to multi-discipline collaboration that participants advocated.

There were similar efforts in other areas of specialization that moved toward Ecohealth objectives. Comparative medicine, a field that studies medical and veterinary medicine, was also evolving beyond the clinical view of disease into a more holistic view of the environment under the framework of One Medicine (Kahn et al., 2009). The evolution of Ecohealth and One Medicine resulted in parallel trajectories that would eventually bring them closer together in the spirit of a SES system initiative. Collaboration in animal and human medicine was determined to be a critical path to getting a desired holistic health goal into research methods (Mobasher, 2015). By 2012, Ecohealth leadership at the International Association for Ecology and Health (IAEH) promoted the convergence of Ecohealth and the OH framework. In 2016, EcoHealth in OH blended in the IAEA mission and strategy. Meanwhile, a new organization emerged and joined in partnership with the IAEA mission. EcoHealth Alliance is an international nonprofit dedicated to an OH approach. This alliance is the result included in the Consortium for Conservation Medicine (“EcoHealth Alliance – About,” 2017) representing medicine, environmental science, and public health interests. In 2017, the convergences of the SES models of health are aligning under OH.

4. One Health

Research within the OH strategy strives to reduce information silos often found in tightly specialized scientific disciplines by encouraging shared data, descriptions, and collaborations. It defines a system of health that is at the intersection of human, animal, and environmental health interactions (Gibbs, 2014; Benelli et al., 2018c) (Fig. 2a). This multi-layered health approach directly embraces the employ of a SES theory. Using OH for examining the transmission of disease pathogens and parasites via arthropod vectors brings a wealth of previously structured organizational thinking, together with an opportunity to propose additional approaches for OH study (Walton-Toews, 2017). The benefit of using an OH strategy is supported by international and national health organizations (Leboeuf, 2011). The OH strategy is emerging as a dominant framework across research areas but is not yet a fully operational research area. Questions about global governance, quality control, laboratory studies, and communication planning all present challenges to developing a reliable network of related science in OH. To better build an operational model, standardized research methods implemented as data is collected will help future research that may need data to be transferable to other areas of investigation (Cantas and Suer, 2014; Davis et al., 2017; Grace, 2014).

Data collection is one part of the approach. Understanding cultural, social, and economic drivers have a place in OH research (Walton-Toews, 2017). OH literature reveals that there are many references to the practice but little consensus on the definition or the scope of OH in 2007. Efforts to correct this have led to proposals of new interpretations of operational needs built from information in the current literature. “One Health Cosmos” is a proposed system dynamic model designed to help refine OH into a new conceptual framework (Xie et al., 2017). The complexity of defining a new research paradigm with OH continues to present challenges for the field.

Connecting OH to the health framework of Ecohealth, which stresses health outcomes associated with development efforts around the globe, acknowledges that OH is a related framework. However, OH is focused on medical and veterinary practice where environmental science is a newer acknowledged area of interest. The general trend, in today’s literature, favors using OH for examining diseases transmissions that move from animals to humans (zoonotic) and the phenomenon of emerging diseases (EIDs). Research efforts in OH also are also being undertaken to consider the impact of OH practices in describing social conditions. For example, a study to determine how OH and traditional public health compares when there is concern about social justice outcomes (Lysaght et al., 2017). Recently published research on zoonoses using an OH strategy include overcoming challenges in public health for low-resource communities (Cleaveland et al., 2017), lowering Brucella infection rates that come from proximity to animals or animal products (Godfroid, 2017), and facilitating conflict that can occur with infectious zoonosis outbreaks (Walton-Toews, 2017). A recent conference paper reports on the successful use of a OH model to measure data compliance practice to analyze data collection strategies and better design arbovirus surveillance (Paternoster et al., 2017).

As the emerging dominant SES framework, the benefits of using OH to describe arthropod vector contribution to disease management and...
related pathogen/parasite transaction has a place in the evolving understanding of OH strategy (Brouqui and Raoult, 2006). Careful considerations of disease transaction variables would enhance the understanding of how epidemiological models work and what additional data would benefit predictive outcomes for zoonotic disease in arthropod-pathogen-parasite disease system. OH connects a wide range of direct human interests including the movement of people, products, vectors, and pathogens/parasites that introduce diseases to new environments. This strategy to converge many areas of interest is the significant benefit connecting OH to epidemiological modeling (Brouqui and Raoult, 2006). This review is embracing the opportunity that OH’s future development is subject to updates and modifications as iterations of the initiative is tested, funded, and implemented.

