



Catastrophe and Climate

# Emerging Risks in the Health Sector: Changing Species Distributions and Seasonality





# Emerging Risks in the Health Sector

## Changing Species Distributions and Seasonality

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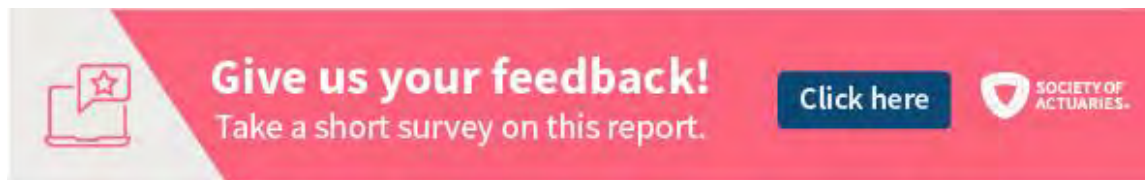
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# Emerging Risks in the Health Sector

## Changing Species Distributions and Seasonality

### Executive Summary

Climate change has the potential to wreak havoc on ecosystems worldwide, with both foreseen and unforeseen consequences. One anticipated repercussion is the change in suitable habitats of vectors, such as mosquitos and ticks, who can transmit serious and even life-threatening diseases to humans. These so-called vector-borne diseases have devastating impacts on human well-being and take a major role in cost to society and insurers. In the context of climate change, new patterns of temperature and humidity along with various biotic and abiotic factors will continue to shape the habitats of these vectors. The complex, non-linear sensitivity of pathogens and vectors to these dynamics make it difficult to develop detailed forecasts of trends of migrations and losses emanating from vector-borne diseases. However, regional and local studies exist that already can inform the actuarial community, especially in the health sector, about these emerging risks from changing species distributions. That is why in this report, we outline major vector-borne diseases, discuss their symptoms and treatment costs, and present the relevant research regarding their evolving spatial patterns due to climate change. This research aims to bring a new level of understanding of this emerging risk to the actuarial community and empower it to model and forecast challenges that will emerge. In the coming years, the joint work between biologists and actuaries will be of paramount importance to shape public policies, institute monitoring, and spearhead awareness campaigns --- all to minimize ensuing social losses.



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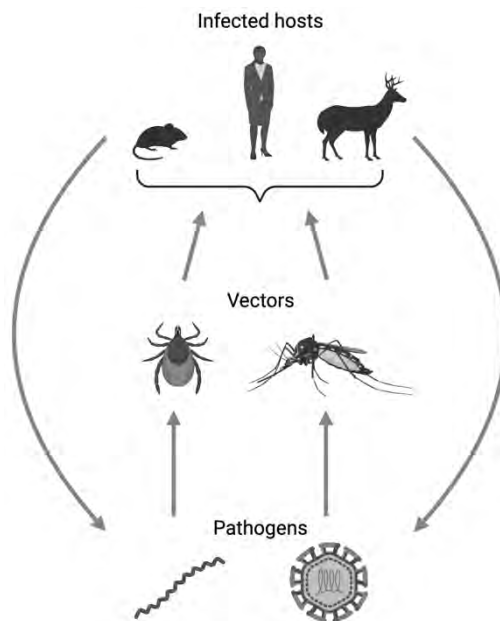
## Section 1: Introduction

Each year, more than 1 billion people worldwide are infected with one of the major vector-borne diseases, such as malaria and dengue (Tozan et al. 2021). In fact, these vector-borne diseases account for 17% of infectious diseases globally (World Health Organization), and each year result in over 700,000 deaths (Tozan et al. 2021). Scientifically speaking, a vector-borne disease is a disease caused by a pathogen, such as a virus or bacterial species, that is transmitted to host animals through one or more other vector species, such as ticks and mosquitos. Well-known diseases in the United States such as Lyme disease and West Nile disease are vector-borne and cause substantial health and economic costs, with \$8 million in medical costs per year for Lyme disease (Limaye et al. 2019) and overall economic impact exceeding \$56 million for severe cases of West Nile. Other serious diseases are less common but increasing in frequency and geographic range, such as Human Granulocytic Anaplasmosis, which causes severe illness in an estimated 11% of cases (Bakken et al. 2006).

The Intergovernmental Panel on Climate Change (IPCC; 2007) ranked increases in vector-borne diseases as one of the most likely changes to result from climate change. This is in large part because major vectors for these diseases, such as ticks and mosquitos, are best able to thrive in temperate to hot climates. Predictions of which regions will be most affected, and when, would enable the actuarial community to prepare for the ensuing health and economic impacts. For this reason, this report reviews recent research on the effects that climate change is likely to have on the hazards to human health due to changes in the spatial distribution and abundance of vector-borne pathogens and their vectors.

Precise modeling of the changing hazards of these diseases depends on a detailed understanding of the complex and interacting layers of factors involved. For example, there is the pathogen itself, the host and vector species by which it reproduces and gets transmitted, the increasingly human-dominated landscapes in which these species live, and patterns of human behavior in those landscapes that drive disease exposure, and, in some cases such as West Nile, the dynamics of outbreaks (Figure 1). Climate change is likely to influence the risks posed by vector-borne diseases through effects on all these layers, both individually and in interaction.

**Figure 1**  
**BIOLOGICAL CYCLE OF VECTOR-BORNE DISEASES**



Pathogen, vector, and infected host species together make up the biological cycle of vector-borne diseases. We discuss bacterial and virus pathogens as transmitted by tick and mosquito vectors, as shown. Infected host species include humans, other mammals, and birds, although in some cases species may be dead-end hosts in the pathogen life cycle (not shown).

Current projections of hazards due to vector-borne diseases generally rely information about where the pathogen, its vectors, and hosts exist now or have existed in the past. This data is used to determine "suitable climate" --- potential ranges where basic features of the environment such as temperature and precipitation are consistent with pathogen reproduction and transmission. Change in climate is expected to drive changes in the geographic range of the pathogen and its vectors. However, which regions of this potential range will actually become occupied with a given disease depend on additional factors such as interactions with other species, changes in land use by humans, and vector-control efforts such as insecticide spraying. Further evolution in pathogens and their vectors can modify their ability to survive and reproduce in different environments, a possibility which has not been considered in ongoing modeling efforts. All things considered, a detailed attribution of health and economic impacts from vector-borne diseases to climate change remains outside the reach of scientific modeling. We focus here on current best estimates of how change in climate will drive changes in where these diseases are likely to be present. For instance, different regions of the United States will be impacted in specific ways: regions with cold winters that were previously uninhabitable by mosquito and tick vectors will become more suitable, and many places that were already suitable will likely experience an increase in vector proliferation. However, some areas that are already suitable may see a reduction in cases due to extreme heat or drought that harms vector or pathogen survival and reproduction.

