A COMPARATIVE STUDY ON EPIDEMIOLOGICAL MAPPING FOR DENGUE CASES IN SINGAPORE AND BANGLADESH

A Thesis Submitted to the Department of Disaster Science and Climate Resilience, University of Dhaka in Fulfillment of the Requirements for the Degree of Doctor of Philosophy

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Under Supervision of
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May, 2024

DEDICATION

To my Parents and Family

DECLARATION

I hereby declare that the research work entitled “A Comparative Study on Epidemiological Mapping for Dengue Cases in Singapore and Bangladesh” has been carried out under the Department of Disaster Science and Climate Resilience, University of Dhaka in fulfillment of the requirements for the degree of Doctor of Philosophy. I have composed this thesis based on original research findings from this study references from published literature and institutional databases. This has not been submitted in part or full to other institutions for any other degree. I also certify that there is no plagiarized content in this thesis.

May, 2024

CERTIFICATE OF THE SUPERVISOR

This is to certify that Md Tauhedul Islam carried out his PhD research under my guidance and supervision, and hence prepared the thesis entitled "A Comparative Study on Epidemiological Mapping for Dengue Cases in Singapore and Bangladesh."

As far as I am concerned, the researcher duly acknowledged the other researchers' materials and sources used in this work. Furthermore, the thesis was not submitted to any other universities or institutions for any other degree or diploma.

It is thus recommended that the thesis be submitted to the Department of Disaster Science and Climate Resilience, University of Dhaka, in partial fulfillment of the requirements for the degree of Doctor of Philosophy. I have read the documents with care and have not found any plagiarized content in this thesis document.

May, 2024

Professor Dr. A S M Maksud Kamal
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ABSTRACT

Establishing the causal relations of any disease or health event is crucial as to its prediction and protection is concerned. Taking dengue as a model case in the city of Dhaka, Bangladesh and Singapore, this study has ventured to apply an innovative step-by-step approach to find out the causal correlations within the climate-vector-disease associations as well as ecological and human variables in the cities of Dhaka and Singapore. The study has discovered a significant correlation amongst climatic variables and vector availability, ecological factors and vector abundance and between vector concentration and dengue occurrence in temporal and spatial dimensions. Also, the study has been able to establish the variation of dengue incidence in different seasons accounted for 30 years, and long-term trends of climate and dengue incidence over a 10-year period, the study developed a bank of applicable data set which could be used by the enthusiastic researches in the field of the effects of climate change as well as ecology on dengue transmission in Dhaka and Singapore and in the regions of the South and South East Asia at large. Based on the findings, a model mapping system was envisioned to predict the future incidence of dengue and thereby, to predict any such disease or health event and devising prevention guidelines thereto at local, national, regional and global level. In one hand, differences of variables in different cities and regions have been proved as to applying one regional model for another region, on the other hand, incorporating crucial variables in one model through a compare and contrast study enabled to frame a relatively common model mapping system applicable for any given entity of a region. It is a huge enabler on global and regional scale to address the outbreak of any given disease in entities with different economic and geographical setting. Devising this technique of mapping and modelling by addressing Spatial variations is an important novelty of this study. Finding out Temporal variations of variables over time, particularly decadal impact of variables is another crucial attribute of the Model to apply it effectively in preventive medicine and urban planning. This research also found that city areas having more built and paved areas and areas with unplanned urbanization had the highest abundance/density of Aedes mosquitoes-the vector of dengue. These results demonstrate that alteration of the ecology in city area is one of the major reasons for the increase of dengue incidence, especially in metropolitan areas. This is a crucial inference as to the dengue prediction and prevention mapping is concerned that, unplanned urbanization, particularly development of shanty slum area is crucial to dengue fever spread. Again, the mapping results of this study has mentionable contributory function to assist in drafting appropriate, differentiated plan, policies and strategies for controlling vectors, i.e. aedes mosquito and preventing the spread of the resultant disease-dengue in the Dhaka city of Bangladesh and Singapore and other vulnerable areas of the regions and the globe at large.

Keywords: Epidemiology, Eco-Epidemiology, Temporal Variation, Spatial Variation.

Chapter One

1. Introduction

1.1 Overview

Modes of human disease vary from coming into contact with infected animals, through contact with the environment (water, air, soil) contaminated by infected animals. Modes of disease transmission also entail indirect communication through vectors, and through modification of this classical disease cycle by ecological aberration. The eco-environmental factors in disease transmission include high rainfall, flooding, natural disasters, population growth, urbanization, and poor sanitation and hygiene [1–4]. Disease risk also depends on individual behavior (e.g. swimming in freshwater, working outdoors), and contact with animals including livestock, rodents, pets, & wildlife [1,3] in case of infectious disease while living in and on polluted milieu for non-communicable diseases and health events. So, the risk factors of etiology of disease and epidemic depend on interactions between humans, animals, and the environment, and vary significantly between locations based on environmental, cultural, and socio-demographic issues [3]. Transmission dynamics are therefore factors of global environmental change of both natural and anthropogenic environments [1,2,4].

Environmental changes have a huge impact on the emergence and re-emergence of certain diseases and health events, mostly in countries with high biodiversity and serious unresolved environmental, social, and economic issues. An extensive literature review revealed a relationship between new health events and diseases outbreaks and climate change events (El Niño, La Niña, heatwaves, droughts, floods, increased temperature, higher rainfall, and others) or environmental changes (habitat fragmentation, deforestation, urbanization, bushmeat consumption, and others).

To prevent and or control this chain of the emergence of new disease and health-related events, integrated surveillance systems and effective outreach programs by developing integrated eco-epidemiological mapping are essential. Due to strong global and local influence on the emergence of infectious diseases, a more holistic approach is necessary to mitigate or control them in low-income nations.

Several studies have described that disruption of the ecosystem has largely been attributed to local environmental change which has acted as drivers of a wide range of life-threatening infectious diseases, including hantavirus pulmonary syndrome, dengue fever, yellow fever, malaria, trypanosomiasis, leishmaniasis, and leptospirosis, and health events eg arsenicosis, spreading of HIV-AIDS, new emergence of ancient diseases, etc. There is strong evidence that some of these environmental changes will intensify shortly if key anthropogenic activities are not controlled. So devising a combined eco-epidemiological mapping is the call of the day [5].

Several aspects of Global environmental change (GEC), including human mobility, climate change, and the trade-in livestock and plants have been explicitly linked to emerging infectious diseases (EIDs) in humans and other species [6–8]. These identified connections between two dimensions of a greater problem; GEC and EIDs matter, but the relevance of most identified factors to future infectious diseases may be dwarfed by factors whose importance is at present far less well appreciated. Indeed, it is possible that circumstances more familiar to earlier human generations could evolve, creating a fertile terrain that could enable the resurgence of currently dormant infectious diseases, of great consequence to our forebears [9].

Climate change does exert its effect on the survival, reproduction, or distribution of disease pathogens and their hosts [10]. According to Patz et al. (2005), correlating the emergence or increased range of infectious diseases with climate change is still not possible due to a dearth of longitudinal, quality data sets and sociodemographic factors [11]. Nonetheless, ample evidence has shown that climate change results in long-term drifts in climate conditions as well as extreme climate patterns and resultant erratic weather events, both of which may threaten human health and well-being [10,12].

A sustained change in weather pattern over a long period of time leading to erratic climate patterns constitutes the basics of climate change. It results in myriads of health problems, including multiplication of the existing health maladies. This study has aimed in examining the evidences of this climate change over health and well-being, particularly on the infectious diseases of human being and animals. It has also ventured to underpin the research progress and gaps with a view to developing preparedness to contain the changes and their impacts. The co-relations between climate change and infectious diseases of human being is evident in literature. It is also evident that, as an agent of the disease causation and as a care giver, human being may effectively contain the spread of the infectious diseases through taking preparedness, including studying and understanding the trends of the climate change patterns, their health impacts on humankind and thereby allocating funds and relocating technologies and technical know-how to protect and promote public awareness and healthy life styles.

Some health effects of climate change may result from indirect impacts on natural ecosystems. For example, altered climatic conditions can change the habitats of vectors such as mosquitoes or rats and affect the parasites they carry. The consequences resulted from global warming depends heavily on preparedness, such as the ability of humans and public health systems to adapt. Human migration and economic stresses from climate variability could threaten human settlement and seriously overwhelm the public health infrastructure [5].

So, newer ways and means have been devised by the scientists to develop better prediction models for different modes of transmissions and etiological sequel of various diseases or health events, giving new thoughts of the foundational mechanisms of the diseases and their causation and spread. They have used two genres of models- time series and spatial methods.

Time series methods use two different approaches- statistics driven traditional methods and mechanisms based dynamic models. Important traditional methods are Generalized Linear Models, Autoregressive Integrated Moving Average (ARIMA) models etc. They use cumulated past values to predict future incidences and have been proved useful in short term predictions in a climatically vulnerable area(s). ARIMA method was successfully applied to study seasonal variability of streptococcus pyogenes infections with relations to the change in the climate variables in Iceland from 1975 to 2010. Dynamics models have been used to examine correlations between humidity and influenza in the United States, rainfall and cholera in Haiti and temperature and mosquito population, and dengue incidences in Maderia, Portugal.

Spatial Methods, on the other hand, use static vis-à-vis dynamic risk maps, which can effectively discern the risk of a given disease or health event on national and regional scale. In the process, the methods depict the result in mapping format utilizing data from the target location. The classic example of this method is the use of Global Risk Map to underpin the effect of El Nino on the spread of Zika Virus in the South America in 2015 [13].

The paragraphs ante underscore that, while the discussed models have been successful in predicting a number of diseases and health events, they are not free from drawbacks as well. The Static models have the shortcomings of not being able for long term assumptions like dynamic models while the later does not offer the short-term accuracy of predictions like static models. Furthermore, both the models need to be fed with experimental data to hone with observed values.

Nevertheless, while researchers continue to adjust and adapt newer techniques and technologies towards continued upgradation of the models, it may be opined that, a better model which may effectively address the research gaps will be key in the days to come for more precision as to the prediction and preparedness of diseases in an ever-changing climate scenario [103,104,105].

Kuate Defo B has summarized the planning, development and sustainable implementation of health policies and health systems ought to be based on precise measurements and understandings of prevalence and incidence of communicable and non-communicable diseases, accidents, and other disabilities, given past and current demographic and epidemiological profiles in societies as well as how they are predicted to change over time [14]. Equally crucial is the need to understand and appreciate the underlying mechanisms and influential factors of these changes. Acknowledging Barthelme's postulates, various theoretical perspectives, notably the epidemiological transition theory [15,16], have been developed and practiced in an attempt to both describe and understand local, national, and global patterns in demographic and epidemiological profiles within and across societies, given the multiple domains of health, diseases, and health events [17].

The planning, development and sustainable implementation of health policies and health systems ought to be based on precise measurements and understandings of prevalence and incidence of communicable and non-communicable diseases, accidents and other disabilities, given past and current demographic and epidemiological profiles in societies as well as how they are predicted to change over time. Equally crucial is the need to understand and appreciate the underling mechanisms and influential factors of these changes, and their monetary and non-monetary costs and implications to individuals, families, communities and governments in the global context. In specific contexts, it may be the interactions between factors from different levels and categories of determinants, and their timing and sequencing during the life courses, which are crucial for public health and the health care systems to be responsive to the need of a society in a rapidly changing environment

In summary, based on the successful prediction Models, pro-active surveillance measures could be taken. Active surveillance is indispensable in preventing disease emergence by identifying areas of risk before they become a threat to human and animal health. Especially in times of reduced budgeting for research funding, it is worth highlighting to policymakers the importance of recognizing anthropogenic drivers, their ecological connections, and the dynamics of specific diseases, reservoirs, and environments. An integrated surveillance system of the health of at-risk human and animal populations should be designed to identify the geographic regions, populations, vectors, and interactions that may result in emerging and reemerging pathogens. This would establish a system of the early outbreak warning system and permit the modeling of spread, analyses, and potentially the application of prompt control or mitigation measures.

So, towards devising effective containment measures, a comprehensive prediction model remains at the core. Spatial and temporal associations between climate and diseases in conjunction with empirical and exercise-driven studies infer that, these factors can affect diseases or health events in a nonlinear fashion, unlike the hitherto linear regression way [18].

The forecasted incidence and prevalence of infectious diseases in the wake of rapidly changing climates heralds an impending social emergency. The predicted increase and distribution of infectious diseases in time and space depicts that, the impact of climate change can impact the entire ambit of epidemiology of infectious diseases in a nonlinear fashion. The Ecological Society of America, in a 2009 Report, mentioned that, many variables will have direct impact on the incidence and prevalence of infectious diseases while many factors might overshadow the consequences of climate change.

This has paved the way as to the usher of new branch of epidemiology-crisis discipline- a new research topic to develop a holistic model of eco-epidemiological mapping embodying all health attributes hitherto unfactored in.

To put the theory into context, particularly to come up with a mapping model, dengue as a test case and its comparative epidemiological studies in Singapore and Bangladesh could be a model study as the disease has been a havoc in these two settings where numerous studies have also been conducted to contain it with a prediction and prevention scheme. It could, in deed, be modelled for other diseases in other country set ups including subnational, regional and global set ups.

Dengue has been one of the most talked about infectious diseases of late. This is a viral disease transmitted through mosquito as a vector. Transmission of dengue virus depends on the presence of Aedes mosquito-the vector. Mosquito generation and development is known to be influenced by the climate. Numerous studies were carried out to examine whether the climatic factors data can be used to predict dengue cases of different tropical countries and cities, particularly in Singapore and Dhaka city, Bangladesh. So, a comparative study of Dengue virus, of its vector Aedes mosquito and of the prediction models posed a unique opportunity towards developing a comprehensive model which might be of great importance as to dengue prediction and prevention in particular cities, at national level, regional level and to compare in regions.

Such a comprehensive modelling of a communicable disease like Dengue might also usher in developing holistic approaches for other communicable and non-communicable diseases and health related states and events. So, the holistic study of Dengue clinical, epidemiological and statistical viewpoints is not only important in preventive medicine but also bear equal bearing as to the national and international policies are concerned for human development.

As described earlier, dengue is a viral fever. It has an incubation period of 2-7 days. Its signs and symptoms include, headache, pain in the eyes, joint and muscle pain, rash and bleeding through different orifices of body. There are two types of the disease:

Dengue hemorrhagic fever:

In this pattern of the disease, there are traditional signs and symptoms of dengue fever along with bleeding manifestations, which is evident by bleeding spots under skin, bleeding from body cavities and reduced number of platelets in blood. There is also leakage of blood fluid (plasma) due to increase permeability of the blood vessels.