Fields are beginning to converge, acknowledging OH as a collaborative strategy. A “One Toxicology” approach rather than being a new initiative, has adopted the OH language. Toxicology has a focus on how chemicals can cause direct and indirect harm to health and ecological sustainability. Toxins in an environment can also alter the behavior of the system from suitable soils to animal behavior. Bringing a OH perspective, with a common goal, is an important perspective for collaboration and sharing of ecological principles and reunitifying toxicology science to a holistic health approach (Beasley, 2009). Taking a broader approach in OH provides for the inclusion of environmental and behavioral influences found in habitat changes, overpopulation, food safety, and ecotourism (Osburn et al., 2009, see also Benelli, 2018a). When developing epidemiological models with a OH strategy, the research examining public health challenges in infectious disease becomes a synergy of holistic thinking and quantitative analysis. Using the framework of OH, the disease model design process can look at opportunities in each area of interest to collect relevant data. The process to identify and quantify dynamic issues across multidisciplinary research results in a more robust model (Luz et al., 2010). The convergence of several fields in a OH approach advocates that stakeholders share the holistic approach to problem-solving as one scientific success. One breakthrough in any scientific query may not be the only solution needed to solve the larger questions of OH. In fact, one breakthrough may lead to new problems and questions, but a shared collaborative approach provides the focus to move beyond one solution and iteratively build a larger understanding. This approach cannot only represent research domains and points of integration but can also focus on transactions that move infections across the processes and critical biological elements in the disease cycle (Coker et al., 2011).

The current framework of OH describes interactions of human, animal, and environment health as co-dependent domains. However, it does not represent active vector-based transactions across or within a domain. With a focus on health within a SES theory, OH can also be used to describe active and intentional disease transmission systems employed by pathogen/parasite-vector interactions. Pathogens and parasites can use direct host-to-host contact as well as indirect contact from the environment (e.g., air, water, soil, and plant parts) to infect new hosts. Active pathogen/parasite transmission across human, animal, and environment domains with arthropod vectors involves more subsystems and variables. OH current description presents an opportunity to advocate for more explicit definitions concerning the data collection around the biological transfer of pathogens or parasites. The current OH representation of animal, human, and environment represent each domain of health interest, but it fails to provide an overall sense of the transactional nature of pathogens and parasites that move across the domains. Risk of health in the OH defined system is not only where the domains cross predictively but also where disruptions crossover expected boundaries. The OH framework representation would be stronger if arthropod vector transmissions were illustrated as a transactional/transmission factor.

OH is not a mature model for global health management. There are calls for stronger international leadership (Zinsstag et al., 2012). There is support for science in the literature, but it is not a coordinated and funded effort with clear governance. As an emerging framework, it depends on established science to collaborate and move the strategy forward. Even with governance and funding unsecured, the health science community is making iterative gains to work in synergy. One important area where multiple inputs are already combined in disease management is the creation of disease models in an epidemiological study.

Epidemiology models are targeted at population level risks using evidence-based data. Models are not intended to replace the data-gathering phase of research, but they are there to provide insights for the evaluation of policy and public health decisions. Models may improve the connections among discrete data sets and help scientists understand a problem (Smith and Ellis McKenzie, 2004). Testing models by changing variables to anticipate or discover critical factors in disease outbreaks are the quantitative tradition of epidemiology. The examination of disease models can provide a quantitative data strategy to be used in modeling OH initiatives focusing on arthropod-borne diseases.

5. Modeling infectious diseases

5.1. Epidemiological modeling

Ronald Ross won a Nobel Prize in Medicine for discovering malaria transmission by mosquitoes in 1902. He is also known as the first advocate for modeling disease in a mathematical way. In his publications on malaria, significant portions of the text included ways to work with variables to understand population risks regarding mosquitoes and malaria (Fine, 1975). This malaria modeling and control work was followed up 50 years later by George Macdonald, who advocated modeling outcomes to direct malaria management (Macdonald, 1961). The Ross-Macdonald model has been the foundation for epidemiological modeling that is taught in public health today (Lessler and Cummings, 2016). When Ross began recommending mathematical modeling for the study of disease, the model’s recommendations reflected his research observations. Because he discovered how malaria transmission occurred by mosquitoes, he accounted for many variables of human, Plasmodium parasite, and vector life. The core of this model is reduced in most descriptions to provide a generic model applied to many disease processes (Keeling and Ross, 2008). Here, we review the fundamental concepts of epidemiological modeling, the connections to a holistic view of disease reflected in model design strategies, and the tenants of holistic medicine as seen in OH. Complexities to disease model functions are introduced to focus on a specific health problem. For infectious disease, additional arthropod vector variables provide significant contributions to building a model for selected pathogens and parasites.

How are vectors factored into disease transmission for modeling efforts in epidemiology? The expansion of systems thinking in disease has begun to consider a more complex role for arthropod vectors in disease. Traditionally the area of epidemiology has focused on the isolation of a single cause of a disease state in a population, though there is growing recognition that biological (with special reference to behavioral traits) and economic factors influence both infectious and non-infectious diseases (Galea et al., 2010; Benelli and Beier, 2017). As the complexities of a disease process build, it becomes necessary to use more evidence-based data from biological and social sources to increase the success of epidemiological modeling outcomes (Morris, 1993; Ajelli, 2017). The success of modern epidemiology intervention in disease management dates back to the 1880s. It was at that time when disease processes once believed to be caused by bad air (e.g., “malaria”, from ancient Italian “mala aria”), or the miasma theory was being replaced by the concept of a causal agent of disease (McMichael, 1999). When disease management is done by not only treating sick individuals but by finding a root cause, the approach reduces current and future risks. This research approach applies to both infectious and non-infectious illnesses.
(e.g., infectious flu and individuals with chronic lung disease).

