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**Understanding climate change as a driver of  
emerging and re-emerging infectious diseases  
in northern Germany**

Bachelor thesis

submitted by

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## Abstract

Anthropogenic climate change affects not only the planet but also its inhabitants. When it comes to human health, it poses various threats, one of which is the rise of infectious diseases. Emerging and re-emerging infectious diseases are a great burden to human lives and it has been observed that with accelerating climate change frequent outbreaks and epidemics occur. Even in Germany emergence of non-endemic infectious diseases is seen.

The aim of this work is to understand to what extent climate change drives emerging and re-emerging infectious diseases in Germany, especially northern Germany.

To examine this, a systematic literature review was conducted. Simultaneously, climate data was collected from local and national institutions to understand this trend and examine the habitat suitability of the observed region under future climate scenarios.

The obtained results show that the change in seasonal duration, microclimate and abiotic factors such as temperature, precipitation, ocean salinity etc. are identified as primary drivers of emerging and re-emerging infectious diseases in northern Germany. These drivers influence the vector-pathogen-dynamics directly, especially the vector-pathogen-density and geographic distribution i.e., the ability to shift geographical ranges in a brief period. The collected climate data not only underlines this but also projects that the habitat suitability of northern Germany is changing favourably for these pathogens and vectors.

Based on the results from the literature review and collected climate data, if current climatic conditions are to prevail, pathogens and vectors causing diseases such as West Nile Disease, Lyme Disease, Dengue, Non-Cholera Vibriosis etc. will have established ecological niches in northern Germany in the future. To address this issue an interdisciplinary approach must be taken. In this work the One Health Concept is presented as it allows different sectors to work in cooperation and thereby ensure human and animal health.

Keywords: Climate change, emerging, re-emerging, infectious diseases, Germany

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## Abbreviations

AIDS – Acquired Immune Deficiency Syndrome

CDC – Centers for Disease Control and Prevention

CHIKV – Chikungunya Virus

COVID-19 – Corona Virus Disease-19

CO<sub>2</sub> – Carbon dioxide

DALYs – Disability Adjusted Life Years

DENV – Dengue Virus

DWD – Deutscher Wetterdienst (German Meteorological Service)

ECDC – European Centre for Disease Control and Prevention

EEA – European Environmental Agency

EFSA – European Food Safety Authority

EIDs – Emerging Infectious Diseases

EVD – Ebola Virus Disease

FBD – Food Borne Diseases

GDP – Gross Domestic Product

HIV – Human Immunodeficiency Virus

IPBES – Intergovernmental Science Policy Platform on Biodiversity and Ecosystem Services

IPCC – Intergovernmental Panel on Climate Change

LF – Lassa Fever

MDR-TB – Multi-drug resistant tuberculosis

MERS – Mediterranean Respiratory Syndrome

RCP – Representative Concentration Pathways

REIDs – Reemerging Infectious Diseases

RKI – Robert Koch Institute

RNA – Ribonucleic Acid

RTOFS – Real Time Ocean Forecast System

SARS – Severe Acute Respiratory Syndrome

SMAP - Soil Moisture Active Passive

TB – Tuberculosis

TBE – Tick-borne Encephalitis

UK – United Kingdom

VBD – Vector Borne Diseases

VZV – Varicella Zoster Virus

WBD – Water Borne Diseases

WHO – World Health Organisation

WND – West Nile Disease

WNV – West Nile Virus

## 1. Introduction

For years, scientists have been warning about the impact of man-made climate change on our planet, ecosystems, and lives. Not until recent years, was this problem seen as an alarming issue by political bodies worldwide. Several activists, students, scientists and organisations have united over this cause, to protect the planet, to protect the future. Depleting forests, melting polar regions, extinction of species, extreme weather events are some of the known consequences of climate change. What is unknown, remains to be a great deal of it. Despite years of understanding the global climate and weather patterns there remains the component of unpredictability. This unpredictability component has become even more challenging with rapid climate change. However, the Intergovernmental Panel on Climate Change came up with a solution of predicting climatic developments based on the emissions levels, also known as the emissions scenarios. “The Representative Concentration Pathways or the RCPs define trajectories representing greenhouse gas and aerosol concentrations for particular climate projections” (National Centre for Climate Services, 2018). These trajectories extend up till 2100, depicting scenarios for various environmental factors. RCP 2.6 shows how the planet might be if the goals of the Paris Agreement and Climate Adaptation measures are met, RCP 4.5 shows the planet’s status with limited mitigation and RCP 8.5 shows how the planet will be if the goals are not met and emission rates increase (NCCS, 2018). To protect the planet and several lives from the impact of climate change and global warming, the emission rates of greenhouse gases must be drastically reduced. This means working towards the scenario RCP 2.6.

When it comes to human health, infectious diseases have been a challenge since ages. 18.4% of global deaths are due to communicable diseases (World Health Organisation, 2022a, P 22). Infectious diseases are a major concern in low-income countries and in the tropics where they are still one of the major killers (Roser, Ritchie & Spooner, 2021). But due to rapidly changing climate, the high-income countries and the temperate zones are also facing huge implications. It has become one of the pressing issues that is driven by climate change, the emergence and re-emergence of infectious diseases. For decades, this relation has been researched by scientists all over the world. It is known that one of the



crucial functions of ecosystems is to regulate pathogen populations and dynamics. Due to the altered environmental conditions driven by climate change, this regulation is disturbed, thereby facilitating the rise of new and previously identified infectious diseases in various parts of the world (Adebayo, 2019, P 6).

Climate sensitive diseases such as West-Nile-Disease, Malaria, Dengue, Chikungunya, Lyme Disease, Salmonellosis etc. have broken out periodically over the years disrupting public health and safety, and national economies. In the recent years, it is observed that the probability of outbreaks of these diseases are increasing. With changing climate, parts of Europe are becoming suitable habitats for these EIDs and REIDs (European Environmental Agency, 2022). For example, in the UK, it is roughly estimated that around 3,000-4,000 new cases of Lyme disease occur annually (UK Health Security Agency, 2022). In Germany, approximately 5,212 confirmed cases of Lyme disease were reported in 2021 (Gesundheitsberichterstattung des Bundes, 2022). These incidences have increased when compared to those from three decades ago. In 2001 there were only 60 cases of Lyme disease in the UK (Cairns et al., 2019, P 4). Similarly in Germany, in 1994 the cumulated number of cases of five states were only 159 cases (Hellenbrand, 2003, P 17). This shows an increasing trend, and it is high time to address the threat of climate change driven EIDs and REIDs to ensure public health and safety.

The aim of this work is to understand to what extent climate change drives emerging and re-emerging infectious diseases in northern Germany. To gain an overall understanding of the topic and gather much information possible, the run-down will be from global level to sub-national level, since the main region of focus is northern Germany. This work therefore presents an overview of this trend up until now (2023) and an outlook on the possible developments in the future for northern Germany.

## 2. Background

Our planet's temperature and heat maintaining system is regulated by the natural greenhouse effect. Greenhouse gases such as methane, CO<sub>2</sub> etc. are responsible for trapping the sun's radiations and storing it in the form of heat within the planet's atmosphere. Therefore, the greenhouse effect and the global warming caused by

it are crucial because without this phenomenon life on Earth would not exist (Campbell et al., 2008, P 1238). Although the naturally occurring greenhouse effect and global warming are crucial for life sustenance, human activities such as burning of fossil fuels, deforestation etc. over the years have led to an increase in the amount of greenhouse gases in the atmosphere and thereby disrupting the natural balance and accelerating global warming. It is prognosed that if immediate measures are not undertaken, by the end of 21<sup>st</sup> Century the CO<sub>2</sub> concentration in the atmosphere will be more than double and the average global temperature will increase by 3°C (Campbell et al., 2008, P 1240). As of 2022, the average global temperature stands at approximately 0.89°C (National Aeronautics and Space Administration, 2023). In lieu of a warming trend several geographical and ecological processes would be disrupted. Melting of glaciers, flooding of coastal regions, warm ocean temperatures, forest fires etc. lead to loss of habitats and species. Climatic changes such as changes in the geographical distribution of precipitation, increasing dryness and arid regions pose a threat to survival of species and sustenance of ecosystems (Campbell et al., 2008, P 1241).

To understand how exactly climate change has an impact on human health and livelihood, first the relationship between climate change and biodiversity must be understood. This relationship is examined further in the following section.

## 2.1. Role of Biodiversity

Biodiversity or biological diversity when simply defined, is a term that collectively describes all living things in a particular area. Although, when investigated, different disciplines of studies have their own definition for biodiversity. A region is said to be rich in biodiversity if it contains an ecosystem with species which are both quantitatively and qualitatively different from other similar regions (Wittig & Niekisch, 2014, P 13). For example, if ecosystem A has three types of plants with three different coloured flowers (white, purple and yellow) and ecosystem B has five types of plants but with only yellow-coloured flowers, it can be concluded that ecosystem A is richer in biological diversity than ecosystem B (Wittig & Niekisch, 2014, P 13).

It is crucial to have an ecosystem with rich biological diversity. The more diverse an ecosystem is, the more stable it is. According to this diversity-stability-

hypothesis, an ecosystem is more stable and resilient to various disturbances and disasters which are environmental, pathological and existential in nature than an ecosystem with less diverse components (Witting & Niekisch, 2014, P 222).

Biological diversity is also extremely crucial for survival (Witting & Niekisch, 2014, 227). This can be explained by the following scenario. In the above paragraph it had been discussed that the variety of species present in an ecosystem constitute the biodiversity of that ecosystem and enables it to function properly. Now, considering a biotope (a habitat) as a unit to describe biodiversity, we shall interpret that a particular ecosystem comprising of multiple biotopes is also rich in biodiversity. During extreme climatic and weather conditions the inhabitants of such ecosystems are more likely to survive than an ecosystem with less diversity i.e., fewer biotopes. For example, in the event of forest fires, the presence of wetland biotopes increases the rate of survival for the inhabitants of that ecosystem (Wittig & Niekisch, 2014, P 227-228).

The role of biodiversity in human lives is extremely important as human beings are completely dependent on ecosystems and thereby it's biological diversity. The relationship between human beings and their ecosystem could be better understood by looking at the benefits received by human beings from their ecosystem. These benefits are coined as *ecosystem services*. These services build the base for mankind's existence. For example, providing fresh oxygen, food, drinking water, raw materials, stabilized habitats, storing excess CO<sub>2</sub> etc. These ecosystem services can be categorized into four types based on the type of service they render i.e., provisional (food, drinking water, stable environment etc.), regulating (regulating climate, protection from diseases, natural catastrophes etc.), cultural (natural attractions, recreational areas etc.) and supporting (soil formation, maintaining nutrition cycles, preserving genetic diversity etc.) (Witting & Niekisch, 2014, P 232-234). In this work the regulating role of biodiversity will be focussed and discussed in the later part.

### 2.1.1. Climate Change and Loss of Biodiversity

According to the sixth assessment report of the Intergovernmental Panel on Climate Change (IPCC), several marine, terrestrial, and freshwater ecosystems have been altered worldwide. Due to the rapidly changing climate, these

ecosystems have gone through biological changes such as growth, abundance, geographical range shift, seasonal timings etc. which are crucial factors that stabilize an ecosystem. Many species of the terrestrial and marine ecosystems have changed their geographical distribution and their seasonal timing. By shifting these two parameters, the dynamics of a stable ecosystem is greatly threatened. According to the assessment conducted by the Intergovernmental Science Policy Platform on Biodiversity and Ecosystem Services (IPBES) the geographical ranges of around 50% of terrestrial non-flying mammals and 25% birds are reducing due to human activities and anthropogenic climate change (Midgley, 2020, P 12). Due to rising global temperatures, several species are moving towards higher altitudes to survive (IPCC, 2022, P 45). But certain rare species which have a much-limited geographical range cannot shift their ranges swiftly because their requirements for favourable conditions might be hard to find. This leads to a loss of these rare species which in the long run leads to their extinction (Midgley, 2020, P 13). This was the case with the Australian rodent, Bramble Cay melomys. The extinction of this species was solely due to human induced climate change (Foden & Wilgen, 2020, P 15). If this rate of change of geographical ranges continues, 20% of wild terrestrial species will face extinction by 2100 (Midgley, 2020, P 13).

The seasonal timings of certain species have also altered in which springtime activities such as breeding are occurring earlier than they usually take place (IPCC, 2022, P 45). Altered breeding patterns result in an altered supply in the food chain of an ecosystem. This in turn leads to a reduction in the availability of prey to feed on (World Wildlife Fund, 2020). These courses of events have led to serious consequences such as restructuring of ecosystems, mass mortality of flora and fauna sometimes even extinction, and great declines in key ecosystem services (IPCC, 2022, P 45).

### 2.1.2. Impacts of Biodiversity Loss on Human Health

Loss of biodiversity can adversely affect human lives and well-being. This can be explained in terms of the ecosystem services. With increasing pollution and toxification of the natural resources such as air, water, land etc., the availability of clean air, water, land etc. is reducing drastically. Proper sanitation and hygiene

become an issue, which are very important for ensuring good health and well-being. Without clean drinking water and fresh supply of oxygen our very existence is at threat. Tampering the natural greenhouse effect and global warming with increased human activities like deforestation, urbanisation, increased land usage etc. has increased pollution levels beyond the natural purification capacities (Adebayo, 2019, P 6).

The second most important ecosystem service that we require for survival is the availability of food. Due to biodiversity loss, food availability and food production may be greatly affected. If key organisms such as bees are threatened or lost, the global production of fruits and vegetables will be reduced massively. Loss of key organisms in the marine ecosystem will affect the availability of fishes and other seafood, which constitute for about 16% of global protein source. This will thereby reduce the source of nutrition, leading to higher rates of global hunger and global malnutrition (Adebayo, 2019, P 6).

The third most important ecosystem service is the availability of resources from which drugs, medicines, antibiotics etc. are obtained. Without the availability of certain plants, trees, microorganisms etc. modern medicine and pharmacopoeia would not exist. Life sustaining drugs such as aspirin, quinine, artemesin-based compounds obtained from plant species such as *Salix alba*, *Cinchona succirubra*, *Artemisia annua* etc. have helped us treat and cure deadly diseases. Antibiotics obtained from microorganisms such as penicillin and erythromycin have saved several lives over the years. It is believed that there might be more plants and microorganisms which could be potential sources of new drugs, which are yet to be discovered. With loss of biodiversity these sources of pharmacopoeia are not only at risk but also the chance of human survival against deadly diseases is reduced, especially with the increase in emerging and re-emerging infectious diseases (Adebayo, 2019, P 5).

Apart from the providing ecosystem services, it has been observed that biodiversity loss has tampered the natural regulating ecosystem services such as regulating pathogens and diseases. This has led to the phenomenon of emergence and re-emergence of deadly infectious diseases. Since certain animal host species have been lost due to climate change, several infectious diseases

have established themselves swiftly in the human ecosystem. High incident rates and sudden increase in mortality due to infectious diseases are a serious threat to global health. The sudden emergence and re-emergence of the West Nile disease and Lyme disease are best examples for this phenomenon (Adebayo, 2019, P 6). There have been several outbreaks accounted for ever since the first discovery of these two diseases in 1937 and 1975 respectively (World Health Organisation, 2017; National Institute of Health, 2022).

In 2.4.2. the loss of biodiversity as a contributing factor of emerging and re-emerging diseases is explained furthermore. But before, the basic dynamics of an infectious disease must be understood. This is explained in the following section, where the pathogenesis and epidemiology of infectious diseases is presented.

