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The Future of Vector-Borne Diseases

A geographical analysis of the influence of climate change on the outbreaks of vector-borne diseases

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Abstract

Since the outbreak of the SARS-CoV-2-pandemic in the beginning of 2020, climate scientists and epidemiologists warn that this pandemic could only be the beginning of a series of large epidemics and pandemics in the future. One factor massively contributing to this development is climate change. Using variables of climate change from the CMIP6 climate projections-catalog and geographic data on outbreaks of eight vector-borne diseases from 1950 to 2020, this study aims to predict the number of outbreaks of these diseases for the years 2050 and 2100 by means of Machine Learning. Even though no other relevant independent variables than the climate-related ones were used for the analysis, the results are clear. Consistent with other studies, the analysis shows that the number of outbreaks of vector-borne diseases increases in regions that already suffer from vector-borne diseases and that neighboring regions will slowly become affected by these dynamics as well.

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1   Introduction

The first half of the 21*st* century will strongly be defined by a catastrophe whose nature and severity almost no person alive has ever experienced before; the SARS-CoV-2-pandemic. The first suspected cases of humans being infected by SARS-CoV-2 were reported in December 2019 in the province Wuhan, China. In January 2020, the new virus string was identified as one of the *Coronaviridae*-family (Organization et al. 2021).

In the following months, SARS-CoV-2 has spread throughout the world and became the most severe pandemic since the Spanish Flu. Starting in March 2020, the first countries implemented political measurements that were previously only known from movies in the cinemas, like strict lockdowns. Millions and millions of people had to isolate themselves and were only allowed to leave the house for the most basic activities, like grocery shopping. Newspapers were filled with news articles, reports and interviews with epidemiologists and statisticians who each week gave forecasts that were worse than the day before. Two years later, the pandemic is still ongoing, however, humans started to live with it and other topics besides the pandemic started to fill the newspapers again.

But, many epidemiologists and climate scientists are warning that this SARS-CoV-2-pandemic is only the start of a series of epidemics and pandemics the world will face in the future. One major reason for their grim forecasts is the human-made climate change. The global temperature is getting warmer and warmer which naturally leads to a shift of climate zones. Climate zones that are already characterized by their warm temperature will become warmer and those that are characterized by rather cold temperature will become warmer as well.

Unlike SARS-CoV-2, many diseases are transmitted by vectors, like mosquitoes. They become the hosts of pathogens by biting and drinking the blood of infected animals. After the vectors become the hosts of the pathogen, they bite humans. This process of biting transmits the pathogen from the vectors into the blood of the bitten humans and humans become infected. After a certain period - the incubation period - the first symptoms of the disease appear. The problem is that the human is infectious even though the symptoms of the disease have not shown up yet. Even though SARS-CoV-2 is not a virus transmitted by vectors, infected humans are infectious before showing symptoms, too.

Many of these vectors, like mosquitoes, breed in warm temperate, (sub)tropic regions like South America, Africa and South East Asia. Prior to climate change, literally all outbreaks of the diseases caused by a virus transmitted by mosquitoes occurred in those regions. Since the human-made climate change, outbreaks of these diseases were reported in other regions as well. Climate scientists and epidemiologists explain this geographic shift by climate change resulting in a higher number of possible breeding grounds for vectors.

In this thesis, I estimate how climate change will affect the number of outbreaks of vector-borne diseases in 2050 and 2100 under the RCP8.5-scenario. Even though the results show a general tendency, they have to be interpreted with caution. Many factors beside climate-related ones influence the spread and severity of outbreaks of vector-borne diseases as well. Furthermore, for simplicity, I only focus on those viruses and diseases that are transmitted through mosquitoes. The main reason for only taking mosquitoes into consideration is that the viruses they transmit are the most familiar and potentially most dangerous ones.

The thesis is organized as follows: Sections 2, 3 and 4 give an overview and explanation on climate change, vector-borne diseases and the connection of climate change and vector-borne diseases. Section 5 walks through the dataset on climate change and the dataset on vector-borne diseases. Section 6 shows the results of the study and section 7 elaborates on the limitation of the study. Finally, section 8 concludes.

2   Climate Change

There exist many definitions of climate change. The most suitable one probably comes from the United Nations Framework Convention on Climate Change which defines climate change as follows:

[Climate Change]...refers to a change of climate that is attributed directly or indirectly to human activity that alters the composition of the global atmosphere and that is in addition to natural climate variability observed over comparable time periods (UNFCCC 2011).

Other institutions and organizations, like the Intergovernmental Panel on Climate Change (IPCCC), define climate change in the same article as not necessarily

human-made. Even though the details of the definitions of climate change differ from organization to organization, one detail is the same in all of them: Human behavior influences it. In order to get a picture of how these dynamics work, I will begin this section with a historical introduction into the scientific research on climate change.

2.1   A History of Climate Change

To fix a date of when research on climate change was first conducted is difficult, but I think a good starting-point to describe the history of the research on climate change is Jean-Baptiste Joseph Fourier. He was a mathematician and physicist who worked for Napoleon Bonaparte in the beginning of the $19th$ century. In 1824, he was the first scientist that described that planet Earth would be a very cold planet if it were not for the Earth's atmosphere that retains the warmth on the planet. To explain this concept in a more picturesque way, Mr. Fourier compared the atmosphere's function to the one of the glass walls of a greenhouse (Fourier 1824).

In 1859, John Tyndall, a British physicist, discovered that while almost all of the gases the atmosphere consists of (nitrogen and oxygen) do not have the ability to trap heat, three other gases (carbon dioxide, ozone, and water vapor) do (Tyndall 1861). In 1938, the British coal engineer George Callendar gathered the data of all measurements on carbon dioxide over the previous 100 years and discovered that the values were increasing. Additionally, he discovered that the increase of the carbon dioxide-values positively correlates with the air temperature (Callendar 1949).

One of the most fundamental projects to monitor the concentration of carbon dioxide in the atmosphere had been initiated by Dr. Charles David Keeling in 1956. He was the first person who was able to show that the concentration of carbon dioxide is positively correlated with the emissions of fossil fuels (Keeling 1973). When Mr. Keeling started to take air samples in order to investigate the amount of carbon dioxide in it, he noticed that the samples he took in the nights contained a higher concentration of carbon dioxide than the samples he took during the days. He concluded that this pattern results from the process of photosynthesis as plants use carbon dioxide during the day to photosynthesize and release it during the nights. Mr. Keeling further noticed that there is a large seasonal pattern as well; the concentration of carbon dioxide is highest in spring, when plants decompose and release gas into the air, and is lowest in autumn, when plants do not photosynthesize anymore and therefore do not need carbon dioxide (this explains the within-year fluctuation in

Figure 1). After the value of Mr. Keeling's work had been discovered, he established a permanent residence at the Mauna Loa Observatory in Hawaii, United States of America to continue his research. There, Mr. Keeling found that the carbon dioxide levels are rising almost every year which he attributes to the rise of fossil fuels (*The Keeling Curve* 2019). In 2005, the physicist Charles F. Kennel honoured Keeling's work that "*They [the data] are the single most important environmental data set taken in the* 20*th century.*" (*Obituary Notice: Climate Science Pioneer: Charles David Keeling* 2005).