While the current scientific understanding of climate change’s effects on the biology of vector-borne diseases has been the subject of a variety of recent reviews, major gaps remain in the information on costs and risks relevant to an actuarial audience. To help address this, this report focuses in particular on two groups of vectors responsible for the majority of cases and severe disease in North America: ticks and mosquitoes. In particular, we review what is known about the likely health and economic effects of climate change on selected pathogens transmitted by these vectors that have substantial health impacts for humans or pose clear emerging threats. We draw primarily on projections for North America to illustrate these effects, but the modeling approaches and biological mechanisms we discuss apply globally. Note that we omit parallel issues for diseases in domestic animals such as horses and cows, which have significant implications for agriculture (e.g., Jacob et al. 2020). We also exclude consideration of malaria, which is a leading global health threat but also declining over the past two decades due to intensive human interventions and therefore are not a clear example for illustrating the effects of climate change; for a recent modeling study see (Ryan et al. 2020). It is also worth acknowledging that vector-borne diseases are a part of the larger group of zoonotic diseases, which includes the SARS-CoV-2 virus responsible for the Covid-19 pandemic. However, the effects of climate change on zoonotic disease risks more generally is outside scope of this work.

**Table 1**  
**LIST OF DISEASES REVIEWED IN THIS REPORT AND THEIR KNOWN VECTORS**

Disease	Pathogen Species	Vector Group	Dominant Vector Species
Chikungunya	Chikungunya virus (Alphavirus)	Mosquitoes	<i>Aedes aegypti</i> , <i>Aedes albopictus</i>
Dengue Fever	Dengue Virus (Flavivirus)	Mosquitoes	<i>Aedes aegypti</i> , <i>Aedes albopictus</i>
West Nile Fever	West Nile Virus (Flavivirus)	Mosquitoes	Multiple species in <i>Culex</i> genus
Zika Fever	Zika Virus (Flavivirus)	Mosquitoes	<i>Aedes aegypti</i> , <i>Aedes albopictus</i>
Human Granulocytic Anaplasmosis	<i>Anaplasma phagocytophilum</i>	Ticks	<i>Ixodes scapularis</i> , <i>Ixodes pacificus</i>
Babesiosis	<i>Babesia microti</i>	Ticks	<i>Ixodes scapularis</i>
Ehrlichiosis	<i>Ehrlichia chaffeensis</i> , <i>E. ewingii</i> , <i>E. muris eauclairensis</i>	Ticks	<i>Amblyomma americanum</i>
Lyme Disease	<i>Borrelia burgdorferi sensu lato</i>	Ticks	<i>Ixodes scapularis</i> , <i>Ixodes pacificus</i>

Adem 2019, Röcklov and Dubrow 2020, Rodino et al. 2020

## Section 2: Climate change has major implications for vector-borne disease costs

### 2.1 NAVIGATING TERMINOLOGY

Across the scientific literature analyzing the effects of climate change on the spatial distribution vector-borne diseases, one can encounter many terms familiar to insurers with a similar or distinctly different meaning or lack of precision. For this reason, caution is warranted when these terms are encountered, as no common set of definitions has settled. Here we outline the terms used in our report, while cautioning the reader that individual paper references might refer to these terms in different ways.

In the context of insurance, there are many possible definitions of risk. One of the classical definitions considers risk to be the uncertainty of future outcomes or events. Pure risk can be defined as a situation where outcomes can be only negative (such as costs, losses, or damages), or neutral, with no positive outcomes (Rejda et al. 2014). In this report, we consider vector-borne disease risk to be the uncertainty of the event of contracting vector-borne disease or not --- which is a pure risk.

In broad terms, we define the event of contracting a vector-borne disease as the union of several constituent events:

1. An individual comes into contact with a vector.
2. The vector bites the individual.
3. The vector transmits a pathogen.
4. The individual has an adverse reaction to the pathogen, i.e., contracts a disease.

In the context of the literature considered, the susceptibility of an individual to contract a vector-borne disease may be viewed as an exposure. However, one can find references wherein by exposure, the probability of contact with or proximity to a harmful agent is meant. For example, Harrigan et al. (2014) and Davis et al. (2018) use the word exposure to describe the probability of a vector becoming a host for the disease, while Belova et al. (2017) and Brown et al. (2015) view exposure as the probability of human being bitten by a vector. Additionally, there are many ways that exposure can be proxied; for example, Duik-Wasser et al. (2020) uses the density of vectors infected with a particular disease as a proxy for exposure. In this report, we refer to population specific exposure, in other words, the probability that an individual from a given population will contract a disease (Rohat et al. 2020). This can also be viewed as the percentage of persons in a population exposed to vector-borne disease risk.

It is not always the case when the vector bites an individual that adverse health outcomes will ensue. We refer to vulnerability as the likelihood of an event where an individual has an adverse reaction (i.e., contracts a disease) when exposed to a pathogen. In particular, certain populations such as the elderly or immunocompromised are more vulnerable to severe illness when exposed to vector-borne pathogens. Areas with more vulnerable populations thus have higher exposure.

It is of particular note that the term hazard is often used in the literature to refer to a potential source of harm or cause of loss (Duik-Wasser et al. 2020), which insurers typically refer to as a peril (Rejda et al. 2014). Here, we reserve the word hazard to refer to a condition that creates or increases the frequency or severity of loss (Rejda et al. 2014). Thus, transferred in the context of vector-borne diseases, increased human activity in an area of high vector density would be considered a hazard, while the pathogen itself can be seen as a peril which is manifested by disease and its potential financial implication. Two different groups of factors are considered that impact both hazards and perils: biotic and abiotic. The biotic factors<sup>1</sup> are all living organisms that can impact other organisms or an ecosystem, while

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<sup>1</sup> See: [https://en.wikipedia.org/wiki/Biotic\\_component](https://en.wikipedia.org/wiki/Biotic_component)

abiotic factors are non-living elements or conditions that affect organisms or ecosystems. Climate change will affect both biotic and abiotic factors with subsequent impacts on the geographic distribution of vector-borne diseases.

We start in Section 2.2 by introducing the biology of vector-borne diseases, and in Section 2.3 we go on to explain the mechanisms by which climate change is currently known to influence the geographic distribution of these diseases. We then describe in Section 2.4 how existing research has measured the health and economic impacts of zoonotic disease and summarize some key general results.

## 2.2 BIOLOGY OF VECTOR-BORNE DISEASES

All vector-borne diseases have three basic biological components — the pathogen, vector organisms, and host organisms — which are linked by the reproductive cycle of the pathogen (Figure 1). In general, infectious diseases are caused by pathogens, such as viruses, bacteria, and other microorganisms, that can be transmitted to humans from a variety of sources. One way that diseases infect human beings is through organisms that serve as “vectors” transporting pathogens to a new host. The broadest definition of a vector is a living organism that transmits the infectious disease to other organisms including humans (Wilson, et al. 2017). Any non-human that transmits infection to a human can be considered a vector (Wilson, et al. 2017).