Dengue shock syndrome

In this variety, all above manifestations are added to failure of blood circulations leading to lack of oxygen in tissue which is manifested by low blood pressure, cold extremities and restlessness.

Dengue is diagnosed clinically based on the above manifestations along with laboratory findings and serological study of the virus. In all the data used in dengue prediction, these criteria are followed.

As to the variables are concerned, daily, weekly and monthly climatic variables such as average temperature, rainfall, sunshine and humidity are usually collected from the concerned Met Offices of the countries/cities. The periodic climate data are then correlated with the data of periodically reported cases of dengue.

Regarding methodology, monthly averages of rainfall, temperature, sunshine and humidity are used as independent variables while monthly dengue incidence numbers are used as the dependent variable. One-way analysis of variance (ANOVA) is used to compare and contrast the data of climate variables in different seasons.

As to development of the Model, an empirical model is usually designed taking negative binomial generalized linear model analysis as the base model. A negative binomial model having a log-link function in the generalized linear model is used to devise the models and methods to calculate dengue incidence cases in relations to the independent climate variables as mentioned above. Since a significant correlation is considered to be present in the numbers and spread of dengue cases across seasons, a season is usually included as a covariate to find out modified models. A negative binomial model is then developed as outcome variables are measured as counts and are usually over-dispersed; i.e., the conditional variance becomes very high when compared to the conditional mean of the variables.

When there are a number of maximum likelihood models are in place, the performance of alternative models on the basis of several likelihood or goodness of fit measures could be compared. Akaike information criterion (AIC) and the likelihood ratio chi-square are the most popular methods in this regard. The model which depicts maximum change in the value of AIC and likelihood ratio chi-square in comparison to the same of the previous models are considered as the most feasible model. Based on the comparative findings of correlation between the climate variables and clinical data, a suitable data could be discerned for appliance in the comparative studies. This is equally applicable whether the models used are applicable to find out whether the models are suitable for annual or decadal of any other time frame comparison of predictions.

These issues are addressed, analyzed, compared and contrasted to draw inferences in different chapters of this thesis. This introductory chapter of the thesis elaborates, inter alia, the background of this research, the research question, objective and scope of the research project, basic framework of the research and study, brief methodology, and contributions of the research to the body of knowledge.

The goals of this chapter are to:

- Review the concept of eco-epidemiological mapping and modeling from different perspectives on specific disease control and prevention context (Section 1.1)
  - Highlight the situation and context: summary of the problem (Section 1.2).
  - Detail the study background (Section 1.3).
- Discuss the research issue along with the background of the research and summary of the problem of research (Section 1.4)
- Propose research questions and objectives (Section 1.5)
- Elaborate the proposed conceptual framework of the study (Section 1.6).
  - Provide scope of the research (Section 1.7).
- Provide significance of undertaking the research (Section 1.8).
  - Research methods and analysis:

Specify the present research setting as a new model addressing all aspects of a probable disease or health events to ensue (Section 1.9).

  - Depict the study in context (1.10).
- Focus on how the research will contribute to the body of knowledge and practice.

(Section 1.11)

- Briefly discuss the limitations of the research study (Section 1.12)
- Elaborate an outline of this write up (Section 1.13)

1.2 Situation and Context: Summary of the Problem

According to the World Health Organization, natural and human-induced threats to human health at global and regional levels include: “climate change, stratospheric ozone depletion, changes in ecosystems due to loss of biodiversity, changes in hydrological systems and supplies of freshwater, land degradation, urbanization, and stresses on food-producing systems” [19]. It is noticeably discernible in tropical and lower climate zones where there is high biodiversity, ecological change is greatest, making these regions potential hotspots for the emergence of new pathogens affecting human, wildlife, and domestic animal health [20,21]. These areas including the sub-tropical and high altitudinal North, where drastic socio-economic and environmental changes are occurring, especially in the form of migration and transportation are particularly vulnerable to the risks of the rapid spread of infectious diseases [22].

The correlation between environmental change and disease causation, particularly infectious disease etiology is a much talked about issue in epidemiology. Some of the postulates in force are higher proliferation and reproduction rates at higher temperatures, extended transmission season, changes in ecological balances, and climate-related migration of vectors, reservoir hosts, or human populations [18,23].

Environmental variables as per the agents of disease causation involved have been incorporated as temperature, humidity, rainfall, and wind speed, etc. while the agent-host relationship has been described as through changes in the duration of agents and agent's life cycles or influences on human, vector, or agent behavior [24,25].

It has been inferred through extensive research that; temperature plays the most crucial role in the transmission of the agent of infectious diseases. The influence of temperatures on vector-borne diseases has been studied by WHO and Gratz. They have shown that a trivial change in temperature imparts a tremendous effect on vector-borne disease transmission and epidemic potential by altering the vector's reproductive or biting rate; by shifting a vector's geographic range or distribution; by altering the extrinsic incubation period of the pathogen; and, by increasing or decreasing vector–pathogen-host interaction and thereby affecting host susceptibility [19,26].

Rainfall is another factor affecting agents of diseases, particularly vectors of infectious diseases. It was depicted that with an enhancement in rainfall there is an increase in available breeding sites which in turn leads to an increase in the population of the vectors -the mosquitoes, while an increase in the net number of adult female mosquitoes increases the odds of a mosquito acquiring a pathogen and transmitting it to a second susceptible host [24].

Humidity lengthens the life span of parasites, insects, and ticks. As they thrive in hot and humid climates and can exploit newly disturbed ecosystems, tropical and subtropical regions experiencing high levels of urbanization and increased deforestation are often the areas at the greatest risk for vector-borne disease epidemics [27].

As the growth and development of dengue vectors has long been established to be dependent on climate conditions, dengue is being studied as a test case in the context of climate change and disease infection co-relation as depicted above. Being a vector-borne disease, the occurrence of dengue infections depends not only on the presence, but also on the density of its vector- aedes mosquito. Substantial studies conducted across the globe have inferred that, climate variables, particularly rainfall, temperature and humidity have a positive correlation with the seasonal variations as to the concentration of Aedes aegypti and occurrence of DENV.

Numerous studies conducted in Bangladesh and Singapore have also established a discernible relationship between dengue incidences and rainfall. This is consistent with some other studies, such as the findings of Focks & Barrera, who opined that rainfall enhances vector density leading to an increase in dengue cases. Rainfall again is the cause of higher humidity which provides an ideal environment for the growth and survival of mosquitoes during wet seasons. However, there are also a few studies in the literature which depicted contradictory findings as to the relationship between humidity and dengue incidence, since the correlation depends on local characteristics, particularly terrain of the area and its latitudinal position.

The correlation between average temperature and dengue incidence was one of the pivotal findings of this study. Karim et al. and Chandy et al. demonstrated similar results while Su reported a negative correlation among the two variables.

Higher temperature is critical as to the limitation of the maturation of the dengue vector. 11.9°C has been proposed as the threshold temperature for the survival of the dengue virus while it has been shown that, the vector of the virus ceases to thrive once temperature falls below 17°C and virus stops multiplication in a temperature below 18°C. It could be opined that, low temperature is not conducive for long term survival of the aedes mosquito which is crucial for its being infected with the virus for transmission to human body. Similarly, virus itself cannot survive in the low temperature to complete its life cycle once it enters host.

Again, a higher temperature reduces the extrinsic period of virus within the vector mosquito, thus increasing the probability of transmitting the disease to human host earlier, leading to epidemic scale of infection. However, a temperature above 30°C has been shown to negate the viral transmission as sweating has been shown to decapitate mosquito from biting human being. Hence temperature study remains at the core of epidemiological understanding of the dengue disease.

The study also underpins the correlations between dengue incidences and relative humidity of a given place. Relative humidity of an area is dependent on temperature and rainfall of the region at large. The combination of these three variables is crucial as to the prolongation of life span of the virus and its vector- the aedes mosquito. Karim at el. and Promprou et al. reported that that there were more dengue incidences in their experiments during monsoon season, which, according to their opinion, was clearly because of high humidity prevailing during wet rainy days. The postulated that, a higher humidity during wet seasons was responsible for the development and spread of mosquitos, thus leading to the rate of their infection. Barbazan et al. have shown that, such increase in mosquito propagation fortifies the frequency of transmissions of virus as high as five times when the survival rate rises from .80 to .95 in a drastic way. Hales et al. have also shown that, the average vapour pressure per annum was considered to be the most crucial climatic predictor regarding dengue occurrence across the globe.

In sum, the combined effect of the three climatic variables- temperature, rainfall and relative humidity significantly influences the tally and duration of blood meal by mosquito, average survival of the vector and the likelihood of the vector being infected with the dengue virus. Hence, the above variables by dint of their impacts on the vector mosquito are important determining factors of the transmission of dengue in a geographic area.

To complicate and ultimately to ease the description of correlation, now it has already been established that ecological factors have been the pivot of changes to the environment [28–

30]. Naomi Oreskes (2004) postulated that there is a systemic and cumulative impact of ecology on eco-environmental change. Of them, anthropogenic environmental change has already been established by evidence-based scientific research [31]. Scientists are using a new terminology called Anthropocene to dub the new geological epoch [32]. Building on the Millennium Ecosystem Assessment definition of drivers of ecosystem defines drivers of ecosystem change as “a complex web of interactions between humans and their surroundings as humans seek to satisfy their basic needs and improve their wellbeing” [33]. Ironically, as scientific progress is speeding up to keep pace with development, so is the emergence of many an anthropogenic driver of environmental changes resulting from economic and social development [34].

Typically, urbanization has a diverse pitfall in developed and developing countries. While in developing countries it results in the development of slum and shanty areas, in the developed society, migrated people are covered with more certain health facilities. In a poor economic setting, it leads to unplanned urban dwellings with high poverty levels, poor dwelling construction, and low education rates, such as the favelas of Brazil [35,36]. Interestingly, despite the lowly health system, urbanization might subside the risk of infection in certain geographical setting, such as in Fiji urban dwellers have a lower risk of infection than those in rural areas, mostly due to differences in exposure to subsistence livestock animals [4,37] which are considered as reservoirs of diseases [3,38–41], although exposure to these animals differs across communities [37] and even for different individuals within the same communities.

Demographic changes due to migration and human mobility are crucial to bringing about new epidemiological change. Unplanned urbanization, particularly the development of shanty and slum areas are important causative factors to facilitate the introduction and dissemination of new infectious agents into a community, in which no previous immunity has been acquired [24,42].

On the other hand, a better-equipped health system, such as screens, medication, and vaccinations can reduce the level of infection in a susceptible group of people, if the provisions are made available and affordable [42].

There is a reverse narrative as to whether climate change causes an enhancement of infectious diseases [11,43–47]. This has partly resulted from a paucity of work using empirical-statistical models to investigate the link between environmental variables and environmental, most importantly, there is virtually no effort to incorporate environmental variables into mathematical models describing malaria transmission [48–50].

Addressing this gap necessitates the development of a new model to incorporate the ecological and environmental factors holistically, which will be process-based in one hand to discern the correlation between the two categories of factors, on the other hand, will give a better understanding as to the effects of complex feedbacks and nonlinear processes typically underlying disease transmission [51]. In this research, we are calling them, dynamic multiplicative processes and thresholds which will explain endemicity and seasonal extinction of a particular disease or health event, as well as disease emergence in new regions as climatic conditions change, provide a credible basis for prediction beyond the range of current climatologic experience. The new Models also represent valuable strategic tools for policymakers evaluating contingency, mitigation, and abatement instead of traditional statistical models [46].

Based on the above uncertainties, we may categorize the epidemiological and ecological factors as those related solely to epidemiological aspects independent of climate, those related to uncertainties associated with climate models themselves, and those related to the interaction between disease and climate. Understanding, quantifying, and improving our knowledge in each of these areas is vital if we are to better understand a develop a model to address all pertinent factors comprehensively [52].

By assessing the estimated risk of leptospirosis infection under different scenarios and for different sub-populations, such as urban versus rural areas, these groups or areas can be targeted with more precise interventions that specifically focus on the key drivers of infection most relevant to them. Common methods used in epidemiology, such as logistic regression models, do not easily allow for scenario analysis and in many cases separate models are required for each scenario, retraining the model each time on a subset of the data [36,40]. Geographically weighted regression models have been used to determine the spatial variation in the relative importance of environmental factors [53], but like standard regression models, they are not designed for scenario analysis.

As such, quantifying uncertainties in climate model predictions is vital to get rid of uncertainties emanating out of transmission-driven models. Out of numerous techniques and methods, multi-model ensembles have occupied special place and attention in climate modeling [54,55] and which is based on full integration of multi-model ensembles of climate and disease models in one hand, on the other hand, which scientifically incorporate the anthropogenic, i.e. human-driven factors of ecology into the model to address the entire gamut of factors involved for a better understanding of prediction and to devise plans for mitigation, adaptation, and control, accordingly.

In this study, venture has been made to take dengue as a test case for the development of a prediction model so as to enable the policy makers towards developing a hassle-free, simple, measurable, realistic and time bound prediction system. The generation of climate-based model was decided, considering the correlations of the climatic variables and dengue incidence, to aide in controlling the vectors, containing the disease incidence and prevalence through proper preparedness and surveillance of the disease and its causative factors. The model is expected to, through the precise prediction, contribute towards early preparedness as to prevention of the diseases in all three triads of the communicable disease paradigm- agent, host and environment level. In this process, it is likely to reduce the burden of the disease in terms of health care giving and also operational, financial and administrative expenses.

Nonetheless, the long-term prediction of dengue incidence remains elusive as the variables vary in time and space, given erratic climate behavior owing to rapidly advancing climate change scenario across the globe. Added to this dilemma, is the development dynamics of nations, particularly unplanned urbanization, afforestation, desertification, reduction of water resources and close proximity of human being and animal, the latter being vulnerable due to their loss of habitats. Therefore, the model might need to be adjusted and recalibrated in the time to come to maintain prediction precision by anticipating the changes in the variables of dengue transmission and distribution pattern, and, but not limited to addition of subtraction of newer factors in the new environmental landscape.