Keeling–Curve (from 1958 to 2021)
Monthly Data on Carbon Dioxide Concentration (parts per million)
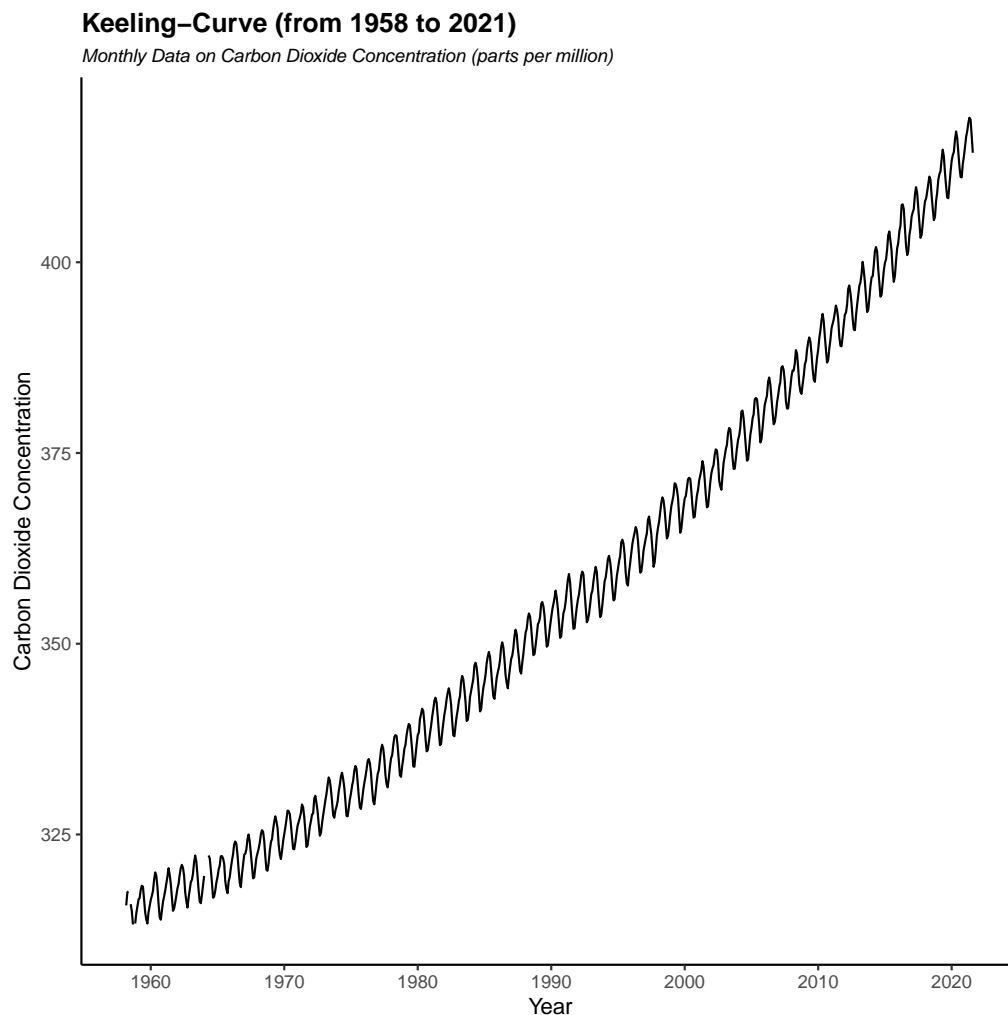
Figure 1: Keeling-Curve: Monthly observations of carbon dioxide concentration in parts per million from January 1958 to August 2021 (Keeling et al. 2005).

Around the same time the impact and value of Mr. Keeling's work had been realized, a number of studies had been conducted that investigated the impact of global warming and climate change. In 1972, Mrs. Yamamoto and Tanaka found that air pollution leads to an increase of the global albedo[1] which led to a cooling effect on the earth-atmosphere system and a temporary stop of global warming (Yamamoto and Tanaka 1972). A number of countries have implemented clean air legislations which reduced air pollution and increased the quality of human life on the one hand, but continued global warming on the other hand. This continuation of the global warming contributed to the emergence of serious weather events, like the Heat Wave in Europe of 2003 which resulted in more than 3,000 deaths (García-Herrera et al. 2010).

The climate change especially affects the Arctic. The Arctic is warming three times faster and in size than the global average. The reason is that the melting of the ice and snow exposes darker surfaces which increases the amount of solar energy absorbed (albedo effect). These dynamics have a tremendous effect on global eco systems and the climate itself. Melting sea ice influences the radiation balance in the global climate system through the albedo effect. The warming leads to changes of the bottom water formation which impacts the ocean systems and the Earth's climate. Melting glaciers lead to a rise of the sea level and the thawing permafrost releases greenhouse gases which are the fuel for global warming (*Climate change in the Arctic* 2021).

2.2   The Drivers of Climate Change

Historically, the climate of the planet Earth varied quite often, even before the human race existed. The sun's energy is one of the most important contributors to climate change because its energy is not constant and this variation influences the climate. Furthermore, the changes of the Earth orbiting around the sun influence climate as well. One last natural driver, I would like to mention is volcano eruptions which, depending on how the sunlight interacts with eruption, warm or cool the surface of the Earth. In the planet Earth's history, these climate changes occurred very slowly, over millions of years. However, the current climate is changing a lot more rapidly and the reason for this are human activities (*What causes the Earth's climate to change?* 2021).

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[1]Albedo is a measure of a surface's ability to reflect sunlight.

I have already discussed in the previous subsection that the massive increase of carbon dioxide - especially since the 1970s - is the huge human-made contribution to climate change. This is because in the 1970s, the consumption of fossil fuels (coal, gas, oil) started to increase massively. Also deforestation played a large part in the increase of carbon dioxide as forests save carbon dioxide and it usually resides there for centuries. Natural processes to restore the balance of the carbon cycle were too slow compared to the rates at which humans produced carbon dioxide. The amount of carbon dioxide therefore accumulates in the atmosphere and will remain there for thousands of years (*Climate Change: Evidence and Causes: Update 2020* 2020).

Global fossil fuel consumption

Global primary energy consumption by fossil fuel source, measured in terawatt–hours (TWh)

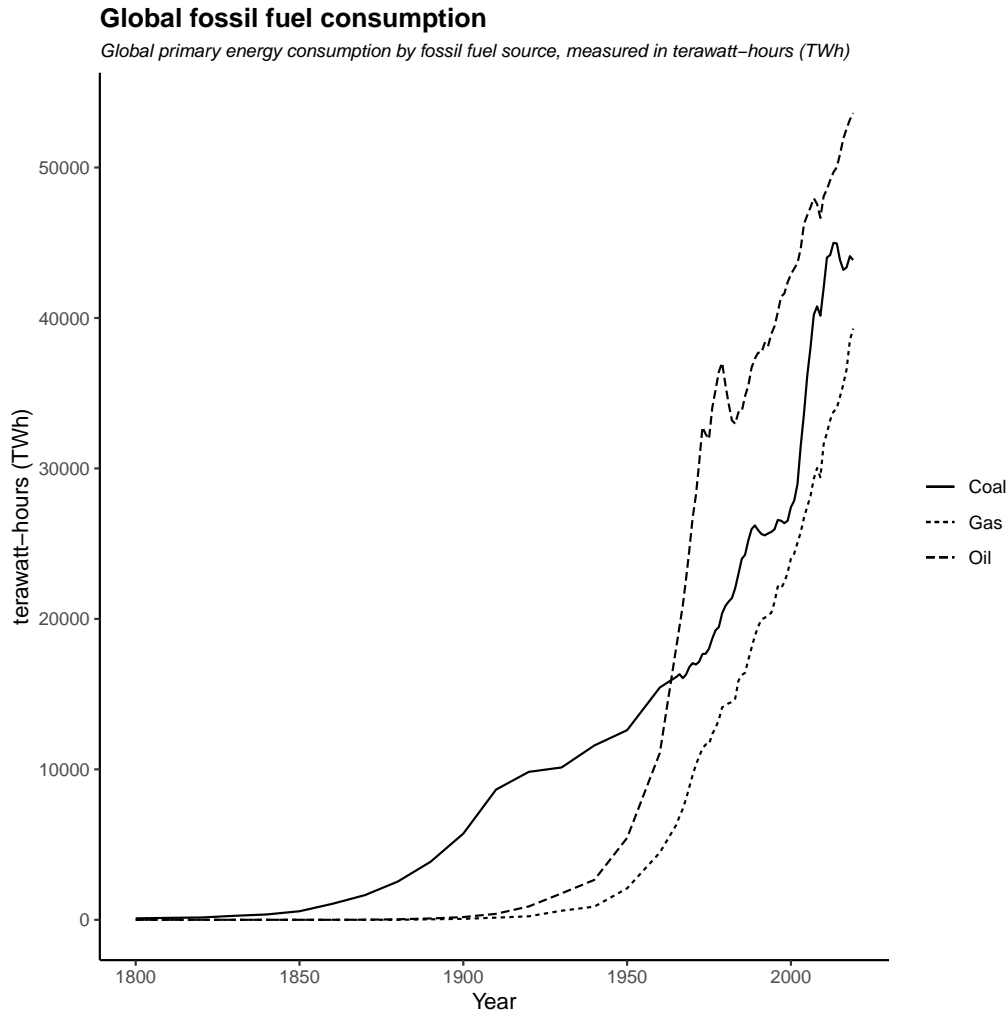Figure 2: Global primary energy consumption by fossil fuel source, measured in terawatt-hours (TWh) (Ritchie and Roser 2020).