The infectious disease, because it can move from one host to another, has a model that identifies sick people and healthy people with a population approach referred to as the SIR model (Jana et al., 2015). SIR accounts for susceptible individuals (S), infected individuals (I), and recovered individuals (R). When there is a latency period of infection were a member is exposed (E) but not yet showing signs of disease the model may be expanded to become SEIR (Li and Muldowney, 1995).

Using the models in population assessment for infectious disease results in a value known as the basic reproductive number (R0), which predicts the likelihood that a disease will spread in a population (Diekmann et al., 1990). When R0 is greater than one (R0 > 1), the infection is spreading. When the population is immune, and one person can no longer make more than one other in the populations ill, the R0 is less than one (R0 < 1) and the disease incidence is not growing. In every example of a model, there are assumptions about what variables can change and at what rate they change. For one case, you may assume that an infected person (I) who enters a population of susceptible people (S) can spread a disease quickly. By modeling rates of infection, the outcomes may contribute to control decisions like resource availability for control or vaccine requirements when available. The models require information not only about the rate of infection from one individual to another, but also the frequency with which the infected person will meet more susceptible people (van den Driessche and Watmough, 2002). Typhoid Mary, who was an asymptomatic carrier of typhoid, is a classic example of one person (I) infecting many other people (S). Her ability to spread disease through food is an example of a specific source of disease and a particular transmission model working together to access susceptible people. She was known as a super-spreader of disease (Paull et al., 2012). Specific diseases require specific data sets to calculate the basic reproductive number (R0). The benefit of using a term like R0 is that it provides decision makers with degrees of risk. A very high R0 number is more contagious and is a more significant threat to human health than a lower R0 number.

In a simplified epidemiology model like SIR (Satsuma et al., 2004) a total population (N) is:

\[ N = S + I + R \]

This description helps model a disease by defining the population regarding disease state. Adding and weighing risk factors for infection, recovery, or death further determine the risks of epidemics. The population may be naïve to the pathogen/parasite and have no immunity. That could greatly accelerate the status of individuals from S to I. The pathogen or parasite rate of infection would also be factored into the model to show the rate of a population changing from susceptible (S) to infected (I). Finally, the reduction of people in the S status relates to the total population by either resistance or removal (R).

The modeling varies in complexity once more when considering the transfer mode of infection. Direct contact resulting from human-to-human or animal-to-human with a rapidly spreading disease requires modeling to weigh the risk and allocate the resources needed to address the outbreak, and prevent or limit direct contact. When there is a vaccine available to force S to I, the R0 values are also used to do vaccine calculations to determine the impact of immune individuals on the progression of an infectious disease in a given population (d’Onofrio et al., 2007). The speed of disease transfer, how quickly can one sick person make other people sick, will determine the epidemic scale of the disease outbreak (Bichara et al., 2015). Modeling a disease with multiple transmission models has practical applications in the public health policy decision process. For example, when the Zika virus was discovered to be both a mosquito-borne transmission (Benelli and Romano, 2017) and a sexually transmitted disease, researchers demonstrated, in a disease model, that the mosquito transmission was a much greater contributor to the Zika virus basic reproductive number (R0) and sexual transmission alone would not contribute as much to disease growth. Therefore, it was a guideline to distribute resources across control efforts that focus on mosquito vectors, environment, and behavioral changes (Gao et al., 2016).

Predictive disease models built to accommodate both vertical and horizontal pathogen or parasite transfers need to factor in environmental conditions, vector behavior, and pathogen or parasite adaptations, to not only work with an ongoing disease outbreak, but also anticipate conditions when the pathogen/parasite can re-emerge from a dormant state (Niu et al., 2012). There are other complex relationships in vector-borne diseases concerning the ability of a pathogen or parasite to moderate at the molecular level in a dynamic process of host selection (Pulliam, 2008). As a vector model of disease, the biological factor participates in a complex set of processes making the selection of variables in epidemiological models more challenging. Therefore, it is important to consider the many levels of adaptation and modification that can take place in a vector-borne disease. It is clear that understanding the risk of emerging disease requires a systems approach at many scales of interaction from molecular flexibility to environmental fluctuations (Geoghegan and Holmes, 2017).

5.2. Pathogen and parasite consideration in modeling

When the focus is about pathogens and parasites infecting humans via arthropod vectors (e.g., mosquitoes, tsetse flies, and ticks, just to cite some major examples), modeling needs to include data about the evolution of the pathogen/parasite-vector pairing, as well as the vector-host dynamics, whenever possible. Because the goal of EIDs and re-emerging infectious diseases (rEID) management is to identify and prevent human epidemics, it needs combined efforts from clinicians and public health planning to treat patients and promote health preserving behaviors (Kilpatrick and Randolph, 2012). Vector-borne pathogens and parasites (VBPs) represent a disease system directly influenced by the actions of the vector and not deliberate host-to-host actions resulting in contact transmission (Onofrio et al. 2015). For example, in vector-borne diseases, the vector host preference may be more important to consider in predicting disease transfer than all available possible hosts. The model needs to allow for the fact that the number of potential hosts for a given pathogen or parasite may not be as critical as the number of preferred hosts for the vector in a vector-borne disease dynamic (Hamer et al., 2011).