For our purposes, we are interested in human diseases caused by viral and bacterial pathogens transmitted by mosquito and tick species. These species feed on the blood of other animals, enabling the pathogens to move from the vector to the host organism. Host animals respond in different ways to the presence of the pathogen. In some cases, for example, the pathogen may not be able to reproduce in the host but can be transmitted back to other vectors feeding on the same organism (Gilbert 2021). In other cases, the pathogen may persist or even reproduce in the host without causing disease symptoms; this can contribute to a standing “reservoir” of non-human species carrying the pathogen in the wild, as is the case for Lyme disease. The Chikungunya virus, for example, originated in Africa with non-human primates as its primary reservoir, but has evolved a second cycle between *Ae. aegypti* mosquitos and humans that enabled its recent spread to South America (Tjaden et al. 2017). If the virus develops a new reservoir of non-human host species in South America, this would substantially reduce our ability to control the virus. Finally, infected hosts may experience disease symptoms. Even symptomatic cases of vector-borne diseases are not generally transmissible directly between infected hosts, however; important exceptions are through contaminated blood transfusions and between mothers and babies during pregnancy.

The species involved in vector-borne diseases come from a taxonomically wide-ranging and heterogeneous group. Although people colloquially refer to “mosquitos” or “ticks” as if they are single units, these names in fact refer to a taxonomic family of 3,500 species (Becker et al. 2020) and a taxonomic order of 800 species, respectively (Gilbert 2021). While a substantial number of these species are vectors for human diseases or have the capacity to become vectors, the majority of mosquito and tick species are not currently responsible for human infectious diseases; only 25 species of tick are known to have major medical or veterinary importance, for instance (Sonenshine 2018). Nonetheless, pathogens are known to be able to acquire new vectors as they spread geographically and continue to evolve. For example, the Chikungunya virus acquired a single genetic mutation in 2005 that increased its ability to be transmitted by the *Ae. albopictus* mosquito species, contributing to one of the largest viral outbreaks observed at that time (Brady and Hay 2020, Deeba et al. 2020).

The biological diversity of vector-borne diseases has important consequences for our ability to understand and predict trends in disease hazards. Each pathogen species, for example, has a particular set of transmission vectors and hosts it infects, which determine its underlying potential for geographic spread. Similarly, each vector species has its own biological features that determine its responsiveness to changes in environment such as temperature and rainfall. Vectors also differ in their feeding behaviors, including preference for humans versus other animal hosts, and in their preferred habitats. Similar density and geographic range of vector species may therefore translate into significantly different levels of exposure and risk of disease for humans. Environmental and epidemiological models of vector-



borne diseases are an active area of scientific research, but outside the scope of our review; for more information see (Sonenshine 2018). Nonetheless, the biological differences among vector-borne diseases are an important reason why modeling the effects of climate change must be done on an individualized basis for each disease (Courret and Benedict 2014).

### 2.3 CLIMATE CHANGE'S IMPLICATIONS FOR VECTOR AND HOST BIOLOGY

As we've seen already, vector-borne diseases are complex socio-ecological phenomena, involving interactions on multiple spatial and temporal scales between pathogens, vectors, hosts, and their environments. Many of these interactions are outside the scope of what science can currently reliably measure or estimate, but a clear foundation for making predictions based on climate change does exist in the effects of temperature and rainfall.

In simple terms, tick and mosquito species are not able to regulate their internal body temperatures (unlike mammals), and so are best able to survive and reproduce when temperatures are neither too cold nor too hot (Tozan et al. 2021). Hotter temperatures in cold regions can expand the time each year that vectors are active and able to transmit disease. The tick species *Ixodes ricinus*, for example, has undergone a range-shift northward in Europe, so that its northern limit is 69° N in Arctic Norway. This constitutes a 400-km northward shift since the 1940s. In Sweden, the same species has spread from below 61° N to 66° N since the 1980s (Gilbert 2021). Similarly, the tick species *Amblyomma americanum* has expanded north to the Canadian border since the 1890s in a manner consistent with models of changing temperature suitability (Gilbert 2021). In a parallel way, moderate rainfall creates habitats for vector organisms and their hosts, while severe drought or flooding can destroy these habitats, reducing population sizes. In tandem, these conditions are commonly known as the climate envelope for a species: “the climatic conditions under which their populations can survive” (Gilbert 2021). Different species, moreover, show substantial variation in their climate envelopes. For example, there are key differences among species in how cold or hot is too much for population survival, and which temperature appears to be optimal (Paz 2015). Temperature also has effects on the speed of pathogen reproduction (Tozan et al. 2021), as seen with the Dengue virus (Brower 2001), which must align with the feeding periods of their vectors in order to be transmitted into a new host (Rocklöv et al. 2019). As a result, a linear increase in average global temperature will generally be transformed by the system dynamics into non-linear health and economic impacts, with some areas experiencing reduced or amplified disease burdens compared to a linear expectation based just on increasing temperature or other variables (Rocklöv et al. 2019). Models are therefore essential.

Long-term projections of vector-borne disease distributions under climate change scenarios are generally made by estimating suitable habitat for the vector (or for the disease directly) based on observations of its current environmental range in combination with standard climate scenario models from the IPCC (2007). These long-term projection models are typically called species distribution models, or alternatively ecological niche models. In effect, the model is trained on what's known about the environmental conditions where the species of interest currently exists. These conditions are then projected into the future using climate models, and the predicted species range is determined by where the trained model identifies suitable habitat will exist in the future. Most commonly the projections are done at the global scale, but some publications have applied this approach to the scales of multiple states or even regions surrounding a city — see Sections 3 and 4 below for references.

Attributing specific range changes or outbreaks of a disease to climate change is challenging, arguably more so than attribution for specific hurricane or wildfire disasters. This is in part due to additional interactions between human behaviors and disease risks (Tabachnick 2010). It's known, for example, that humans have had powerful effects on habitats for vectors: for example, when humans started storing water in containers, it created a new niche for the *Aedes aegypti* mosquito species (Tabachnick 2010), which is now one of the major vectors for West Nile, Chikungunya, and dengue. Increased globalization of trade and travel has also created new opportunities for pathogens to spread into novel regions and hosts (Tidman et al. 2021). Thus, the species distribution models we described tell us about where a species is likely to be able to exist (i.e., its climate envelope), but many additional factors are involved in

determining what portion and regions of that possible range will be occupied in the future. Moreover, while current research has focused primarily on how climate change will act through changes in temperature and rainfall, it may also have indirect effects on disease through its effects on human land use (Diuk-Wasser et al. 2020) and mobility patterns (Gardner et al. 2018, Soriano-Paños et al. 2020).