3   The Connection of Climate Change and Epidemics

It is scientific consensus that climate change impacts infectious diseases. Generally, the current climate change in the form of global warming is predicted to lead to more frequent and severe disease impacts, however, a subset of pathogens could also

decline with global warming as well (Harvell et al. 2002).

Interestingly, those studies suggest that climate change does not necessarily expand the suitable habitat of species that are often hosts of infectious diseases but rather shifts the geographical range. This can be explained as species often have an upper and lower limit of tolerating temperatures. Another reason that speaks in favor of geographical shifts is that an increase of the habitat's suitability does not necessarily result in an increase of geographical distribution because other factors besides climate change like competition and predation among those species come into play. It is possible that past control efforts to prevent the spread of a disease and reduction of biodiversity through climate change might even lead to a net decline of infectious diseases (Lafferty 2009).

Most likely, climate change will affect the vector stages of pathogens, or *vector-borne diseases* as rising temperatures will affect the distribution of the vectors, the parasite development, and the transmission rates (Harvell et al. 2002). Cook 1992 found that an increase of the mean ambient temperature in central Africa by 2°C would result in the tsetse fly[2] relocating from the Middle Belt of Africa (mainly Nigeria) southwards spreading to the Forest Belt in Western Africa. The increase of temperatures also affects the behavior of the vectors itself. It has been found that the vector reproduction rate, vector population growth, biting rate and the period of infectivity positively correlates with temperature (Harvell et al. 2002). A study conducted by Linthicum et al. 1999 reveals that it is possible to forecast Rift Valley Fever[3]-epidemics in East Africa five months prior to the outbreak by using data on abnormally high rainfall, abnormal Pacific and Indian Ocean sea surface temperatures and satellite normalized difference vegetation index data.

Scientifically, there apparently exists strong evidence that climate change leads to geographic shifts in the number of outbreaks of vector-borne diseases. Before I elaborate on how I approach the analysis of this connection methodically, I give a general overview on vector-borne diseases and briefly present the eight diseases used in this study.

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[2]The tsetse fly is, among others, the host of the Sleeping Sickness (T. brucei gambiense/rhodesiense).

[3]The Rift Valley Fever is a virus transmitted through two mosquito vectors - *Culex tritaeniorhynchus* and *Aedes vexans*.

4 Vector-Borne Diseases

According to the World Health Organization, vectors are organisms that are able to transmit infectious pathogens either between humans or from animals to humans. A majority of these vectors are insects that absorb disease-producing microorganisms during a blood-meal from an infected host. When this disease-producing microorganism (pathogen) has replicated, the vector transmits the pathogen through biting into a new host. These transmitted pathogens can take the form of parasites, viruses, and bacteria and cause - if the new host is a human - human illnesses (vector-borne diseases). Globally, more than 700,000 deaths are caused by vector-borne diseases every year. More than 50% of these deaths (400,000) are caused by the parasitic infection Malaria with estimated 219 million cases annually. The most prevalent viral vector-borne disease is Dengue with estimated 96 million symptomatic cases and 40,000 deaths per year (*Vector-borne diseases* 2020).

The list of vectors that transmit vector-borne diseases is long. For this study, however, I will only focus on mosquitoes as the diseases they transmit are among the most well-known and the most dangerous ones. Table 1 gives an overview on the most important mosquito-types in this setting and the diseases they transmit.

Vector		Disease Caused	Type of Pathogen
Mosquito	Aedes	**Chikungunya**	Virus
		Dengue	Virus
		Lymphatic filariasis	Parasite
		Rift Valley Fever	Virus
		Yellow Fever	Virus
		Zika	Virus
	Anopheles	Lymphatic filariasis	Parasite
		Malaria	Parasite
	Culex	**Japanese Encephalitis**	Virus
		Lymphatic filariasis	Parasite
		West Nile fever	Virus

Table 1: Excerpt of a non-exhaustive list of vector-borne diseases transmitted by mosquitoes, ordered according to the type of pathogen that causes the disease in humans (*Vector-borne diseases* 2020).

Unfortunately, a record of the appearance of vectors does not exist which is the reason why I will only focus on the diseases transmitted by mosquitoes. As otherwise this study would go beyond the scope of a master thesis, I will only focus on the eight diseases highlighted in Table 1. The rest of this section gives a brief overview on each these eight vector-borne diseases.

4.1   Chikungunya

The Chikungunya-virus has first been described during an outbreak in Tanzania 1952 and led to occasional outbreaks in Africa and Asia in the following half decade. In 2004, an outbreak of Chikungunya in Kenya spread to locations in the Indian Ocean and further to India where around 1.5 million people got infected over the following years.

In 2007, the first transmissions in Europe were reported during an outbreak in Italy. This incident confirmed the theory that outbreaks of Chikungunya are plausible in Europe. 2013 is the year with the first documented outbreak with autochthonous transmissions in the Americas, more specifically on the Caribbean island Saint Martin. Europe faced the highest number of Chikungunya infections in 2014 with 1,500 confirmed cases.

The mosquitoes which are most commonly involved in the transmission of Chikungunya are *Aedes aegypti* and *Aedes albopictus*. While Aedes aegypti's breeding ground are coconut husks, cocoa pods, bamboos stump, tree holes and rock pools in the tropics and subtropics, Aedes albopictus live in a range of water-filled breeding sites in temperate and cold temperate regions.

The illness induced after the bite of an infected mosquito usually occurs within four to eight days. The characteristic of Chikungunya is the abrupt onset of fever which is many times accompanied by joint pain. As this joint pain can last for a few days but also for years, the Chikungunya-virus can cause an acute or a chronic disease. Usually, the symptoms are mild and the infections go unrecognized or is misdiagnosed which is rarely fatal as Chikungunya is hardly life threatening. Even though the joint pain can last for months or even years for some patients, the majority of patients fully recover from the disease. Furthermore, it is likely that recovered humans are immune from future infections (*Chikungunya* 2020).

4.2   Dengue

The spread of Dengue exploded only in the recent decades. Prior to 1970, only nine countries had officially reported severe Dengue epidemics. Today, Dengue is endemic in more than a hundred countries on basically every continent except Europe and Oceania.

However, unlike in the past decades, the threat of an outbreak now also exists in Europe. In 2010, France and Croatia reported their first local transmissions and imported cases from the two countries were detected in three other European countries. After an outbreak of Dengue on Madeira islands with 2,000 cases in 2012, even ten European countries reported imported cases.

Equivalent to Chikungunya, Dengue is transmitted to humans through bites of

an infected female mosquito, mainly by the Aedes aegypti.

The majority of humans infected by Dengue show no or mild symptoms and the disease only seldomly leads to death. The incubation period lasts for four to ten days and the symptoms last for two to seven days. In severe cases, Dengue leads to high fever (approximately 40°C) and is usually accompanied by symptoms like severe headache, pain behind the eyes, nausea or swollen glands (*Dengue and severe dengue* 2022).