## 2.2. Infectious Diseases

Diseases have co-existed in our environment since ages. The beginning of the infectious diseases, also known as communicable diseases, dates to the early 16<sup>th</sup> Century. Our discovery of malicious microorganisms in the 19<sup>th</sup> Century was the first scientific breakthrough in understanding the origin of these diseases. This discovery nullified the previously widely accepted miasma theory, which stated that “an illness or disease was caused by miasma, an ill-defined emanation from a rotting organic matter” (Last, 2007, P 237). As of today, we know that infections are caused by infectious agents such as micro- and macro-organisms and sometimes even prions, which may or may not be malignant. Infectious disease, on the other hand, is a state of illness caused by one particular infectious agent or its by-product which has been transmitted directly or indirectly through a host medium such as a plant, animal, vector etc. from an infectious source such as an infected person, animal, or a reservoir (Barreto, Teixeira, Carmo, 2006, P 192-193). Infections do not always develop to become an infectious disease. A person can be infected, i.e., the infectious agent has entered and developed in the individual’s body, but the individual still might not have experienced any symptoms or illness. When the infection starts compromising the individual’s immune system, that is when the illness occurs. But this changing point is different for different infectious agents (Barreto, Teixeira, Carmo, 2006, P 192-193).

The burden on human lives due to infectious diseases have decreased over the years. In 2000, the global mortality rate due to communicable diseases was 30.7%, whereas in 2019 it stood at 18.4% (World Health Organisation, 2022a, P 22). This accounts for almost a 50% reduction in number of deaths due to communicable diseases globally. This is due to the improvement in treatment, detection, monitoring and cure. Although there have been improvements in the management of communicable diseases, there is an alarming need to address a novel trend, emerging and re-emerging of infectious diseases. Re-emerging infectious diseases (REID) can be defined as previously identified and controlled infectious diseases which reappear from time to time (Barreto, Teixeira, Carmo, 2006, P 194). Emerging infectious diseases (EID) on the other hand are defined as infectious diseases which are newly identified in a population or suddenly increasing in incidence or have existed previously but in a different region and now has shifted its geographical range (McArthur, 2019, P 297). The increase in REIDs and EIDs poses a threat to human lives due to their unpredictable nature. Their ability to spread rapidly, cross biological and geographical barriers and the economic burden implicated with it, makes them even more a major concern. The most recent example to this is the outbreak of the novel coronavirus (COVID-19) in the later part of 2019 killing almost 3.3 million of the global population by the end of 2020. This estimated mortality rate is said to be an undercount of the actual death toll (WHO, 2020). The economic impact due to the Covid-19 pandemic is off the charts and the estimations are still underway. Considering recent events, it is high time to address REIDs and EIDs and to mitigate their impact swiftly as possible. The following section will explore the pathogenesis of infectious diseases, including REIDs and EIDs, followed by their epidemiology.

### 2.2.1. Dynamics of Infectious Diseases

The genesis of every infectious disease depends on several factors. This can be explained with the help of The Epidemiological Triad model (Fig. 1). The Epidemiological Triad model or the Agent-Host-Environment model was postulated to explain the interactions between the three main factors (agent, host, and the environment) which determine the dynamics (virulence, contagiousness etc.) of an infectious disease. In a given ecosystem, host organisms (plants, animals, birds, humans etc.) and infectious agents aka pathogens (bacteria, viruses, prions,

parasites, protozoa etc.) are coexistent. Under certain environmental conditions these two organisms come in contact, and it is these environmental conditions that determine the level of exposure and interaction between the host and the infectious agent. Frequent exposure and interactions between these two organisms may lead to an infection which in turn may lead to disease and then to recovery or death (van Seventer & Hochberg, 2017, P 22).

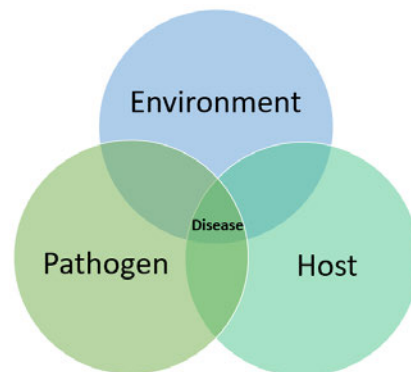


Figure 1, The Epidemiological Triad Model, based on van Seventer & Hochberg, 2017, P 22, own illustration.

The origin of every infection and disease is different. For this, aspects such as pathogen source and reservoir, modes of transmission and host function must be understood.

**Source of Pathogens or Reservoirs:** The primary source of pathogens is called the reservoir. A reservoir is an ecological niche with stable and favourable conditions for the infectious agent to survive, multiply and sustain itself. Upon contact with a susceptible host, the infectious agent then transmits from the reservoir to a new location i.e., the susceptible host. Reservoirs can be abiotic (food, water, air, soil and substance), biotic (plant, animal and human) and zoonotic (animal) (Barreto, Teixeira & Carmo, 2006, P 193; Krämer & Wille, 2003, P 40). There is another reservoir, known as the nosocomial reservoir and this corresponds to the pathogens that are transmitted from hospitals and clinics. These pathogens are usually drug-resistant due to their environmental conditions (Fritsche, 2016, P 254).

**Modes of transmission:** Now that the pathogen has a reservoir, the next stage of the host-pathogen interaction is transmission. Transmission could be either direct or indirect. Direct transmission occurs when the pathogens are spread directly



from the reservoir. This could be through secretions, air and water droplets, bites etc. Indirect transmission occurs when the pathogens are spread through a vehicle (aka vectors) and infected objects (aka fomites). Vector-transmission is mostly carried out by invertebrates such as flies, mosquitoes, worms, ticks, fleas etc. (Krämer & Wille, 2003, P 40).

**Types of hosts:** A host is any organism, simple or complex, that is the target of a pathogen. There are two types of hosts depending on their function. Hosts in which the infectious agent matures and reproduces are known as definitive hosts or primary hosts, whereas hosts in which the infectious agent is still in its vegetative phase i.e., larval or asexual phase, are known as intermediate hosts or secondary hosts (Barreto, Teixeira & Carmo, 2006, P 193). For example, in the life cycle of the protozoan Plasmodium, the female Anopheles mosquito is the definitive host and human beings are the intermediate hosts (Last, 2007, P221 & 291). Based on the above information, the host-pathogen interactions could be mapped out and integrated with the Epidemiological Triad Model for better comprehension (Fig. 2).

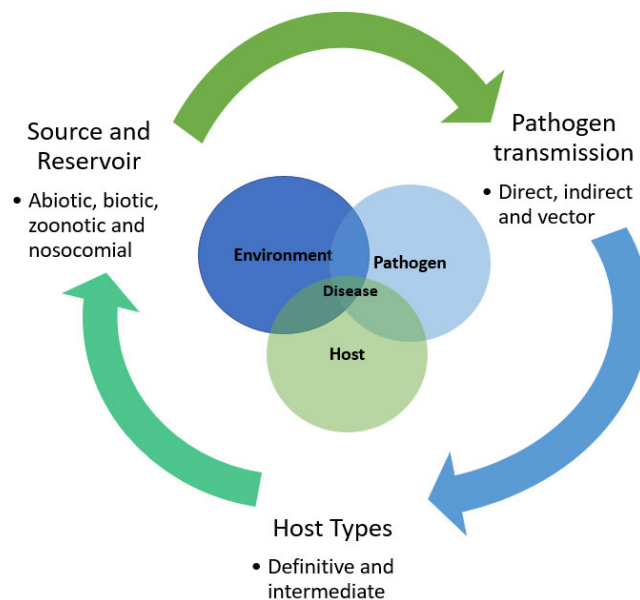


Figure 2, Updated version of the epidemiological triad, own illustration.

For a host to be infected, the different stages of infection must be gone through. The first stage of infection after the pathogen has come in contact with the host is *colonization*. Upon entering the host body through a physiological portal i.e., skin or the mucous membranes of the digestive, respiratory, urogenital tract, the agent

tries to multiply rapidly and hence *colonizes* (van Seventer & Hochberg, 2017, P 22). This stage is not an infectious stage. The next stage is the attacking of the host tissues or the *infecting* stage. Although this stage may cause some disruption in the bodily functions of the host, it doesn't always lead to disease (van Seventer & Hochberg, 2017, P 22). Host immunity is a very important factor here and therefore not all infections develop into a disease. The next stage is the *disease* stage. Here, the infection has managed to overtake the host's immune system thereby compromising it. As the level of disruption in the host's body has exceeded the host's capacity to fight the infectious agent, the onset of symptoms occurs and finally the disease. The symptoms shown in a host are subjective whereas the signs of illness are objective (van Seventer & Hochberg, 2017, P 22). This means that the expression of symptoms may vary from host to host, but the signs of illness itself are expressed in all infected hosts. The final stage of an infection is *recovery* or *death*. Recovery can be either complete, in which the infectious agent and the disease caused by it are no longer detectable in the host's body, or incomplete in which the host has recovered from the disease, but the infectious agent is still present in its body thereby leading to chronic and latent infections. In case of a chronic infection the agent is still traceable for a long period of time. In case of latent infections, the agent is in a dormant state in the host cells and could be reactivated anytime. Latent infections pose a risk since they can transmit anytime as they serve as a silent reservoir of pathogen (van Seventer & Hochberg, 2017, P 22).

In addition to the cascade of stages of development of an infection, there are certain factors that determine if an infection develops into a disease or not. These determinants can be categorized into pathogen/agent determinants, host determinants and environmental determinants.

**Agent Determinants:** The agent determinants include infectivity, pathogenicity, and virulence (van Seventer & Hochberg, 2017, P 22). The probability that an exposed host will be infected is known as *infectivity*. *Pathogenicity* on the other hand is the ability of a pathogen to cause disease in an infected host (van Seventer & Hochberg, 2017, P 23). *Virulence* is the severity of the disease caused and the intensity of pathogenicity (Fritsche, 2016, P 253).

**Host Determinants:** The host determinant *susceptibility* is also crucial for an infectious agent to be able to infect the host upon exposure. Based on their biological predisposition a host can either resist infections and diseases or not. The more susceptible a host is, the more likely is the host to be infected and more disruptions due to infections and diseases it experiences. Susceptibility is however influenced by intrinsic genetic factors, acquired factors i.e., acquired immunity (active or passive) and other biological factors such as age, sex, pregnancy, underlying diseases, nutritional health, stress, etc. (van Seventer & Hochberg, 2017, P 23).

**Environmental Determinants:** Physical, social, behavioural, cultural, political, and economical factors fall under environmental determinants. These factors directly affect the host-pathogen-interaction and determine the likelihood and the degree of vulnerability of the hosts to pathogens. Apart from that environmental determinants can also affect the host's susceptibility to infections where it might even induce some physiological changes in the host, making it more susceptible and vulnerable (van Seventer & Hochberg, 2017, P 24). For example, a smoker with low socioeconomic resources is more susceptible to flu-like infections than a non-smoker with better socioeconomic resources.

Following the stages of infection are the stages of development of a disease. After a host has been infected, the first disease stage or the *incubation period* begins. The incubation period extends from first exposure to the occurrence of first symptoms. This stage is usually a non-infectious stage. The incubating period varies from pathogen-to-pathogen and host-to-host. Sometimes it overlaps with the latent stage (of an infection) and sometimes its followed by the latent stage (Fig. 3). But both these stages are non-infectious in nature. The second stage of disease is the period of *clinical illness*. This period extends from first signs of symptoms to the last signs of illness in the host. This stage is either infectious or non-infectious depending on other factors i.e., environmental factors and susceptibility of other hosts that interact with the infected/diseased host. Following this is the period of *infectiousness* or the period of *communicability*. This is the period where the diseased host is capable of transmitting infectious agents and infecting other hosts (van Seventer & Hochberg, 2017, P 24). This stage is highly contagious. Each stage of disease may extend over different periods of time for

different infections. Again, there are different factors which influence the expression of disease in a host just like different factors which determine if an infection will develop into a disease or not. Factors such as host susceptibility, pathogen infectivity, infectious dosis, virulence, route of exposure etc. are crucial for disease occurrence and in understanding them. Knowledge of the stages of disease is essential in detecting a particular disease especially REIDs and EIDs and in developing strategies and measures to control their spread (van Seventer & Hochberg, 2017, P 24). For example, when an individual is infected with varicella zoster virus (VZV) it develops into what we know as chicken pox. The stages of disease for chicken pox are such, that the period of incubation and the latency stage of infection overlap i.e., occur at the same time. Shortly after the latency stage the transformation from a non-infectious phase to an infectious phase occurs. The individual may not be showing any signs of symptoms but might be capable of transmitting infectious agents. Thus, becoming a carrier of disease. A carrier might be healthy or ill depending on their biological disposition, but they can still infect the population unknowingly and thereby facilitating the spread of infectious agents (van Seventer & Hochberg, 2017, P 24). Following this asymptomatic infectious stage, appears the first signs of clinically detectable illness. This stage overlaps with the infectious stage, where the diseased carrier is actively capable of transmitting pathogens.

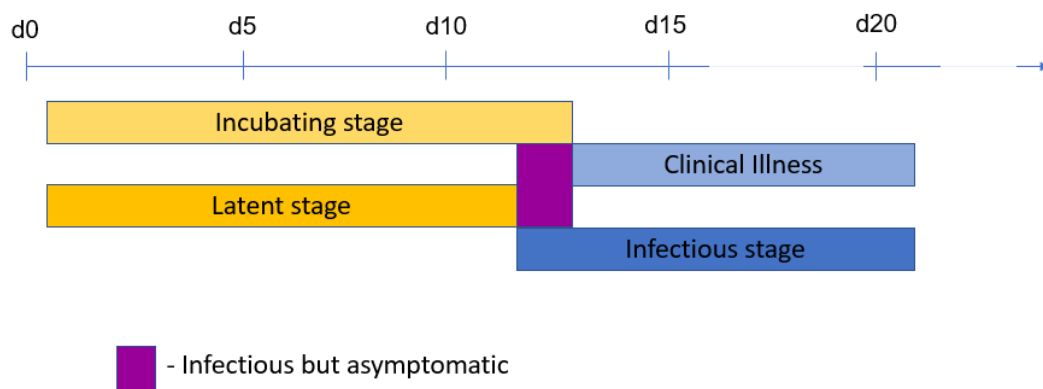


Figure 3, Stages of disease - chicken pox, based on van Seventer & Hochberg, 2017, P 26, own illustration.

Knowing the different stages of a disease and the duration of each stage gives us enough information to strategically avoid massive spread, outbreaks and protect populations. A disease outbreak can be classified into different categories depending on the population size, geographical and temporal parameters.

### 2.2.2. Epidemiology of Infectious Diseases

Outbreaks of infectious diseases pose a great threat to global health since it affects populations uncontrollably. Depending on certain factors such as the duration, geographical range etc., they can be classified into various types. Based on the source of the outbreak, it can be either propagated or a point source outbreak. A point source outbreak occurs when there is a mass exposure to an infectious source at a particular place and time (Rothman, Greenland & Lash, 2008, P 552). This means that the infection is confined to one place and a certain period of time. A point source outbreak can also be an ongoing outbreak if it is not limited to a place or time i.e., the population is being exposed prolongedly. Food borne diseases are an example of point source outbreaks. Propagated outbreaks on the other hand occur if the exposure is due to transmission from person-to-person. It could also be from object-to-person as in nosocomial infectious diseases (Rothman, Greenland & Lash, 2008, P 552). Based on the pattern, duration and geographical range, an outbreak can be endemic, epidemic, or pandemic (Fig. 4). An outbreak is endemic when the disease has spread in a particular region (eg: a town or city) among a particular group of people (eg: infants) over a particular period of time (eg: summer season). When the exposed/infected population are young, then it is known as holoendemic and when the exposed/infected population belong to all age groups then it is known as hyperendemic. An endemic develops into an epidemic when the disease has spread beyond the initially estimated geographical barriers (eg: a state, country, or continent). Pandemic occurs when the disease has spread over various continents or globally (Barreto, Teixeira & Carmo, 2006, P 193).