When and how a vector and an infectious agent come into contact provides opportunities to look at geographic and spatial models of disease. Both have range limits dictated by environment and landscape that will influence infectious agent-vector pairing. Models using the spatial occurrence of a disease have been utilized to assess environmental factors that directly or indirectly impact the pathogen/parasite or the vector, and ultimately contribute to risk analysis and disease control measures. New technologies that can manage large data inputs can select spatial and space-time modeling, high quality epidemiological relevant data, operational parameters for disease control and communication to stakeholders, to build new approaches to limit vector-borne diseases in resource-poor environments (Eisen and Eisen, 2011).

While the outcomes and approaches vary for different types of pathogens and parasites, they all cause some level of harm to the host (Casadevall and Pirofski, 1999). Pathogens and parasites also have strategies that are arthropod-specific to assure the infectious agent fitness and successful transmission beyond a single vector’s life. A pathogen/parasite using the vector biology to assure survival can move horizontally and vertically to new vectors. Horizontal is moving from one vector host to another vector host. Vertical transmission is when the infectious agent is transferred to the next generation of a host. The ability to use mixed modes of transmission (vertical and horizontal) allows pathogens and parasites to persist under diverse conditions (Lipsitch et al., 1996). The transfer of the pathogen/parasite to the next generation of hosts can confound the disease model. The model may
indicate the disease has disappeared in the primary hosts, but the pathogen or parasite survives in a dormant or inactive form of the next generation (see also Ward and Benelli, 2017). The trigger for vertical transmission mode includes food, available resources and reproductive success (Agnew and Koella, 1999). Other combinations of environmental, taxonomic, evolutionary and physiological factors can evoke vertical transfer (Lequime et al., 2016). In practical applications of disease prediction models, this accounts for the fact that some mosquito-borne arboviruses disappear from a landscape; the disease pathogen remains the area, but there is no disease reported in animals or humans. Rift Valley Fever Virus (RVFV), a disease currently limited to eastern Africa, is a high-consequence pathogen (Belay and Monroe, 2014) with the potential for international distribution (Kenawy et al., 2018). It can infect both animals and humans. In young animals, RVFV has a high mortality rate. In humans, severe illness may occur in 1–2% of infected people. There is considerable concern that this virus may be able to travel to new areas like North America and locate native mosquito species potentially acting as competent vectors (Bird and McElroy, 2016). RVFV, in Africa, has a transmission cycle that moves from the infected mosquito female to the eggs. The eggs of the mosquito can remain viable during dry periods. The virus will stay infectious for several years during egg dormancy. Rainfall creates the aquatic environment needed for egg hatching, and when the mosquitoes emerge, they have an active virus that will multiply and infect the saliva of the biting females, continuing the cycle (CDC, 2016; Kenawy et al., 2018).

The infectious agent ability to trigger dynamic evolutionary changes is a factor to consider when establishing the agent’s ability to successfully exploit highly competent arthropod vectors. A pathogen or parasite assimilating to transport by an arthropod vector must adapt to survive the arthropod defense system, potentially amplify itself within the arthropod body, and then exit the arthropod to enter a new host. When using an intermediate vector, the pathogen/parasite success depends on the vector staying viable. The infectious agent generally will do little harm to the vector’s health (benign) to provide the vector the best opportunity to find new hosts for the infectious agent. Many pathogens and parasites use a vector to amplify and deliver a higher dose during the next transfer. Their evolution, using amplification strategies, may favor greater virulence in infectious agents spread by arthropod vectors to their destination host (Ewald, 1994a).

The strategies for pathogen and parasite adaptation evolve over generations, but they may also be in the genetic flexibility built into the infectious agent genes to change dynamically to new environmental challenges. That flexibility can provide more optional strategies to survive and adapt to the life cycle of any one pathogen/parasites life (Sharakhov and Sharakhova, 2015). More data about the vector and infectious agent relationship makes stronger epidemiology models that can consider how vector control management will influence an epidemic outbreak or how a new invasive arthropod could expose a susceptible host population to the danger of a vector-borne disease.

5.3. Arthropod consideration in modeling

Proving that arthropods carry diseases is a breakthrough credited to the discovery of Texas Cattle Fever’s transmission by ticks in 1893 (Smith and Kilborne, 1893). This was followed by the discovery the mosquito role in the transmission of malaria (Ross, 1911). The understanding of arthropod vector role in disease revealed that a new dimension public health management was possible, vector control. With significant investments of time and expense, vector elimination programs began across the globe to address public health risks (Gubler, 1998). Some were landscape modifications to reduce vector breeding while others focused on killing adults in chemical campaigns that dominated control efforts after the discovery of DDT (Benelli et al., 2018a).