4.3   Japanese Encephalitis

As the name of the disease indicates, Japanese Encephalitis was first document in Japan in 1871 and has become the most important cause of viral Encephalitis in Asia. It is estimated that there are approximately 68,000 clinical cases of Japanese Encephalitis every year with 17,000 deaths. This virus primarily affects children as most adults have a natural immunity after being infected in childhood.

The Japanese Encephalitis is transmitted to humans through bites of the mosquito species *Culex*. Currently, 3 billion people in 24 countries in South East Asia and the Western Pacific region experience an increased risk of transmission.

Most of the Japanese Encephalitis-infections progress with no symptoms or only mild ones, like fever and headache. However, around 0.4% of all infections result in clinical illness. Mild clinical cases suffer from gastrointestinal pain and vomiting whereas severe cases are characterized by neck stiffness, disorientation, seizures and death. Of the 70% who survive the disease, 20 to 30% end up with a permanent disability like paralyses, recurrent seizures and the inability to speak (*Japanese encephalitis* 2019).

4.4   Malaria

Unlike the other vector-borne diseases I investigate in the thesis, Malaria is the only one caused by a parasite instead of a virus. These parasites (*Plasmodium*) are transmitted through bites of female *Anopheles* mosquitoes to humans.

Malaria is one of the most widespread diseases with half of the world's population

at risk in 2020. In the same year, there were more than 240 million cases of Malaria with around 627,000 deaths. Especially Africa has an extremely high Malaria death toll with Subsahara Africa accounting for more than 90% of the worldwide Malaria deaths. Negatively impressing is the fact that only four African countries accounted for half of the global Malaria death toll in 2020 with Nigeria (31.9%), the Democratic Republic of the Congo (13.2%), United Republic of Tanzania (4.1%) and Mozambique (3.8%).

The challenge in diagnosing Malaria is that the first symptoms of Malaria which are fever, headache and chills are often mild and therefore not recognized as being symptoms of Malaria. When left undetected and untreated, Malaria can lead to severe illness and death within 24 hours (*Malaria* 2022).

4.5   Rift Valley Fever

The Rift Valley Fever is a zoonosis that primarily affects animals, but it is also capable to infect humans. As this type of virus mainly affects animals, high economic losses result in the geographic area as the infected animals need to be slaughtered in order to prevent animal-to-animal and animal-to-human transmissions.

The virus was first detected in an epidemic among sheep on a farm in the Rift Valley in Kenya in 1931. In the aftermath, the virus was named after this geographical region. Since its discovery, many outbreaks have been reported in Subsahara Africa. In 1977, a large outbreak of the Rift Valley Fever was reported in Egypt after livestock got infected along the Nile irrigation system. In September 2000, infected livestock from the horn of Africa spread the Rift Valley Fever-virus to Saudi Arabia and Yemen leading to the first reported cases of this disease outside Africa.

Most of the human infections are a result from humans being in direct or indirect contact with the organs and blood of animals infected by the Rift Valley Fever-virus. However, there are reports that show that human infections resulted from bites of infected mosquitoes (Aedes and Culex), too.

Humans infected by the Rift Valley Fever-virus usually experience no to mild symptoms like flu-like fever, muscle pain, joint pain and headache. Neck stiffness, sensitivity to light and the loss of appetite are also possible symptoms. It is also possible for humans to experience the severe form of the Rift Valley Fever with one of

the following symptoms: ocular (eyes) diseases, meningoencephalitis or haemorrhagic fever. Most infected humans that suffer the severe form of Rift Valley Fever die if they develop a haemorrhagic fever (*Rift Valley Fever* 2018).

4.6   West Nile Fever

The West Nile Fever-virus can jump to humans during the transmission cycles between birds and mosquitoes. As with many other viruses, the West Nile Fever-virus got its name from the location of its detection; it was discovered in a woman in the West Nile district of Uganda in 1937. In 1999, the West Nile Fever-virus was imported from Israel and Tunisia to New York which ultimately led to a dramatic spread and outbreak on continental United States of America. Also Europe was not spared from the disease with large outbreaks occurring in Greece, Romania and Russia.

As explained in the beginning of this subsection, the human infection results when a mosquito bites a human after feeding on an infected bird. Until today, no human-to-human transmission through casual contact has been documented.

80% of humans infected with the West Nile Fever-virus experience no symptoms. The remaining 20% develop the West Nile Fever with symptoms like fever, headache, tiredness, body aches, nausea and swollen lymph glands. The severe form of West Nile fever which occurs in 0.6% of the infected patients additionally includes symptoms like neck stiffness, disorientation, coma and paralysis (*West Nile virus* 2017).

4.7   Yellow Fever

Yellow Fever originates in Africa and South America and is endemic in 47 countries. The Yellow Fever-virus is also transmitted by mosquitoes from the Aedes-species. The name of the disease comes from a phase of the illness some infected patients experience.

Generally, most humans infected with Yellow Fever do not show any symptoms. If humans have symptoms, the most common ones are fever, muscle pain with back ache, loss of appetite or vomiting. A minority of the patients enter a more severe phase during the recovery of the previously mentioned symptoms. In this second

phase, the fever returns and the liver and/or kidneys get affected. If this happens, the skin and eyes of the patients will turn yellow ('yellow' as in yellow fever) and the patients develop dark urine and abdominal pain with vomiting. It is also possible that patients in this severe phase bleed from the mouth, nose, eyes or stomach. 50% of the patients who enter this second phase die within seven to ten days (*Yellow fever* 2019).

4.8   Zika

Primarily, the Aedes aegypti is responsible for infecting humans by biting them. The mosquitoes themselves become hosts of the Zika-virus by biting infected monkeys. The Zika-virus was first detected in monkeys in Uganda in 1947. Five years later in 1952, the first humans infected by the Zika-virus were identified in Uganda and the United Republic of Tanzania. 60 years after discovering the Zika-virus in monkeys, the first reported outbreak of Zika occured outside of Africa, namely on the Island of Yap (Federated States of Micronesia) in 2007. In the beginning of 2015, a large outbreak of Zika was reported from Brazil and later that year, associations between the Zika-virus and the Guillain-Barré syndrome and microcephaly and other congenital abnormalities were made.

Most of the patients infected by the Zika-virus do not develop any symptoms. If a person develops mild symptoms, they are usually fever, muscle and joint pain, malaise and headache. However, it has been found that many complications during pregnancy have occurred in association with the Zika-virus like fetal loss, stillbirth and preterm birth (*Zika virus* 2018).

In the first three sections, I gave an overview on climate change, vector-borne diseases and how they are connected with each other. The following sections will now elaborate on the framework and the approach I used to investigate how climate change affects the distribution of vector-borne diseases. Section 5 gives an extensive overview on both the dataset on the climate change-variables and the dataset on the number of outbreaks of vector-borne diseases, followed by the results (Section 6), the limitations of the analysis (Section 7) and the conclusion (Section 8).

5   The Datasets

5.1   Climate Change

As discussed in subsection 1.2, the massive increase in fossil fuel-consumption in the 1970s led to the climate change, we are faced with today. So, humans were the largest driver of climate change and therefore, humans also influence how climate change develops by adapting their behavior. Climatologists are aware of this relationship and take it into consideration when computing climatic models.

In the $5th$ Assessment Report of the IPCC of 2014, the so-called 'Representative Concentration Pathways (RPC)' were first used as a basis for the report's findings[4]. These RCP's capture future trends of fossil fuel-consumption and make predictions of how the concentrations of the greenhouse gases will develop in the future as a result of the human activities of today.

There exist four RCP's that range from low to high future concentrations of greenhouses gases. Table 2 gives an overview on the four RCP's.

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[4]In the previous IPCC reports, 'Special Report on Emission Scenarios (SRE)' were used to determine how socioeconomic circumstances influence the emission rates and their impact on climate. RCP's - on the other hand - fix the trajectory of the emission rates rather than the socioeconomic circumstances.