## 2.4 HEALTH AND ECONOMIC IMPACTS

The pattern of recent outbreaks in vector-borne diseases have unsurprisingly been accompanied by reverberating economic impacts, with reverberating impacts primarily for health and life insurance. For example, the 2002 outbreak of West Nile Virus in Louisiana resulted in 329 recorded cases, with an estimated cost of \$20.1 million. This included \$4.4 million in medical costs and \$9.2 million in public health response costs (Zohrabian et al. 2004).

Impacts of these outbreaks however are not purely economic. Even though mortality for each of these diseases is below 1% (CDC 2021), they can take a devastating toll on the quality of life for many of those affected. One metric for quantifying this type of human loss due to a specific cause or illness is in terms of Disability-Adjusted Life Years. Briefly, the Disability-Adjusted Life Years<sup>2</sup> (DALYs) of an illness is the sum of the years of life lost due to premature mortality (YLLs) and the years of healthy life lost due to disability (YLDs).

In addition to point in time aggregate estimates of economic costs and DALYs, various studies have attempted to model the dynamics of these metrics during outbreaks over space and time. Understanding the potential economic ramifications can help insurers be prepared for an increase in claims and even catastrophic losses resulting from these events, especially in the context of climate change. To that aim, the essential factors to consider in modeling disease spread include projections of the climate envelope of species affected, along with human factors such as demographics (for example, income and education levels), urbanization, travel, preparation of healthcare systems, and potential for herd immunity (Gubler et al. 1998, Wilder-Smith 2008, Mammen Jr. et al. 2008; Guzman et al. 2010, Shepard et al. 2014; Jourdain et al. 2020). When quantifying subsequent economic and human impact, it is vital to realize that each disease has different associated symptoms, long-term health effects, and subsequent impacts on mortality. To fully account for these factors, models for spatio-temporal disease spread based on climate change projections, together with models for the expected number of cases and models for economic impact, are needed.

In the following sections, we will lay out what is known about the factors for disease spread and health implications for each disease, which can be used to further make predictions on economic costs and DALYs. There are many similarities in these factors seen across the discussed diseases — for example, all have some degree of common symptoms, such as a fever, headaches, muscle pain, joint pain, and a rash. A large number of cases of these diseases are mild or even asymptomatic, but they can pose a significant risk in vulnerable demographics, especially if left undiagnosed and untreated. While treatment of the acute diseases when caught early are relatively straightforward, long term effects can be disabling, requiring long term use of health services, medications, and treatments. Thus, the costs associated with these diseases are heavily impacted not just by the severity of the acute disease and mortality rates, but the long-term repercussions for quality of life. In addition, many of the symptoms of these vector-borne diseases resemble other common diseases, delaying the recognition of a spreading epidemic (Senn et al. 2011; Caputo 2020). For example, after the 2007 epidemic in Italy, less than 1/3 of surveyed general practitioners were able to identify key information about the disease, such as the symptoms, potential complications, incubation period, and means of transmission (Caputo 2020). Thus, the level of awareness for individuals and healthcare workers in areas of emerging risk can have down the line impacts on costs. Other current measures being used in an area to prevent disease spread, such as mosquito and tick control programs or reducing exposure by individual use of insect repellents should also be considered (Diuk-Wasser et al. 2020).

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<sup>2</sup> See: <https://www.who.int/data/gho/indicator-metadata-registry/imr-details/158>

Unfortunately, to our knowledge, no continuous encompassing models projecting the spread of particular diseases worldwide are available. Further, the underlying historical data for the expected number of cases and deaths can be significantly impacted by underreporting (Shepard 2011, 2013; Gibbons et al. 2014), resulting in high variability in the existing modeling projections (Guzman 2010, Shepard 2014). For example, one study estimated that 2010 saw 96.0 million cases of Dengue globally (Bhatt et al. 2013), while another estimated only 0.2 million (Shepard 2014). Effective models need to account for these issues using so-called expansion factors (also called multiplication factors), which adjust for under and over-reporting (Bhatt 2013; Gibbons et al. 2014; Shepard 2014). When a lack of data is present, consolidation of information from empirical studies and expert opinion can provide meaningful guidance (Bhatt 2013; Shepard 2013). Despite the limitations, in Sections 3 and 4 we will present key findings of the impact studies that have been conducted thus far.

## Section 3: Mosquito-Borne Diseases

In this section, we review projected impacts from climate change on four vector-borne diseases caused by viruses carried by mosquitos. Some recent general reviews of note are (Franklinos et al. 2019, Röcklov and Dubrow 2020, Tidman et al. 2021).

### 3.1 PROJECTIONS FOR MOSQUITO VECTORS

Mosquito species frequently serve as vectors for multiple pathogens. This is the case for *Ae. aegypti* and *Ae. albopictus*, for example, which figure centrally in three of the diseases we review below: Chikungunya, Dengue, and Zika. Projecting how these vector species will respond to climate change can therefore provide a basis for informing more specialized models addressing each disease. Developing scenarios for what will happen with the vector can also help us understand what will happen for emerging diseases where disease-specific projections are absent, such as for some tick-borne diseases we discuss in Section 4. Before discussing Chikungunya, Dengue, West Nile, and Zika in detail, we therefore review what's known about their principal vectors.

The *Ae. aegypti* species originally evolved in sub-Saharan Africa as a species that fed on multiple non-human animal species before being carried across the Atlantic Ocean to the Americas by Europeans in the 1400s (Jones et al. 2020). *Ae. aegypti* then evolved to live with and off of humans, and now has persistent reproductive populations in the Americas and the Asia-Pacific, including along the southern border of the U.S. and the East Coast. By contrast, *Ae. albopictus* was restricted to Asia until the 1980s and has expanded its territory rapidly since then, establishing reproducing populations in over 40% of the world's landmass (Jones et al. 2020), including in the eastern half of the U.S. (Cromar and Cromar 2021). In the *Culex* genus, the species *C. quinquefasciatus*, *C. restuans*, and *C. tarsalis* are vectors for West Nile in North America but differ in their competence as vectors for the disease, which may substantially effect transmission patterns in different regions (Dunphy 2019). The first two are regularly found in urban habitats, while *C. tarsalis* lives in rural settings. *C. quinquefasciatus* is spread throughout the tropics and lower temperate regions, including the Southern U.S. and Florida. *C. restuans* and *C. tarsalis* both range from central or lower Canada into Mexico.

Modeling studies generally agree that climate change will expand the suitable habitat for mosquito vector species in North America (e.g., Kraemer et al. 2019, Liu-Helmersson et al. 2019, Monaghan et al. 2019, Ryan et al. 2019, Iwamura et al. 2020, Rohat et al. 2020, Uddin Khan et al. 2020). *Ae. aegypti* is projected to experience an improved climate across the Southern border of the U.S. in the coming decades, with multiple models (Monaghan et al. 2019, Uddin Khan et al. 2020) suggesting a widespread expansion across latitudes as far north as southern Illinois, for example. Model projections for *Ae. albopictus* indicate expansion beyond its currently established range in the southeastern U.S. in multiple directions, including along the Pacific Coast, to the east and south of Nebraska, and into New England (Monaghan et al. 2019). In the U.S., *C. quinquefasciatus* has been observed to already be present along the entire

border with Mexico and the southern Atlantic coast, and Samy et al. (2016) projected the species’ suitable range of habitats would expand northward under all climate scenarios considered.