In the past, the eradication of arthropod vectors was seen as a viable strategy. After the successful elimination of the yellow fever mosquito, *Aedes aegypti* L., in most of the Americas using DDT and land management, the idea that mosquito populations were no longer an issue was a common belief (Gubler, 2005). In fact, in 1965, researchers were considering how to maintain research colonies of *A. aegypti* in the face of total elimination of the species in the field. Dr. George B. Craig of Notre Dame made a case for the maintenance of *A. aegypti* as a research tool (Craig, 1965). Those assumptions were incorrect. *A. aegypti* was able to rebound and establish itself back in the tropical areas of America because of insecticide resistance and re-invasion of the species (Kotsakiozi et al., 2017). Today it is more universally understood that eradication is not practical due to cost, environmental issues, and unexpected outcomes of species eradication (Hardy and Barrington, 2017; Nauen, 2007).

Diseases that require arthropod vectors to transfer a pathogen/parasite to humans are often managed controlling the vectors (Benelli and Mehlhorn, 2016). With the elimination of a vector species no longer considered a viable goal for vector control, the research collected on arthropod vectors are more focused on how to interrupt other weak links in a disease cycle in addition to vector death. The data on arthropod vector dynamics are complex, and, in many cases, being re-discovered. Epidemiological modeling has to adjust to the new reality of disease transmission in arthropod vector modeling (Wonham et al., 2006).

Accounting for arthropod vector-borne disease modeling requires new ways of thinking. Arthropod vectors have complex life cycles where host preferences can change. First, it is no longer realistic to reduce the complexity of how an arthropod-vector population influences a disease cycle by merely controlling the population at one stage of vector life. Even with adequate controls used for disease management, the vector population can quickly recover and reintroduce the disease. Second, the elimination of an arthropod vector population was often not species specific (Benelli et al., 2016). Today, more consideration is given to the wide range of species in the environment, as well as to potentially becoming invasive species. Many factors, including the age, reproductive potential, and species distribution influences on arthropod vector competence are again under investigation (Lord, 2010).

Both pathogens/parasites and vectors respond to the environment in ways that may not be advantageous for pairing. Climate may influence where a vector may lay eggs and alter the population of available vectors. Some mosquitoes lay eggs in clean water, others prefer water with high content of organic matter, and others place eggs close to a waterline and hatch after the eggs immersion in water following a rainstorm (Lord, 2004). An arthropods’ success in reproduction, hatching, and adulthood is a baseline for disease models, and can vary with climate and species needs. These types of biological and environmental variables, with the possibility of many more, would alter the probability of a vector becoming infected with a pathogen/parasite in the first place. If the pathogen/parasite finds the vector successfully, many conditions impact the vector’s competency in infecting a host.

With current vector management and control strategies, new sets of processes are active in vector control. Integrated Pest Management (IPM) – and Integrated Vector Management (IVM) as well – have taken on new dimensions of control efforts with a particular focus on urban controls (Knudsen and Slooff, 1992; Benelli and Beier, 2017). Looking at IVM approaches allows researchers to consider multiple scales of intervention from species management to community health programs. Programs to educate people about personal behaviors to avoid contact with arthropod vectors are shown to have an impact on disease and are an influence on outcomes in disease risk models.

The concern for EIDs is global. A host with a pathogen/parasite can carry disease away from its original location, and arthropod vectors can easily move unnoticed. The possibility of the distribution of pathogens and parasites via arthropods raised concerns over a century ago (Nuttall, 1899). Creating a strategy to manage and monitor vector-borne disease risk requires cross-boundary stakeholders to effectively
solve problems and achieve desired outcomes. In parts of the world embroiled in political, social, and economic crisis, misuse of vector control tools may create new problems. The frequent overuse of insecticides and antibiotics to fight vectors and infectious agents, respectively, is not well monitored, and the number of drug-resistant pathogens and parasites, as well as insecticide-resistant vectors, is fast growing and spreading worldwide (Eisler et al., 2003; Hemingway et al., 2016). Global health risk, defense from bioterrorism, and enforcement of rules about surveillance once again raise concerns about the governance of health regulations (Fidler, 1999).

The pathogen/parasite host preferences are not always the same as the arthropod vectors. Zoonotic diseases occur in two forms, and each will influence the arthropod vector impact on disease transmission. Some can originate in animals, and then mostly occur as human infections, which can therefore move from human-to-human directly (arthropogenic). Other zoonotic diseases reappear from animal reservoirs (obligate zoonoses) (Cleaveland et al., 2007). In most cases of obligate zoonoses, the pathogen/parasite is not able to use a human host to infect an arthropod vector with the disease because the pathogen/parasitereproductive ability in humans does not reach an infective level. The infection stops with the human and creates a dead-end host for the infectious agent. Humans can continue to be infected as vectors developing on an animal host reservoir bites a human. This host preference (or lack of host specificity) also requires the disease modeling strategy to account for the likelihood of an arthropod vector seeking out multiple hosts during one lifecycle (Dobson, 2004).