The pen picture sketched above depicts that, a mapping model for the prediction of dengue, and to that connection to any communicable disease, could be studied from different perspectives, particularly factors of temporal and spatial dimensions. It, therefore, warrants a comparative study of the model in different settings. Selection of Dhaka, Bangladesh and Singapore was the principal logic to quench this quest of an ideal research work. The present study, however, explores a holistic approach to study the variables of ecology and epidemiology having a direct bearing on the causation of dengue, with the aim in view to envision a new model to design an eco-epidemiological mapping based on the existing research gap, as revealed by the dengu data analysis in Bangladesh and Singapore.

Based on above, the conceptual definition of eco-epidemiology and eco-epidemiological mapping adopted for this comparative epidemiological study of dengue in Dhaka, Bangladesh and Singapore are:

a . Eco-epidemiology: The study of natural, environmental factors as well as human modifiers influencing agent, host, and environment in the causation of dengue.

b. Eco-epidemiological mapping: A model of mapping combining environmental, clinical, and ecological factors as well as quantification of their gaps to assess and predict dengue incidence in decadal temporal prediction to devise control and preventive measures.

1.3 The Study Background:

The etiology and epidemiological factors are crucial to treat, contain and prevent the emergence of any health-related state and event, particularly communicable diseases. Of particular importance is the geographical prevalence of a given health condition, which, unfortunately, because of erratic data and method of interpretation of data, is absent so to speak. More so, if one unique model could be devised based on accurate epidemiological data, it could be emulated to address control and prevention of numbers of other diseases [56].

It has now been well established that infectious diseases transmitted within human habitat with human host populations represent almost 75% of the infectious diseases that have (re-)emerged in human populations in the last century [57,58]. As these pathogens are typically transmitted to multiple host species [59], wildlife is often an important component of such systems [60], as is illustrated by the novel coronavirus SRAS-COV-2 which is thought to have emerged in seafood markets in Wuhan, China [61].

It has been estimated that more than 1400 species of infectious agents have been reported to cause disease in humans [62–65]. These include pathogens for some 347 diseases of sustained clinical importance with established clinical diagnosis, epidemiology, and therapy, as a decision-support tool for clinicians [66]. Among these, 110 diseases pose a threat to non-immune travelers [66]. Sixty-two of these clinically significant diseases can be prevented by vaccination; 19 usually as routine childhood immunizations [66–68]. However, all these clinical procedures are rendered meaningless when the diseases get community-level dimensions, if not epidemic with the rapidly advancing climatic and ecological make-ups. So, clinical diseases, with the climate and ecology factoring in, are no longer clinical scenario solely, their containment, prevention, and control, and most importantly their evolution in newer forms and dimensions have been the topic of epidemiology and ecology [65].

Although many factors modulate agent, host, environment cycles of any health event, particularly the dynamism of a any communicable disease, it is important to discern the correlations between the propagation of diseases and eco-epidemiological factors to address them holistically. A better realization of this relation sis of crucial importance to devise accurate models, which could increase the precision and usher into a more robust and result-oriented control and prevention system. Metcalf at el. seconds the opinion that, a precision model based on holistic approach of the study of the variables can better address the preparedness and preventive measures. [69].

There remain a good number of reasons for wanting to map the geographical distribution of an infectious disease. Mapping is a primary goal in spatial epidemiology [65,70–78]. Maps of disease distribution and intensity allow immediate visualization of the extent and magnitude of the public health problem. When based on empirical evidence, maps can support carefully weighted assessments by decision-makers on the advantages and disadvantages of alternative courses of action [79–81]. These may range from helping plan national scale intervention strategies [82] to advice for individuals on whether to vaccinate and/or provide prophylaxis before travel [67,83]. These maps can also document a baseline from which intervention success or failure can be monitored.

The purpose of spatial modelling in animal and public health is three-fold: describing existing spatial patterns of risk, attempting to understand the biological mechanisms that lead to disease occurrence and predicting what will happen in the medium to long-term future (temporal prediction) or in different geographical areas (spatial prediction). Traditional methods for temporal and spatial predictions include general and generalized linear models (GLM), generalized additive models (GAM) and Bayesian estimation methods. However, such models require both disease presence and absence data which are not always easy to obtain. Novel spatial modelling methods such as the Model of Maximum Entropy (MAXENT) and that of Genetic Algorithm for Rule set Production (GARP) require only disease presence data and have been used extensively in the fields of ecology and conservation, to model species distribution and habitat suitability. Other methods, such as multicriteria decision analysis (MCDA), use knowledge of the causal factors of disease occurrence to identify areas potentially suitable for disease. In addition to their less restrictive data requirements, some of these novel methods have been shown to outperform traditional statistical methods in predictive ability (Elith et al., 2006). This research provides details of some of these novel methods for modelling disease distribution, highlights their advantages and limitations, and identifies studies which have used the methods to model various aspects of disease distribution.

Maps of disease distribution and intensity allow immediate visualization of the extent and magnitude of the public health problem. When based on empirical evidence, maps can support carefully weighted assessments by decision-makers on the advantages and disadvantages of alternative courses of action

Besides, as modes of data gathering evolve and improve (for example, through enhanced electronic surveillance [79] and Internet-based health reporting [84], including HealthMap/ProMED [85,86], BioCaster [87,88], and Argus [89,90]) and techniques developed to exploit these data (for example, semi-automated rapid mapping), these geographical distributions (often referred to in this literature as baseline disease risk assessments) can also provide a 'normal' against which real-time outbreak alerts can be assessed for international bio surveillance [91–93].

Furthermore, as the portfolio of infectious disease distribution maps expands and their fidelity improves, the public health community will be better able to evaluate the factors that predispose a time and place to the origin [94,95], and the emergence of infectious disease outbreaks [20,64,65,96–102].

Previous models have been successful in predicting the spread of certain illnesses, while they failed to depict or predict many health events accurately. As evident, different types of models have their shortcomings. Static models have limitations as to predict the same long-term reliability of dynamic, mechanistic models. On the other hand, the latter does not always provide the short-term accuracy of traditional, static methods. Besides, in dynamic models, disease incidence and prevalence need to be incorporated to reveal real-time observed reality [105].

Dr. Andrew Farlow of Oxford and his team unveiled such a unique system during the innovation session of a seminar organized by Trans-NIH Global Health Working Group. The model was originally designed to map dengue fever but, as the team claimed, could be applied to many of the 350 infectious diseases currently registered by the Global Infectious Disease and Epidemiology Network. Only about seven have been fairly well mapped by other methods, he noted in his talk, "Disease Mapping and the Economics of Vaccines: Opportunities and Challenges" [56].

The mapping model entails several input factors, depending on a particular disease or health event. For the dengue model, the research team selected factors like population density and movement, vegetation, and urbanization because the main vector mosquito thrives in densely populated suburban environments. Average monthly rainfall, temperature, and humidity were used as independent variables and the number of dengue cases reported monthly was used as the dependent variable. One-way analysis of variance (ANOVA) was used to determine whether each of the climate variables differed significantly between seasons.

"Incorporating all data together, the model was generated which could predict the probability of occurrence of an infectious disease of any given disease which was intended ultimately to target more effective surveillance strategies."

The first model map was able to identify dengue's presence in 128 countries, including 36 previously classified as dengue-free by the WHO. However, the general of the dengue mapping was a huge undertaking, requiring five years of work, 15 staffers, and 22,000 parasite rate surveys, and not to mention, highly expensive [56].

The model was encouraging for dengue, but it didn't last as first it was a herculean effort and most importantly it lacked accuracy as it could not incorporate all the basic data needed to develop a general model for any given disease.

This research explores four key questions about statistical models developed to describe the recent past and future of vector-borne diseases, with special emphasis on dengue: (1) How many variables should be used to make predictions about the future of vector-borne diseases? (2) Is the spatial resolution of a climate dataset an important determinant of model accuracy? (3) Does inclusion of the future distributions of vectors affect predictions of the futures of the diseases they transmit? (4) Which are the key predictor variables as to the causation and spread of vector-borne communicable diseases at present and in the days to come? Examples are given of dengue models using one, five or 10 meteorological variables.

However, the result of the failure of generalization of this study was crucial: we need to generate an atlas of the disease factors and disease together in addition to quantifying statistical uncertainties in each case. This is the essence of the eco-epidemiological mapping model [106]. The following sub-chapter will detail this Research Problem.

1.4 Research Problem:

It is evident that there continue to be gaps in the methods as well as information available, so experimentation and devising of a new holistic approach is a call of the day. A combination of the two models, as well as quantifying the gaps of the two different methods seem to be the option ahead which can equally be applicable for short-term disease prevention and long-term planning [56].

However, in the past, cartographers were poised with many problems. First, the authors did very rarely use the reference of the baseline study during mapping. Second, cartographic errors were obvious as the GPS was yet to be invented in those days. These errors were magnified enormously when working on a global scale. Third, no assessment of the fidelity of the map was done and spatial and temporal differentiation was never assessed. These limitations constrained significantly the public health utility of the maps. However, despite the continuity of the limitations and advent of newer problems, these old issues to a greater or lesser extent have been addressed in many of the contemporary mapping efforts reviewed here [65]. A particular example regarding Dengue epidemic in Bangladesh worth mentioning here. Dengue epidemic impinged on Bangladesh, a country of the South Asia in 2000 after three decades of sporadic and seasonal presence, particularly in monsoon[107]. From 2000 to 2009, out of 64 districts, reports were available from only 29 districts, of which 91% cases were from the capital city of Dhaka [108] presumably due to paucity of confirmatory laboratory diagnosis under the changing criteria [107,109].

In the city of Dhaka too, the reporting cases lacked proper threshold of epidemic, although the clinical cases were everywhere. Mohammad Zahirul Islam showed that, the monsoon season of 2000 witnessed the first ever epidemic of dengue in the history of the city of Dhaka which resulted in 5,521 officially reported cases, with only 93 fatalities [110–112].

To summarize, there is a clear gap as to Baseline Risk Assessments for routine public health, improve bio surveillance and provide better long-term preparedness by improving fundamental eco-epidemiological understanding [92].

This is, needless to mention, is the research problem, which, in the following section, will be put forward in the form of Question and Objective of the Research.

1.5 Research Questions and Objectives:

The research undertaken would like to address the fundamental question: “First, from 2000-2010, what natural imbalances occurred in the nature leading to epidemiological and ecological changes leading to upsurge of dengue in the epidemic form, secondly, how can those changes be depicted and thirdly, how could they be generalized to use for the prediction and prevention of any health event [113]**.**

Based on a holistic approach to address the research problem and background as elaborated above the research question is:

How a holistic model of epidemiological mapping could be developed, which will

a. General Prediction Mapping: Address the short-term forecasts (e.g. Like Static ARIMA methods) by modelling by using the weighted sum of the values of past incidences to estimate prospective values in future of any health event or communicable diseases, dengue in Bangladesh and Singapore in this case;
b. New Precise Prediction Mapping: Will quantify and address the gap between the clinical data and the prediction values emanated out of model outputs from epidemiological variables based on the decadal data by adding new epidemiological and ecological factors;
c. Spatial Mapping: Generalize a Model by fine tuning the best suitable model to forecast dengue incident on a broader regions and global scale, by a comparative study of different models in Bangladesh and Singapore
d. Temporal Mapping: To finetune the time gap-annual, biennial or decadal- in a Model required for the variables to factor in accurate future prediction

It goes without saying that, hitherto, there were no study of daily temperature variation and disease variance, no correlation study of dengue and rainfall, population density or humidity, not to mention the study of impact of human induced factors e.g., unplanned urbanization, air, water and soil pollution, global warming and son on directly impacting not only on the disease progression, but also on the climate. This model development research is intended to take into account all these factors of the city of Dhaka, including some nouvelle issues like anomalies in Sea Surface

Temperature (SSTA), an index of El Nino-Southern Oscillation (ENSO) responsible for the erratic behavior of climate in the South Asian Region [107,114,115].

It should be borne in mind that, the policy makers in public health sectors, be in the government or Non- Government Organizations (NGO) or Community Based Organizations (CBO) would be in a better positions in terms of time, resources and preparedness if there are better models in place. It would aide them in better preparedness to bolster preparation, which will lead to a healthier society in an ever-changing climate and ecology [65].

Not to mention, this remains the ultimate objective of any epidemiological study now a days. This research is no exception.

1.6 Proposed Conceptual Framework:

In the previous sections, the possible causation and consequences of climate change on human health related states and events, in particular communicable diseases have been summarized [116]. In addition to climate change, health states and events are generally impacted by socio-economic and ecological factors such as human mobility, erratic urbanization, and habitat issues etc. Woodward et al. (2011) and Confalonieri et al. (2007) elaborated climate and ecological effects on health into two major categories i.e. direct and indirect [116,117]. Changing weather pattern s imparts direct impact on human health while it results in indirect ecological consequences through food and water quality and quantity, agriculture, among others. In sum, climate and ecology could affect human health through three ways: directly, indirectly and through social and economic disruptions [10,118–121].

From the discussions presented earlier, inference could easily be drawn as to the determination of the variables concerning specific diseases or health events. However, there are some variables that not only have direct bearing on particular communicable diseases, but also play a mediating role towards its full fruition. Accordingly, the proposed framework in Figure 1.1 depicts a stepwise relationship and Framework Planning, about the chosen disease, i.e., dengue infection in a chosen area, i.e., district of Dhaka of Bangladesh and the city state of Singapore to ultimately develop a general model of prediction and prevention.