Within this broad agreement about growth at the extremes of species’ current ranges, however, it is important to consider how climate change will have locally or regionally varying effects. For example, Kraemer et al. (2019) projected declining suitability for *Ae. albopictus* in parts of Texas and Oklahoma due to increased dryness. On the global scale, Iwamura et al. (2020) projected an accelerating spread of environmentally suitable areas for *Ae. aegypti* especially in China and the U.S., at a rate of 2.4–3.5 times faster by 2050 than estimated during 1950–2000. As a consequence, we should expect to see sudden shifts at the leading edge of the vectors’ ranges (Iwamura et al. 2020, 6). Human behaviors can also reverse anticipated effects: while generally one might expect higher precipitation creates more stagnant pools for larvae to grow, “during the 2015–2017 ZIKV [Zika virus] outbreak, there was an inverse relationship with precipitation: drought led to greater transmission because increases in household water storage were associated with increased Zika cases” (Ryan 2021). Similarly, *C. tarsalis* may be able to withstand extreme droughts by relying on agricultural irrigation practices in rural areas (Dunphy et al. 2019).

### 3.2 CHIKUNGUNYA

In most infected individuals, Chikungunya presents as a fever that develops within a week, followed by severe joint pain and stiffness (CDC 2021). While most patients recover from the initial illness in a few days (Pialoux et al. 2007; Burt et al. 2017), many of those affected suffer from chronic and disabling joint pain (polyarthralgia) that can last for weeks, months, or even years after the infection (Abdelnabi 2017; Schilte et al. 2013; Trentini et al. 2018). Since the 1960s, there have been recurring outbreaks of Chikungunya (CHIKV) in Asia and Africa (WHO 2020; Yergolkar 2006). However, in 2007 there was the first reported local transmission in continental Europe (Rezza et al. 2019) and in 2013 the disease was transported to the Americas (Khan et al. 2014). Recent outbreaks in new regions have sometimes exceeded a million cases (Tjaden et al. 2017), as happened in India in 2005-2006 (1.4 million cases reported) and in 45 different countries in the Americas in 2013 (1.7 million suspected cases). Local transmission of CHIKV was reported in the U.S. for the first time in 2014, with 11 identified cases in Florida (Kendrick et al. 2014).

Most of the U.S. and Canada are projected to remain unsuitable for Chikungunya, but a recent study projected increased transmission under both higher and lower carbon emission scenarios for the Gulf Coast, southern Florida, Cuba, the Yucatan peninsula, Sinaloa, and across much of Central America (Tjaden et al. 2017, 2). Another study found 1-2 months per year could become suitable for transmission in southern coastal British Columbia under a high-emission climate scenario (Ng et al. 2017).

While mortality rates for Chikungunya are low, economic burden and DALYs associated with Chikungunya are significant, particularly due to chronic joint problems, which occur in an estimated 15–60% of individuals (Schilte et al. 2013; Abdelnabi 2017; Trentini et al. 2018; Hsu et al. 2019; Caputo 2020; CDC 2021). In 2016, Bloch estimated \$83.6 billion in direct medical costs throughout the Americas, \$68 million in perinatal costs, and an additional economic impact of \$101.4 billion in indirect costs (Bloch 2016). Total DALYs in the Americas were estimated at 2,432 per 100,000 people. Another study estimated that from 2010 to 2019, CHKV DALYs globally were around 106,000 (Puntasecca et al. 2021).

**Table 2**  
**ESTIMATED IMPACTS OF MOSQUITO BORNE DISEASES IN U.S.**

Disease	% Symptomatic	% Hospitalized	Mortality <sup>9</sup>	Direct Cost per Case	Annul DALYs (per 100,000)
Chikungunya	50%-97% <sup>1</sup>	0.5%-10.7% <sup>5</sup>	>1%	\$15,722 <sup>10</sup>	14 <sup>10</sup>
Dengue Fever	25% <sup>2</sup>	18% <sup>6</sup>	>1%	\$1,146 <sup>11</sup>	10 <sup>11</sup>
West Nile Fever	20% <sup>3</sup>	67% <sup>7</sup>	>1%	\$36,738 <sup>12</sup>	*
Zika Fever	20% <sup>4</sup>	2% <sup>8</sup>	>1%	\$7,047 <sup>13</sup>	7.7 <sup>14</sup>

1. Staples et al. 2009, Ayu et al. 2010; 2. Bhatt et al. 2013, Grange et al. 2014; 3. Paz 2015; 4. Rawal et al. 2016; 5. Kumar et al. 2016; Rolle et al. 2016; Vairo 2018; Hsu et al. 2019; 6. Shepard et al. 2014; 7. Walensky, et al. 2021; 8. Dirlikov et al. 2016; 9. CDC 2021; 10.

Bloch 2016; 11. Global Health Estimates 2020, Peterson et al. 2012; 12. Staples 2014 13. Lee et al. 2017 14. Global estimate from Puntesecca et al. 2021 \*There have been no comprehensive studies of the DALY from West Nile Virus (Zhang, Bi, and Hiller, 2007; Badawi 2018).

### 3.3 DENGUE

Dengue fever does not occur in most individuals infected with the Dengue virus, however when present it is often accompanied by a headache, rash, and/or muscle and joint pain that last around a week (CDC 2021). An estimated 2% to 5% of infected individuals will develop so-called severe Dengue, which is characterized by severe plasma leakage or bleeding, impaired consciousness, or heart impairment (Halstead and Wilder-Smith 2019; CDC 2021). These life-threatening symptoms require costly emergency care. Persisting fatigue and depression continue to affect some patient's quality of life for months (Seet, Quek, and Lim 2007).