Apart from the disease outbreaks in a human population, there are outbreaks in the non-human population which also tend to influence an outbreak in the human population. They can be classified as enzootic, epizootic, and zoonotic outbreaks. Enzootic is analogous to endemic but occurs in the animal population and epizootic is analogous to epidemic i.e., when the epidemic has not crossed the biological barriers and is restricted to a non-human population (van Seventer & Hochberg, 2017, P 31; Barreto, Teixeira & Carmo, 2006, P 193). On the other hand, zoonotic outbreaks are caused by animal-to-human transmissions. That means, that the infectious agents have successfully crossed over the biological

barriers and have established themselves in the human ecosystem. The source of zoonotic infectious agents can be both domestic animals and wildlife (van Seventer & Hochberg, 2017, P 31).

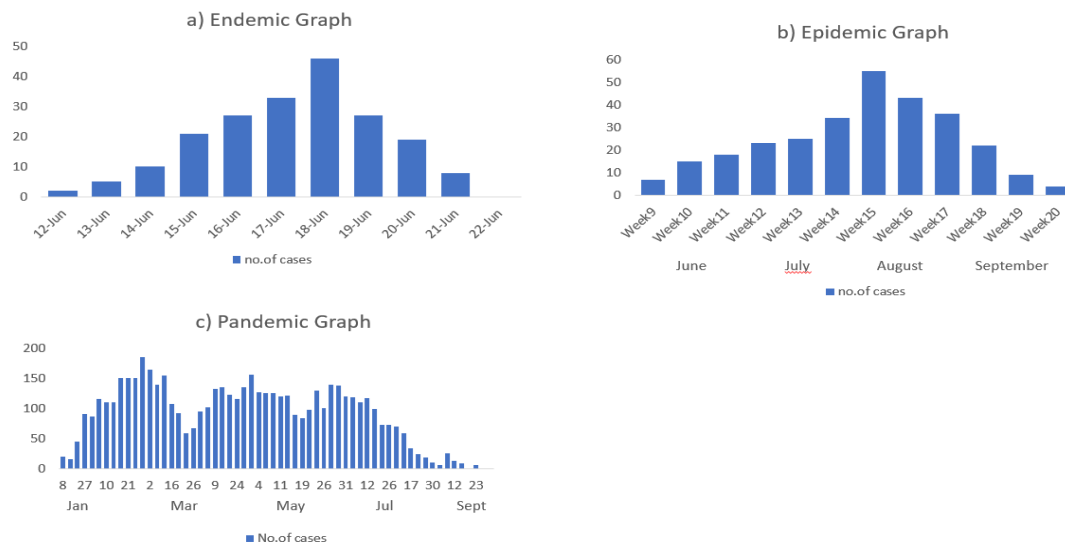


Figure 4, Types of disease outbreaks, graphical representation based on Reintjes & Grein, 2003, P 76, own illustration.

### 2.2.3. Epidemiology of Re/Emerging Infectious Diseases

It has been observed that over the years a majority of EIDs are zoonotic in nature. Almost 75% of human pathogens are of zoonotic origin. Currently, it could be said that almost all the human pathogens are transmitted from animals (van Doorn, 2021, P 659). For a pathogen to jump from species-to-species, it must have gone through various modifications and mutations to overcome interspecies and interhuman barriers. During the pre-industrial times this might have been somewhat of a challenge for pathogens to accomplish a successful species jump. Nowadays this has become “easier” or has been “facilitated” by human activities such urbanization, land usage etc. which have altered the transmission patterns of pathogens relatively fastly. So far, there has been four great shifts facilitating the human-pathogen interface. All these shifts could be explained by the human activity that had taken place around that time (van Doorn, 2021, P 660). During the prehistoric times, there were zoonotic interactions but on a much smaller scale and were mostly interspecies i.e., the pathogens were not well-established in the human ecosystem. The first big shift took place around 5000 to 10,000 years ago which was mainly localised. This was due to the first agricultural activities and animal rearing. The second shift took place around 1000 to 3000 years ago and

was intracontinental. The major human activity around this period was the invention of trade routes and wars among kingdoms within a continent. The third shift took place in the 16<sup>th</sup> Century, and this was the first time when the zoonotic interactions were on an intercontinental scale. This major shift could be traced back to human activities such as European exploration and imperialism. The fourth shift is the current change that is still taking place. Here, activities such as globalization, urbanization and human-induced climate change are the major drivers for emergence of infectious diseases (van Doorn, 2021, P 660). Secondary factors such as lack of public health services, poor medical infrastructure, frequent war and famine etc. exacerbate the burden caused by REIDs and EIDs (Mukherjee, 2017, P 3).

Apart from the EIDs and REIDs of zoonotic origin, the re/emergence of communicable diseases from non-zoonotic sources also threaten the global health. The biggest prognosis on this is the rise of antimicrobial drug resistant diseases (van Doorn, 2021, P 661).

Drug resistance is a major concern as it could setback all the years of clinical advancements made in treating infectious diseases. Re/emergence of drug resistant strains of tuberculosis, AIDS, malaria and other nosocomial diseases are a great threat to populational health due to their enhanced virility and pathogenicity. It has been estimated that in the future antimicrobial and antibiotic resistant diseases will create an immense health and economic burden if active measures are not taken (van Doorn, 2017, P 661).

### 2.3. EIDs and REIDs of the 21<sup>st</sup> Century

According to WHO, the following infectious diseases are among the top emerging diseases that are highly likely to cause full-scale epidemics, if not addressed at the right time (WHO, 2015; Mukherjee, 2017, P 2). In 2015, the World Health Organisation published a list of EIDs and REIDs and in that, the top priority diseases includes haemorrhagic diseases such as Crimean Congo fever, Marburg fever, Lassa fever, Ebola fever, respiratory syndromes such as Middle Eastern Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS), vector-borne diseases such as Nipah and Rift Valley diseases. Secondary priority list contains known killers such as Tuberculosis, Malaria, Zika, Dengue, AIDS,

Avian Influenza such as A (H1N1, H7N9, H5N1, H5N6 etc.) and Chikungunya (WHO, 2015; Zumla & Hui, 2019, xv). Although the list of top priority R/EIDs may seem compact, there are many more infectious diseases which appear from time to time and have not been included or “considered” to be a top concern. In addition to that there are other infectious diseases which may not yet have been “discovered” as a re/emerging infectious disease. For example, there are some diseases that have been recently identified to have/have had impact on human lives. SARS-CoV-2 and Monkeypox in humans, nosocomial Covid-19 etc. are some of them (Centres for Disease Control, 2022, P 1945-2139). In the following, the epidemiological profiles of certain diseases will be presented.

### 2.3.1. Emerging infectious diseases

#### a) Haemorrhagic Viral Diseases/Fever

Haemorrhagic viral fevers pose a great threat to human lives. Due to their lethal characteristics, they have been a major public health concern. The viral haemorrhagic fevers are zoonotic in origin and are caused by enveloped single-stranded RNA viruses. There are six families of viruses that cause viral haemorrhagic fevers (Zumla & Hui, 2019, xv).

They are as follows,

- Filoviruses – Ebola and Marburg fevers
- Arenaviruses – Lassa, old World and new World arenaviruses
- Hantaviruses
- Nairoviruses
- Phenuiviruses (Crimean Congo fever, Rift Valley fever etc.)
- Flaviviruses (Dengue, Yellow fever etc.)

#### i) Ebola Virus Disease – Filoviridae: *Zaire ebolavirus*

The first outbreak of Ebola Virus Disease (EVD) was identified in 1976 in Democratic Republic of Congo near the Ebola River. Since then, Ebola has been on the spotlight due to its highly lethal nature and its ability to develop into an epidemic in a short period of time. One of the mysteries of the Ebola virus is that its reservoir is still unknown (CDC, 2021; Löscher & Prüfer-Krämer, 2003, P 19). In



1976, almost 284 people were affected, and the mortality rate stood at 53%. Since then, there have been multiple EVD outbreaks with short intervals and less incidence until 2013. In Democratic Republic of Congo, it is still an ongoing epidemic. The first ever large-scale epidemic was noted in 2013 lasting for about two years (2014 to 2016) in West Africa. EVD reached a pandemic potential when it was detected in the United Kingdom, Spain, United States and Sardinia following this epidemic. This incident marked the growing pandemic potential of EVD and has ever since been a top-priority disease especially in research and development (Zumla & Hui, 2019, xv).

ii) [Lassa Virus Disease or Lassa Fever – Arenaviridae: \*Lassa mammarenavirus\*](#)

The Lassa Fever (LF) was first documented in 1969 in Nigeria. Until now several LF outbreaks have been documented. The main reservoir of the virus was found to be the multimammate rat (*Mastomys natalensis*), a native rodent of sub-Saharan Africa (Löscher & Prüfer-Krämer, 2003, P 19). LF has reaped many lives over the years. About 300,000 to 500,000 infected cases have been documented of which 5 to 10,000 deaths are recorded. As of now, multiple cases of LF have been recorded in the United States, United Kingdom, Canada, Netherlands, Israel, Sweden, and Germany (Zumla & Hui, 2019, xv). Under favourable conditions, a full-scale pandemic of LF could be expected.

iii) [Dengue – Flaviviridae](#)

The dengue virus (DENV) is an RNA virus as mentioned in 2.2.3.2. and causes the dengue haemorrhagic fever in humans. It is transmitted by vector, female *Aedes aegypti* or *Aedes albopictus* mosquitoes. Dengue can be caused by four types of antigenic serotypes i.e., DENV1, DENV2, DENV3 and DENV4. This infectious disease is also a tropical disease because the tropics provide the favourable conditions for the virus to survive, incubate and multiply. The ambient temperature for the virus to multiply rapidly is around 25-28 degrees. This explains as to why dengue is epidemic to south-east and south Asia, the Caribbean and the Oceania and is a leading cause for deaths and hospitalizations (Löscher & Prüfer-Krämer, 2003, P 25; WHO, 2022b). In the past couple of decades, dengue has spread over continents and still prevails as a leading cause of death in Asia and

Latin America. There is a steady growth in its incidence and has affected more people than it was first discovered. In 2019, 5.2 million people were infected with DENV. The current infection rate and death toll is still to be determined because of the ongoing SARS-CoV-2 pandemic (WHO, 2022b). This alarming trend is of high importance as it clearly poses great threat to global populations.

## b) Viral Respiratory Syndromes

The viral respiratory syndromes are majorly caused by coronaviruses. They are large, enveloped, single stranded, positive sense RNA viruses. Of the four sub-groups of coronaviruses ( $\alpha$ ,  $\beta$   $\gamma$  and  $\delta$ ), only  $\alpha$  and  $\beta$  groups are found to infect humans (CDC, 2020). In the past couple of decades there have been three major coronavirus outbreaks, the latter surpassing the damage caused by their predecessor.

### i) Severe Acute Respiratory Syndrome – SARS (SARS-CoV-1)

The first coronavirus outbreak causing the severe acute respiratory syndrome (SARS-CoV-1) occurred in 2002 in China. The natural reservoir of SARS-Cov-1 is believed to be from a particular bat family found in the caves of Yunnan Province in China, which was then passed on to palm civets and finally spilling over to humans (Cui, Li & Shi, 2019, P 182). This lethal pandemic was the first airborne disease to spread uncontrollably globally and lasted for two years until 2004. Around 8,098 people globally were infected and around 774 were dead (Zumla & Hui, 2019, xiv).

### ii) Middle Eastern Respiratory Syndrome – MERS

The MERS-Coronavirus outbreak occurred first in 2012 in Saudi Arabia. In 2015, MERS-CoV caused a severe epidemic in the country especially due to nosocomial and person-to-person transmission. Just like SARS-CoV-1 the natural reservoir is believed to be of bat origin but the intermediate host for MERS-CoV was found to be camels, especially the taxonomical families found in the Middle East and Asia (Cui, Li & Shi, 2019, P 188). MERS shows high epidemic potential and still terrorizes the Middle East with recurrent outbreaks in the community and in hospitals. It could be classified as an ongoing epidemic of the Middle East. There was about a total of 2458 cases reported to WHO (as of 2019), of which 848

deaths were recorded mounting up to 34% mortality (Zumla & Hui, 2019, P 14-15). MERS-CoV was/is known to cause an epidemic and impact human lives.

Although, it has not really crossed geographical boundaries (exception: South Korea), it should be noted that, its mortality rate is distinctively higher than SARS-CoV-1 (Zumla & Hui, 2019, xiv-xv). Given the fact that they are both caused by  $\beta$  coronaviruses, it must be noted that over the years, this virus sub-group could have managed to mutate, where its virility could have possibly been enhanced.

### iii) Severe Acute Respiratory Syndrome – SARS-CoV-2 or CoViD-19

The Covid-19 outbreak occurred first in December 2019 in China and it has been the most devastating outbreak ever, killing millions of people worldwide. SARS-CoV-2 is a distinct  $\beta$ -viral strain in comparison to SARS-Cov-1 and MERS-CoV and is far more lethal than the others. Due to its high contagiousness and several other factors, it soon reached pandemic proportions (WHO, 2022a, P 3).

Covid-19 infected about 504.4 million people worldwide of which around 6.2 million people were dead (WHO, 2022a, P 3). Unlike SARS-CoV-1, Covid-19 was asymptomatic and difficult to diagnose. This led to rapid spread of the virus, as many individuals who were infected and reservoirs of the virus, didn't show or experience any symptoms. The natural reservoir of the virus is believed to be of zoonotic origin, but investigations are still being conducted to pinpoint the exact origin (Sheervalilou et al., 2020, P 8874). Since its first discovery, Covid-19 has caused subsequent pandemics from multiple mutations. The fact that its mutants also possess a pandemic potential, if not the same lethality, must be noted.

### c) Acquired Immune Deficiency Syndrome – AIDS

AIDS is caused by the Human Immunodeficiency Virus (HIV) and is a highly fatal sexually transmitted disease. HIV was first discovered in 1981 in the United States, even though evidence suggests that HIV was present since mid-1970s. Its origin is still debatable, but first cases were first reported in West Africa and the United States (Myers, MacInnes & Myers, 1993). HIV belongs to the viral family of Retroviruses and is transmitted through direct contact in the form of exchange of body fluids. It must be understood that it cannot be transmitted through saliva or droplets but via blood, breast milk, semen, and vaginal secretions. AIDS by itself doesn't lead to death but with concomitant diseases such as tuberculosis, malaria,

bacterial pneumonia, and other diseases it could lead to death as observed in most cases. Since its discovery AIDS has taken away about 40.1 million lives. Today, about 1.5 million people are infected with HIV and around 650,000 deaths were due to HIV-related causes. There is no cure until now to completely eradicate HIV, but it could be managed and the life span of the patients could be extended with proper therapy. It is has become a co-existing pandemic or a more like a health condition (WHO, 2022c). But it must be kept in mind, that drug-resistant HIV is being reported and have shown tendencies of being more aggressive.