Type of RCP	Effort to curb emissions	Energy generation	New technology	Transport	Temp. 2081 - 2100	Sea level 2081 - 2100	Extreme weather 2081 - 2100	Adaption required
RCP 2.6	High	Renewable	Emissions capture	Bicycles, public transport	1.0°C	0.4m	Small increase	Low level at low cost
RCP 4.5	Medium	Renewable		Mix	1.8°C	0.47m	Moderate increase	Medium level at medium cost
RCP 6.0	Medium	Mix		Mix	2.2°C	0.48m	Moderate increase	Medium level at medium cost
RCP 8.5	Low	Coal-fired power		Cars, trucks	3.7°C	0.63m	Large increase	High level at high cost

Table 2: Overview on the four RCPs defined in the 5th Assessment Report of IPCC in 2014 (*What are the RCPs?* 2017).

This study is limited to the 'RCP 8.5'-scenario. One reason for this limitation is that looking at the remaining three scenarios as well would go beyond the scope of this thesis. Second, the most recent (6th) IPCC-Report evaluated that exceeding the 1.5°C level in the near term (i.e., 2021 to 2040) is very likely under the very high greenhouse gas emission-scenario, which is defined as the 'RCP8.5'-scenario (Masson-Delmotte and (eds) 2021).

However, the development of the temperature alone is not sufficient when analyzing the spread of a disease, as Rogers and Randolph 2006 explain in section 4.2 of their paper where they investigate the effect of climate change on the spread of Malaria, namely pressure and rainfall. So, the subsequent research for a dataset evolved as being rather complicated. First, it was required that the dataset does not contain the temperature only but also other variables like pressure and rainfall. Second, the dataset needed to be as granular as possible. As I try to predict the number of outbreaks of vector-borne diseases on a regional level and not nationwide, the research for a suitable dataset ended up being very difficult.

After many days of research, I have finally found a suitable dataset in the data store of Copernicus (*About Copernicus* 2022). Copernicus is an Earth observation program implemented by the European Union and managed by the European Commission. It stores worldwide data from satellites and ground-based, airborne and seaborne measurement systems and provides the data free and openly accessible to users once the user is registered to the store.

The data catalog is from the 'CMIP6 climate projections' which provide information on daily and monthly global climate projections from a large number of experiments, models and time periods computed in the framework of the sixth phase of the Coupled Model Intercomparison Project (CMIP6) (*CMIP6 climate projections - Overview* 2021). The main reason why I have used this dataset for the analysis is that it is the baseline for the 6th IPCC-Report. Using Rogers and Randolph 2006 as an inspiration in terms of which types of variables I should consider relevant for reflecting changes in the climate to which vectors react sensitively, I have declared the six variables in Table 3 as relevant to analyze how climate change affects the spread of vector-borne diseases. Certainly, it is highly unlikely that these six variables are sufficient to predict the number of outbreaks of vector-borne diseases accurately. However, on the one hand, these variables have the possibility to show up a certain tendency in which direction the relationship between climate change and outbreaks of vector-borne diseases are headed. On the other hand, the computation time on these six variables has already been so time-consuming that including more variables

would have gone way beyond the scope of the thesis.

Name	Units	Description
Near-Surface air temperature	Kelvin	Temperature of air at 2m above the surface of land, sea or inland waters. 2m temperature is calculated by interpolating between the lowest model level and the Earth's surface, taking account of the atmospheric conditions.
Daily minimum near-surface air temperature	Kelvin	Daily minimum temperature of air at 2m above the surface of land, sea or inland waters.
Daily maximum near-surface air temperature	Kelvin	Daily maximum temperature of air at 2m above the surface of land, sea or inland waters.
		Continued on next page

Table 3 – continued from previous page

Name	Units	Description
Evaporation including sublimation and transpiration	kg m^{-2} s^{-1}	The transfer of latent heat (resulting from water phase changes, such as evaporation, condensation, sublimation and transpiration) between the Earth's surface and the atmosphere through the effects of turbulent air motion. Evaporation from the Earth's surface represents a transfer of energy from the surface to the atmosphere. It indicates a vector component which is positive when directed downward (negative upward).
		Continued on next page

Table 3 – continued from previous page

Name	Units	Description
Precipitation	kg m^{-2} s^{-1}	The sum of liquid and frozen water, comprising rain and snow, that falls to the Earth's surface. It is the sum of large-scale precipitation and convective precipitation. This parameter does not include fog, dew or the precipitation that evaporates in the atmosphere before it lands at the surface of the Earth. This variable represents amount of water per unit area and time.
Surface air pressure	Pascal	The pressure (force per unit area) of the air at the lower boundary of the atmosphere. It is a measure of the weight that all the air in a column vertically above a point on the Earth's surface. It is calculated over all surfaces - land, sea and inland water.

Table 3: The main variables used on global climate data (*CMIP6 climate projections - Overview* 2021).

For each variable, two files have been used; one for the historical records and one for their projections. CMIP6 provides data from 1850 to 2014 for the historical and numbers from 2015 to 2100 for the projected data. As the 6*th* IPCC-Report claims that the RCP8.5-Scenario is the most realistic one, the projected data is

computed under this scenario. The model I have selected for all variables is the CNRM-CM6-1-HR-model from France as this is one of the climate models which has all the information required for the analysis.

Each of the files is organized in grid cells with 360x720 observations on a monthly level from January 1850 to December 2100. Figure 3 gives the visual representation of how the data is organized by showing the average temperature of the grid cells in December 2014 if the world would be divided into 259,200 grid cells.

**Global Average Temperature according to
CNRM−CM6−1−HR−model (France)**

Measured in Kelvin, December 2014, RCP8.5−scenario
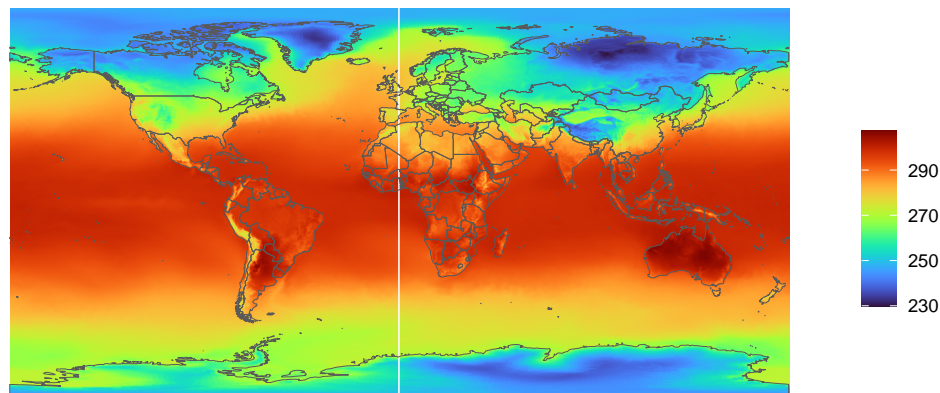
Source: Copernicus

Figure 3: A visual representation of the average global temperature in December 2014 of the CNRM-CM6-1-HR-model under the RCP8.5-scenario, measured in Kelvin.

In order to get annual data, I have calculated the mean over the months. Furthermore, out of two reasons, I have not used the full historic records of the datasets starting in 1850. First, it is quite unlikely that records of diseases around 1850 either exist or are trustworthy. Second, considering all annual observations from 1850 to 2100 would increase the computation time immensely. Therefore, for the analysis, I

only consider the data from 1950 to 2100 in a five year-rhythm[5].

5.2   Vector-borne diseases

Acquiring a historical record on outbreaks of all the eight vector-borne diseases in which I am interested turned out to be a more challenging task than previously expected. The problem is that publicly and especially free available data is scarce and not as granular as required for the analysis. Having information on outbreaks of vector-borne diseases merely on a national level was too general to me as the dataset on global climate change is quite detailled. Fortunately, I came up with an idea to maneuver around these complications.