There has been a dramatic increase in the number of Dengue cases worldwide reported to the WHO over the last two decades (Brady and Hay 2020, WHO 2020). It is estimated that half of the world's population — 3.9 billion people — is at risk of infection (Brady et al. 2012), with around 25% of exposed individuals contracting the disease and developing clinical symptoms (Bhatt et al. 2013). Countries in both South and Central America have experienced major outbreaks in recent years, with 3.1 million cases of Dengue fever reported by the Pan American Health Organization in 2019 (Robert et al. 2020). Transmission has intensified in past decades with outbreaks increasing in frequency, magnitude, and geographic occurrence (Gubler 1998; TDR/WHO 2009)

Brady and Hay et al. (2020) note “a lack of consensus on the magnitude of the threat of future potential spread of dengue but some agreement that areas at the fringe of the current distribution of dengue in the southern United States, the Mediterranean basin, and southern China are likely to be most at risk” (Brady and Hay et al. 2020). A recent modeling study by Messina et al. (2019) predicted that much of the Southeastern U.S. would become suitable for Dengue by 2080, for example, but overall found “minimal changes” to the overall global area at risk. In Europe, for example, northern areas may see increased risk from warming and higher rainfall while southern areas will experience decreased risk from warming and drought (Tidman et al. 2021). Two further concerns not driven directly by climate change are whether the Dengue virus becomes endemic in the 50 U.S. states — local transmission is already established in Puerto Rico — and whether it moves into other wild non-human species in the Americas, which would provide it with a larger reservoir of hosts and greatly reduce the effectiveness of trying to eliminate mosquitos in human-inhabited areas.

### 3.4 WEST NILE

Currently the most widely geographically distributed mosquito-borne virus in the world (Paz 2015), West Nile entered the U.S. in 1999 in New York City and spread rapidly from there, becoming endemic across most temperate regions of North America (Paz 2015). West Nile has symptoms that are also common with Chikungunya and Dengue, such as headaches, body aches, joint pains, vomiting, diarrhea, and/or a rash. However, 1 out of every 150 people develops West Nile neuro-invasive disease, which typically manifests as meningitis, encephalitis, or acute flaccid paralysis (McDonald et al. 2021). Among these patients, estimated hospitalization rate jumps to 94%, with a 9% fatality rate (McDonald et al. 2021). Long-term fatigue and weakness are frequent complications (Pepperell et al. 2003; Klee et al. 2004). Costs per severe case of West Nile can be over \$700,000, with an estimated annual cost across the country of \$56 million (Staples et al. 2014; Barrett 2014).

Despite the similar symptoms, West Nile has some distinctive biological features relative to the other three mosquito-borne diseases. In particular, birds serve as non-human reservoirs for the virus while humans and horses are dead-end hosts, meaning that the disease is not transmitted from infected people or horses to other hosts. Research suggests outbreaks occur when the virus becomes amplified among bird hosts early in the summer when daily temperatures are above average (Paz 2019). Migrating birds carrying the virus long distances along their routes also contribute a distinctive spatial factor to West Nile outbreaks.

The effects of changing temperature and precipitation on West Nile are variable by region, in part due to which mosquito vector species are dominant in an area and whether the changes push the climate toward or away from the optimal values for that vector. For example, Paz (2019) found that below average annual precipitation was associated with increased West Nile disease in most of the U.S.'s eastern regions and the Northern Rockies and Plains, but higher than average total precipitation was associated with increases in the Western regions. One study, which only considered temperature effects and not precipitation, projected an additional 590 cases of severe illness — specifically, from West Nile neuro-invasive disease — per year in the U.S. by 2050 under the moderate climate change scenario of RCP4.5 (Belova et al. 2017). Although approximately half of U.S. counties reported cases of West Nile during 2004-2012, the most significant increases they projected for neuro-invasive disease cases were along the southern border with Mexico, e.g., in California, Texas, and in the Southeastern U.S.

### 3.5 ZIKA

Like Chikungunya and West Nile, the Zika virus has greatly expanded its geographic range in recent years (Weaver et al. 2016). Since 2013, the virus has spread to at least 49 countries and territories, and Brazil alone has experienced an estimated 150,000–500,000 cases, leading to at least 3,000 cases of microcephaly (Ryan 2021). Small outbreaks involving local transmission were reported in the U.S. during 2015–2017, including in Texas and Florida, but no cases of transmission were reported in 2018 and 2019 in the continental U.S. (CDC 2021). However, many public health agencies in the U.S. have begun planning for Zika outbreaks as a credible threat (Carlson et al. 2018). Zika is likely to show distinct dynamics from other diseases we survey here in several respects (Asad and Carpenter 2018, Li et al. 2021). The large 2016–17 outbreak in the Americas showed rapid spread through a human and mosquito transmission cycle, but then a large reduction in cases since, possibly due to increased human immunity in highly affected areas. Dengue, by contrast, is known to exist in four varieties called serotypes that do not provide cross-immunity for hosts after infection. Zika is also known to be carried and transmitted by a wider range of mosquito vectors than Chikungunya or Dengue, leading to a more complex biological story for geographic spread and persistence.

Carlson et al. (2018) has provided a unique and valuable consensus study of projections from four different models for Zika in the U.S. They observed wide variation in the predicted number of people at risk, but concluded there was rough agreement on the areas predicted by other methods to be at the greatest risk from Zika virus, with southern California and the Gulf Coast most significantly represented as hotspots. However, this consensus was limited to along the coasts and Southern U.S., e.g., in Los Angeles County and the southernmost part of Florida. Building on this work, Ryan et al. (2021) provided global population-at-risk projections for Zika in 2050 and found over 700 million people could experience new, year-round climate suitability for transmission. As they wrote, “Net changes in risk are dramatic, largely because there are very few areas where climate warming will drive future temperatures to become unsuitable (too hot) for at least one month of the year, but many areas where the climate will become newly suitable” (Ryan et al. 2021, 67).

The most concerning aspect of Zika is the potential for severe birth defects (occurring in between 1 and 30% of cases) when contracted during pregnancy (Vorona and Lanni 2016; Krauer et al. 2017). One small study found that 69% of infants with congenital Zika virus develop microcephaly (Moura et al. 2016), with complications such as impaired cortical development, abnormalities of the Corpus Callosum, spinal cord, or skeleton, and hydrocephalus (Leão et al. 2020). Infants also can have irritability, seizures, and dysphagia (Moura et al. 2016). The onset of Guillain-Barre syndrome has also been reported, which can sometimes result in paralysis (Krauer et al. 2017). A 2017 study estimated that under a .01% attack rate, direct medical costs in the U.S. would be around \$117.1 million, and under an attack rate of .025% this estimate jumps to \$198.6 million (Lee et al. 2017; see also Frenzen 2008).

## Section 4: Tick-Borne Diseases

In 2017, ticks accounted for 90% of the vector-borne illnesses in the United States (Molaei et al. 2019). Lyme disease stands out by far in terms of case numbers, but other diseases such as Anaplasmosis are growing rapidly in cases and geographic range while also having severe health consequences if not diagnosed and treated appropriately. Many of these less common but emerging tick-borne diseases do not have specialized climate projections available. As a result, we must rely on projections of effects on their principal vectors, recognizing that this leaves dynamics due to the pathogen itself out of the picture. Nonetheless, tick-borne diseases have been shown to be more seasonally predictable than mosquito-borne illnesses, allowing for better modeling and predictions, in part because ticks travel relatively less distance than mosquitos to breed or feed (Eisen, 2020). Some recent reviews of note are (Sonenshine 2018, Eisen and Paddock 2020, Rodino et al. 2020, Gilbert 2021; see also Table 1 in Porter et al. 2021).