#### d) Lyme Borreliosis – *Borrelia burgdorferi*

Since early 20<sup>th</sup> Century Lyme disease was identified as an emerging disease with epidemic potential. This vector-borne disease is caused mostly by the bacterial species *Borrelia burgdorferi*. The other species of the Borrelia family such as *B. afzelii*, *B. garinii* etc. have been discovered but are not more pronounced than *B. burgdorferi* when it comes to infecting populations. It was discovered that many decades ago the bacteria had successfully established itself in its vector i.e., the tick population especially the Ixodes species. These ticks along with their pathogen were identified to be present predominantly in north-eastern parts of the American continent, central Europe, and Russia (Löscher & Prüfer-Krämer, 2003, P 17). Currently, Lyme disease is very present in the United States, western and central Europe and in parts of eastern Europe. According to CDC, annually approximately 476,000 cases are diagnosed in the US and in Europe over 200,000 cases are diagnosed every year (CDC, 2022).

### 2.3.2. Re-emerging infectious diseases

REIDs are diseases that have been known for a long time which, after a sudden disappearance or decline in incidence, are spreading again either globally or regionally, causing more frequent outbreaks or epidemics. Some of the REIDs are tuberculosis, malaria, dengue, etc. (Löscher & Prüfer-Krämer, 2003, P 20).

#### a) Tuberculosis – *Mycobacterium tuberculosis*

Tuberculosis (TB) was or still is one of the major killers since centuries. It is believed that the first origins of the tuberculosis bacterium date back to 150 million years ago. Archaeological evidence and ancient books and scriptures show that

tuberculosis was present worldwide (Barberis, Bragazzi, Galluzzo & Martini, 2017, P 9-10). It wasn't until mid-19<sup>th</sup> Century advancements in understanding the pathogenesis of the tuberculin bacterium was made. With combined efforts of scientists, the BCG vaccine and drugs to cure tuberculosis were developed. It was found that TB mainly affected people at a young age (15-21 years) and was transmitted through droplets and fomites. In many individuals the infections were latent, and the bacterium had a full life span (Barberis et al., 2017, P 11). This is crucial information because the bacterium can live for a very long time, thereby infecting many, if left untreated.

Since its first clinical discovery, TB is one of the major causes of death, especially in developing countries. It is the 13<sup>th</sup> leading cause of death and the second leading infectious killer worldwide. In 2021, 10.6 million people were infected of which 1.6 million people died due to TB (WHO, 2022d). This highly contagious and highly lethal disease also appears as opportunistic disease in patients suffering from HIV/AIDS. Due to the immunosuppression caused by HIV and the high contagiousness of TB, patients are often doubly burdened. Nearly 187,000 people died from HIV associated TB in 2021 (WHO, 2022d). Another burden on patients is drug resistance. In 2018, around 558,000 people were estimated to be with MDR-TB but only a part of them could be diagnosed. It is a growing concern that these numbers might be increasing (Zumla & Hui, 2019, xvi). Multidrug-resistant TB (MDR-TB) contributes to the deceleration of the TB treatment. This occurs to due poor drug quality, inappropriate care provided by health care professionals, premature termination of therapy by patients. Although MDR-TB is treatable and manageable, it is very cost-intensive (WHO, 2022d). But with development in drug production and supply the burden due to MDR-TB can be alleviated.

#### b) Malaria – *Plasmodium falciparum*

Malaria is one of the most important tropical diseases that is still terrorizing populations. This vector-borne infectious disease is caused by the protozoan parasite of the *Plasmodium* family. Malaria can be caused by four different species of *Plasmodium* namely, *P. falciparum*, *P. vivax*, *P. ovale*, and *P. malariae*. Of the four *Plasmodium falciparum* causes the most lethal type of malaria which has reaped millions of lives over the years. Following that is *Plasmodium vivax* which is found in non-tropical regions. After infecting its actual host, the female

Anopheles mosquito, the protozoan matures in the mosquito's body. Human beings are the intermediate hosts, who are infected through mosquito bites. For the protozoan to survive the temperature conditions must be at least 20 degrees (P. falciparum) or 15 degrees (P. vivax). This is the main reason for malaria to be endemic to tropical countries, especially the African continent (Löscher & Prüfer-Krämer, 2003, P 23). Under favourable conditions, malaria is a super-spreader. According to the world malaria report, 241 million cases of malaria were confirmed of which 627,000 deaths were recorded. About 96% of reported deaths originated from the African continent (WHO, 2022e). There have been fluctuations in the incidence of malaria but not exactly a reduction. It is therefore necessary to address this issue.

c) Mpox (Monkeypox) – Poxviridae: *Orthopoxvirus*

Monkeypox virus was first discovered in monkeys from Asia and Africa in 1958. Back then, this zoonotic virus was observed only in the animal ecosystem until the first human monkeypox cases were reported in 1970 in West and Central Africa. Unlike smallpox, which is caused by VZV, monkeypox was found to be caused by a distinct virus from the family *Poxviridae* called the orthopoxvirus. They have wide range of natural hosts which are mainly non-human primates, squirrels and animals that were arboreal and found in the tropical rainforests. By 1986 there were a total of 338 cases of monkeypox recorded which was followed by its disappearance in the following years. It was even mentioned that monkeypox may be termed as a disappearing disease (Fenner, 1993, P 176-183). This would have held true if it had not reappeared in 2003 in the United States (WHO, 2022f). Although, its reappearance in 2003 did not last long, Mpox was still monitored for future reappearances. It was not until 2022, multiple cases of Mpox were reported in several parts of the world. Even though it is not as lethal as smallpox and the smallpox vaccine can be used to mitigate mpox transmission, it still needs to be addressed as it shows tendency of exceeding endemic proportions. Recent information shows that the transmission chain may extend from 6 to 9 generations. This means that in communities with declining immunity towards pox (small or monkey), the impact might be bigger than imagined. As of the 2022 outbreak, 78,236 cases have been confirmed of which 38 deaths were reported (WHO, 2022f). As of the data collected in 2023, so far 96 deaths have been recorded

globally of which 81 deaths were recorded in countries with no previous mpox history (CDC, 2023). This highlights the fact that there is much need for research in understanding the potential of monkeypox.

#### d) West Nile Disease – West Nile Virus: *Flaviviridae*

West Nile Disease (WND) is a vector-borne encephalitic disease caused by the West Nile Virus (WNV) of the *Flaviviridae* family. In nature, it is maintained in a bird-mosquito-bird cycle and the main vector organism in this cycle is *Culex* mosquitoes. The first human case of WNV was discovered in 1937 in Uganda. In 1953, WNV was detected in birds in the Nile region (WHO, 2017). Since then, WNV was traced in some human and horse population groups with symptoms of mild fever and almost no neurological complications. It wasn't until the latter half of 1990s several concurrent outbreaks in Algeria, Tunisia, Morocco, France, Israel etc. occurred, causing severe neurological complications and even death in infected individuals. The 1999 outbreak in the United States brought attention to the virulent WNV strain (Rossi, Ross & Evans, 2010, P 2-3). WND can be classified as neuroinvasive or non-neuroinvasive depending on the severity of the disease. In the United States, currently 863 cases are reported of which 70% are neuroinvasive and 30% non-neuroinvasive (CDC, 2022). Though there have been some fluctuations, WNV is prevalent worldwide.

## 2.4. Climate Change and Infectious Diseases

It is observed that anthropogenic climate change is a leading driver of the re/emergence of infectious diseases. In this section, the different consequences of human induced climate change in relation to the re/emergence of infectious diseases will be explored.

### 2.4.1. Abiotic factors and zoonotic disease emergence

Human activities such as intensive land usage, mining, deforestation, urbanization, burning fossil fuels, mass production of meat, etc. emit great amounts of greenhouse gases into the atmosphere. Excessive emission of these gases results in increased global temperature. High global temperatures lead to series of adverse events such as melting of glaciers, extreme and altered weather patterns, heavy rains, frequent forest fires etc. Changes in weather patterns and micro-

climate results in change of abiotic factors of an ecosystem such as change in humidity, high temperature, heavy rains, more wind and so on. This change in abiotic factors alter the host-pathogen interaction and the vector dynamic drastically which results in the re/emergence of deadly infectious diseases. (Ellwanger et al. 2021, P 6). For example, a change in rain patterns and temperature help vector borne diseases like Malaria to flourish. As explained in 2.2.3.3. the parasitic protozoan *Plasmodium* can thrive in areas with a temperature of at least 20 degrees Celsius. With rising global temperature and availability of breeding medium for the female Anopheles mosquito (stagnant water puddles, marshes etc.), this creates most favourable conditions for the parasite to multiply and transmit rapidly on a global scale. The extreme climatic events caused by anthropogenic climate change increase the geographic range of pathogens which were previously endemic and also facilitate the proliferation of vectors that transmit diseases. It has been observed that with accelerating climate change frequent epidemics occur (Ellwanger et al. 2021, P 6).

#### 2.4.2. Biotic factors and zoonotic disease emergence

It is crucial that an ecosystem is rich in biodiversity to reduce the risk of emergence of infectious disease. The interactions between living things in an ecosystem determine the biotic factors of that ecosystem. Presence of certain plant species, certain microorganisms determine the behaviour, distribution and abundance of animal species, regulation of prey-predator interactions etc. In turn, the interactions between humans and animals determine the diversity, abundance, and distribution of microorganisms in an ecosystem. All these together determine the ecology of pathogens (Ellwanger et al., 2021, P 6). As explained in 2.1. the stability of an ecosystem is determined by its biodiversity. The more stable the conditions in an ecosystem i.e., stable climate, no mass migration etc., the less opportunity for lethal pathogens to spill over. Due to human activities such as mass deforestation, there is a huge loss of biodiversity, thereby destabilizing ecosystems. In addition to that, destruction of several forests and habitats lead to disappearance of key organisms or the “bridge” organisms and geographical range shift of endemic or enzootic pathogens (Ellwanger et al., 2020, P 6-7).



Loss of habitats due human activities (e.g., Deforestation) and consequences of anthropogenic climate change (e.g., Forest fires) may force the wild animals and vectors and related pathogens out of their ecological niches. As a result, animals tend to migrate towards regions with better conditions to survive (e.g., food abundance, higher altitudes etc.). These regions could be urbanized or de-urbanized. Sometimes it may even cause the wild animals and vectors to invade urbanized areas, thereby encountering domestic animals, livestock and even humans. With this migration, the pathogens are also carried with them. The pathogens then adapt themselves to new “bridge” species or intermediate hosts (e.g., pets such as dogs and cats or farm animals). This accelerates the process of pathogen spillover in human ecosystems. Pathogen spillover is when a series of host-pathogen interactions have taken place for the pathogen to have finally crossed multiple physical, molecular, and ecological barriers by jumping between different hosts and can establish itself in the human ecosystem given the conditions are favourable for further development. It depends on factors such as phylogenetic distance between hosts, frequency and intensity of these interactions and the genetics of both pathogen and hosts (Ellwanger et al., 2020, P 6-7). Another adverse event of climate change induced habitat loss is the loss of animal biodiversity that are crucial in maintaining pathogen dynamics. For example, in a habitat a particular prey species could act as a reservoir for pathogens. Due to habitat loss, if its predator population is lost, it may lead to an overpopulation of this prey. This increases the chances of proliferation of the blood-borne vectors and facilitates the transmission of the pathogen (Ellwanger et al., 2020, P 14).

### 2.4.3. Burden on human health and health systems

Communicable diseases are a great burden to societal health and governing bodies. They cause socioeconomic disturbances and potentially collapse the economic growth of a country. Therefore, it is very important to be best prepared for any outbreaks to avoid high mortality rates and economic losses. The most precise way to calculate the global burden of infectious diseases is to calculate it in terms of global death rate. To assess the global health outcome the mortality and morbidity of infectious diseases need to be calculated. Its sum i.e., mortality and morbidity, provide the burden of that disease and is measured in DALYs (Disability Adjusted Life Years). DALY is a standardized metric for loss of health

over time. It allows to measure the burden of a disease and draw comparisons based on countries, age, sex, and other parameters. For example, one DALY means one year of good health lost due to illness, premature death, disability, or injury. As of 2019, 670 million DALYs due to communicable, neonatal and maternal diseases has been recorded. This has indeed decreased over time. In 1990, the global burden due to infectious diseases was approximately 46.40%. In 2019, this rate dropped to 26.35% (Roser, Ritchie & Spooner, 2021). Although this reduction does show that the burden of infectious diseases is being mitigated over the years, it shows that infectious diseases still have a huge impact on our health systems. Also, it must be noted that this data has not considered the impact of R/EIDs. With hindsight of recent events, the DALYs must be re-calculated to determine the current global disease burden. The economic burden on the other hand, has always been dramatic. From bubonic plague to the Covid-19 pandemic, the socioeconomic losses have been beyond initial estimations. Conventionally, the economic losses were estimated by calculating the basic direct costs (i.e., health care expenses) and indirect costs (i.e., absence at work due to illness/disability, reduced income, etc.) (Smith et al., 2019, P 2). This although is not efficient, as it does not provide a broader view of the total expenses. It must be understood that in the event of an outbreak three stages of economic impact takes place. The *prevention and disease preparedness stage* which includes educating population about preventive methods to mitigate risks and the provision of prophylaxes. The *outbreak stage* which includes disruption of international businesses and supply chains, travel and trade bans and public isolation to avoid further spread of disease, treatment of infected population etc. Finally, the *aftermath stage* which includes loss of employment, businesses and gaps in education, bankruptcy, closure of public markets, stigmatized food and agricultural products, possibility of being orphaned etc. (Smith et al., 2019, P 2). For example, the Zika virus outbreak in the United States led to estimate the approximate lifetime direct medical costs of a child with Zika virus. For children diagnosed with microcephaly the costs were about \$179,760 USD, for children with the Gillian-Barre Syndrome the lifetime costs were \$56,863 USD and a severe case of Gillian-Barre Syndrome was \$500,000 USD. This varies from country to country. The estimates for South America and the Caribbean were around \$7-18 billion USD in just 2015-2017. Apart from the direct costs, the different costs in different

sectors depending on the different stages of an outbreak, as explained above, must be drawn into calculations (Smith et al., 2019, 2-4). For example, the agricultural sector, trade and retail sector, travel and tourism sector, societal and environmental impacts (see Tab. 1).

*Table 1, Economic burden of infectious diseases, based on Smith et al., 2019, P 2-4, own illustration.*

Sector	Disease	Example for economic burden	Economic burden in \$
Agriculture and animal food production	Rift Valley Virus	The somalian meat export and livestock market collapsed. Over 75% of exports resulted in loss and the GDP of Somalia suffered a 25-36% reduction ensuing that.	Loss of over 300 million USD
	Nipah Virus	1.1 million infected livestock (pigs) were culled in Malaysia leading to a drastic loss which is still being accounted for until today.	Initial loss of 97 million USD. Indirect costs such as trade loss, control programs etc. lead to an overall loss of 365 million USD.
Tourism and Travel	SARS-Cov-1	Almost 68% of tourist visits to Hong Kong fell when the SARS-Cov-1 pandemic broke out. Singapore tourism fell by more than 70%	Asia Pacific carriers faced a loss of about 6 billion USD. North American airlines lost about 1 billion USD. Global economic loss was around 40 billion USD.
Tourism and Travel	MERS	South Korea and Saudi Arabia lost a huge part of their international tourists.	South Korea lost about 10 billion USD. Saudi Arabia lost around 5 billion USD per year.
Trade and retail sector	SARS-Cov-1	GDP of Hong Kong and China dropped by 2.6% and 0.8% respectively.	
	Nipah Virus	The Malaysian pork industry took a great hit during the nipah virus outbreak.	The pork industry faced a loss of about 15 million USD.

The social and environmental impacts are often neglected while calculating the economic burden of infectious diseases as they are non-marketable or non-tradeable goods. For example, ecosystem services, availability of resources, educational facilities, job opportunities and so on are not accounted for. They must also be included in the evaluation since they provide prognostic data on the duration and magnitude of the disease burden. To improve this, new evaluation methods must be developed (Smith et al., 2019, P 3-4).