In 2020, I did an internship where I have worked with data whose details on the outbreaks of infectious diseases that would suit the previously explained requirements for this analysis. The provider of this data is GIDEON. GIDEON is an online-tool that stores and provides information on more than 350 diseases and its global outbreaks on a country- and if available on a subcountry-level. GIDEON has many well-known and influential customers like the World Health Organization, the ECDC and Munich RE which further increased my encouragement to use GIDEON's data, even though it is not provided for free (*GIDEON* 2022).

After the registration-process was finished, I have started to document the number of outbreaks and the number of cases per outbreak for each of the eight diseases and for each (sub)country. As explained in the previous subsection, I have considered the timeframe starting at 1950 up to 2020.

The most time-consuming part when preparing the dataset on the outbreaks of vector-borne diseases was geocoding the outbreaks. To achieve this, I have separated the dataset of one disease into a dataset consisting of all outbreaks on the national and another dataset consisting of all outbreaks on the subnational level. In order to find the geocodes for the dataset with the national outbreaks, I have used the R-Packages 'rnaturalearth' and 'rnaturalearthdata'. Geocoding the subnational outbreaks turned out to be more time-consuming and complicated because the reported subnational locations of the outbreaks sometimes varied in their hierarchical NUTS-level. Furthermore, especially when an outbreak was reported in a region of

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[5]This reduces the total amount of observations from 64,800,000 down to 7,776,000 for each of the six variables.

an African country, the reported subregion sometimes did not exist anymore because of political reasons, the geographical range of the region had been changed or the region was renamed. The reason for this discrepancy lies in the way, GIDEON gathers its data. Besides many other sources, GIDEON extracts the numbers of cases of an outbreak and its location by analyzing scientific articles. As some of these scientific articles are decades old, the names and borders of the investigated geographical regions might not be up-to-date anymore. To overcome this issue, I manually had to correct for these discrepancies.

As the R-packages 'rnaturalearth' and 'rnaturalearthdata' do not provide geo-coordinates on a subnational level, I have used Admin 1-data from Natural Earth[6] (*Natural Earth* 2022).

5.3   Merging the Global Climate Change- and the Vector Borne Diseases-dataset

The last step before setting up a Machine Learning-Model was to merge the dataset on global climate change and the dataset on the outbreaks of vector borne diseases. The challenge I have faced here is that the spatial features of both datasets are different; the dataset on global climate change is organized as a raster file with the world divided into 360x720 grid-cells with equal size whereas the dataset on outbreaks of vector-borne diseases is a spatial dataframe with points as the geometric label.

The approach to merge the two datasets was to find the square(s) of the dataset on global climate change that covers as much area as possible of the area of where the outbreak occurred in the dataset on the outbreaks of vector-borne diseases. Graphically, this looks like Figure 4.

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[6]https://www.naturalearthdata.com/downloads/10m-cultural-vectors/

Figure 4: The idea of how the dataset on global climate change and the dataset on the outbreaks of vector-borne diseases were merged. In this example, if a national outbreak in Brazil was reported, all grid cells would be assigned the value 1 which had a certain area of Brazil inside the cell. Here, all highlighted grid cells are assigned the value 1 whereas all non-highlighted grid cells are assigned the value 0. The red lines show the structure of the dataset on climate change, the black dots show the structure of the dataset on the outbreaks of vector-borne diseases.

As a simplification, I have looked at each reported outbreak without taking the reported number of cases into consideration. Even though predicting the number of cases of vector-borne diseases into the future would have been an interesting task as well, the data provided by GIDEON does not report the number of some old outbreaks and for many outbreaks, the reported numbers are estimates. In my analysis, it is further important to note that if in the same year an outbreak were both reported nationwide and on the subcountry-level, the whole country was assigned the value 1 whereas the subcountry was assigned the value 2. For example, if there was

one reported outbreak in Brazil and one reported outbreak in Estado da Bahia - which is a federal state of Brazil - in the same year, Brazil would be assigned the value 1 and Estado da Bahia would be assigned the value 2.

Furthermore, I have summed up all outbreaks that occurred in a certain raster and in a certain year. For example, if there was one outbreak of Zika and one outbreak of Chikungunya reported in Brazil for the year 2015, the value for this observation would be 2. Naturally, if in this scenario there were two outbreaks of Zika reported, the value for this observation would be 2 as well.

6   Results

After all of the data was merged and the final variable with the total number of outbreaks of vector-borne diseases was calculated, I calculated the predictions of the total number of outbreaks for the years 2050 and 2100. The Random Forest-model was trained using the observations on the climate change- and vector-borne diseases-data from 1950 to 2020 in a sequence of five years. Even though the climate change-data on the years 2015 and 2020 are predictions themselves, I have decided to allow them being used in the historic dataset. The main argument for this decision was that on the one hand the predictions will be rather accurate as the observations of the climate model ended in December 2014 and the predictions started with January 2015. On the other hand, many outbreaks of vector-borne diseases were reported in the 2000 to 2020-period. Not including the 2015- and 2020-data on climate variables would have meant not including important observations on outbreaks in these years.

Ultimately, the full dataset compiled of 3,888,000 observations with ten variables. Out of these ten variables, eight were used for the Random Forest-model, one was used as a label for the year and one was used as the dependent variable. The full dataset was divided into a training- and a test-dataset with a random 75%-to-25%-ratio. The Random Forest-model on the training-dataset gives the result that approximately 96% of the variance in the data can be explained by the model and an overall out-of-bag prediction error of 0.5% was calculated.

Additionally, Figure 5 shows the importance of the variables included in the Random Forest-model in terms of their individual contribution to the mean decrease in the sum of squared residuals when the variable is included in a tree split.

Random Forest – Variable Importance Plot

Presented as the mean decrease in the sum of squared residuals
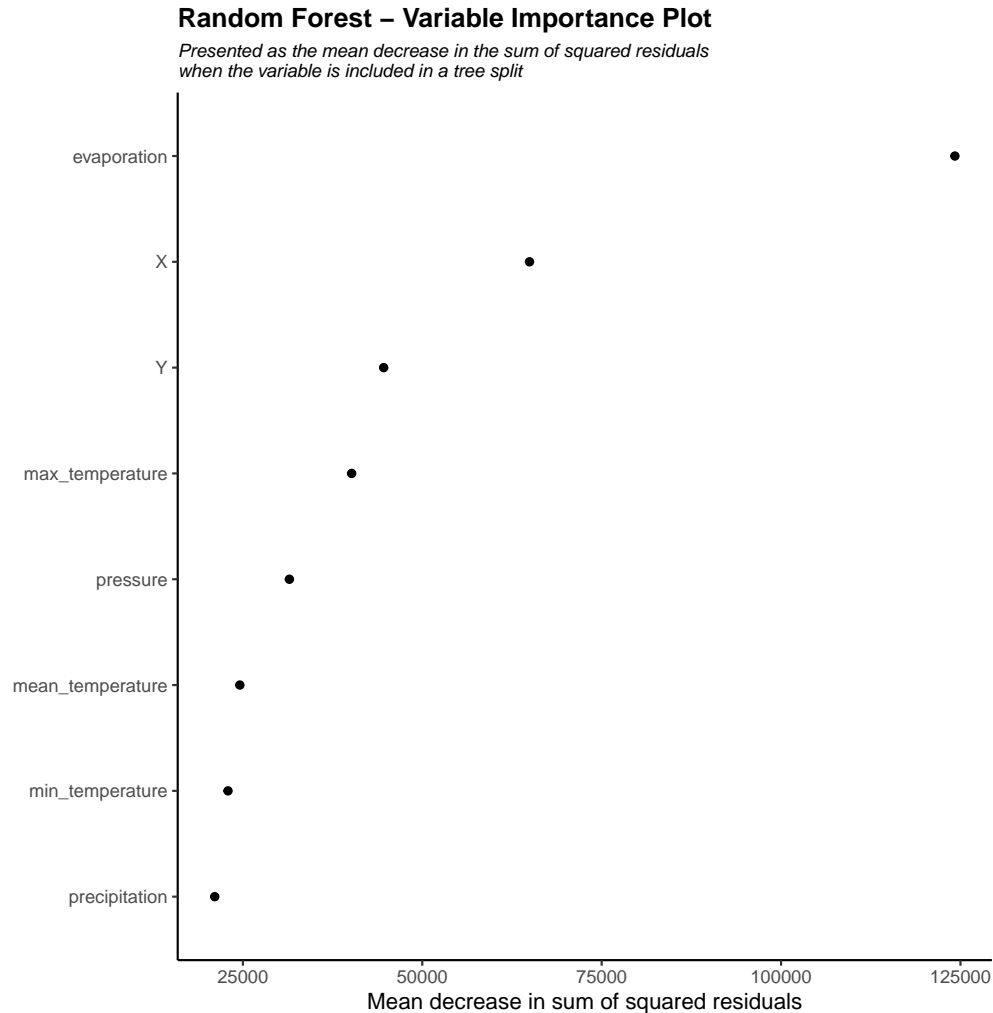*when the variable is included in a tree split*