### 4.1 PROJECTIONS FOR TICK VECTORS

As was the case for mosquito vectors, tick species are frequently competent to transmit multiple diseases to humans. We focus on three in particular here: *I. scapularis* (black-legged tick), *I. pacificus* (western black-legged tick), and *A. americanum* (lone star tick). *I. scapularis* and *A. americanum* have been shown to be re-inhabiting the areas that they previously occupied but had been deforested by human land development (Molaei, et al. 2019). *A. americanum* has also expanded its geographic range into the Northeast and Midwest (e.g., Iowa, Wisconsin, and Michigan) of the U.S., where southern New Jersey had been its historical northernmost limit (Molaei et al. 2019). By contrast, *I. pacificus* has not changed its range substantially in the past 100 years, and is located in states along Pacific Coast (Washington, Oregon, California) and in some counties near the shared borders of Nevada, Utah, and Arizona (Eisen et al. 2016). Of the three, *I. scapularis* is a vector for the most pathogens and is also highly widespread — it was documented in 1,420 counties in 37 U.S. states, more than double two decades prior (Eisen and Paddock 2020).

In terms of climate change, both *I. scapularis* and *A. americanum* are well-positioned biologically to take advantage of northward expansion in their climate envelopes, while *I. pacificus* may experience contractions or expansion in different regions depending on the scenario modeled. *I. scapularis* in particular is a generalist in terms of animal hosts it feeds on, and so it is less likely to be limited by the range of any particular host as its climate envelope expands. For example, it might shift from white-tailed deer in the U.S. to reindeer (caribou) in Canada (Gilbert 2021). A recent genetic study of *A. americanum* suggests its recent northward expansion may be due in part to local evolutionary adaptation, as the new northern populations exhibit genetic differences compared to those in its historical range (Monzón et al. 2016).

Model projections agree on northward expansion for both *I. scapularis* and *A. americanum* into southern Canada (Springer et al. 2015, Sonenshine 2018, Sagurova et al. 2019, Raghavan et al. 2019). *I. scapularis* has already been advancing north at a rate of about 46 kilometers per year in Ontario and westward in the U.S. (Sonenshine 2018). Raghavan et al. (2019) find that “the increasing occurrence of lone star ticks [*A. americanum*] in the upper midwestern states of Minnesota, Wisconsin, and Michigan may be an early indication of climate change-mediated northward shifts.” Models for *A. americanum* conflict over projected losses in its range in eastern Texas and Florida, though (Springer et al. 2015, Raghavan et al. 2019). A recent study of *I. pacificus* found substantial regional variation reflecting the sensitivity of ticks to both temperature and desiccation (MacDonald et al. 2020).

### 4.2 LYME DISEASE

Lyme disease is the most common vector-borne disease in the U.S., with most reported cases occurring in the Northeast, Wisconsin, and Minnesota. Kugeler et al. (2021) estimated 480,000 patients were diagnosed and treated for Lyme disease annually in the U.S. during 2010–2018. While directly reported cases of Lyme disease have increased fourfold since the 1990s, from 10,000 to 40,000 per year, there is little evidence for climate change directly driving this growth in areas such as the Northeast U.S. that already had established populations (Gilbert 2021). Other

ecological factors, such as the abundance of white-tailed deer, may be dominant drivers in that region, but major uncertainties and debates are ongoing about which factors are most important generally (Kilpatrick et al. 2017). Nonetheless, there is support for temperature and precipitation effects of climate change enabling the northward expansion of Lyme disease's principal vector species, *I. scapularis*, carrying the disease with it (Gilbert 2021). One recent study suggests that climatic variables have the opposite effects on cases in Wisconsin and Minnesota versus Northeastern states, while landscape variables in both regions have similar effects (Couper et al. 2021). Another study found that the start date of Lyme disease season was associated with higher cumulative growing degree days, lower cumulative precipitation, and higher humidity (Rocklöv and Dubrow 2020), providing further evidence that climate change may shift Lyme disease cases earlier in the calendar year (Monaghan et al. 2015).

Health costs associated with Lyme disease arise not only from treatment of the acute disease and its potential complications, but also continuing treatment of Post-Treatment Lyme Disease Syndrome (PTLDS) which occurs in an estimated 10-20% of cases (CDC 2021). During early stages of the disease, patients usually present with a rash along with a fever, chills, headache, fatigue, muscle and joint aches, and swollen lymph nodes, and are treated with antibiotics. However, if treatment is delayed, the bacteria may enter the heart (Lyme carditis), joint tissues (Lyme arthritis), or nervous system. Lyme carditis can be particularly dangerous, requiring immediate hospitalization, IV antibiotics, and at times a temporary pacemaker. Further damage to nerves and joints can be permanent if the disease is not treated early. Thus, while treatment of the acute disease seems straightforward, overall treatment costs for Lyme disease can be particularly high. Adrion et al. (2015) provide an excellent retrospective study of costs, determining that from 2006 to 2010 in the United States, a Lyme disease diagnosis was associated with a \$2,968 (95% CI: 2,807–3,128,  $p < .001^3$ ) increase in overall health care costs per individual for a year, with patients having 87% more outpatient visits during that time (further supported by Obel et al. 2018). Those who experienced PTLDS symptoms such as ongoing fatigue, musculoskeletal pain, and neurocognitive issues saw an additional \$3,798 (95% CI: 3,542–4,055,  $p < .001$ ) in costs. Further, individuals with comorbidities and those that develop PTLDS report a significantly lower quality of lifelong term than the general population (Aucott et al. 2013, Wills et al. 2016). One study estimated costs in the U.S. of around \$8 million (2018 dollars) for 1 year of LD associated issues (Limaye et al. 2019) This included \$2.8 million in costs for private insurance, \$3.7 million for Medicare, and \$1 million for Medicaid.

### 4.3 EMERGING DISEASES LACKING CLIMATE PROJECTIONS

A number of tick-borne diseases are known to be increasing in geographic range and number of cases but to our knowledge have not received modeling studies to determine the possible effects of climate change. Nonetheless, some information can be gained from studies of climate change effects on their known principal vector species, discussed above. In this subsection, we highlight and briefly review three diseases — Anaplasmosis, Babesiosis, and Ehrlichiosis — as important emerging North American vector-borne diseases in need of more extensive study in light of climate change.