#### 2.4.4. Climate Change and R/EIDs – Status in Europe

In 2018 the European Parliament published an infographic created by the European Environment Agency (EEA) about the impacts of climate change on Europe. According to this graphic, different regions of Europe are/will be affected differently (EEA, 2021). The regions are categorized into the Arctic, Atlantic, Boreal, Mountain, Mediterranean, Continental, and Coastal and seas. Each region faces extreme events such as forest fires, flooding, heavy rains, droughts, high temperatures, storms etc. and their corresponding economic burden in different sectors such as energy, food and electricity production, tourism and travel etc. (European Parliament, 2018). For example, the surface temperature in Europe is found to be above the average global surface temperature. In just the last decade, the average annual temperature in the European continent was 1.9 to 2.01 degrees warmer than the pre-industrial era, whereas the global average annual temperature was 0.62 to 1.04 degrees warmer than the pre-industrial era (EEA, 2022). The overall annual precipitation and flood levels in Europe have been increasing since 1970. Indicators have been showing different precipitation levels in different regions i.e., northern, central and southern Europe have different precipitation levels (EEA, 2021). Such climatic changes have a direct impact on many ecosystems such as the altering of timing and duration of seasonal biological events, migration of species etc. In addition to that many vector organisms, infectious agents, host species and pathogen dynamics are also affected, since they are highly climate sensitive. They also cause changes in human behaviour which leads to increased susceptibility against infectious diseases. Climate change is an important driver of the re/emergence of infectious diseases (European Centres for Disease Control, n.D.).

In the past few decades, several tropical and sub-tropical infectious diseases which were not endemic to Europe were observed to infect and cause fatalities in the European continent. These diseases are climate sensitive and can be categorized into three groups based on their transmission i.e., vector borne diseases (VBD), food borne diseases (FBD) and water borne diseases (WBD). Climatic changes such as increase in average surface temperature, humidity and vegetation spurt influence vector dynamics greatly, because most vectors are arthropods, and these cold-blooded organisms thrive in warm, humid conditions

(Semenza & Paz, 2021, P 2). As a result, VBDs such as WNV, Dengue, Chikungunya, Zika and Leishmaniasis and Lyme disease broke out concurrently in Europe in the past years. The biggest WNV outbreak was observed in 2018 in southern and central Europe. Almost over 2000 cases were recorded. From 2018 until 2020, multiple cases and even deaths have been recorded in different countries from different regions of Europe. In the South, the countries affected were Spain, Italy and Greece; in the East, Romania, Bulgaria and Hungary were affected and, in the North, Germany was affected. This could be explained by the high temperatures in early spring and high precipitation in late winter to early spring in those years. In addition to that, drought like conditions due to high temperatures and the absence of wetlands in the European terrain, forced birds and mosquitoes to settle on water bodies such as lakes, ponds, rivers etc. The combined effect of these two phenomena facilitated the proliferation of the vectors during spring and thereby facilitating the WNV outbreak in Europe. Similar trends were observed when outbreaks of dengue, chikungunya, Zika and Leishmaniasis broke out in countries such as Spain, France, Italy, parts of Germany and eastern Mediterranean countries such as Greece, Cyprus and Turkey (Semenza & Paz, 2021, P 4-5).

Equally, FBD are more prevalent in European countries. Pathogens causing FBD are more persistent, sometimes heat-resistant and are highly infectious with minimal dose. The most reported FBD by developed countries is caused by the bacteria *Campylobacter*. Over 220,000 cases are reported per year. It was observed that *Campylobacter* thrived in high temperatures, humidity, rainfall and was seasonal. Following that are the *Salmonella* outbreaks which constitute the second highly reported FBD in European countries. *Salmonella* is also highly seasonal and the infection rates are clearly higher in summer than in winter amounting up to almost 87,000 cases per year (Semenza & Paz, 2021, P 5).

Europe has a history with WBD. After successful containment of several WBD outbreaks, there are some which are being triggered by climate change. The circulation of water or also known as the hydrological cycle is being altered by climate change continuously. This results in unpredictable events such as storms, heavy rains, depressions and so on. This cascading effect of extreme weather events (e.g., altered hydrological cycles and rising surface and ocean

temperature) could accelerate the transmission of certain pathogens in which they are flushed into waterways, drinking water, urbanized areas and recreational areas (e.g., river rafting areas, natural pools etc.). WBD like Leptospirosis and Cholera break out when favourable conditions are available and spread exponentially (Semenza & Paz, 2021, P 6). Other emerging and re-emerging diseases such as TB, AIDS, Malaria etc. are also prevalent in Europe. However, they are not in alarming proportions as compared to the global incidence. As explained above, climate change poses a potential threat to human health in many ways. Facilitating infectious diseases and causing them to re/emerge is one of the top concerns. But this problem can be tackled if disease preparedness and advanced controlling and monitoring measures are adopted. Good news is that institutions like ECDC, EU-Commission, EEA etc. and other national institutions are keen on addressing this issue. In the following part of this work, the effects of climate change in facilitating the re/emergence of infectious diseases will be studied on a regional level. For this purpose, the country chosen is Germany and the region chosen will be northern Germany.

### 3. Methods

An extensive systematic literature review was conducted to examine the nature of the relationship between climate change and R/EIDS in northern Germany and to determine which EIDS and REIDS are primarily driven by it. Following this, a climate data analysis was conducted to understand this trend and project future trends. Northern Germany was chosen as the geographical scope. As northern Germany comprises of many states, the scope was restricted to the states of Schleswig-Holstein, Hamburg and Mecklenburg-Vorpommern. Since the geographical scope was on a sub-national level, databanks such as LIVIVO, Cochrane, HAW-Catalogue, and other university library catalogues were searched. Keywords and search terms included were “climate change”, “emerging infectious diseases”, “vector borne diseases”, “food borne diseases” “water borne diseases” “Germany” and “human”. Both English and German were chosen in the language criterion to avoid overlooking valuable contributions. Other inclusion criteria such as time frame (2012-2022), accessibility, relevance to the topic were used. 117 studies returned as results and after adding the exclusion criteria such as redundancy and topic irrelevance, 23 studies were drawn for closer inspection.

Upon thorough review 10 studies were chosen. Apart from the above-mentioned databanks, other institutional websites like ECDC, EFSA, RKI were also accessed to gain more information (e.g., vectors maps, no. of reported cases etc.). Tools such as the Surveillance Atlas, Vibrio Map Viewer, Ocean Viewer were used. The second part of the analysis was the collection of climate data from local and national institutions and to hypothesise possible trends in disease dynamics. Institutions such as the German Meteorological Service (DWD) and Northern German Climate Monitor (Norddeutscher Klimamonitor) were chosen. The obtained results are presented below.

## 4. Results

### 4.1. Literature Review

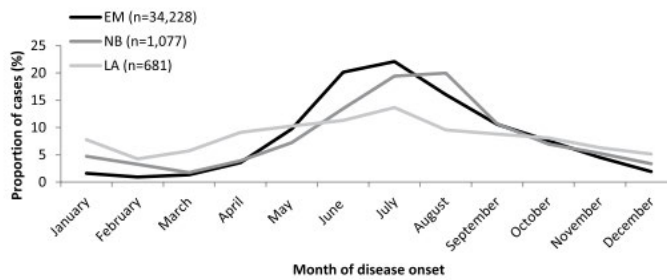
First, the results from the literature review are presented. The results from the 10 chosen studies show that the incidence of EIDs and REIDs are clearly facilitated by anthropogenic climate change in northern Germany. Altered natural environment, climate, microclimate and vegetation constitute as important primary drivers (Semenza & Paz, 2021; Blazejak et al. 2018). This corresponds to the altered seasonality and seasonal durations, and changes in abiotic factors such as temperature, precipitation, ocean salinity etc. Apart from them, travel, tourism, trade and outdoor recreational activities such as hiking, camping, swimming etc. are also identified as contributing drivers (Blazejak et al. 2018). These drivers affect the pathogen and vector dynamics such as vector-pathogen density, geographical range shift and their distribution. The most commonly present EIDs in the observed regions of northern Germany are VBDs: Lyme disease, Tick-borne-encephalitis (TBE), FBDs: Campylobacteriosis, Salmonellosis, and WBD: Non-cholera-vibrio infections. The vectors present are however varied. These vectors and pathogens carried by them are highly climate sensitive. REIDs such as malaria, tuberculosis and WND and EIDs such as HIV, SARS, travel-acquired Dengue and Chikungunya etc. are either mitigated yet ongoing or their pathogens are absent in human ecosystem (as in the case of DENV & CHIKV). There are several cases of Monkeypox reported in the observed states of northern Germany. In Mecklenburg-Vorpommern 6 cases, in Hamburg 184 cases and in Schleswig-

Holstein 28 cases are reported. So far, no deaths have been reported in Germany (RKI, 2023). In the following the most important results and identified trends will be summarized.

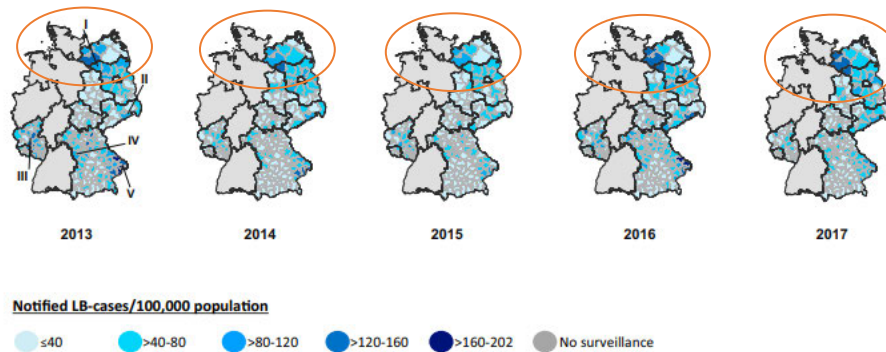
#### a) Seasonality and Vector-Pathogen-Density

Both pathogens and vectors rely on habitat conditions for survival. Most pathogens and vectors thrive under warm and humid conditions, especially, pathogens causing diseases such as Dengue, Chikungunya, West-Nile fever, Meningitis, Encephalopathy etc. and their vectors such as mosquitoes like *A. aegypti*, *A. albopictus*, *C. pipien*, and ticks like *I. ricinus* etc. (Fischer et al., 2013; Koch et al., 2016; Blazejak et al., 2018; Jenkins et al., 2022). In the case of northern Germany, tick-borne diseases such as encephalitis, Lyme disease and meningitis precede the rest of the EIDs and REIDs. It has been observed that over the years the tick population had not only increased but also the incidence of tick-borne diseases rose during warm seasons. Acute Lyme borreliosis shows a pronounced seasonality due to the temperature-dependent activity of the ticks. The incidence rises from April with a peak in August and then drops again (Frank et al., 2014, P 564). According to the report by Enkelmann et al. published in 2018, there was a marked seasonal trend in the incidence of Lyme borreliosis. From 2013-2017 around 57% of the reported cases showed the onset of the disease from June to August with a peak in July and July-August. The disease distribution in northern Germany was spread extensively in Mecklenburg-Vorpommern and in the city of Schwerin. Schleswig-Holstein and Hamburg were not mapped since they were out of scope (Fig. 5) (Enkelmann et al., 2018, P 2-3). In addition to that, the prevalence of *B. burgdorferi* in ticks in northern Germany, especially along the Baltic coast and in Hamburg was observed i.e., 3.1% along the Baltic Coast and 34.1% in Hamburg. A new strain of the Borrelia virus, *B. miyamotoi* was detected in northern Germany (Blazejak et al., 2018, P 2&9).





**Figure 3.** Proportion of LB cases by month of disease onset and clinical manifestation in 9 German states, 2013–2017.



**Figure 4.** Notified LB incidence by district of residence ( $n = 56,011$ ). Based on equal distance between lowest and highest recorded incidence, we formed 5 incidence categories. 435 cases with tick exposure in a foreign country were excluded. Among the remaining 33,153 cases with information on place of tick exposure in Germany, district of exposure corresponded with district of residence in 90.6%, 4.9% reported exposure in another district in the same state and 4.5% in another state in Germany.

Figure 5, Seasonal and geographical distribution of Lyme Borreliosis in Germany, Enkelmann et al. 2018, P 2.

Following tick-borne diseases are the mosquito-borne diseases. Most of the mosquito-borne diseases in Europe, including northern Germany are transmitted by the Aedes mosquito *A. albopictus*. This species carries pathogens such as the DENV and CHIKV. The other mosquito species which poses a threat to northern Germany is the *C. pipiens* which is responsible for the transmission of WNV (Semenza & Paz, 2021, P 4). These pathogens and vectors are highly season and climate sensitive. Currently, the diseases spread by these two vectors in northern Germany are not as severe as in other parts of Europe or the world but works of Koch et al., 2015 and Fischer et al., 2018 show a detailed prognosis of the disease trend if the current climatic conditions are to prevail or worsen. *A. albopictus* is an excellent proliferator and is known for its ability to establish new ecological niches in a short period of time. If the future climate scenario of northern Germany consisted of warm and wet climate, there is a possible risk of this vector to establish an ecological niche in northern Germany (Koch et al., 2015; Fischer et al., 2018).

Food-borne diseases are one of the most reported diseases in Germany altogether. Infections due to *Campylobacter* and *Salmonella* which develop into diarrheal diseases or food poisoning are predominantly frequent during warm seasons. These pathogens are climate sensitive and thrive in warm temperatures. Since 2005, there has been an upward trend in Germany of food-borne bacterial diseases especially campylobacteriosis. It was also found that the incidence began during January and peaked in summer. In 2018, around 67,872 cases of campylobacteriosis were reported in Germany (Oberheim et al., 2020, P 1-2).

The emergence of water borne diseases caused by non-cholera vibrios has been recently reported. Over 13 non-cholera vibrios are known to cause infections and diseases in humans and are mostly present in the tropics and sub-tropics. In previous decades, these pathogens were absent in the Baltic Ocean and North Sea of Germany. But over time, their presence is gradually increasing. Due to climate change and the combination of increasing ocean temperature and decreasing salinity of oceans, pathogens like *V. vulnificus* are found in the coasts of northern Germany. It was observed that its presence was particularly high during summer seasons. As of 2020, a cumulative total of reported cases due to *V. vulnificus* from 2003-2020 stands at 120 from both North and Baltic seacoasts of Germany (Brehm et al., 2021, P 878-883).

#### b) Geographic Vector-Pathogen-Distribution

Currently, only certain pathogens and their vectors are present in northern Germany. Among the well-established pathogens and their disease carrying vectors, *B. burgdorferi* and its vector *Ixodes ricinus* take precedence. Due to rising temperature, this vector-pathogen duo has shifted its geographical range both latitudinally and altitudinally over the years (Semenza & Paz, 2021, P 5). As of the vector map published by ECDC in March 2022, the geographic distribution of tick-borne encephalitis has manifested entire Germany including northern Germany. This map when compared with the map from the tick-borne disease outbreak report (2012-2016) by Beauté et al., 2018 shows a clear change in the geographic distribution (Fig. 6).