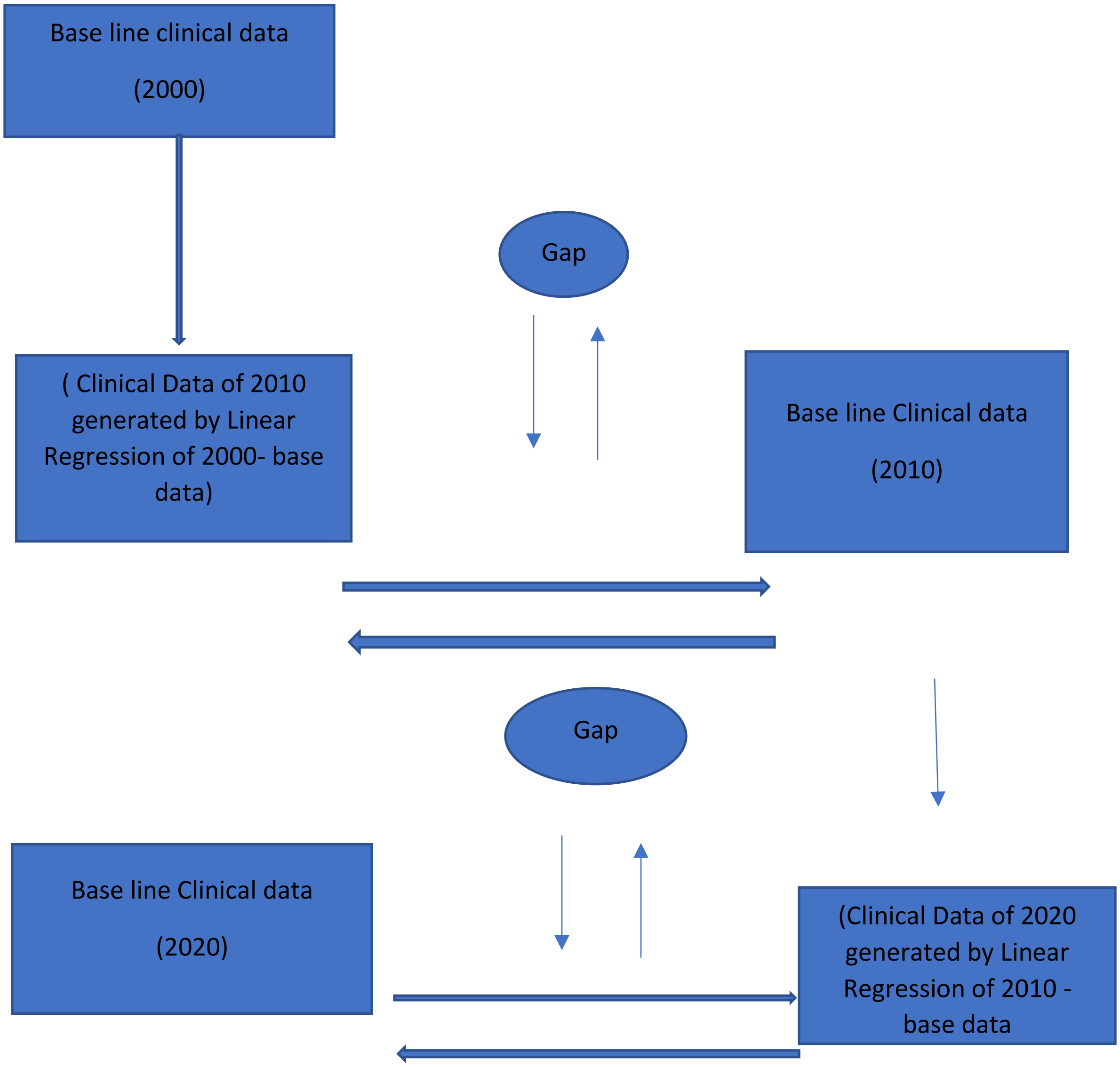


Figure 1.1: Chart for individual clinical data in temporal variations.

It is, needless to mention that a base-line gap is inevitable in Figure 1.1 based solely on clinical data, which warrants the impacts of climatic variables on the progression of the communicable diseases. There have been numbers of different models across the globe to for the prediction of the distribution of dengue in response to climate change in the days to come [11,122,123]. However, there is paucity of studies to identify the association between weather variables and dengue transmission with particular regard to the South Asia, the most affected and vulnerable area of dengue fever [114,115,124–126]. Shahera Banu et al. have endeavored to undertake experiment on the potential impact of changes in climate on the pattern of dengue in Dhaka [114].

Taken all these into considerations, the research will similarly study the impact of base line data of climate change in two separate occasions of temporal zones to find out possible solutions as to gap of Figure 1.1 is concerned. So, the Figure 1.2, to study the climate impact on dengue associations, will echo the similar study framework as Figure 1.2. It is mentionable herewith that, there will still be a gap between the deduction data and field data, which remains to be addressed yet by any study conducted so far. This will be the crux of the current study to minimize this gap of data before developing a model mapping system. To address this gap, a weighted variable as to the ecological factors are concerned, have been planned in Figure 1.3 as below: Adding the variable closest to the existing gap, the ultimate model will be figured out. It has also been revealed that, the added variables which were expected to fill the gap between clinical findings and statistical deductions, vary in temporal and spatial lines. New factors are added over time with the changing paces of human mobility, new host-agent-environment relationships and newer evolutions of climate and anthropogenic variables in time and space.

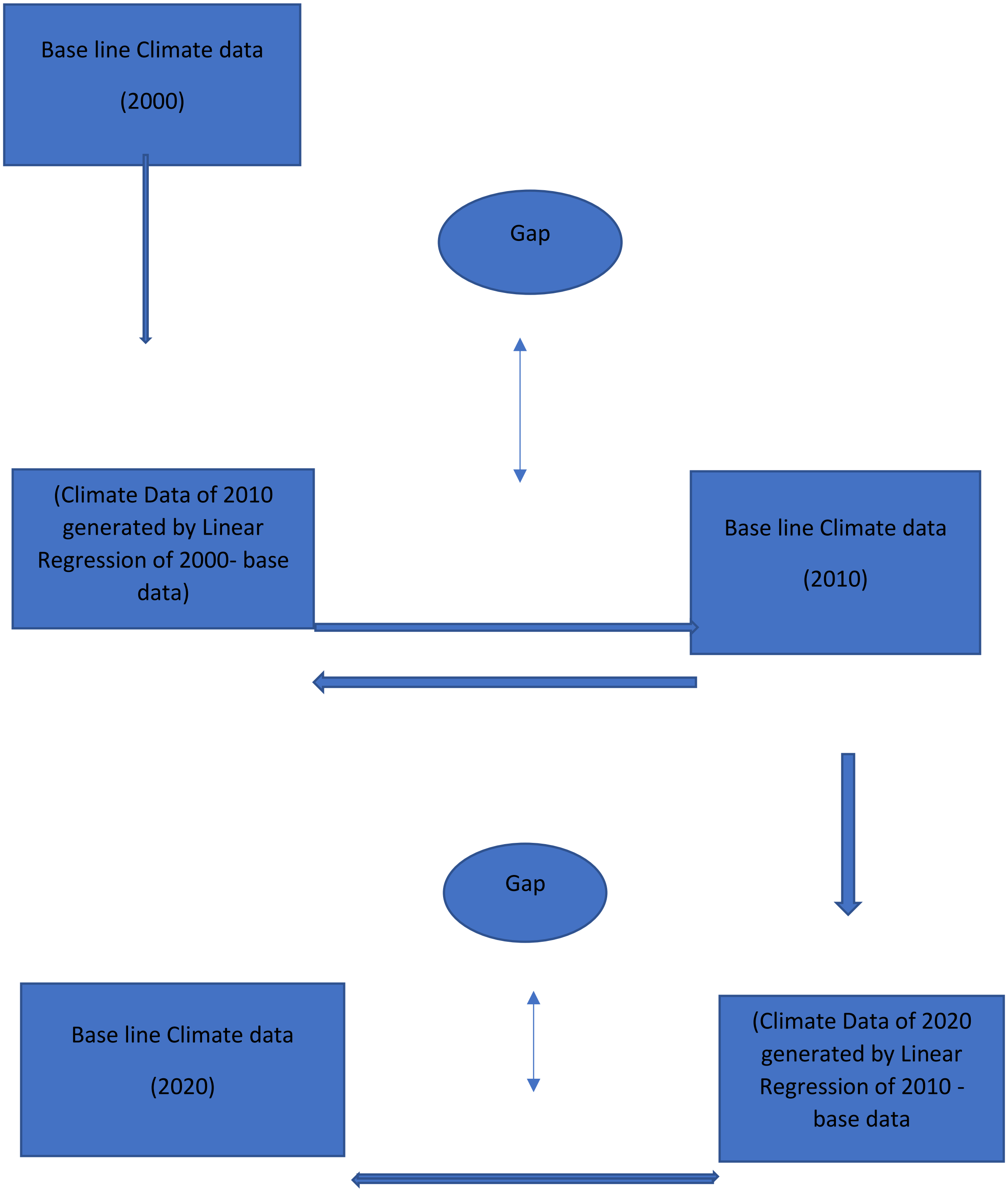
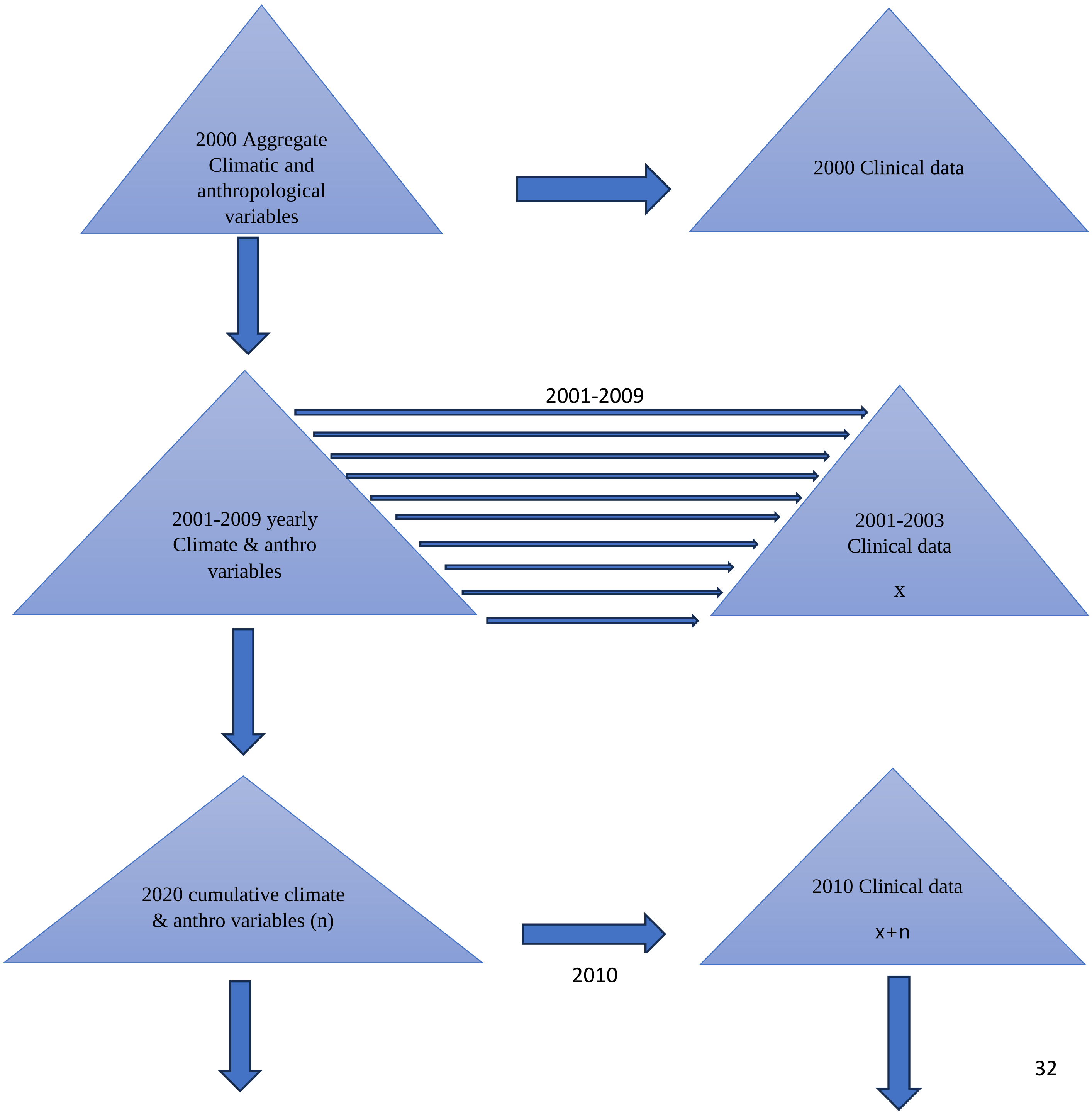


Figure 1.2: Chart for individual climate data in temporal variations.

Figure-1.3: Paired and weighted variables of anthropogenic (anthro) factors.

So, two most important nouvel findings of the research needed to be conceptualized as under:

Temporal variation scheme: Cities and habitat usually develop on unique geographical disposition, although there may be variation of geography and spatial difference amongst different cities and habitats of a country or continent. However, in a given city or habitat, there exists variation of climatic variables in different seasons and over time, given rapidly advancing impact of climatic and ecological changes. Socio-economic development of an area also plays a cumulative role towards a change of agent-host-environment relationship of an entity (city or country). Needless to mention, unlike the seasonal variation, this temporal variation takes time to impart its effect on the responsible variables. This is a fascinating finding of this study that, a decadal variation, rather a yearly variation of the factors was evident amongst the factors, most probably owing the impact time required for these variables to exert their impact. Here is a schematic presentation of this finding:



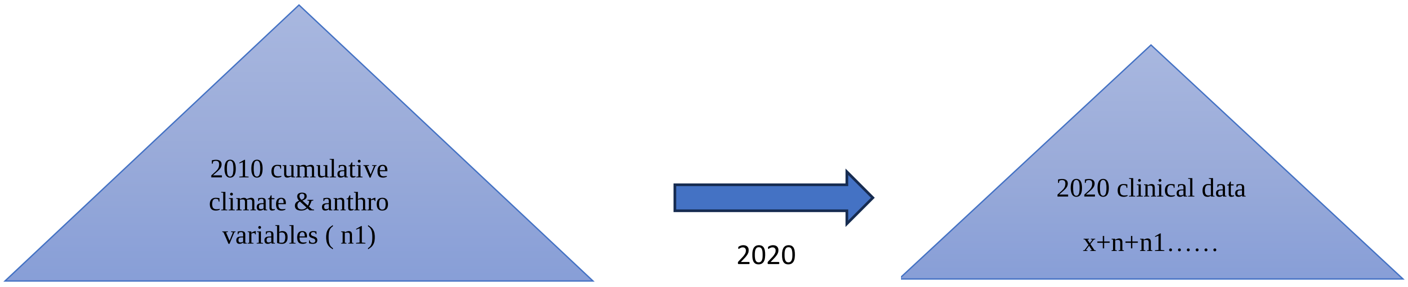


Figure-1.4: Yearly versus Decadal resultants in temporal variations

Spatial variation scheme: Depending on altitude, latitude, terrain, geographical disposition and urban development, the climatic and host-vector variables vary from city to city, country to country and region to region. Incorporation of the same variables in the same model thus pose questions as to the region-specific authenticity of the modular output. Indeed, it has been discerned that, every entity, be it a city or a country has a few own variables which in one hand differ from those of other entity, but on the other hand, play a crucial role to the output of the Model mapping in that entity. In sum, one city or country specific model is not ideal for another city or country, rather a regional modelling structure, incorporating the common variables of different entities seem realistic for a region-wide mapping model, if not a global one. Indeed, a unique global model might never be feasible, given wide range of variance of the variables across the globe. Development of such region-specific model, which ecstatically, differ from sub-regional or city model is an interesting finding in this study which were deduced from differential findings in the modular study of the Cities of Dhaka and Singapore. The following scheme depicts this regional model, vis-à-vis traditional national or city model:

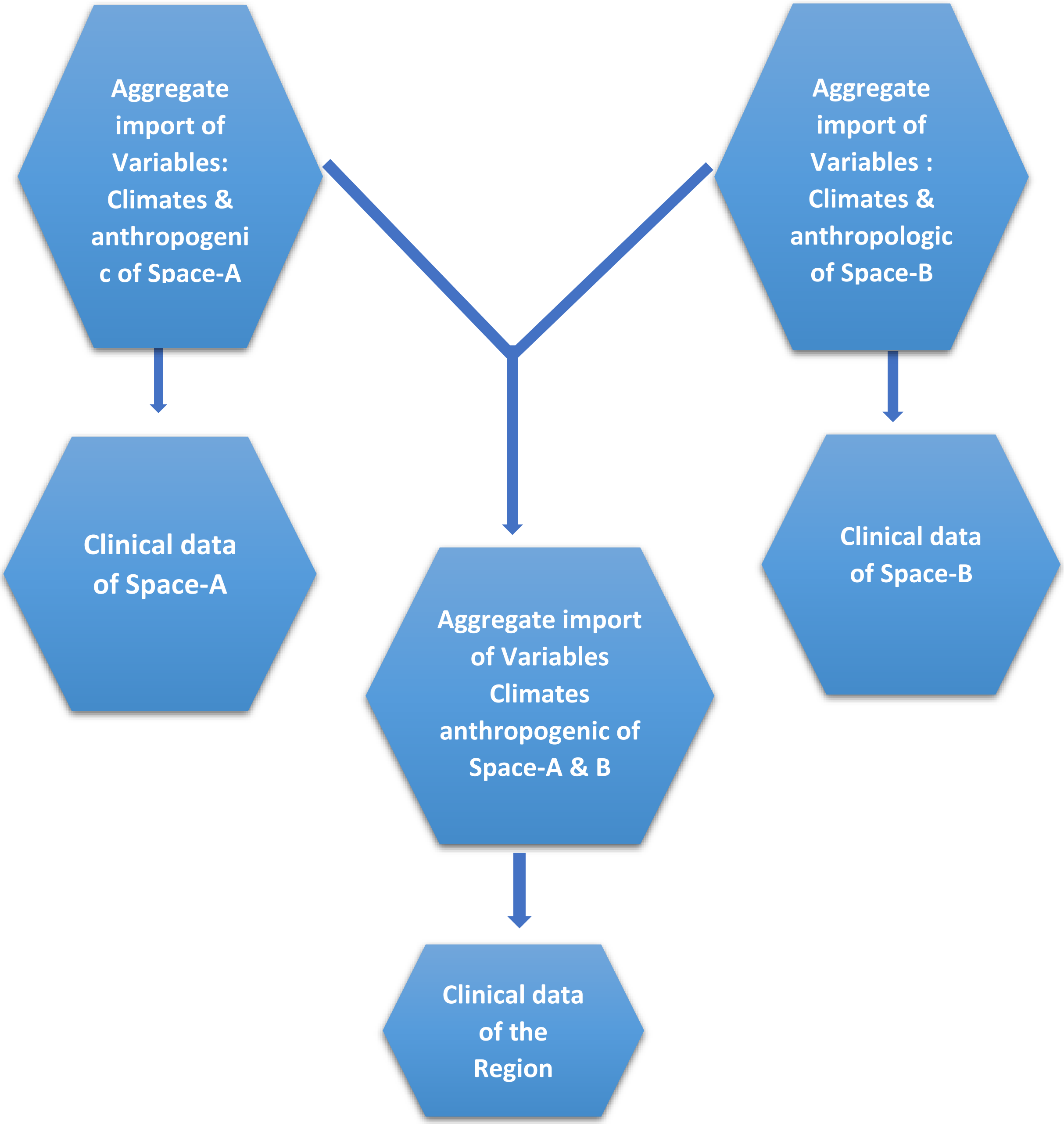


Figure-1.5: Spatial variations of variables and methods

1.7 Scope of the Study:

This study is aimed at developing a holistic model of eco-epidemiological mapping of a given disease, particularly an infectious disease so as to enable the concerned authorities for the prediction and prevention of the event. As a reference case, the incidence of Dengue fever in the cities of Dhaka of Bangladesh and Singapore have been taken in the time duration of 2000 to 2020. Although the study variables, initially taken, were limited to clinical and climatic factors, to address the gap as per the motion of hypothesis, ecological factors of the two regions were incorporated to develop the comprehensive model [113].

As repeatedly described earlier, the four dengue viruses, the agents of dengue fever and dengue hemorrhagic fever in humans, are transmitted predominantly by the mosquito Aedes aegypti in the urban settings, while Aedes albopictus in the rural settings. The abundance and the transmission potential of both the vectors are influenced by temperature and precipitation. While there is strong biological evidence for these effects, empirical studies of the relationship between climate and dengue incidence in human populations are potentially confounded by seasonal covariation and spatial heterogeneity. Using 20 years of data and a statistical approach to control for seasonality, we show a positive and statistically significant association between monthly changes in temperature and precipitation and monthly changes in dengue transmission in the study areas. We also found that the strength of this association varies spatially, that this variation is associated with differences in local climate, and that this relationship is consistent with laboratory studies of the impacts of these factors on vector survival and viral replication. These results suggest the importance of temperature and precipitation in the transmission of dengue viruses and suggest a reason for their spatial heterogeneity. Thus, while dengue transmission may have a general system, its manifestation on a local scale may differ from global expectations.

There have been a good number of studies to unveil the relationship between climate and dengue in various spatial and temporal directions. While temperature and rainfall has been attributed to etiology of dengue viral out surge [127], erratic climate has been suggested to have direct effect on the biology of the vector mosquitoes of dengue namely, *Aedes aegypti* and *Aedes albopictus*

[128–130]. Exclusive studies have shown that, high rainfall and temperatures can provide the conditions for oviposition, stimulation of egg-hatching, high vector development and a decrease in the reproductive period of the virus in the mosquito [128–130]. In separate studies, it was seen that, high temperatures were associated with dengue in Brazil [131], China [132], Costa Rica [133], Indonesia [134], Mexico [135], Puerto Rico [127], Singapore [136], Taiwan [137] and Thailand [138] and high rainfall with dengue in Barbados [139], Indonesia [134], Mexico [135], Puerto Rico [127], Taiwan [137], Thailand [140], Trinidad [141] and Venezuela [142]. Some studies have suggested an association between dengue epidemics and El Niño [143–146].

So, dengue has posed ample scope to study as a topic disease to study and develop the proposed model to predict and prevent any given infectious disease and or health event.

So, dengue has posed ample scope to study as a topic disease to study and develop the proposed model to predict and prevent dengue in the two study areas. It has given scope to have a comparative study as to the variables' selection and differentiations of the two regions, to find out their spatial and temporal variations and finally, to have a unified narrative for the model applicable in general.

1.8 Significance of the Study:

Although it is yet to be discerned whether difference in socio-economic status led to variation of disease incidence, particularly dengue incidence and prevalence in Bangladesh and Singapore, it has already been established that, socio-demographic profile of the population is a major facilitating factor to transmit dengue transmission in the study areas [147].

Sharmin et al. has conducted a study on the slum dwellers of the six major cities of Bangladesh, namely, Dhaka, Chittagong, Khulna, Rajshahi, Barishal and Sylhet. They found that, an estimated number of 35.2% of the city dwellers live in slum and shanty areas., where improper waste disposal, sanitation and swage together with contaminated water supply and shanty habitats create favorable breeding sites for aedes aegypti and aedes albopictus-two important vectors of dengue fever in Bangladesh [148,149].

Notified cases of dengue infections in Singapore reached historical highs in 2004 (9459 cases) and 2005 (13 817 cases) and the reason for such an increase is still to be established. A mathematical model for dengue infection that takes into account the seasonal variation in incidence, characteristic of dengue fever showed that the result mimics the 2004-2005 epidemics in Singapore.

Bouts of dengue epidemics are expected to ensue in future in the absence of any preparedness or preventive measures, let alone intervention or prophylaxis. With the pace of unplanned urbanization, there is a continued changes in city population along with habitat of virus, vectors and the environment itself, which all together may contribute to uncertainty regarding future risks of dengue surge. While plausible climatic changes, including increase rainfall in monsoon and more frequent episodes of drought pose future risk factors for epidemics, ecological factors such as changes in demography, habitat and other anthropogenic issues are likely to contribute to more dengue break outs in future. High fertility rate in poor economic setting with poor hygiene and habitat resulting in an increased percentage of the shanty dwellers with naïve immunity will also increase the risk of dengue incidence in future. Added to the sore is continued unplanned urbanization in the pace of erratic human mobility are likely to exacerbate disease risk. So, a proper surveillance-based prediction and prevention tool is instrumental to address the issue holistically [148].

However, haphazard and passive public health surveillance and current containment plans are insufficient to address future risk. In the absence of a reliable vaccine or prophylactic measure, behavioral impact programs are crucial which too, are yet to be planned and executed in the absence of a model health prediction and prevention strategy [148].

To impart protective behavioral and attitudinal adjustments a pro-active Standard Operational Procedure (SOP) in the form of a Knowledge, Attitude and Practices (KAP) is mandatory. Md. Siddikur Rahman has elaborated that, ‘KAP surveys are representative of a specific population to collect information on what is known, believed, and done in relation to a particular topic and are the most frequently used study tool in health-seeking behaviour research [150]. However, almost all dengue KAP research has been area-based and conducted in several countries, except for some studies conducted at the university level [151–153].

So, a scientific model of eco-epidemiological mapping system is long due in the study areas and the region, if not at global scale.

1.9 Research methods and analysis:

As stated, ante, the model development was intended for addressing prediction and prevention of any health event, particularly infectious disease, and the study subject was specifically discerned and devised for dengue infection and epidemic in Bangladesh and Singapore, and the South Asia and the South East Asia at large.

At the outset a working definition of the variables, most importantly, diagnostic criteria of the disease in subject, i.e. Dengue fever, characteristics to single out the variables causing dengue outbreak in space and time in Dhaka and Singapore were discerned. In this regard, the Multi Criteria Design Analysis (MCDA) process was adopted. MNCDA involves the following stages:

1) Defining the objective, 2) Identifying factors and constraints using different information sources (e.g. expert opinion, a literature search and analysis of historical data), 3) Defining the relationship between the factors and the vulnerability of a location for dengue, 4) Transforming or standardizing the values of the factors on a relative scale to allow comparison between each criterion, 5) Weighting the criteria based on their relative importance to vulnerability, 6) Combining and aggregating all the layers/criteria to produce a final weighted estimate of vulnerability in each location and, 7) Conducting sensitivity analysis and validating the results [154].

This study was conducted for a period of 20 years in two separate sessions from 2000-2010 and 2010-2020 period in the specific hospitals of Dhaka, Bangladesh and Singapore. The study population comprised individuals of all age groups, attending the outpatient and inpatient departments of tertiary hospitals in the cities of Dhaka and Singapore. Inclusion and exclusion criteria were developed for the clinical dengue patients for linear regression study. Monthly details of total rainfall, temperature, sunshine and relative humidity for all the months of the study period were obtained from Meteorological Department and retrospectively analyzed in relation to total number of dengue cases. According to the intensity of the rainfall, temperature, humidity and sunshine, weather data was divided in two periods namely, Pre-Monsoon (Off period) and Monsoon (On- period) [125].

A person diagnosed with dengue on discharge from the hospital was designated a study case. The physicians in each hospital diagnosed dengue fever from those patients who were admitted with acute febrile illness following a clinical case definition of dengue fever, as mentioned in the WHO guideline for dengue fever [110,155].

A trained data extraction team consisting of a study medical officer and a research associate and two volunteers extracted dengue case records from all major catchment hospitals of Dhaka City Corporations and Singapore Metropolitan area. The data extraction team had had an exhaustive exercise to find out individual file of each study case based on the criteria for the study period, which they tabulated in the supplied pro-forma [156].

In separate operation, the data for the cities of Dhaka and Singapore were obtained from Center for Disease Control (CDC), which monitors situation of infectious disease and health events across the respective country. CDC predicts, monitors and supervise the diseases situation throughout the countries by collecting information through its control room cell, which is now is now designated as the National Health Crisis Management Centre (NHCMC), DGHS. Dengue surveillance is mostly conducted actively either by communicating directly with the public and private health facilities or passively through "Hot Line" daily. Besides, at the end of the month, each facility produces a cumulative report of morbidity and mortality on the dengue situation and submits it to the CDC. The team obtained all the data pertinent to dengue infection in the cities of Dhaka and Singapore during the same period than made a confidence interval by comparing with the field data obtained from the city itself. In this way, it collected a fine-tuned data for all major cities of the country as stated above and for the country itself, at large [113].

Similarly, we obtained average daily weather data including temperature, rainfall, sunshine and humidity recorded in the weather station of the district office of Bangladesh and Singapore Meteorological Departments (BMD) located in Dhaka for the city of Dhaka and Singapore respectively. Then, the daily average maximum and minimum temperatures, average rainfall, sunshine and relative humidity data were obtained from the Met offices of Dhaka and Singapore over a period of 10 years (2000-2009) and (2010-2020) for Dhaka and Singapore which later were compared and with the national data obtained from BMD for each district and zones of Bangladesh and Singapore to get a mean value as done in dengue study case [110].

For data analysis and interpretation, SPSS software (version: 20) and other mapping models were used. The plan was simple and included running frequency tables and some cross tables. Prediction analysis was done based on MCDA process with weighted values of each variables, which is the crux of the study, elaborated at length in the Methodology and Data Interpretation Chapters [113,154].