If a health population represents a stable health system, a new or reemerging zoonotic disease creates measurable disruption in the health system dynamics. The system dynamics model provides for adjustments to small changes in the system leading up to a disease disruption. In that circumstance, even before a disease outbreak, system conditions change, and arthropod vectors of zoonotic diseases adapted to those changes. Pathogens, parasites and arthropods evolve and modify regularly, and with a rapid reproduction rate, a switch in specificity, and disease dynamics can seem sudden if the process remains unmonitored. With a high frequency of opportunity for adaptation, a pathogen/parasite-vector pairing can infect new hosts or expand their range to access unchallenged host populations. This constant iteration of disease efficacy requires medical professionals to remain up to date on the risk of emerging pathogens or parasites and their potential arthropod vectors (Colwell et al., 2011).

Human populations shift and change also. As the number of people increases in a place, the risk of infectious disease rises. Geographic shifts and growing populations often result in high human density and low sanitation standards. Arthropod vector species can change or shift with environmental dynamics. Overcrowding and slum conditions lead to higher disease risk and a need for public health action (Snyder et al., 2017). Those risks include arthropod species that thrive in urban environments (Ajelli, 2017).

In blood-feeding arthropods, the adaptations used for successful blood feeding have also evolved to meet the needs of the arthropodevolutionary survival. Female mosquitoes, for example, rely to cues like CO2 and volatile skin compounds (Takken and Scott, 2003) when seeking a vertebrate blood meal. When a pathogen or parasite and an arthropod become a vector (as a pair), each is required to adapt to the other without the adaptation being fatal, requiring evolutionary fitness. The dynamic is complex, costly to each organism, and has been described as a co-evolutionary arms race (Ciota, 2017). The impact of the pathogen/parasite infection may also change the arthropod’s behavior, which can result in higher (or lower) levels of infection in a host population (Leelvra et al., 2007). For example, a pathogen/parasite may interfere with blood intake during a single bite encounter between the mosquito and a mammalian host. Feeding interference can result in the mosquito needing to bite more than once to satisfy her need for a meal. That behavior provides the pathogen/parasite more exposure to multiple hosts during a feeding event and increases pathogen transmission success (Stanczyk et al., 2017). A pathogen or parasite may also change a vector’s behavior in a way that reduces transmission to a host. In some mosquito species, the infectious agent actively infecting the mosquito can slow feeding behavior and decrease the pathogen distribution (Vogels et al., 2017). The dynamic of pathogen/parasite finding a new potential vector is a critical area of study that calls for more research, particularly in regards to public health (Murdock et al., 2017). This interface of pathogen/parasite and arthropod contains many potential modes of intervention that could control or prevent the spread or amplification of the infectious agent, possibly resulting in vaccine creation or vector control options.

Changes in climate can also impact vector-borne disease dynamics. Specifically, the biting rate, vector development rate, and pathogen/parasite replication increase with higher temperatures. The results are not linear because temperature alone is not the only variable. High temperatures without water could also create moisture stress that could increase vector survival/abundance (Kilpatrick and Randolph, 2012). Arthropod adaptation includes reactions to climate stress, as seen in some mosquito species which adapt to dry weather by having drought-resistant eggs that will emerge when the moisture levels return (Reiter, 2007). To capture the dynamics requires a complete investigation of the biological processes in disease transmission. The process can be highly variable and very detailed. In mosquito vectors, virus transmission variables included the duration of human infection, mosquito biting rate, pathogen transmission success from humans to mosquitoes, virus replication time in the mosquito (extrinsic incubation period, EIP), mosquito density and survival, a mosquito to human transfer of the virus, and detection of the illness in humans (Marcheva and Prosper, 2013).

Perhaps one of the most critical considerations for looking closely at arthropod vectors of diseases within the OH initiative is the potential severity of these diseases on human hosts. Pathogen and parasite evolution with their biological vectors has been found to lead to more virulent infectious agents resulting in a more severe disease condition, due to the need of a pathogen/parasite to be able to rapidly reproduce in both the vector and the host to make the infection transfer possible (Wang, 2017). Some evolution theory suggests that the evolutionary tendency of selection may encourage pathogens and parasites to evolve using only human hosts (Ewald, 1994b; Kilpatrick and Randolph, 2012). This evolutionary trend is a critical event in planning for pandemic disease by monitoring arthropod vectors for new pathogen/parasite strains that may indicate a new disease pattern. Whenever a pathogen/parasite from the category of zoonotic disease (animal-to-human) adapts/transforms to a human-to-human (H2H or anthroponoses) transmission the risk of severe health outcomes is greater (Richards et al., 2017; Zouache and Failloux, 2015).