Anaplasmosis is thought to be transmitted principally by *I. scapularis* (CDC 2021), which is widespread across the U.S. and experiencing a northward expansion of its range. Eight states account for almost 9 in 10 cases, although some cases have also been reported throughout the U.S., possibly due to travel or misdiagnosis (CDC 2021). Many individuals have mild or moderate symptoms within the first few days such as fever, chills, headache, joint and muscle pain, vomiting and diarrhea (Bakken et al. 2006). However, almost half of patients require hospitalization (Bakken et al. 1996). In 11% of cases, patients will go on to develop severe, late-stage illness that can result in renal or respiratory failure, nerve damage, bleeding problems, rhabdomyolysis, organ failure, and even death (Bakken et al. 2006; Heitman et al. 2016; CDC 2021). Due to current available treatments, mortality in the U.S. is around 1%, however delayed

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<sup>3</sup> P-value, indicating <99.9% confidence level of interval estimate



treatment with antibiotics significantly improves risk (Kuriakose 2020; CDC 2021). Most studies of the monetary costs of Anaplasmosis are analyzing the costs to livestock rather than human infections.

Babesiosis is best known for its impacts on livestock, but it is also an emerging zoonotic disease for humans with an incomplete understanding of vector species within the *Ixodes* tick genus (Gray et al. 2019). Similar to Anaplasmosis, most cases have occurred in Northeastern states, Wisconsin, and Minnesota in the U.S. (Kumar 2018; Krause 2019). A recent study noted increased diagnosis in Pennsylvania and confirmed increased case numbers and geographic spread in the state (Ingram and Crook 2020). A second study found a nearly 17-fold increase in incidence rate in the Upper Hudson Valley region in New York (Joseph et al. 2020). Many cases of Babesiosis are asymptomatic, and do not require any treatment. However, symptoms can appear weeks or even months after exposure (CDC 2021). Symptoms are usually generally flu-like, including a fever along with chills, body aches, and fatigue (Jiang et al. 2015). However, complications of Babesiosis include hemolytic anemia, which can lead to an enlarged spleen and liver, and jaundice. Such severe cases can result in blood clots, unstable blood pressure, respiratory distress, a heart attack, and organ failure (Krause et al. 2008). These complications may require more intensive and costly treatments such as blood transfusions or dialysis (CDC 2021). Overall mortality from the diseases is around 1% of cases, but among hospitalized patients this rate jumps to 3% to 9% (Krause 2019).

As a disease, Ehrlichiosis is defined to be caused by three known pathogen species in the *Ehrlichia* genus of bacteria: *E. chaffeensis*, *E. ewingii*, and *E. muris eauclairensis*. (See Rodino et al. 2020 for more information on its definition and relation to Anaplasmosis.) Annual case numbers have increased steadily since 2000, growing from 200 that year to 1,800 in 2018 (CDC 2021). The principal vector for *E. chaffeensis* and *E. ewingii* is *A. americanum* (Heitman et al. 2016). Ehrlichiosis is most frequently reported from the southeastern and south-central United States, from the East Coast extending westward to Texas, but in 2018, four states (Missouri, Arkansas, New York, and Virginia) accounted for more than half of all reported cases of Ehrlichiosis (CDC 2021). A recent spatial model analyzing environmental factors for cases in Kansas found significant county-level risk effects for the variables of poverty status, relative humidity, and the interaction of diurnal temperature range with mixed forest area (Raghavan et al. 2014). Within the first few days after contracting Ehrlichiosis, individuals typically have general symptoms such as a fever, chills, a severe headache, muscle aches, nausea, vomiting, diarrhea, and loss of appetite. Additionally, around 1/3 of individuals develop a rash, typically about 5 days after the fever begins. Delayed treatment can lead to severe complications, such as damage to the brain and nervous system, respiratory failure, uncontrolled bleeding, and organ failure. Overall mortality from the diseases is around 1% of cases (CDC 2021).

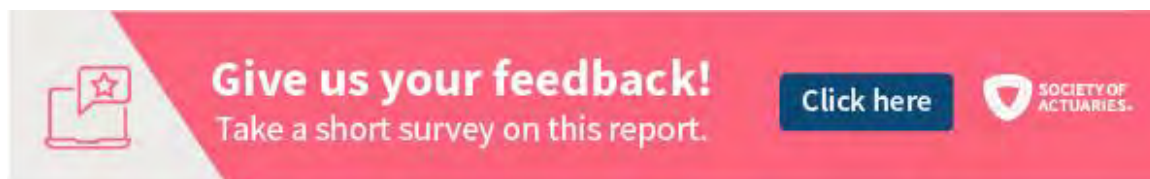
## Section 5: Conclusion


Climate change is projected to expand the geographic ranges of many of the most important tick and mosquito vectors for diseases in North America. This expansion will be constrained as key variables affected by climate change, including temperature and precipitation, are biological constraints on where ticks and mosquitoes can survive and reproduce. However, due to many other relevant biotic and abiotic factors, also affected by climate change in non-linear ways, it remains challenging to determine how responsible climate change is for recent disease trends happening within the existing ranges of vectors. Processes such as globalization and land-use change also significantly affect what parts of the potentially suitable habitats for vector-borne diseases will see outbreaks or growth in cases each year. Thus, quantifying climate change responsibility for overall trends in vector-borne diseases is an ongoing challenge for basic science.

Nonetheless, by combining climate, ecological, and epidemiological models (Belova et al. 2017) there are significant opportunities to gain a more precise and accurate understanding of how climate drives regional disease dynamics. Regionally, more nuanced data sources and model elements can be more readily gauged, either for existing sources or with certain investments. Given that temperature and precipitation factors typically have non-linear effects on vector survival, reproduction, and competence to transmit disease, geographically focused rather than global models


might have a better chance of capturing these complexities (e.g., Dong et al. 2020, Couper et al. 2021). Thus, with highly developed skills in risk modeling, actuaries working together with biologists are poised to make rapid advances in the near-term prediction of burdens of vector-borne diseases. In the near future, an important aim for biologists is to identify key ecological variables that impact tick or mosquito abundance. The [Ecological Forecasting Initiative](#) is one of those places where modelers from these two worlds can meet.

From a larger perspective, to build models linking climate to biology to health and economic impacts, researchers will need adequate data to estimate, for example, how increased vector abundance translates into higher disease risk and how transmission to humans translates into health outcomes and costs. Inconsistent reporting of disease cases is a major obstacle in this respect for general researchers, hampering accurate risk modeling, proper diagnosis and treatment, and public health response. In addition, many of the diseases we've discussed are challenging for clinicians to diagnose correctly. This is especially true when awareness of an emerging threat in a geographic region is low. Getting the correct diagnosis early can substantially improve patient outcomes and reduce the need for long-term treatment. Cost-benefit analysis for interventions and mitigation strategies are quite lacking (Greig et al. 2018; Davidsson et al. 2018), and as most of these diseases have no vaccine or limited vaccine effectiveness and safety, mitigation through public awareness and vector population control is crucial (Silva et al. 2020). Thus, working in parallel on forecasting disease trends, supporting awareness campaigns, developing reporting mechanisms, and insisting on better tools for early diagnosis can be valuable investments for actuaries and insurers to help mitigate more significant losses (Alfaro-Murillo et al. 2016; Stefopoulou et al. 2018).



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