1.10 Study in Context:

Since the time of Eon, human mobility is an integral attribute of human being. The pull factors for human migration include economic necessity, better living standards, better and safer society and social factors e.g., health, education and humanitarian dimensions. Important push factors are environmental deterioration, man-made and natural disasters. Movement across borders and internal displacement also take place for economic, cultural, social and political reasons. Unfortunately, though, human mobility also entails movement of viraemic people and infected vectors expanding the range of the infected diseases. Along with human movement, comes the behavioral patterns and attitudinal perspectives of different communities which bring around newer health event or state in a new society. Dengue spread, while remains a classic case in the cities of Dhaka and Singapore in this regard, government's agencies' helplessness to contain it despite all out efforts is also noteworthy [148,157,158].

In the past , dengue used to occur in the city of Dhaka sporadically from 1964 until a discernible epidemic in 2000 established the disease as a new phenomenon in the societal and state psyche. The first introduction of dengue in this city and the country at large was traced back so as to single out the sources and factors likely to contribute future episodes of the diseases here. It was found that, the surge in 2000 was likely the result of the import of the strain of the virus from a nearby endemic country, probably nearby region of the South East Asia or ASEAN region. This prompted us in selecting Singapore, an ASEAN country, which is also a City State, as the other study area. In the study areas, the highest incidence of cases was reported in 2002, following which there was a general decline in the annual surge, although there were enhanced incidences in the alternate years subsequently. The decline in the incidence might have been because of increased public awareness, which is a general reaction of any population towards a new disease or health events, which resulted in a reduction of the propagation of mosquito and an increase in the herd immunity. Also, there is a subsequent change in outbreaks' incidence with mandatory introduction of serological diagnosis in the case reporting of the dengue disease in clinical set ups. Further, many of the dengue cases didn't report to the hospital as only a few of the total dengue fever requires hospitalization. So, the apparent reduction of the dengue incidence was a fallacy of the surveillance system. Serological testing of patients in hospital testifies that, dengue incidence is on the rise and it did never decline. In the days to come, paucity of intervention and prophylaxis, rapid urbanization, erratic environmental factors and human mobility with ecological changes might fortify the incidence of dengue. Predicted rise in global temperature and rainfall may exacerbate it further.

the largest number of cases was notified in 2002 and since then reported outbreaks have generally declined, although with increased notifications in alternate years. The apparent decline might be partially due to public awareness with consequent reduction in mosquito breeding and increased prevalence of immunity. However, passive hospital-based surveillance has changed with mandatory serological confirmation now required for case reporting. Further, a large number of cases remain undetected because only patients with severe dengue require hospitalization. Thus, the reduction in notification numbers may be an artefact of the surveillance system. Indeed, population-based serological survey indicates that dengue transmission continues to be common. In the future, the absence of active interventions, unplanned urbanization, environmental deterioration, increasing population mobility, and economic factors will heighten dengue risk. Projected increases in temperature and rainfall may exacerbate this.

For both study areas, while there is strong biological evidence for these effects, empirical studies of the relationship between climate and dengue incidence in human populations are potentially confounded by seasonal covariation and spatial heterogeneity. Using 20 years of data and a statistical approach to control for seasonality, we show a positive and statistically significant association between monthly changes in temperature and precipitation and monthly changes in dengue transmission in the areas concerned. We also found that the strength of this association varies spatially, that this variation is associated with differences in local climate, and that this relationship is consistent with laboratory studies of the impacts of these factors on vector survival and viral replication. These results suggest the importance of temperature and precipitation in the transmission of dengue viruses and suggest a reason for their spatial heterogeneity. Thus, while dengue transmission may have a general system, its manifestation on a local scale may differ from global expectations.

Climate change is likely to profoundly modulate the burden of infectious diseases. However, attributing health impacts to a changing climate requires being able to associate changes in infectious disease incidence with the potentially complex influences of climate. This aim is further complicated by nonlinear feedbacks inherent in the dynamics of many infections, driven by the processes of immunity and transmission. Here, we detail the mechanisms by which climate drivers can shape infectious disease incidence, from direct effects on vector life history to indirect effects on human susceptibility, and detail the scope of variation available with which to probe these mechanisms. We review approaches used to evaluate and quantify associations between climate and infectious disease incidence, discuss the array of data available to tackle this question, and detail remaining challenges in understanding the implications of climate change for infectious disease incidence in the years to come. We point to areas where synthesis between approaches used in climate science and infectious disease biology provide potential for progress in future.

There have been a methodological approach to outline mechanisms underlying climate and infectious disease associations in non-human pathogens [159,160], reviewed conceptual challenges in detection and attribution [161], and provided an overview of core knowledge gaps [162]. A similar Standard Operational Procedure (SOP) for human pathogen and health events have been tried to work out in this research.

Here, endeavors have been made to review the mechanisms by which climatic variables might affect infectious disease transmission (dengue as the subject disease), issues and challenges involved in linking climate drivers to infectious disease (dengue) transmission, codify a unified system incorporating statistical and mechanistic models that can be used to quantify these connections, and finally inference were made as to how these might contribute to generating future projections, prediction and prevention of the effects of ecology and epidemiology on the given disease and or health event [69].

1.11 Major Areas of Contributions:

The study is expected to add new dimensions to the body of knowledge of the field. The major areas of contribution are:

- In theory, establishing the causal relations of any disease or health event is crucial as to its prediction and prevention is concerned. Taking dengue as a model case in Dhaka, Bangladesh and Singapore, this study has ventured to adopt a stepwise approach to establish the correlations amongst the triad of disease causation, i.e., host-agent-environment. It also explored the ecological and anthropomorphic factors responsible for the outbreaks of dengue in the cities of Dhaka and Singapore.
- The study was able to deduce a significant correlation between climate variable and availability of the vector, ecological factors and vector density and between vector abundance and dengue occurrence in temporal and spatial dimensions.
- Also, the study undertook extensive analysis of the annual, seasonal and decadal variation of climate factors and dengue incidences thus generative a useful data set for future study and research on the effects of climate change as well as ecology on dengue transmission in Dhaka and Singapore, in the regions of the South and South East Asia at large.
- Based on the findings, a model mapping system was envisioned to predict the future incidence of dengue and thereby, to predict any such disease or health event and devising prevention guidelines thereto at local, national, regional and global level
- In one hand, differences of variables in different cities and regions have been proved as to applying one regional model for another region, on the other hand, incorporating crucial variables in one model through a compare and contrast study enabled to frame a relatively common model mapping system applicable for any given entity of a region. It is a huge enabler on global and regional scale to address the outbreak of any given disease in entities

with different economic setting. Mapping and modelling by addressing Spatial variations is an important novelty of this study.

- Finding out temporal variations of variables over time, particularly decadal impact of variables is another crucial attribute of the Model to apply it effectively in preventive medicine and urban planning.
- This research also found that city areas with more paved roads and concrete buildings and infrastructures did exhibit a higher number of aedes population. The results depict that, rapid changing in urban ecology, particularly unplanned urbanization may pose a big threat for the accelerating spread of dengue, especially in metropolitan areas. This is a crucial inference as to the dengue prediction and prevention mapping is concerned that, unplanned urbanization, particularly development of shanty slum area is crucial to dengue fever spread.
- Again, the mapping results of this study have important contributory function to aide in taking appropriate, differentiated policies for containing multiplication of vectors and propagation of dengue disease in Dhaka, Bangladesh and Singapore, the region and the globe at large.
- Finally, through the integrated dengue management framework based on a model eco-epidemiological mapping system is expected to play a pivotal role in upgrading national health sectors of the cities of Dhaka and Singapore and can contribute towards policy guidelines for any health event or disease across the country, the region and the world in general.

The contributions of this Study have further been detailed in Chapter 7 (Summary and Implications).

1.12 Limitations of the Study:

As any other vigorous research study, this research also faced with numbers of limitations, which, nevertheless, will act as torch bearer for further research in this field. Some of the limitations are:

First, continuous time-series data on dengue infected cases, the viral information and vector epidemiology difficult to retrieve from public depository, which the study team had to prepare impromptu by themselves based on the secondary data available.

Secondly, owing to paucity of resource, time, and data, this study was unable to investigate the relationship between climatic variables, ecological factors and vector breeding. The seasonal variations could not therefore be analyzed.

Thirdly, keeping out the private hospitals out of the research areas remain a limitation of the study, as gradually more and more private sectors are being involved in the health management of the both the study areas.

Fourth, framing a detailed questionnaire on institutional (governmental and NGO) control measures beyond the scope of this study, as it was not crucial for model development. However, further study and research on these issues, with a holistic approach to incorporate public and private sectors alike in the effective vector and dengue prevention and control will be important as to devising a better control program of the disease.

Fifth, surveillance data on aedes mosquito or dengue disease incidences in Dhaka, Bangladesh and Singapore were not tailored for longitudinal analysis. Moreover, in the absence of a statutory principle, the limited data available were not ready to be used in general as there is no data sharing policy procedure in place across the different administrative authorities of the study areas. This posed the most serious limitation while conducting this study.

Sixth, although, dengue mapping model was almost a unique one, it could easily be deducted that, the model could be applicable for all vector borne diseases, however as to other diseases, agent-host-environment needs to be weight- adjusted which remains a crucial limitation, as well as lesson, from this study prior to delving into development of a Map for any given disease or health event. A few studies on such a few diseases or health events could have been more fitting to show the implications of the Model.

1.13 Thesis Outline:

- Fundamentally, the presentation of this thesis abides by the structural guidelines of the doctoral thesis espoused by Perry (1998). The study kick started by outlining the broad view of theoretical gap and practical new normal leading to the core issue of the research. The identification of the problem then follows a conceptual framework being supported by the theory and literature to testify it empirically and conceptual validation. The overall framework as well as organizational outline of this thesis is elaborated in this section. The thesis comprises **eight chapters** and each of the chapters is introduced as under:
- Chapter 1: **Introduction** describes the concept of the topic, background of the research and problem, research question, objective of the research, a framework based on background literature, scope and significance of the study, brief methodology, research context, expected contributions and finally, limitations of the study.

  Chapter 2: **Literature review** explores major perspectives which solidify the review of the theories, general focus in different types of studies concerned, mainstream studies of the topic and review of the identified antecedents.

Additionally, this chapter discusses the literature related to the antecedents of the topic from diverse angles and dimensions than simply from the context of new research question.

- Chapter 3: **Conceptual framework** develops and finalize a conceptual model based on a comparative and contrastive relationships of different variables of the core topic and a framework for conceptual insight to explore the unfolding dimensions of the topic, ie model generation and its development process based on qualitative data. This chapter further proposes a competing model to verify the mediating impact of the new factors along with plausible paucity of the old and existing correlations.
- Chapter 4: **Methodology of the study** pens the relevant scientific, statistical and numerical research approaches to be followed in this study. These include the rationale for the qualitative and quantitative approaches for this study, population and sample, response rate, unit of analysis, selection of key informants, measurement of constructs, research instrument, survey data, analytical tools of quantitative data, qualitative data collection, protocol and analytical approach of qualitative data.
- Chapter 5: **Sample profile, measurement model development and testing the proposed models of Singapore data.** The sample profile details the sample demographics, responses, data cleaning and descriptive statistics. Secondly, in the process of measurement validation, all construct measures have been assessed individually in myriads of models available. Finally, proposed and competing models have been tested and compared with the overall measurement

model to verify the overall fit to the data and the theory.

- Chapter 6 discusses the same things about city of Dhaka, Bangladesh aspects.
- Chapter 7 differentiates the **findings** of Singapore and Dhaka, Bangladesh study.
- Chapter 8 gives the summary and implications of the research, most specifically, the novelty of this study. To crystalize the answer to the research question and to innumerate the objective, this chapter synthesizes the overall findings, which follow the implications for researchers and practitioners of the days to come. Detailed contributions to the theory and the body of knowledge have also been discussed here. Being obliged by the present research findings and background, several future research directions have been suggested herewith. Finally, the limitations of this research have also been depicted to be overcome by future workers in this field.

In sum, this chapter has elaborated the background and overview of the thesis. The background study explicitly explores the research gap that emanated from the literature review. The research problem, research question and objective, and justification of the study highlight the importance of undertaking this research. This chapter also provides an outline of the research framework, methodological approach, and areas of contribution. Given the framework of this thesis, the following chapter contains a comprehensive discussion that emerged from a detailed, critical, and exhaustive review of the literature focusing on infectious disease predictions from various perspectives.

Chapter Two

2. Literature Review

2.1 Overview:

Since the time of Eon, even before the basic ideas and notion of the causative agents of infectious diseases, people were aware that climatic change had had a relationship with epidemic. The Roman orthodox leaderships used to take refuge in mountainous abode in summer to avert malaria, while the South Asian discovered that, foods cooked with strong curry items could deter diarrheal diseases [163].

A vast number of the infections are benign and even have benevolence for both the host and vector. Only a meagre number of them do cause adverse impact on hosts, thus bearing the name 'infectious diseases. In the long sojourn of human cultural and social advancement along with human mobility and interaction, the patterns of theses infectious diseases have also evolved diversely. So are the impact of agricultural evolution and livestock's herding which have had a direct bearing on the course of infection and infectious diseases [163].

Now a days, keeping pace with socio environmental changes in both low- and high-income settings, human mobility has become the prime mover of rapid spread of infectious diseases [21]. Particularly in the low altitude areas in both sides of the Equator, the traditional regions of high biodiversity, emergence of newer pathogens are discernible with the rapid change of ecology [20,164].

Anthropogenic interactions of habitat and habitants are important modifiers of transmission of endemic infections to epidemic scales. These drivers range from water-land-air pollution, rapid and unplanned urbanization, deforestation, road and dam constructions, agricultural encroachment, erosion of river and ocean and human migration [165].

Socio-economy, health and hygiene, body immunity are amongst the most important factors that modulate the transmission of infectious diseases [23]

Climate conditions have been sensitively corelated with numbers of infection-their agents, vectors, reservoir, and their biological replications [105]. To explain these correlations, several theories have been developed over time. These include high multiplication and reproduction at high temperature, extension of transmission seasons owing to change in climate, change in ecology and its balances with nature, vectors migration, changes in hosts and reservoirs of pathogen in relation to climate change. So, a careful assessment and analysis is warranted as to any discourse and decision between climate change and infectious diseases [23].