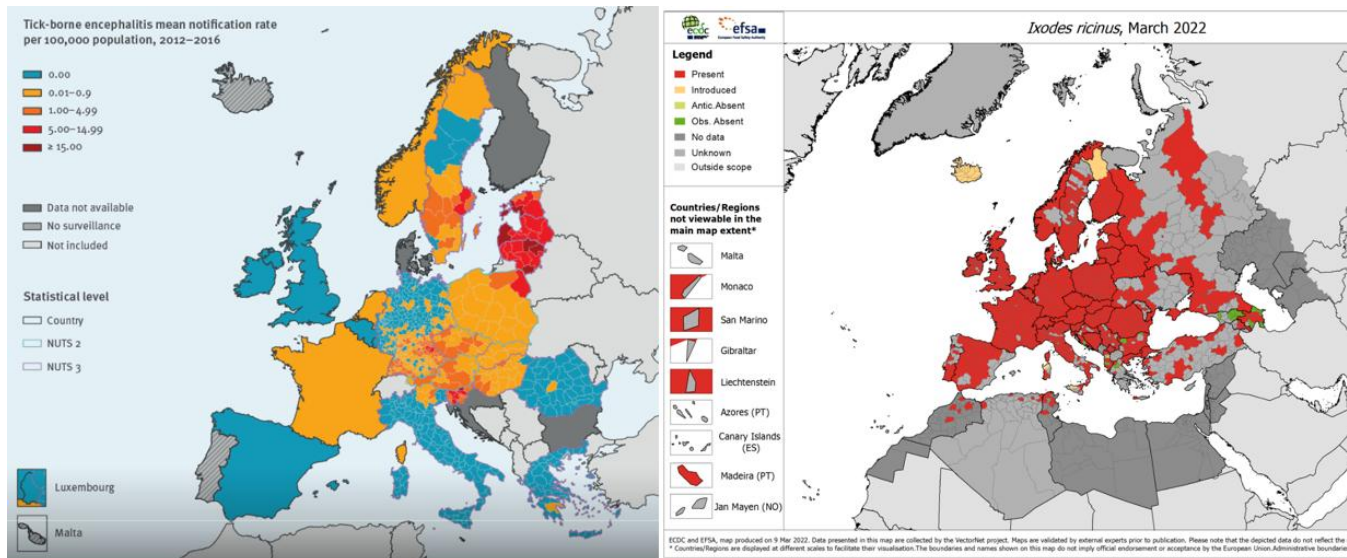


Figure 6, Geographic distribution of tick-borne encephalitis from 2012-2016 produced by ECDC, adapted from Beauté et al., 2018 (left), Geographic distribution of tick-borne encephalitis from March 2022, ECDC, 2022 (right).

According to the geographic distribution map of the surveillance data from 2012-2016 (left), it is seen that there was almost no presence of TBE (except parts of the Hamburg/Mecklenburg-Vorpommern border) in northern Germany. However, according to the map from March 2022 (right), the presence of tick-borne encephalitis is well-established in the observed region (see Fig. 7).

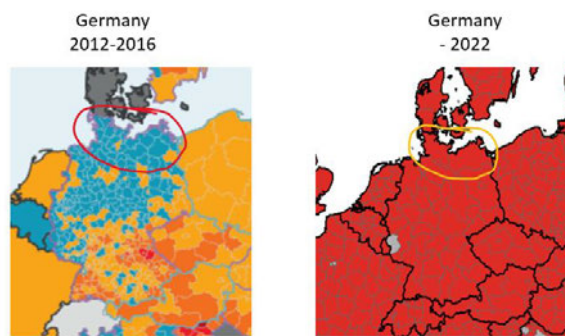


Figure 7, Germany zoom-in with northern Germany in focus, Beauté et al., 2018; ECDC, 2022.

The geographic distribution of mosquitoes such as *A. aegypti* and *A. albopictus* carrying diseases like Dengue, Chikungunya and Zika viral disease is not yet observed in northern Germany. Comparatively, the species *C. pipiens* is widely distributed in northern Germany. *C. pipiens* is known to be the carrier of WNV, Usutu Virus, etc. In 2014, there were only nine cases of WNV reported in Germany and it was found that the disease was acquired during travel (Frank et al., 2014, P 561). In 2018, the first WNV outbreak in Germany was recorded in southern Germany following which it gained importance (Semenza & Paz, 2021, P 4).

Currently, though no new WNV outbreaks have been reported, there is a distinct change in the geographic distribution of its vector *C. pipiens* (Fig. 8).

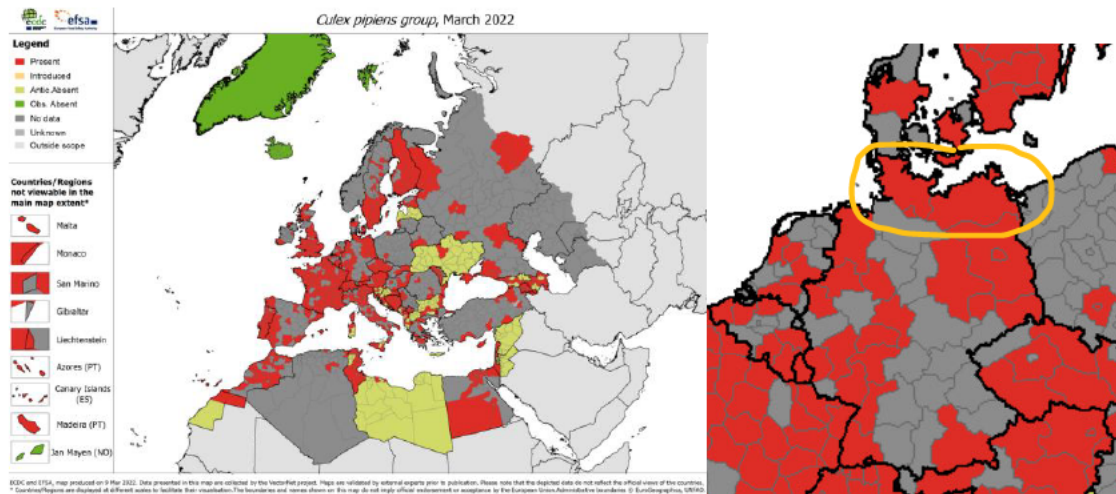


Figure 8, Geographic distribution of *C. pipiens* in Europe (left) and in Germany (right), ECDC 2022.

Data on the geographical distribution of pathogens causing food-borne diseases such as campylobacteriosis and salmonellosis were not found.

Water-borne diseases or infections caused by non-cholera vibrios pose a threat in the future. They, like other pathogens, have managed to expand their geographic range and shift to other climate zones which were previously inhabitable for them. In northern Germany a similar trend was observed. With the help of tool mentioned in Brehm et al., 2021 (Vibrio Map Viewer) and the Ocean Viewer Tool, the geographic distribution of non-cholera-vibrios was traced. It clearly shows the changes in both, geographic distribution and pathogen density (Fig. 9).

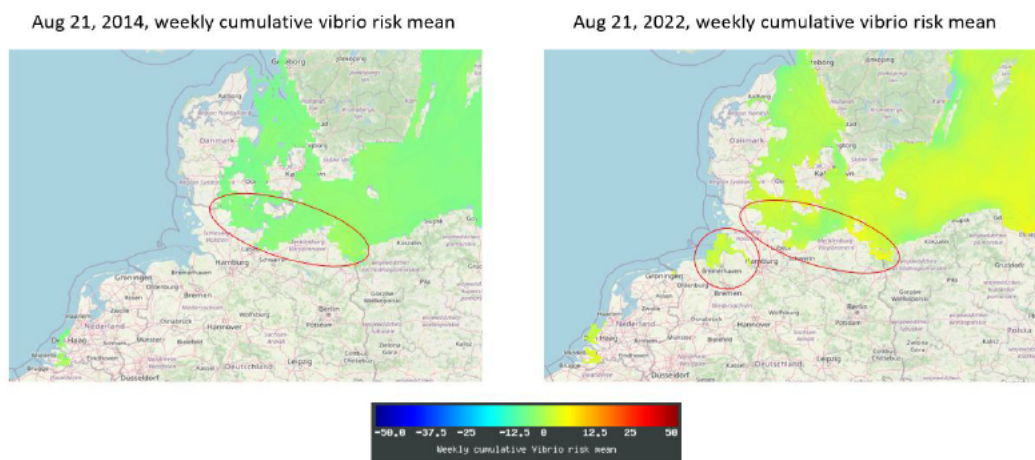


Figure 9, Geographic distribution of non-cholera vibrios by assessing the weekly cumulative vibrio risk mean in 2014 (left) and in 2022 (right), Ocean Viewer, 2022.

## 4.2. Climate Data

The climate data of the chosen northern German states were observed for different emission scenarios to determine or to be able to predict the habitat suitability of certain vectors and pathogens. As mentioned previously in this work, change in abiotic factors such as temperature, precipitation, ocean salinity etc. alter the vector-pathogen dynamics. So, looking at these indicators, the relation between EIDs and REIDs that are driven by climate change could be better understood. Therefore, climate maps created with temperature, precipitation and ocean salinity as variables are presented.

### a) Temperature

The average annual surface temperature of Germany was observed under different emission scenarios i.e., 2.6; 4.5, 8.5 RCP over different time periods i.e., past (1970-2000), present (-2022) and the future (2050-2080). To understand the annual and seasonal climate changes, the months April (Spring), August (Summer) and November (Autumn-Winter) were chosen for closer observations. The maps were created with the help of the online tool developed by the German Meteorological Service (Fig. 10). According to the illustrated maps, the temperature has increased over the years during all seasons i.e., spring, summer, and late autumn-early winter. Currently, the average temperature range in northern Germany has increased to 6°-10° Celsius. In the future it is prognosed to increase by a range of 2°- 4° Celsius. A similar trend has been predicted by other datasets such as the dataset from the ENSEMBLES project (Fig. 11).

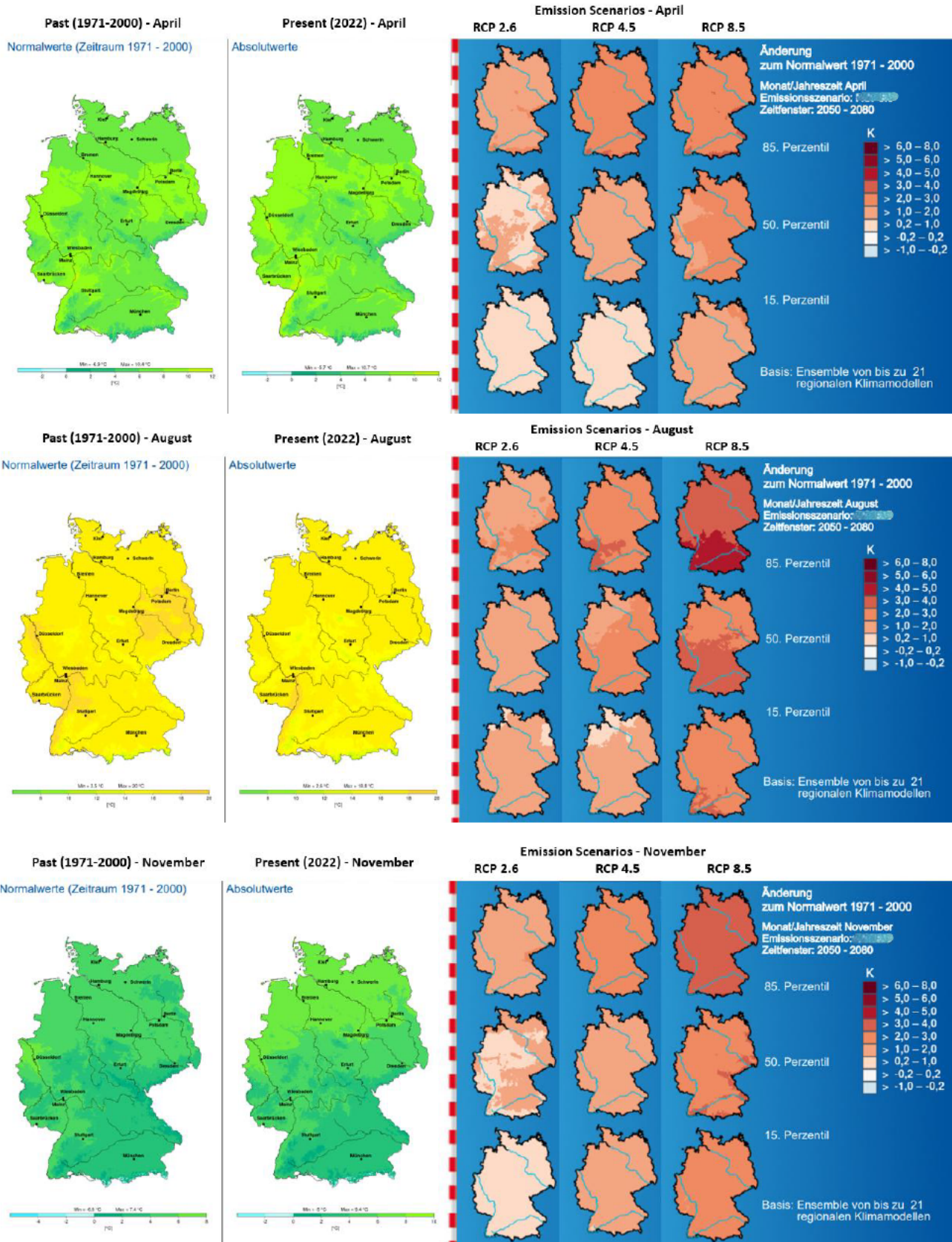
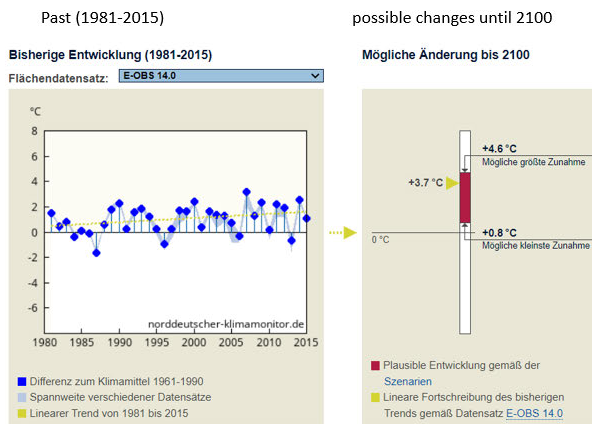


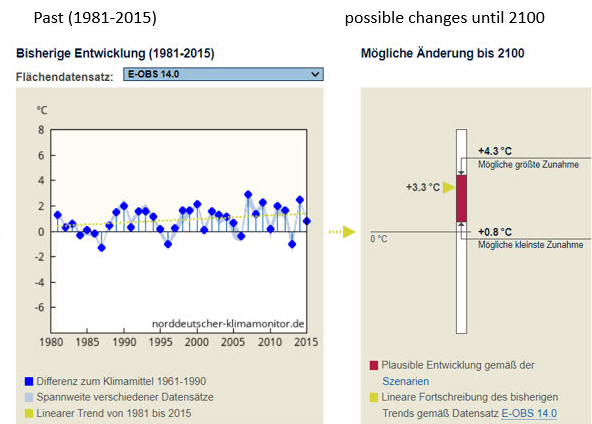
Figure 10, Changes in average annual temperature in the past (1971-2000), present (2022) and future (2050-2080). The prognosis for future is depicted under different emission scenarios, German Meteorological Service, 2022.