6. Aggregating data for One Health

Acquiring meaningful data on arthropod vector dynamics in a disease system is a major challenge within the SES. Acquiring or aggregating data that were obtained as an outcome of an isolated study may not provide enough context for inclusion into a disease theory. The OH framework is well suited to address the areas of interest for the pathogen/parasite-vector dynamics via epidemiological modeling by addressing data outcome quality. Methods developed for a given species population may need to be reviewed for suitability in other studies. Repeating experiments may be minimized if the OH guidelines can provide some assurance of data applicability across studies. These areas of interest, concern, and methodology of theory are steeped in a dynamic world of changing landscapes of ecology and data. As more information is available, a framework can organize and focus the researchers on common solutions. In the next section, understanding data sources and graphic representation of complex ideas are suggested to help support a strategic approach where arthropod vector data will contribute to disease strategies.
7. Distributed data

The volume of actual and potential data sources continues to grow and presents both challenges and opportunities for systems to alert, respond, and predict EIDs (Khan et al., 2010). “Nowcasting” is a term used in social media studies to describe the current state of an event by monitoring and amalgamating social media cues (Johansson et al., 2014). With reference to infectious diseases, Google Flu® was launched with the intent of tracking search terms on the Internet to locate flu hotspots. The experiment has not been as successful in detecting outbreaks as hoped, but it pointed out the idea that hotspots, key nodes in a social network, can be exploited in the near future to combat infectious diseases early (Lazer et al., 2014).

There is a worldwide recognition that EIDs are a threat and that tracking and managing information about vectors is a vital data component (Myers and Patz, 2009). In United States, reporting of mosquito-borne viral diseases is done via ArboNet, which is hosted by the Center for Disease Control (CDC). Funding for the project began after West Nile Virus outbreaks in 1999 (Lindsey et al., 2012). Health official and surveillance specialists must request access and submit data at will. When data submission is a voluntary activity, the quality of information is likely to change over time. Governance of a surveillance system requires funding to monitor quality and compliance. Federal funding for CDC vector surveillance has been decreasing, and the system relies on less robust sources of data as time goes on (Hadler et al., 2015).

In the European Union (EU), there is a VectorNet project for data collection that has been designed as a broader repository for arthropod vectors responsible for animal and human diseases (Schaffner et al., 2016). Collaborative studies have been conducted to test and address gaps in the system and assess the predictive factors that work in disease management. In a project to track the highly invasive Asian tiger mosquito, Aedes albopictus (Ste toysmaia albopicta) (Skuse), a competent Zika virus vector (Benelli and Romano, 2017), data in VectorNet documented the movement of the mosquito and matched against models of regional climate suitability for the species (Petrić et al., 2017). This data strategy is an example of how modeling for a disease can benefit from detailed data on arthropod vector behavior and climate adaptation before a pathogen or parasite has arrived at a new location.

HealthMap is a global view of disease outbreaks. The network has aggregated information from a variety of freely available sources (Freifeld et al., 2008). In the spirit of social media reporting that focused on the current state of a selected disease (the “now” in nowcasting), HealthMap provides graphical views of diseases and news reports about trending diseases of all types. It also provides a daily news update as well as a twitter feed for disease news worldwide.

With a large number of sources for disease data, the OH framework provides an opportunity to establish guidelines for researchers developing methods to reuse data for various health analyses. A proposal to integrate data into OH by creating a Checklist for One Health Epidemiological Reporting of Evidence (COHERE) is in the peer-reviewed literature. The goal of reporting guidelines is to improve data quality and promote data integration (Davis et al., 2017). OH research design proposals are also being generated as process flowcharts with recommended practices to guide research practices (Lebov et al., 2017). The general direction of health reporting research is to move towards collaboration. Better collaboration allows researchers to leverage many data collection efforts and do the analysis that will produce results in reusable formats that can help build disease prediction tools.

8. Distributed decisions

With many data sources available, the decisions to act on a disease outbreak are a combination of factors both from science and social decision-making. Completely preventing an EID may be impossible at this time but health policy should plan methods to minimize harm until prevention is possible. Infectious diseases are often detected after they have impacted some individuals. In animal health, that can influence food value, animal survival, and economic outcomes. In humans, an infection can cause morbidity and mortality in vulnerable populations (Narrod et al., 2012; Benelli et al., 2018a). Minimizing adverse consequences is one reason why disease models exist. They can provide guidance about limited resource allocation. If they are to evolve into predictive models, they must embrace a diverse range of data about a disease, travel, social contact, and pathogen/parasite-host-vector networks. Some variables may be known, some varied over time and some may need to be assumed (Johansson et al., 2014). The quality and value of the data used in decisions about health are often influenced by the stakeholder’s point of view. In this framework, key questions are: what is the cost or value of an intervention to control disease? How do you reach a plan of action when you have multiple points of view?

A multi-criteria decision analysis (MCDA) approach to health system research can be applied to a OH frame. The MCDA strategy has evolved as a way to analyze multiple streams of dissimilar information (Baltussen and Niessen, 2006) and how to evaluate arthropod-borne disease responses in a multi-stakeholder decision framework. MCDA was used as a tool to investigate and build a shared understanding of how decisions can be supported to manage and prioritize infectious disease strategy (Hongoh et al., 2016). In that study, stakeholders were asked to prioritize disease criteria and give weight values to solutions. The result of which was a participatory decision-making process that highlighted social concerns and resource-related prioritization for public health actions in reaction to disease threats. It created a model where facts and variables determined from the quantitative research mix with social and economic values and criteria. It provides a social framework for decision-making and also provides a place for evidence-based science to be weighed in a social value framework.