Keeping pace with the forces of urbanization, there have been rapid change in human life and habitat, ranging from working conditions, consumerism, population aging, changes in social norms and values, cultures and behavior, and health service techniques and technologies. With these, there are emergence of new diseases and manifestations of old diseases including their spread and virulence in newer forms to adapt with the new ecology, environment and human nature [166].

Unlike other health events, infectious diseases are very much dependent on climate sensitive entities like biology and behavior of both hosts, agents, and environment. So, with the change of global climate and day to day environment, it is likely to impinge on disease pathology, progression, and impact on human life. It is likely to manifest in depths and dimensions, particularly in transmission and expansion in newer time and space lines, in the coming years and decades as the newer change in global climate become more and more evident. Along with the climatic changes, are the changes in social, economic, behavioral and habitat factors which are equally contributory to the factors and processes of infectious disease causality, transmission, and impacts [166].

The World Health Organization (WTO), brought into fore the plausible causes of communicable diseases and health events with respect to human environment and ecology through a report published in 2017. The discernible causes enlisted include, climate change, stratospheric ozone depletion, changes in ecosystems due to loss of biodiversity, changes in hydrological systems and supplies of freshwater, land degradation, urbanization, and stresses on food-producing systems.

The symbiosis of human being with domesticated animals and wildlife poses important links as to the causation of infectious disease outbreak in the past centuries [167]. However, the etiological link between host and pathogen varies with species diversity and diversity of the composition of the community [168]. Therefore, it is of crucial importance to realize the correlation between the effects of fragmentation of habitat and other changes in ecology on host–pathogen interactions [164,169].

In 1878, during one of the strongest El Niño episodes on record, one of the most severe summertime outbreaks of yellow fever took place in the southern United States. In the Northern hemisphere, it is now an established fact that, mid-winter is the season of recurrent influenza epidemics every year [163].

Emerging infectious diseases (EIDs), in line with the historical perspectives, continue to pose global threats with rapid dissemination [170,171]. Therefore, it is the call of the day that, to efficiently device EID prevention and control plans and programs, the complex and un-orthodox relationships among myriads of hosts and pathogen, environmental change, and members of humankind ought to be understood [172]. Only a developed and specific surveillance systems could provide better understanding for analysis of the emergence of newer diseases [164,173].

This review of the extant literature is devised to study the theoretical foundation highlighting different studies conducted as to the causal relationships of disease, agents and environment to predict and prevent future incidence of such disease and health events, with particular regard to Dengue infections in Bangladesh as a subject case to develop a general model applicable to all health events and states. This attempt also ventures to solidify the antecedents of evolving gap so as to design a model to address such gap. In this chapter, all these directions have been exhausted in the context of narrowing the research gap to answer the research question. The aims of this chapter are to:

- Review the relevant theories and their rational arguments into a new theoretical paradigm (Section 2.1.1)
- Review the supportive streams that provide more insights for this study (Section 2.1.2)
- Consolidate the comparative and contrastive studies of modelling methods which have provided a clear indication of antecedents of new ideas in this regard (Section 2.2.3)
- Review the relevant literature related to the identified antecedents of Modelling and to specify their probable impact on new model designing (Section 2.2)

- Synthesize the review to consolidate the antecedents mapping and modelling methods. (Section 2.3)

2.2 Review of the Fundamental Research Streams:

The main purpose of this review is to develop a theoretical grounding of the study of dengue, its host, vectors and environment to discern the correlations amongst the variables so as to identify antecedents of epidemiological and ecological approaches for devising a comparative method of predicting the disease incidence. Initially the review consolidates literature on relevant theories before discussing the literature pertinent to epidemiology, ecology, mapping, and modelling. Further, the review identifies some of the key studies that have examined either of these issues. Therefore, the following sub-sections review following fundamental research streams for this study; the theoretical foundation, a brief review of the pertinent studies, studies of prediction models and methods.

2.2.1 Study on theoretical foundation:

Of late, transmission of infectious diseases from animal to human being have phenomenally enhanced, such as HIV-AIDS, tick-borne diseases, mosquito-borne diseases, and most importantly bat-induced Covid-19 global pandemic. While these have a huge and devastating impact on human health and development, primary negligence as to the early reporting of such cases have not been conducted historically lest it had impacted regionally or globally [170].

Humankind strived for finding ways of salvation from the scourge of infectious diseases without any avail. However, by the late 20th century, with the invention of modern techniques as to diagnostics and therapeutic inventions, the prevalence of infectious diseases went down to a great extent. But unfortunately, despite the discovery of antibiotics and sophisticated treatment methods, newer arrays of infections ushered in under the pretext of bioterrorism, population mobility, erratic climatic behavior and unequal distribution of health facilities (in line with wealth cycles of the state and society). It has thus warranted a second thought as to giving prevention and control of infectious diseases a place ahead of treatment [174].

Environmental change lies in the epi-center of emergence of newer infectious diseases and re-emergence of ancient world's infection, as postulated by modern day public health scientists [175–177]., the real causology as to the establishment of relationship between diseases and key factors of environment and ecology is still evolving. Some put more emphasis on proximal environmental characters such as agent-host-ecology cycles than the distal factors like habitat development, water and land use, biodiversity loss etc. for the causation of prevalence, distribution and severity of infectious diseases [178].

Human ecology is classically dubbed as the study of interactions amongst individuals and groups and their aggregate and segregate actions with the environment they live in. Thus Disease Ecology , which entails medical geography and epidemiology is of critical approach as to understanding emergence and resurgence of diseases, particularly infectious diseases [179,180]. Again this human interaction is very much a politico-economic and social issue. Starting from land and resource distribution, addressing environmental preservation vis-à-vis economic development are all dictated and discerned by socio political governance. Thus Political Ecology and Political ecologic approach has gradually been developing as a new tool for interpretative framework for new disease emergence and their prevention and control (Political Ecology vs Disease Ecology – new approach to framework of disease epidemiology) [181].

2.3 Epidemiological theories:

The definition of Environmental Health, to be more specific, the Environmental dimension of Health has tracked a tortuous and serpentine route in its evolution from ‘bad, toxic air’ theory to ‘germ theory’. Surprisingly, though seemingly funny, the former theory emphasized a great deal on environmental protection in comparison to the lately evolved postulate. According to the ‘bad, toxic air’ or Miasma theory, foul smelling environment emanating out of a bad environment was causative agents of infectious disease, thus putting more impetus on environmental cleanliness and biodiversity management. However, following the postulate of scientific Germ Theory that, microbes lie in the core of causation of all infectious diseases, the social environment and its determinants’ contributing roles in the etiology of diseases supplanted resulted in an ear of negligence towards the environment, in the age of so called first and second industrial revolution. However, of late, the very role of environment, particularly its interaction with humankind under the guise of ecological exchange has been established as the pivot of infectious agents’ life and thrive in the environment to impart infection in human beings. So the combined role of environment and ecology as to the prime mover of infectious disease prevalence, spread and containment has now again taken its firm seat in public health domain [182].

The rather side line benefits of Miasma theories such as reducing the spread of habitat of mosquitos in the wetland by water removal during dry season, removing raw waste from river and pond beds, thus reducing water-borne diseases and relocating habitat in fresh location continued till late 1800. Later on, with the advent of germ theory, all these but went to die down completely after their very recent rejuvenation from long hibernation after the renewed emphasis of environment and ecology as to the causation of spread of diseases [183].

Over the years, scientists have developed two basic systems to quantify the disease occurrence and causal factors-the risk factor approach and biological approach. The former is based on association of disease occurrence with factors ranging from environmental, behavioral, ecological, and genetic attributes. In this approach, an odds ratio or relative risk is calculated based on presumed factors of causation so that preventive measures could be taken apriori. On the other hand, the biologic approach, which has evolved since 1980s is a statistical method based on evolutionary dynamics of host pathogens interactions, which is essentially a function of fundamental biology of host and agents such as, mutation, gene flow & migration, contact & transmission rates leading to a complex but natural disease patterns in time and space. Since this phenomenon is derived from underlying dynamics of host and pathogens, it is of crucial importance as to understanding deeper causal mechanisms in addition to predicting disease patterns. Not to speak, the future discourse of disease epidemiology will revolve round this approach as it seems to be the holy grail the scientists have been expounding over ages [174].

In the contemporary public health age, biomedical thoughts and praxis have evolved in a different dimension based on previous experiences of Miasma or Contagion versus Germ theory of disease causation. The former approach led to the innovation of healthy practices such as sanitation, hygiene, habitat and food & nutritional dimensions of health leading to giant leaps in extended life expectancy and longevity[184], even though the proper scientific pathophysiological and patho-epidemiological studies were yet to be discerned under the auspices of this method [185].

In contrast, with the invention of the Germ theory of disease causation, a reductionist trajectory developed in public health domain which, inter alia, emphasized on vaccinations, antibiotics and therapeutics, pesticides and larvicides and biological barriers to infection. This praxis has resulted in wonderful improvement of public health with regard to communicable diseases' spreading.

Given the fact that, establishing the ecological and environmental factors as to the causation and impact on disease prevalence is not based on empirical studies, the study of natural pattern changes in disease modality (although, mostly caused by epigenetics) and subsequent preventive measures seem to be the call of the day and of future in Public Health and Epidemiology. This research is intended to establish this trajectory of future preventive medicine in epidemiology based on a comparative studies of contrast of eco-epidemiological causation in different scenarios, while synergistic statistical changes in disease patterns in those varying environment [178].

2.4 Ecological theories:

Keeping pace with the advancement of civilization and development, newer and newer diseases are surfacing. These emergences of diseases are attributed to either the resurgence of hitherto unknown diseases, thanks to newer technology and technical know-how or due to spread of old diseases in new domains in both time and space [176]. Both causalities have largely been resulted from a number of factors ranging from social, economic, scientific, environmental and demographic dimensions [186]. For instance, human mobility has been attributed to many new diseases in the course of human development, such as small pox, plague, cholera and covid19 in recent times. So newer infections will continue to be discovered while old infections will go on changing in virulence, frequency, and geographical dispersion [187].

Although the agent-host-environment relationship is yet to be discerned holistically, it is understood that, the three components of infectious disease cycle remain in a dynamic equilibrium under normal situation. Newer diseases ensue when this equilibrium is breached, mostly owing to ecological disturbances, such as changes in land use, human mobility, building new structures etc. Historically, the European and American explorers were witnessing victims of this ecological imbalances, perpetrated mostly by themselves [188–192]. Contemporary examples include, flare up of Schistosoma infections following the construction of Aswan Dam in the Nile in Egypt, increases in malaria after Volta River project in African heartland, increase in malaria following deforestation in Malaysia for rubber plantation and most lately, reforestation (!) of sub-urbs in the US Mid-East resulting in increase of Lyme's disease, by bringing the deer-the bearer of vector(Tick for Borrelia burgdorferi) to close proximity of human habitat [181].

To address the causality factors for increasing trends of infectious diseases in space and time, a number of interdependent socio-political, economic and environmental issues have been discerned. These include, increasing in number of populaces, unplanned urbanization, migration, in equal distribution of resources and facilities, climate change, loss of biodiversity and lack of infrastructure etc. [193]. It is hoped that, once the causal relations are established, it will lead to a framework action as to prevent or contain the incidence of newer disease, curtail the emergence of newer infections and the prediction, detection and control of future diseases and thereby minimizing their impact [172,193].

Human mobility, mode of transportation and population concentration has directly been attributed to spread of infectious diseases in space of time through empirical studies. The human migration, both forced and opportunistic may equally contribute to the dispersion of diseases. It may happen either by the conveyance of diseases with the migrant themselves or through their vulnerability to a new pathogen faced by them in the new setting. Means of transportation has become yet another factor contributing to migration of diseases. For example, the postulate of ' airport malaria' which is a concept of malarial outburst amongst the people living in vicinity of the airport areas in the United Sates, England and the Nordic Countries (National Research Council, 2001), Asian dengue vector-Aedes albopictus, reported to be air borne to Houston in wet tires of consignment carrying wagons etc. are mentioned worthy in this regard [121,194].

Community ecology aims to identify the factors that govern the structure, assembly, and dynamics of ecological communities. This study describes how analytical and conceptual approaches from this discipline can be used to address fundamental challenges in disease research, such as (i) managing the ecological complexity of multi host-multi parasite assemblages; (ii) identifying the drivers of heterogeneities among individuals, species, and regions; and (iii) quantifying how processes link across multiple scales of biological organization to drive disease dynamics. It shows how a community ecology framework can help to determine whether infection is best controlled through “defensive” approaches that reduce host suitability or through “offensive” approaches that dampen parasite spread. Examples of defensive approaches are the strategic use of wildlife diversity to reduce host and vector transmission, and taking advantage of antagonism between symbionts to suppress within-host growth and pathology. Offensive approaches include the targeted control of super spreading hosts and the reduction of human-wildlife contact rates to mitigate spillover. By identifying the importance of parasite dispersal and establishment, a community ecology framework can offer additional insights about the scale at which disease should be controlled [195].

Based on hitherto discussion, gradually there have been development of a new discipline to study the issues governing structure, aggregation, and dynamics as to the communities in ecology. It has primarily been named as Community Ecology. It entails, inter alia, study of topics, such as management of multiple hosts and agents interactions in a given ecological setting, identification of diversities amongst host, agents and environments, quantification of disease dynamics in complex linkages. Gradually, two holistic approaches of prevention and containment of infectious diseases have evolved under the paradigm of Community Ecology namely Defensive and Offensive Approaches. The former espouses strategic use of diversity in the wild and its livelihood to shackle spread of vector, pathogen and host interactions, thereby using the opposition of inmates of hosts' symbiosis to curtail growth and pathogenesis of the microbes. The offensive approach, on the other hand, target the superfluous spreading of hosts and their contact with wildlife to mitigate the infection rates. Community Ecology, thus offers the measurement of the scale of controlling the infection to impart a permanent impact on the disease spread in the long run [195].

2.5 Mapping models

Stocking myriads of data is a prerequisite of disease mapping. The first and foremost information required is the scientific study of host-pathogen relationship for the causality of a disease or a state of health. Secondly, the trend of spatial and temporal expansion of disease is a crucial factor to map a disease. The third information is how this trend is influenced by environmental and ecological factors. The fourth and most important factor is the reliability, robustness and contemporariness of the gathered data which is essential to predict and formulate a nearly real mapping of a disease or health related state and event of a given entity [196–198].