Figure 5: A visual representation of the importance of the variables included in the Random Forest-model in terms of their individual contribution to the mean decrease in the sum of squared residuals when the variable is included in a tree split.

As shown in Figure 5, besides the six variables related to climate change, the x- and y-coordinates were included in the Random Forest-model as well. The reason for including these two variables is to take spillover-effects into account. Leaving out the x- and y-coordinates theoretically could have led to the result that there will be an outbreak of a vector-borne disease in Antarctica in 2050 if the climate change related variables would have allowed for that. However, geographically, this evolution would

have made no sense at all. Therefore, according to the Variable Importance-Plot, the coordinates played an important role for predicting the future number of outbreaks of vector-borne diseases. Unsurprisingly, the maximum temperature played a more important role than the remaining two variables on temperature as mosquitoes rather breed in warmer and more humid areas.

Afterwards, I have predicted the outbreaks of vector-borne diseases for the test-dataset. In order to see how accurate the predictions on the test-dataset were compared to the actual observations, I have calculated the Root Mean Squared Error between the predictions and the observations which resulted in around 0.05.

Figure 6 gives the visual representation of the number of predicted outbreaks in 2050 compared to the number of observed outbreaks in 2020. In order to get a clearer visualization, only those grids are colored with a higher number of predicted outbreaks in 2050 compared to the observed ones in 2020. The results are in many parts consistent with existing literature and with the data provided by GIDEON. According to the model, especially South America with Brazil and South East Asia with India will be the regions and countries that are expected to face the largest increase of the number of outbreaks of those vector-borne diseases investigated in this thesis. Other regions that are expected to face an - even if not that large but still significant - increase of the number of outbreaks are Central America including Mexico and the southern states of the United States of America as well as the Caribbean, the eastern and southern parts of Africa as well as China and Mongolia and the islands and peninsulas of the very South East of Asia. Geographic regions with only a small probability of facing an outbreak of one of the investigated vector-borne diseases are mainly the ones from the northern hemisphere.
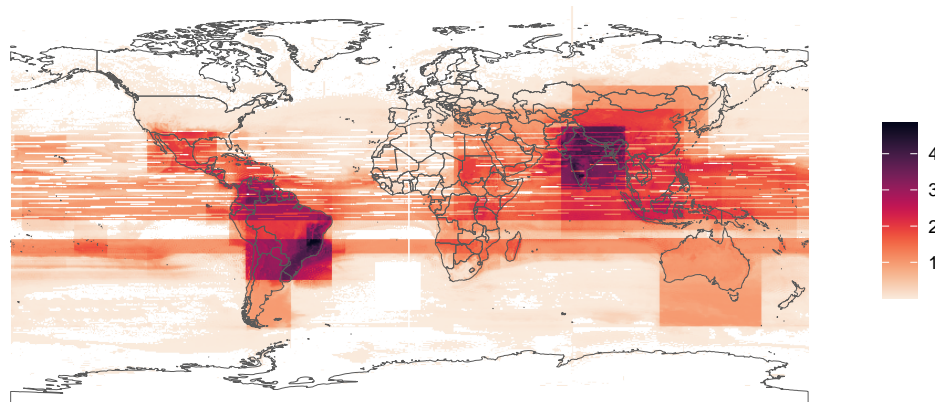
Number of predicted outbreaks of vector−borne diseases
Difference between 2050 and 2020

Figure 6: The difference between the predicted number of outbreaks of
vector-borne diseases in 2050 compared the observed number of outbreaks in 2020.
The darker the colour, the more outbreaks are expected in the corresponding grid
cell in 2050 compared to 2020, the lighter the colour, the fewer outbreaks are
expected. The white cells indicate that the difference in the number of outbreaks
stays the same or is negative.

Figure 7 which compared the number of outbreaks between 2100 and 2020 draws
a similar picture to figure 6. However, the band formed from the colored grid cells is
broadening. This indicates that more regions will face the risk of (more) outbreaks

in the 2100 to 2020-comparison relative to the 2050 to 2020-comparison. Specifically, the number increases to the south down to Southern Argentina and South Africa and the north up to the central states of the United States of America and South Europe.

Number of predicted outbreaks of vector–borne diseases
Difference between 2100 and 2020

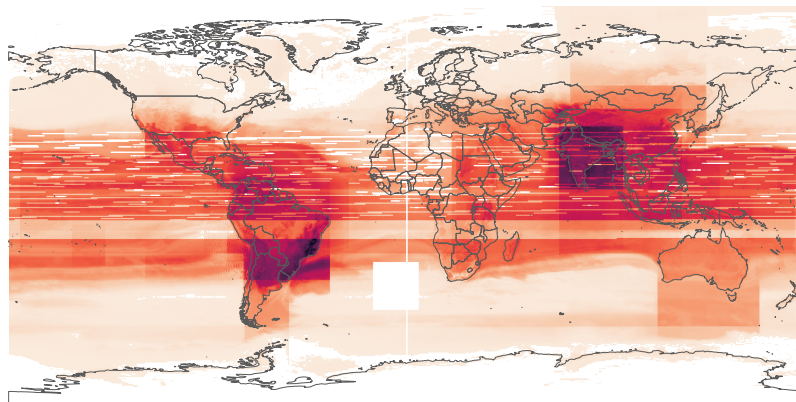Figure 7: The difference between the predicted number of outbreaks of vector-borne diseases in 2100 compared the observed number of outbreaks in 2020. The darker the colour, the more outbreaks are expected in the corresponding grid cell in 2100 compared to 2020, the lighter the colour, the fewer outbreaks are expected. The white cells indicate that the number of outbreaks stays the same or is reduced.

Figure 8 shows the difference in the number of projected outbreaks of vector-borne diseases between 2100 and 2050. It is initially surprising that those regions that were colored the darkest in the Figures 6 and 7 are now white, like Brazil, East Africa, and India. However, this observation is consistent with the scientific literature (see Lafferty 2009) which found that climate change does not necessarily *expand* the breeding ground of - in our case - mosquitoes, but rather *shifts* the geographic range of the breeding ground. Therefore, the colored band in the center of the plots in Figures 6 and 7 manifest into two thinner bands towards the southern and northern hemisphere.

According to this comparison, especially geographic regions of the northern hemisphere will be exposed to a higher probability of facing an increase of outbreaks of vector-borne diseases. Namely, these are the middle states of the United States of America, Western Africa, Southern Europe as well as Central Asia.