9. Data representation

Representing data graphically helps people to synthesize information and enhances people to detect the expected and discover the unexpected in large data sets (Thomas and Cook, 2006). A common representation of OH is a three-circle Venn diagram where each domain is represented by a circle that interacts with other domains (Fig. 2b). Interfaced areas (where the domains cross) represent areas of relating factors. The ability of a biological vector to move within, between and among the domains represents an opportunity to add another layer to the Venn diagram, which would represent transactions mediated by biological vectors. The representation of OH as three circles is intended to represent each of the domains, but it fails to provide a sense of the transactional nature of pathogens and parasites that move across the domains. To provide the graphic with more “representational insight”, the illustration could also convey vectors as an active agent in the graphic. This would provide additional dimensions into the OH process by illustrating the presence of transaction in the graphic (Uttal and O’Doherty, 2008).

In Fig. 2b, the OH framework is represented on the left by the domains of human, animal, and environment within the SES. The representation on the right shows two arrows representing active disease transfers that are functioning in a OH dynamic. Zoonotic pathogens or parasites moving from animals to humans are represented with an arrow, and the circular arrow represents the dynamic transactions taking place in a biological vector transfer of a given disease.

Building the evidence for arthropod vector data to be a part of a transactional factor in OH begins with looking at OH as a general strategy for health studies. Human, animal, and environment health are areas of concern that can interact (domains represented as solid circles). The disease moves across these domains in the areas of intersection and social-ecological processes influence that dynamic. In both diagrams, SES encloses the OH domains. SES are systems that work under dynamic conditions and when systems and subsystems interact. The red
arrow in Fig. 2b showed zoonotic pathogens or parasites moving from animals to humans. The circular purple arrow represents the arthropod vector acting impacting all domains.

Arthropod vectors are not simple pathogen/parasite carriers. As a blood-feeding arthropod is biting and one or more hosts when infective agents are present, there are at least three distinct organisms interacting: the arthropod, the pathogen/parasite(s), and the host. Each has evolved to survive the encounter as often as possible (Halbach et al., 2017). In the dynamic interactions of host and pathogen/parasite, there is a co-evolution at work (Woolhouse et al., 2002). Understanding or at least appreciating the factors at work in arthropod vectors of disease provides the input into a OH initiative that goes beyond the transfer of a pathogen or parasite across the environment, animal, and human interfaces. Additional arthropod vector data, including basic biological knowledge (Benelli et al., 2018b), collected meaningfully and applied to zoonotic disease models can enhance modeling development as well as disease prediction.

10. Conclusions and potential applications “in the real world”

Overall, the research question addressed in this review explicitly references arthropod vector data to improve zoonotic disease prediction. The system to obtain quality data, reference a disease cycle, manage human factors, and share the results across research areas, will benefit from a SES/OH framework. It is still conventional wisdom to break the arthropod vector disease cycle at the weakest link by removing the vector from the environment. Frequently this has resulted in environmental changes, where landscapes are modified, or pesticides are applied to manage arthropod vectors of disease. Narrowly applying solutions to one problem in isolation will create change in another system or subsystem process. The result can be finding new issues at another point in the SES system.

Within a OH strategy driving disease model design, the roles of vectors, pathogens, parasites and hosts are studied as individual agents and as integrated processes. All data gathering is done under the premise that information obtained and shared about one factor can be used to understand the larger fields of disease predictions across all of the OH domains. The analysis moves into areas of public health, integrated and biological control of vectors, and government investments in resources, to construct a broader solution. When health problems are studied, understood as individual components and placed into a larger multi-process program, there are priorities selected based on the goals of the system under study. Those priorities then factor into what actions and what outcomes are initiated to achieve desired outcomes. Collaborative decision-making provides more opportunities to successfully work and communicate in a complex, evidence-based ecosystem and help re-imagine a way to understand the relationships among multiple species at multiple scales of interaction (Waltner-Toews, 2017).

Understanding the dynamics of vector-borne diseases helps to break away from past disease management paradigms where health problems are viewed in isolation and solutions are often distributed as a “one and done” event. The OH framework begins to set a value on information from evolutionary adaptations in pathogen/parasite-vector, host, and pathogen/parasite-host success as well as modeling interactions of multiple environmental variables. This understanding not only leads to a better understanding of current disease states but also adds data robust to epidemiological models.

Conflict of interest

The Authors declare no competing interest.

Acknowledgements

Dr. G. Benelli is grateful to the One Health Initiative (www.onehealthinitiative.com) for hosting him as supporter. Dr. B. Kaplan and Dr. L. Kahn kindly provided the map used in Fig. 1 and the One Health scheme used as Fig. 2a.

References