### Average surface temperature trend In Spring

#### Schleswig-Holstein & Hamburg

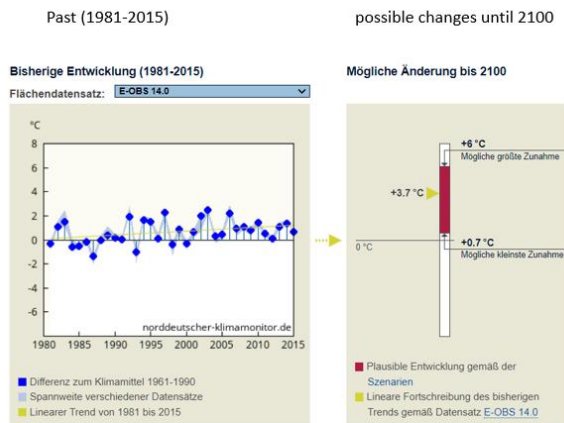


#### Mecklenburg-Vorpommern

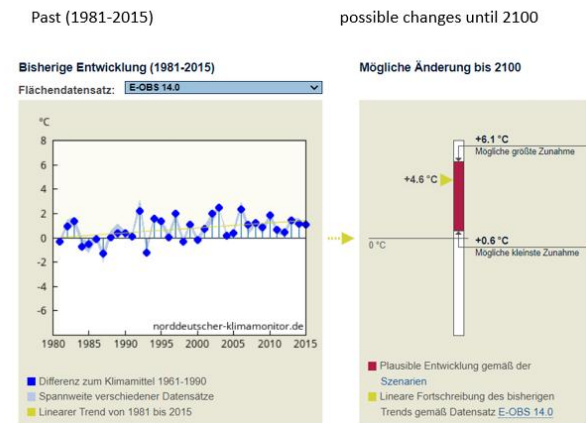


### Average surface temperature trend In Summer

#### Schleswig-Holstein & Hamburg

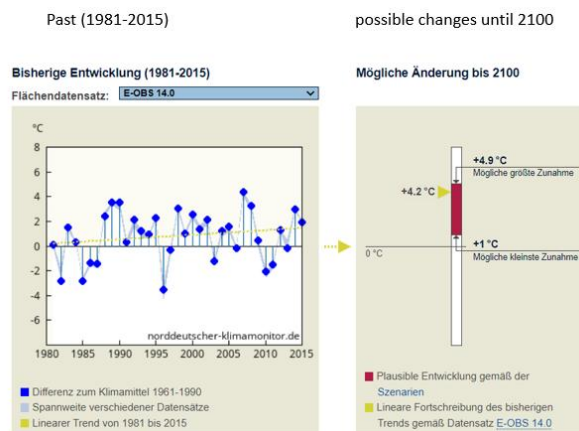


#### Mecklenburg-Vorpommern



### Average surface temperature trend In Winter

#### Schleswig-Holstein & Hamburg



#### Mecklenburg-Vorpommern

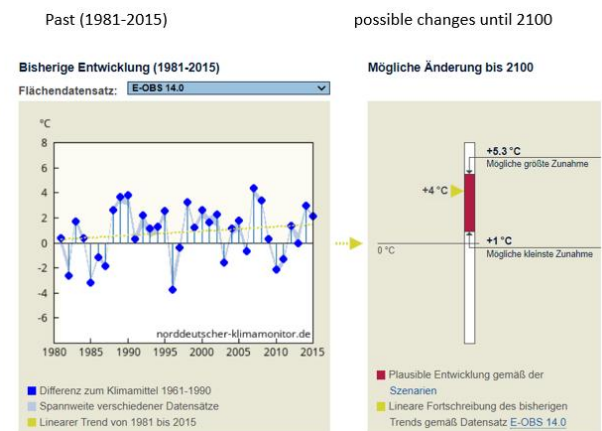


Figure 11, Changes in average surface temperature in the past (1981-2015) and possible changes in the future (-2100), based on data from the ENSEMBLES project, Norddeutscher Klimamonitor, 2022.

In the future, the states of Schleswig-Holstein, Hamburg and Mecklenburg-Vorpommern are predicted to have warmer springs, summers, and winters. In Schleswig-Holstein and Hamburg, the temperature is prognosed to increase by 3.7°C(0.8°C-4.6°C) in Spring, by 3.7°C(0.7°C-6.0°C) in Summer and by 4.2°C(1.0°C-4.9°C) in Winter. In Mecklenburg-Vorpommern the temperature is prognosed to increase by 3.3°C(0.8°C-4.3°C) in Spring, by 4.6°C(0.6°C-6.1°C) in Summer and by 4°C(1.0°C-5.3°C) in Winter.

#### b) Precipitation

The annual seasonal precipitation levels were determined using the tool provided by the German Meteorological Service. The changes in precipitation seasonally are based on the data collected from 1881 until 2022 (Fig. 12). Overall, the precipitation levels show a 'slightly' decreasing trend irrespective of fluctuations during certain years. As of 2022, the precipitation levels recorded during spring in the observed states are as follows: Hamburg with 125L/m<sup>2</sup>, Schleswig-Holstein with 135L/m<sup>2</sup> and Mecklenburg-Vorpommern with 70L/m<sup>2</sup>. These values are lower than the previously recorded average seasonal precipitation i.e., Hamburg (163L/m<sup>2</sup>), Schleswig-Holstein (155L/m<sup>2</sup>) and Mecklenburg-Vorpommern (134L/m<sup>2</sup>). A similar trend was observed during autumn same year. 2022 was recorded as year of ninth-driest spring and third warmest and driest autumn since beginning of data collection in 1881 (DWD, 2022). During summer, the precipitation curve is significantly showing a downward trend whereas during winters the curve traces an upward trend (Fig. 12).

Prognosis of the precipitation trends in the future (2023-2100) were made with respect to different emission scenarios (RCP 2.6, RCP 4.5, and RCP 8.5). According to the dataset from DWD and the ENSEMBLES project, developments like the current precipitation pattern has been observed. For example, the prediction model of the E-OBS 14.0 dataset (ENSEMBLES) shows that in Hamburg and Schleswig-Holstein future springs will be -87% wetter than the reference period (1960-1990) and in Mecklenburg-Vorpommern -74% wetter than the reference period (1960-1990) (Northern Germany Climate Monitor, 2022).



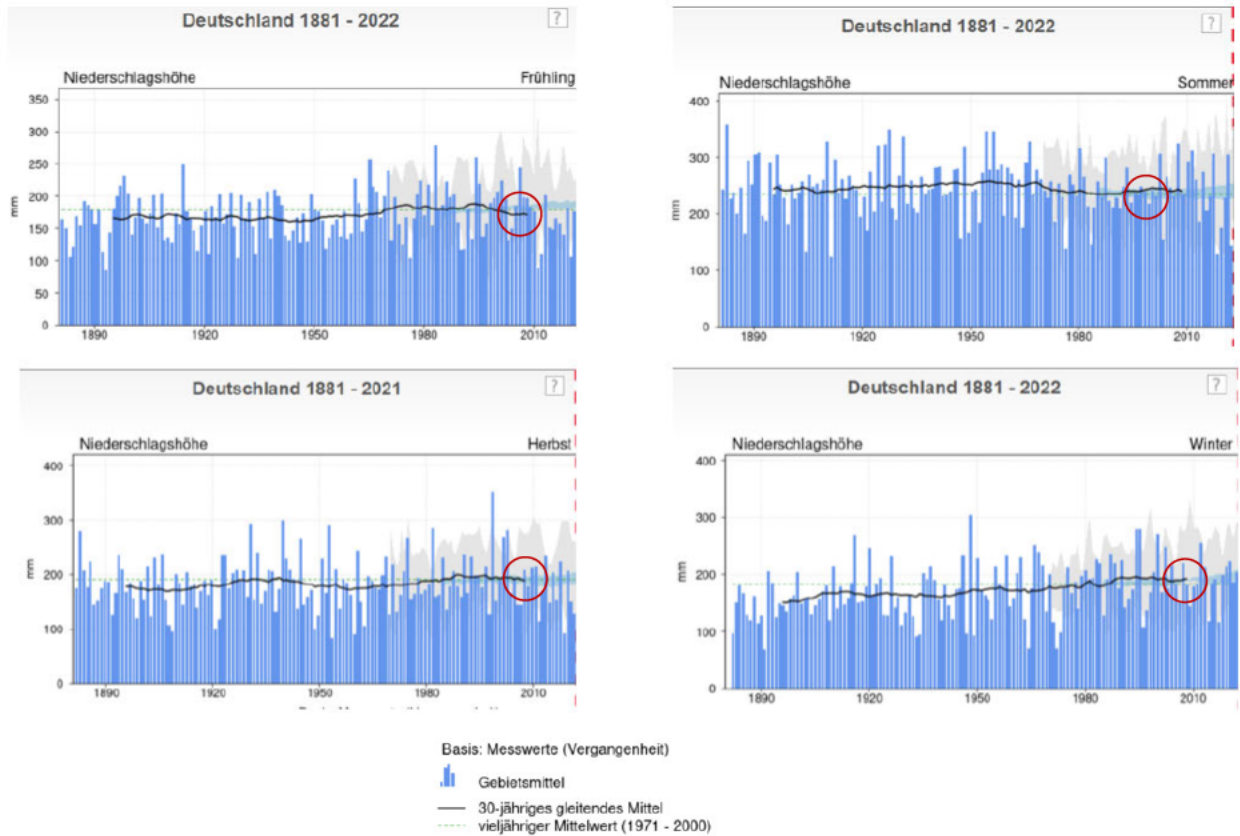


Figure 12, Precipitation level trends during different seasons in Germany from 1881-2022, German Meteorological Service, 2022.

Furthermore, a prognosis on the occurrence of days of heavy rain was considered. Again, here the dataset E-OBS 14.0 and DWD were chosen. According to the predicted trends, the number of days of heavy rain in Schleswig-Holstein, Hamburg and Mecklenburg-Vorpommern are tabulated below.

Table 2 Prognosed no. of days of heavy rain until 2100 in northern Germany, Norddeutscher Klimamonitor, 2022.

States	DWD REGNIE dataset		E-OBS 14.0 dataset	
	Seasons	No. of days of heavy rain	Seasons	No. of days of heavy rain
Hamburg	Spring	0	Spring	-1
	Summer	+3	Summer	+2
	Autumn	-1	Autumn	0
	Winter	+1	Winter	+1
Schleswig-Holstein	Spring	0	Spring	0
	Summer	+4	Summer	+4
	Autumn	-2	Autumn	-2
	Winter	0	Winter	+1
Mecklenburg-Vorpommern	Spring	-1	Spring	-1
	Summer	+2	Summer	+1
	Autumn	0	Autumn	0
	Winter	+1	Winter	+1

### c) Sea Surface Salinity

The changes in sea surface salinity especially of the North Sea and Baltic Sea which stretch through the coast of northern Germany were assessed. The Ocean Viewer tool was used. Data collected by the soil moisture active passive (SMAP) satellite and the real time ocean forecast system (RTOFS) were used. Since the data from RTOFS was available only from 2020 to 2022, the SMAP was used to assess the information from 2015. The changes in sea surface salinity are illustrated below (Fig. 13). The illustration depicts the reduction in ocean salinity over the years and in the coastal regions of northern Germany. According to SMAP, in August 2015 the range of sea surface salinity was 34.84 – 32.65 psu in the North Sea. In August 2022 based on RTOFS this range has declined to 33.76 – 29.50 psu (National Ocean and Atmospheric Administration, 2022).

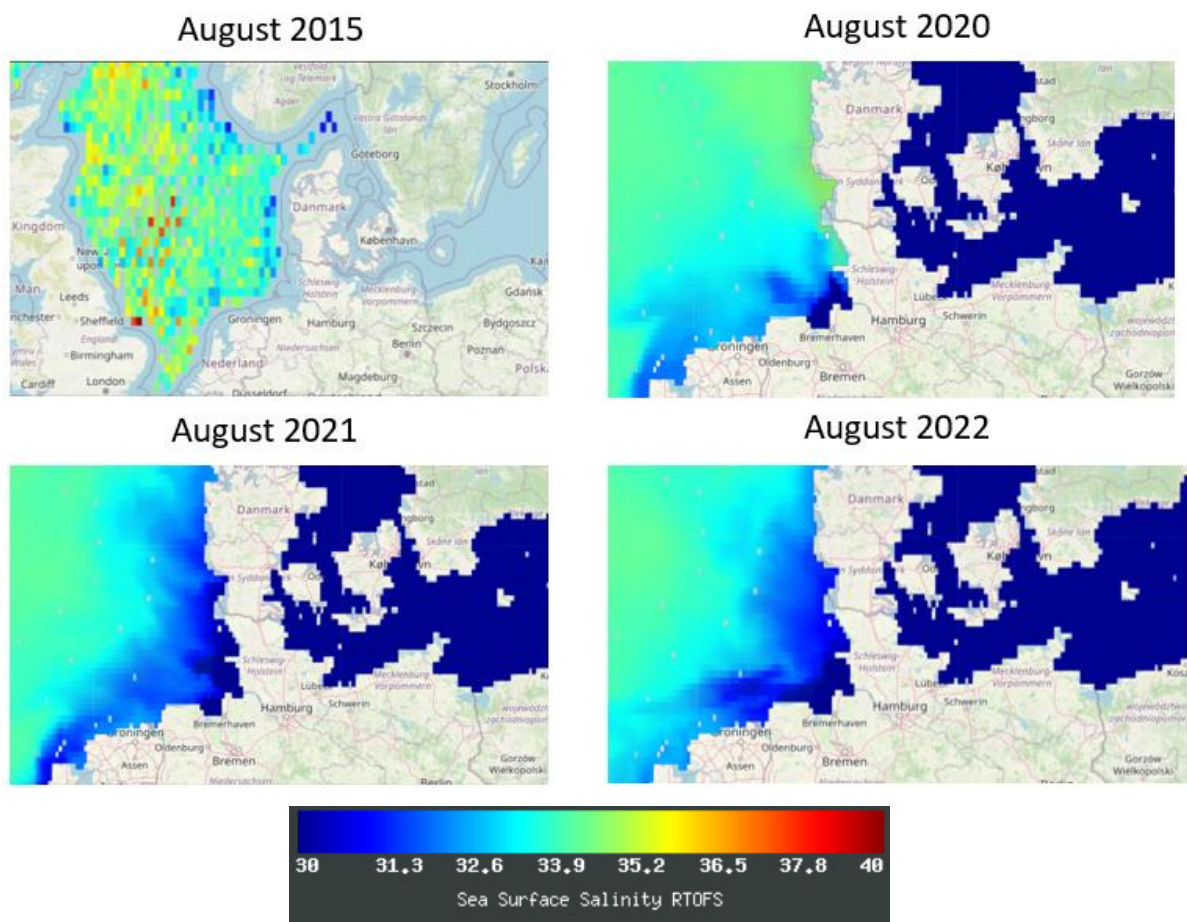


Figure 13, Sea surface salinity of the coast of northern Germany in 2015 (SMAP), 2020 – 2022 (RTOFS), NOAA, 2022.

## 5. Discussion

### 5.1. Interpretation of results and prognostics

As mentioned earlier, rapid climate change alters the fine tunings of an ecosystem. Based on the literature review conducted it is well established that changes in abiotic factors affects the dynamics of pathogens and vectors, thereby influencing EIDs and REIDs in northern Germany.

A key finding that resulted from the literature review was that altered duration of seasons caused by anthropogenic climate change facilitates the re/emergence of infectious diseases. Longer periods of warm temperature facilitate the incubation of pathogens and the proliferation of vectors. Ticks causing Lyme disease, mosquitoes causing haemorrhagic fevers, bacteria causing food poisoning and infections flourish under these prolonged warm conditions. Under current climatic conditions, vectors that are accustomed to the temperate belt such as *Ixodes ricinus*, *A. albopictus*, *C. pipiens* etc. will proliferate formidably. Under future climatic conditions, vectors that are more suited for higher temperatures such as *A. aegypti*, Anopheles mosquitoes, water-borne bacteria will proliferate in northern Europe (including northern Germany), given they are introduced in this region. Rise in annual temperature of about 6-10°C makes the northern hemisphere habitable for climate sensitive vectors and pathogens and thus creating a new ecological niche. Infected vectors will increase in population therefore causing several outbreaks of infectious diseases.