Number of predicted outbreaks of vector−borne diseases
Difference between 2100 and 2050
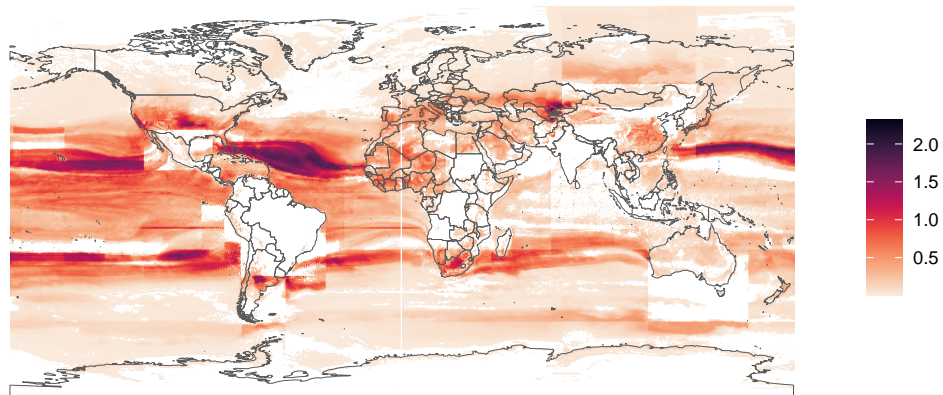
Figure 8: The difference between the predicted number of outbreaks of vector-borne diseases in 2100 compared the predicted number of outbreaks in 2050. The darker the colour, the more outbreaks are expected in the corresponding grid cell in 2100 compared to 2050, the lighter the colour, the fewer outbreaks are expected. The white cells indicate that the number of outbreaks stays the same or is reduced.

7 Limitations

The analysis of the research question of my master thesis is very complex and prone to improvements. Therefore, this section will be divided into two parts. First, I will elaborate on how the analysis could be improved with the datasets used for this analysis. Then, I will carve out how this study is externally limited.

7.1 Internal Limitations

The analysis makes use of two datasets; data on indicators of climate change and data on the number of outbreaks of vector-borne diseases. In my opinion, adaptations can be made to both datasets.

7.1.1 Data on indicators of climate change

As explained in the previous sections, I have used the dataset of the CMIP6 climate projections-catalog from which I have decided to analyze the projections provided by the CNRM-CM6-1-HR model from France. However, Copernicus provides a selection of 57 other models as well provided by nations from all over the world. It is highly unlikely that these models have projections that are significantly different from the model I have used for the thesis. In order to get stable results, one could replicate my study using the average projections of all 58 models provided by Copernicus. However, this would go beyond the scope of the master thesis and it would be a challenge for the work performance of my computer.

Furthermore, I have only used six variables to measure the effect of climate change on the number of outbreaks of vector-borne diseases. Taking only these variables into consideration was inspired by the paper 'Rogers and Randolph 2006' where they explain how they have used five similar variables in one of their earlier studies to predict the distribution of malaria. However, depending on the selected model of the CMIP6 climate projections-catalog, it is possible to analyze up to 51 climate variables. Certainly, some of these variables will probably be not relevant in analyzing this thesis' research question, like 'Snowfall flux' or 'Land ice area percentage'. But, variables like 'Capacity of soil to store water' or 'Specific humidity' could be used in addition to the six variables that I have used. As previously explained, the preparation of the

variables used for the study has already been very time-consuming. Adding more variables to the study would have further prolonged this process.

Finally, I have decided to look at climate data from 1950 to 2100 in a rhythm of five years. Considering all of the years in the 1950 to 2100-period would definitely result in more accurate predictions because especially in the last twenty years, outbreaks of vector-borne diseases were reported almost on an annual basis for a lot of countries. The reason for not analyzing all the years is, once again, the limitations of the working power of my computer.

7.1.2   Dataset on outbreaks of vector-borne diseases

In my study, I have projected the number of outbreaks of vector-borne diseases which are only transmitted by mosquitoes. However, there are many other types of vectors as well which transmit other forms of vector-borne diseases[7]. GIDEON also provides information on historic outbreaks of these diseases, however, this would also go beyond the scope of the master thesis.

As a last point, I would like to elaborate on the quality of the reported outbreaks of vector-borne diseases provided by GIDEON. Even though the provided data is very detailed, more accurate reports in terms of the geographic distribution of outbreaks would have been desirable. For example, a nationwide outbreak of Zika will probably not have affected all of the regions of the country; a detailled documentation including the names of the affected regions of the country would have been ideal. But, the fact that this type of information is most definitely not public and/or time-consuming and difficult to gather increases the value of GIDEON's work immensely.

7.2   External Limitations

This study analyzes the research question of how climate change will affect the outbreak of vector-borne diseases by looking at climate related-variables only. However, the one factor without which no outbreak of vector-borne diseases among humans is possible is not included in the analysis; humans.

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[7]The full list of vector-borne diseases with the according vector from which Table 1 is an excerpt of can be found under https://www.who.int/news-room/fact-sheets/detail/vector-borne-diseases

With the pure existence and the social character of humans, they are responsible for the human-to-human-transmission of (vector-borne) diseases. The increased frequency and size of outbreaks of vector-borne diseases documented in the past twenty to thirty years will further be advanced with population growth, the continuing growth of urbanization and the human-made climate change. Furthermore, other factors like the quality of sanitation facilities should be included in the study in order to increase the quality of the predictions. Unfortunately, records of these types of data on a grid-cell level does not exist publicly and neither do their predictions into the future. Even if these data would exist, its preparation would be too time-consuming for one person to conduct this analysis.

8   Conclusion

Especially since the start of the SARS-CoV-2-pandemic in the beginning of 2020, the fear of big epidemics and pandemics in the future increased. Even though for most people this pandemic came surprisingly, for climate scientists and epidemiologists the outbreak of this pandemic was only a matter of time looking at the frequency of the outbreaks in the past twenty to thirty years, mainly the outbreaks of vector-borne diseases. Vectors are very sensitive when it comes to the disturbances or changes in the climatic surroundings. Therefore, it stands to reason that climate change influences the outbreak of vector-borne diseases.

This study is devoted to measure the effect of climate change on the number of outbreaks of vector-borne diseases, restricted to mosquitoes. The data on climate change consists of the historical records and projections of the CNRM-CM6-1-HR-model from France from the CMIP6 climate projections-catalog in the form of grid-cell levels provided by Copernicus. The selection of the six variables were inspired by Rogers and Randolph 2006. The time-span I use for the study are the historic records from 1950 to 2010 and their projections from 2015 to 2100 under the RCP8.5-scenario which is according to the $6th$ IPCC-report the most likely one to become reality. In order to relieve the work performance of the computer, I only take every fifth year of the time-span into consideration.

The data on the outbreaks of vector-borne diseases is provided by GIDEON, an online-tool that stores and provides information on more than 350 diseases and their global outbreaks on a country- and if possible on a subcountry-level. I have looked

into the outbreaks of eight of the most well-known vector-borne diseases and matched their coordinates to the data on climate change.

Ultimately, I have set up a Random Forest-model and used it to predict the number of outbreaks for 2050 and 2100 for each grid-cell. The results are unsurprising and consistent with research already conducted on the relationship between climate change and the outbreaks of diseases. Comparing the number of outbreaks between the years 2050/2100 and 2020 shows that especially Southern America, East Africa and South East Asia will be the most affected regions in terms of the number of outbreaks of vector-borne diseases. Investigating the difference between 2100 and 2050 reveals that the previously mentioned regions are not expected to experience an increase of the number of vector-borne diseases. However, their neighboring regions to the north (United States of America, Southern Europe) and the south (South Argentina, South Africa) are expected to face an increase in the number of outbreaks of vector-borne diseases between 2050 and 2100.

It is crucial to note that these results have to be interpreted with caution. As the study looks at a time-frame in a five year rhythm, the increased number of outbreaks of vector-borne diseases which were on an almost annual basis in the past twenty to thirty years is not considered due to extensive computation times. Furthermore, I only analyzed the effects of six climate-related variables. However, Copernicus provides information on 45 more climate-related variables which could be considered in a follow-up study. Lastly, climate is not the only factor that influences the number of outbreaks of vector-borne diseases. Population growth, urbanization and the quality of sanitation facilities is likely to play an important role as well. For reasons of lack of availability, variables on these factors are not included in this analysis.

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