Expansion of geographic range and increase in vector-pathogen-density was also a key finding from the literature review. Certain regions of earth which were once inhabitable for some pathogens and their vectors will become habitable and these previously non-identifiable pathogens will become endemic to these regions. These pathogen and vector dynamics are facilitated by secondary drivers such as trade, travel, tourism etc. but driven by primary factors such as increasing temperature (surface and ocean), fluctuating precipitation levels, and decreasing sea surface salinity. Under current climatic conditions and future climatic conditions, it can be expected that infectious diseases that are identified in other parts of the world might emerge in northern Germany and the existing infectious

diseases might re-emerge seasonally causing seasonal outbreaks. Diseases that have not yet broken out in human ecosystem indigenously (pertaining to northern Germany) like WNV, DENV, CHIKV and Zika might cross the species barrier under future climatic conditions. As seen in Fig. 8, the geographic range of the *Culex* mosquito has expanded. Although currently the viruses (WNV, DENV etc.) have been identified only in farm animals, it must be noted that it is only a matter of time and influence of environmental factors for the pathogen to spillover. FBDs such as Campylobacteriosis and Salmonellosis did not show any geographical shift. This is understandable since FBD outbreaks are point source outbreaks in most cases (Refer 2.2.2.). WBDs caused by bacteria and protozoans (in northern Germany: non-cholera vibrions) may expand their range as well and might be detected in inland waters. As illustrated in Fig. 9, the vibrions have expanded their geographic range over the years. To predict the future outcomes of the vibriion population in the coasts of Baltic Ocean and North Sea, environmental factors must be observed closely.

Based on the observed temperature and precipitation trends from 1881-2022, it can be concluded that regions of northern Germany or Germany altogether have become warmer, wetter, or in some parts drier. Long periods of warm and wet conditions have made northern Germany habitable for the above-mentioned pathogens and vectors. This explains why there have been several outbreaks of the observed EIDs in recent years. Looking at the data for the coming years, certain outcomes of future climate scenario can be expected. Future climatic conditions indicate that springs and autumns are drier, whereas winters are wetter, and summers might fluctuate between wetter and drier conditions. An increase in surface temperature by 2-4°C in northern Germany is predicted for the future. Overall precipitation has reduced over the years and is '*declining*' i.e., regions of northern Germany may face moderate to severe water shortage in the future. According to the dataset E-OBS 14.0, -87% in Schleswig-Holstein and Hamburg and -74% in Mecklenburg-Vorpommern show that precipitation levels might decrease 87% in Schleswig-Holstein and Hamburg and 74% in Mecklenburg-Vorpommern when compared to the precipitation levels in the past (reference period: 1960-1990). According to the graphs produced by the tool developed by DWD (Fig.12) a similar trend is observable. The graph curves for spring, summer

and autumn show a downward tendency, whereas the graph curve for winter shows an upward tendency. To cross-reference with the observations made above, another environmental factor was also taken into consideration. The number of days of heavy rain in the future were observed. In all three states, the no. of days of heavy rain during spring and autumn are lower than the no. of days of heavy rain during summer and winter. This projection is similar to the observation made based on the E-OBS and DWD data for seasonal precipitation. These results could be used to hypothesise that future climatic scenarios consist of wet-warm winters, arid-warm springs and autumns and summers with high temperatures and frequent yet shorter periods of high and low precipitation. These conditions might provide a suitable condition for incubating pathogens, proliferating vectors, facilitated transmission, and spread of infectious disease in human ecosystems.

Sea and ocean salinity was observed to be able to predict and understand the possible developments of water-borne diseases in the northern Hemisphere especially in northern coasts of Germany. As illustrated in Fig. 13, the sea surface salinity has clearly reduced over the years. From 2015 to 2022 the ocean salinity has reduced by a range of 1.08-3.15 psu. Under future climatic conditions this might reduce further. With reducing ocean salinity, the heat capacity of the oceans and seas will also reduce. As a result, the ocean temperature will increase. This scenario could also be interpreted vice-versa i.e., with increasing ocean temperature the ocean/sea salinity recedes, since ocean temperature and ocean/sea salinity are interrelated. This phenomenon provides favourable conditions for certain pathogens to proliferate and establish an ecological niche and as a result, an increase in outbreaks can be expected (for example those caused by non-cholera vibrios). These outbreaks might be more frequent during summer than during other seasons. Although, if the ocean temperature during future autumns and springs continues to stay warm, infections/outbreaks of non-cholera vibrios during springs and autumns can be expected as these pathogens are climate sensitive.

Diseases such as HIV, Monkeypox, SARS etc. which are fundamentally acquired through travel and trade might not become indigenous in northern Germany but

might continue to prevail as epidemics or pandemics. So far there is almost no evidence suggesting that HIV, SARS and Monkeypox are driven by environmental factors in northern Germany. The possibility of mitigating and eradicating these deadly diseases exists, given that advancements in the field of public health are made.

Under previous climatic conditions, northern Germany was not one of the global hotspots for emerging and re-emerging infectious agents and diseases. Therefore, most of the infectious diseases were travel-acquired or behaviour-acquired. Currently, even though northern Germany is not one of the global hotspots for infectious agents and diseases, changes in climate and microclimate allows the pathogens and vectors, which were formerly travel-acquired, to habituate and proliferate, thereby finding new ecological niches. Under future climatic conditions, it can be hypothesised that these ecological niches might be more pronounced and more in number, making northern Germany a suitable habitat. Whether northern Germany will become an infectious disease hotspot or not, is still far-fetched.

## 5.2. Limitations

This work allows to gain an overall understanding of the past, current and future status of the northern German states with respect to EIDs and REIDs. However, most of the significant EIDs were mostly arboviral i.e., vector borne with focus on tick- and mosquito borne diseases. Other arthropod vectors such as phlebotomies and mammals such as rodents were not investigated. Due to the chosen geographic scope not much data was available on REIDs such as Malaria, Monkeypox, etc. and their development over the years.

This work focuses on the environmental factors of climate change that drive the emergence and re-emergence of infectious diseases. Although the environmental factors are primary drivers for disease emergence, secondary drivers of climate change were not explored in detail. Increased human activity due to globalization and urbanization are important secondary drivers since many non-indigenous EIDs and REIDs were/are introduced to northern Germany through travel, trade, tourism etc. Best examples of this are outbreaks of SARS (Cov1 and Cov2),

Malaria, WND, Monkeypox etc. Apart from the environmental perspective, a social perspective must also be noted. For example, more outbreaks or infections occur/might occur frequently during summer and warm conditions, because people tend to spend more time in nature and undertake outdoor recreational activities than in winter or cold conditions. This increases the chances of disease contraction, -transmission and its spread.

In addition, EIDs and REIDs caused due to antimicrobial drug resistance and those that are nosocomial in nature have not been explored in this work. It must be noted that re-emergence of deadly diseases such as drug-resistant TB and HIV due to rise in antimicrobial drug resistance is of increasing importance and will have great burden on health systems and populations in the future, if not addressed in time.

The collected climate data delivers not only an overlook of the climate trends in northern Germany but also provides information on the future climate scenarios for northern Germany. It must be noted that there might be deviations since the dataset accessed from Norddeutscher Klimamonitor dates only until 2015 unlike the data obtained from the German Meteorological Service which is up to date. In addition to this, the interpretations made based on the regional data is somewhat in contrast to the predictions made by the European Environmental Agency (EEA). The EEA published in 2020 that the consequences of climate change for the European continent will be as grave as the rest of the world. The frequency, duration and severity of meteorological and hydrological droughts were projected to be prominent in most of Europe, except parts of northern Europe which are more likely to be flooded in the following years. Projections of severe drought and drought induced loss by 2100 in southern Europe were made. Following this, projections of forest fires in Scandinavia, heavy rains and flooding in Central Europe, severe drought in the Mediterranean, coastal flooding in port cities like Venice, storms and hurricanes surges in France in the next 50 years were also made (EEA, 2020). Based on the data collected, the outlook for northern Germany in the future consisted of wet-warm winters, arid-warm springs and autumns and summers with alternating dry-warm and wet-warm periods. To gain a better understanding of this difference, microclimates must also be drawn for closer

inspection. Both regional and national climate scenarios must be further investigated so that precise predictions and forecasts can be made.

This work focuses only on certain environmental and climatic factors such as surface temperature, precipitation and ocean salinity. It fails to explore other environmental factors which are also highly caused due to anthropogenic climate change i.e., air pollution, fine particle emission etc. Research in understanding how these factors might influence the dynamics of infectious diseases is needed.

### 5.3. Recommendations – an interdisciplinary approach

To control and prevent the impact of infectious diseases on human health, several strategies and clinical advancements were made over the centuries. Beginning from adopting better hygiene practices and proper sanitation in living spaces to discovery of vaccines and drugs, various methods have been developed to ensure health. But recent pandemics and epidemics show that a much more unified approach should be adopted since controlling infectious diseases is multi-disciplinary. Therefore, in this work the One Health Approach will be chosen to explore the various factors governing the control and prevention of R/EIDs. The One Health Approach highlights that the understanding of the interaction between human health and wildlife health and the environment is a crucial component of global disease prevention, surveillance, control and mitigation, especially zoonotic infectious diseases (Mackenzie & Jeggo, 2019, P 1). Several factors such as animal food supply chain, human induced climate change, geographic range shift of certain species etc. are found to be drivers of the emergence of zoonotic infectious diseases. By understanding these interactions and assessing the intensity of these interactions, a much rapider response to controlling the factors which lead to the emergence of zoonotic infectious diseases is possible. The Swedish University of Agricultural Sciences in cooperation with One Health Sweden developed a pictorial representation to better understand the concept of One Health (Fig. 14). For example, the factors that lead to the emergence of food-borne infectious disease such as the one caused by *Salmonella* or *Campylobacter* can be controlled rapidly by implementing measures based on the One Health Approach. Revised (animal) food safety procedures, advanced surveillance systems, better rearing environment for livestock etc. must be adopted to control



the emergence of a *Salmonella* or *Campylobacter* outbreak. For this to be achieved, an interdisciplinary cooperation of sectors such as Public Health (disease mitigation, monitoring and surveillance, and investigating disease emergence), Agriculture and Animal Husbandry (detecting infected livestock, curing them and improving infrastructures), Food Safety and Regulations (detecting infected product and stopping further distribution), Veterinary Science (curing diseased livestock and understanding the disease), Climate Science (understanding environmental changes and factors that facilitated the disease development), Molecular and Microbiology (understanding the infectious agent), etc. is needed.

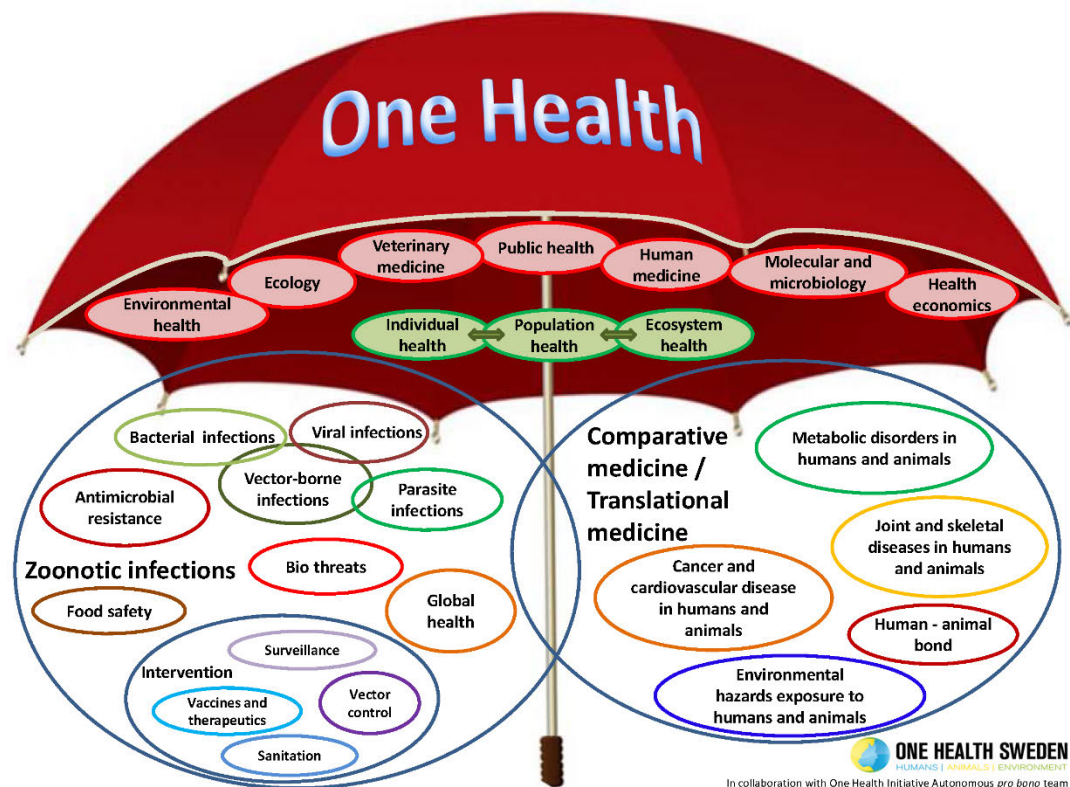


Figure 14, The One Health Umbrella, Mackenzie & Jeggo, 2019, P. 2.

## 6. Conclusion

It is clear that the emergence and re-emergence of infectious diseases are driven by climate change. Extreme weather conditions and rapidly changing environment directly affect the biodiversity, ecosystems and with that the phylogenetic composition of pathogens. As a result, several infectious diseases emerge and re-emerge over time, impacting human and animal health. Although statistically

infectious diseases represent a smaller fraction of causes of global mortality when compared to non-communicable diseases, their unpredictability and uncontrollable nature of infectious disease outbreaks makes them lethal as ever, thereby causing a huge burden on human lives. Recent example for this is the SARS-Cov-2 pandemic. Based on the findings of this paper, the burden of EIDs and REIDs driven by climate change is and will be great on human health and well-being. In the case of northern Germany, arboviral and bacterial EIDs and REIDs will be preceding the others predominantly. Since the pathogens and vectors identified in northern Germany are climate sensitive, the change in vector-pathogen density, geographic range and distribution, seasonality can be expected. Travel-acquired EIDs and REIDs for example, respiratory or immune disorder syndromes might not become indigenous to northern Germany i.e., undergoing phylogenetic mutations and breaking out as new strains or diseases in northern Germany. In contrast, their prevalence and incidence might increase. However, there remains a possibility that under future climatic conditions this supposition might alter. Therefore, the need for preparedness and swift response to control and mitigate the spread of infectious diseases exists and is of top priority. One of the best approaches for being prepared for catastrophes that is driven by climate change would be the One Health Strategy. This interdisciplinary approach as explained previously is not only sustainable but also essential since human/animal health and the environment are interrelated. Therefore, cooperation from various fields such as developing advanced technology for better prognosis on unpredictable and extreme weather events, better risk and crises management and warning systems in case of global pandemics and catastrophes, discovering innovative drugs, vaccines, and therapy options, etc. would help mitigating the burden on human and animal lives. In addition to the above-mentioned points, it must be understood that it is not realistic to assume that EIDs and REIDs can be completely eradicated. But with preparedness and development in the field of public health the burden of EIDs and REIDs can be alleviated.

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## Declaration

I hereby declare that I have written this thesis independently and have not used any sources or aids other than those indicated, that all statements taken verbatim or in spirit from other writings are clearly marked and that the thesis was not part of a course or examination in the same or a similar version.

Jeyasree Rameshanand



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Hamburg, 13.03.2023