A variety of mapping are in force in epidemiology. Point data mapping is used practically to showcase prevalence data or incidence data from a geographical perspective. Occurrence data map, on the other hand is the graphical presentation of an observation of any disease or health state or event in time and space in a given geographical entity {HealthMap/ProMED [82,199], BioCaster [87,88] and Argus [89,200]}.

The principal achievement of a mapping endeavor is to find out an accurate measurement of endemicity of a given disease in a given area [201]. This endemicity is a function of prevalence of a disease in an area and fraction of the cases and control in the populace concerned in time and space. This , in turn, enables the authorities to afford variations of operations and endeavors of public health interventions, such as measurement of clinical burden [79,202], national reproductive number measurement [80,203] which in turn, lead to a national feasibility assessment and action plan.

Based on Point Observation of Occurrence, this study, has endeavored to develop a method of mapping, named Boosted Regression Trees (BRT) method, with the prime objective of discerning the basic niche of the target pathogen in relation to host and environment [204]. To be more specific, the environmental, ecological, and clinical factors directly impacting the pathogen and pathogenicity of the disease were enumerated and depicted in the map to have a direct impact study. The factors that paved the way of decision towards this method, include,

A. Out of a number of study, BRT method has topped in terms of accurate evaluation of Area Under Curve(AUC) and Correlation statistics [78,205];

B. Both continuous and categorical data of all kinds of predictor variables could be easily accommodated in this Method.

C. It is user friendly and pretty easier to understand and implement.

D. It includes a ranked codes of environmental and ecological predictors, which do not need further justification [65].

Important usefulness of mapping include:

i. Determining crucial baseline estimates of diseases [206–211];

ii. Transmission factors of diseases [212–214];

iii. Clinical burden in the society [81,202,215,216];

iv. Surveillance system and outbreak tracking undertaken by the stake holders [86,217];

v. Resource allocation at micro, meso and macro levels [82,218–221];

vi. Local, national, regional and international travel restrictions [222–224] etc.

In contrast to the easier system of developing mapping, there has always been a gap between the data available and the map drawn to use for preventive and surveillance medicine. To address this issue, a software named the Atlas of Baseline Risk Assessment for Infectious Diseases (ABRAID) has been developed over time which can use continuously updated data and do depict situation mapping accordingly in an automation fashion. For individual infectious disease, disease specific methodological data or spatial inference method as and when necessary, are used to tailor the disease specific map [224,225].

The databases in force have two major setbacks. The first is mainly resulted from irregular pattern of collection of data when different countries need data on a given time. This is crucially needed when subnational and regional data required to be discerned from methodical periodic census data of individual country [226]. The second constraint is unavailability of the specific epidemiological information of the population mapped under a census data-base. So different data sets need to be incorporated and integrated into mapping before being produced from census data [226,227].

The classic example of spatial analysis of epidemiological data in the Soho area of London in 1854 to detect the source of cholera in the area-the infame water pump and its subsequent removal to cutdown the cholera infection in the area, constitute the basic premises of spatial mapping and its significance [228]. Routine datasets which are gathered in hospital setting might usher in new era of epidemiological diction if they were inclusive of the area and habitat of the cases and cohorts. The relation between geographic context and incidence of any given disease is not only important from predicting or preventing a communicable disease in a given area, it could equally been applicable in other health states and events, such as pollution or radiation in relation to childhood leukemia and other relevant diseases [229–237]. So a simple tools and application should be designed and developed so that, health professionals in general can easily be contributive as well as beneficiary in formulation of the spatial mapping by applying spatial dimensions of diseases and health states [238].

Chapter Three

Conceptual and Theoretical Framework

3 Theories of new model:

The contemporary modelling techniques for mapping of diseases and health states revolve round the Presence and Absence databases as and when necessary. The Presence data are of particular importance in geographical distribution in both time and space of factors concerning planning, epidemiology, ecology and evolution of communicable species [239–244]. General-purpose statistical methods are used in depicting both Presence and Absence database [242,245]. Presence only data are modelled in conservation purpose while Absence databases are used in poorly sampled data of tropical and high-altitude areas [246–248].

If we are to develop a model, or more specifically a mapping model, the fundamental principle would be co-relating the set of occurrence localities with environmental variables which are likely to determine the suitability of the environment to thrive a species in a particular locality [249,250]. Traditionally, the geographical location is discerned by its latitude-longitude pair which is applicable to all such locations in the globe, where similar environmental suitability ought to persist, which will act as the function of environmental variables required for the livelihood of a given species or health state [247,251].

A niche-based model is the representation of the approximate ecological niche in each environmental facility. Therefore, there might be two sets niches – the fundamental niche and the realized niche. The former denotes the conditions, if persists, would cater the full realization of a species' thriving to the fullest form, while the later niche, the realized niche is the manifestation of the observed datasets in the given environmental conditions [252].

Over ages, it has been observed that, the realized niche is supposed to be smaller than the fundamental data due to factors like human influence (such as preventive measures), biotic and symbiotic interactions or geo-physical barriers which often hinders the dispersal, colonization, and habitation of the species in question [253,254]. However, with the advent of human influence in nature, particularly global warming and erratic climate behavior, some realized niche are becoming larger than the fundamental niche, indicating the excessive growth and dispersion of pathogen and health states, in a newly revived environment due to human activity. Revival of malaria in hitherto sub-tropic zones of Europe is a classic example in this regard.

In practical situations, the departure between the two niches is not discernible. However, from scientific and epidemiological context, if the two niche do not coincide, the modelling algorithm will not be representative of the occurrence localities. So , the intention of this study is to incorporate both the factors-environmental, fundamental factors and realization-influencing, ecological factors to develop the potential nice modelling which will be almost close to the reality [255].

Of late, a copious number of methods have been exercised and put into practice with a view to study biodiversity research [256], biology of conservation [257] and invasion biology [258]. These devices include, MaxEnt, GARP, CLIMEX, BIOCLIM, BRT, GLM, GAM etc. Out of them, MaxEnt has extensively been used on study based on Prsence-data only, such as, the study of climatic study of giant African snails (Achatina fulica Fe´russac, 1821) [259], Eastern grey squirrels (Sciurus carolinensis Gmelin, 1788) [260] and different xerophyte species such as orchids (Epipactis helleborine) [261].

MaxEnt has superiority over other methods in the following domains:

1. It does not need a comprehensive datasets, it only requires Presence-only data [205];

2. The MaxEnt software better user-friendly and economical via-a-vis other approaches [205];
3. It has been proved robust in modelling even scare numbers of data sets [262,263].

MaxEnt methodology is described underneath in a nut shell:

1. The software has been developed to measure incidence or prevalence of species by Presence-only data by tallying environmental data on given areas with known occurrences of a particular species. A target landscape or a model background is fixed for the comparison of the data [264];
2. All statistical sets such as , linear, quadratic, product , threshold and hinge methods are applicable in MaxEnt feature typology;
3. A continuous map is generated with an estimated Presence-only data in a 0-1 scale regarding prevalence probability;
4. A jackknife test is used to test the P value, i.e. Significance of the each of the variables

(To run the model, the convergence threshold (10−5), maximum iterations (5000) and max number of background points (10000) are used. The MaxEnt model is, at the outset, generated based on the 10-fold cross-validation method.)

The AUC of the Receiver Operating Characteristic (ROC), was used to estimate the performance of the model [265]. AUC values range from 0 to 1, where a value of 0.9 indicates high performance [240,266]. To improve the displays of prediction in this study, the continuous suitability maps predicted by MaxEnt were converted into suitable/unsuitable area (binary habitat) by applying a threshold value. Here, maximum training sensitivity plus specificity was used to define habitat and non-habitat for P. solenopsis. This threshold has been used in many primary studies [267–270].

Maxent has strong similarities to some existing methods for modeling species distributions, in particular, generalized linear models (GLMs), generalized additive models (GAMs) and machine learning methods such as Bayesian approaches and neural networks. GLMs, GAMs, Bayesian approaches and neural networks are all broad classes of techniques, and we refer here only to the way they have been applied to presence only modeling of species distributions. Theoretically, Maxent is most similar to GLMs and GAMs [271]. A frequently-used GLM is the Guassian logit model, in which the logit of the predicted probability of occurrence is

$$\alpha + \beta 1f1(x) + \gamma 1f1(x)\ 2 + \ldots + \beta nfn(x) + \gamma nfn(x)\ 2$$

where the fj are environmental variables, α, βj and γj are fitted coefficients, and the logit function is defined by logit(p) = ln (p 1−p). The expression in (6) is the same form as the log (rather than logit) of the probability of the pixel x in a Maxent model with linear and quadratic features. A common method for modeling interactions between variables in a GLM is to create product variables, which is analogous to the use of product features in Maxent. In the same way, if probability of occurrence is modeled with a GAM using a logit link function, the logit of the predicted probability has the form

$$g1(f1(x)) + \ldots + gn(fn(x))$$

where the fi are again environmental variables. The gi are smooth functions fit by the model, with the amount of smoothing controlled by a width parameter. This is the same form as the log probability of the pixel x in a Maxent model with threshold features, and regularization has an analogous effect to smoothing on the otherwise arbitrary functions g1. In both cases, the shape of the response curve to each environmental variable is determined by the data. Despite these similarities, important differences exist between GLM/GAMs and Maxent, causing them to make different predictions. When GLM/GAMs are used to model probability of occurrence, absence data are required. When applied to presence-only data, background pixels must be used instead of true absences[272]. However, the interpretation of the result is less clear-cut—it must be interpreted as a relative index of environmental suitability. In contrast, Maxent models a probability distribution over the pixels in the study region, and in no sense are pixels without species records interpreted as absences. In addition, Maxent is a generative approach, whereas GLM/GAMs are discriminative, and generative methods may give better predictions when the amount of training data is small [273]. For a joint probability distribution p(x, y), a discriminative classifier models the posterior probability p(y|x) directly, in order to choose the most likely label y for given inputs x. Typically, a generative classifier models the distribution p(x, y) or p(x|y), and relies on Bayes' rule to determine p(y|x). Our unconditional Maxent models are generative: we model a distribution p(x|y = 1) [255].

The basic essence of Maxent models is probability measurement of species presence by observing the dispersion and distribution of the maximum entropy (i.e., closest to uniform), with constraints poised by the empirical values of actually observed spatial distributions of the species and the climatic variables data of the given area [274].Maxent models generally rely on presence only data. They have extensively been applied to develop model for species distribution and have exhibited excellent predictive performance vis-à-vis other structured decision making models, particularly those models relying o presence-absence data [205,275]. Moreover, These models have also been applied in the distribution of project species given a rapidly changing climate milieu in future. [276,277].

Point Sampling is another model approach used to predict species distribution when only vector presence data are available [278]. It involves assigning the presence data in a random location within a given county or location. Then explanatory data are estimated at that point and assigned to the presence data for modeling with Maxent. To minimize the uncertainty emanated out from random data, the experiment is repeated time and again and the mean prediction value is calculated at each pixel.

Validation and evaluation of models are done by splitting the data into two parts randomly: training and validation datasets. In practice, 75% of the presence data are randomly selected to act as training data, with the remaining 25% acting as validation data [277,279]. To minimize the uncertainty resulting from training and validation set splits, the model results are repeated several times for each species and all data are used to make the final predictions. Point sampling model methods were first successfully used for malaria prediction when the above methods were separately and repeatedly used for all four species of anopheles mosquito -the vector of malaria juxtaposed to other climate variables responsible for the transmission of the parasite and propagation of the vectors [280].

The research approach here was to first analyze the mutual interactions of the epidemiological triad of agent-host and environment, subsequently to find out individual impact of the variables on each other, such as effects of climatic variables on dengue abundance, then subsequently analyze the effect of year/time on dengue incidence. The meteorological, ecological and dengue case data were analyzed in two stages:

3.1 Model 1: Analysis of climate & Ecological factors versus dengue case incidence:

At the outset, mean temperature (MT), mean relative humidity (MRH), mean rainfall (MR) and mean sunshine (MS) were calculated, apart from the ecological variables. We then attempted to find relationships between climate variables (MT, MR, MRH, and MS) and the number of confirmed dengue cases from clinical data. As the values were obtained by counts, the following Poisson Regression method was applied to model the correlations between climate variables and dengue incidence of study period (2004-2020):

$\log(\mu)= \beta 0 + \beta 1 *MT + \beta 2 * MRH+ \beta 3 *MR+ \beta 4 *MS + \beta 5* EF + error$ ----------------------- (1)

where; μ is the mean case count; $\beta 0$ is the intercept; $\beta 1$, $\beta 2$, $\beta 3$, $\beta 4$ and $\beta 5$ are the coefficients of MT, MRH, MR MS and EF respectively.

3.2 **Model 2:**

Analysis of estimated dengue cases over time/year: Here, we emphasized examining the relationship between predicted confirmed dengue cases over year. The following Linear regression model was used to predict the number of dengue cases over the upcoming year:

$Y_t= \beta 0 + \beta 1*X_t$, ------------------------------ (2)

where; Y_t is the estimated mean count dengue cases and X_t is the time/year.

3.3 Synthesis:

The above depictions result in a number of inferences, concerning climate data as well as ecological data. Therefore, further study needs to be undertaken to address this gap and provide empirical assessment which might aide in realization and understanding of predicting dengue cases and death resulting from dengue fever over the years.

Chapter Four

4. Methodology

4.1 Study Area and Design

Singapore**,** city-state located at the southern tip of the Malay Peninsula, about 85 miles (137 kilometers) north of the Equator. It consists of the diamond-shaped Singapore Island and some 60 small islets; the main island occupies all but about 18 square miles of this combined area. The main island is separated from Peninsular Malaysia to the north by Johor Strait, a narrow channel crossed by a road and rail causeway that is more than half a mile long. The southern limits of the state run through Singapore Strait, where outliers of the Riau-Lingga Archipelago—which forms a part of Indonesia—extend to within 10 miles of the main island.

The average monthly temperature varies from about 81° F (27° C) in June to 77° F (25° C) in January. The daily range is somewhat greater, averaging about 13° F (7° C). Singapore's maritime location and constant humidity, however, keep maximum temperatures relatively moderate: the highest temperature ever recorded was only 97° F (36° C). The seasons are defined by the relative incidence of rainfall, which, in turn, is determined by the movements of the monsoon air masses. The wettest and windiest period is during the northeast monsoon (November–March), with rainfall reaching an average monthly high of more than 10 inches (250 millimeters) in December. Conversely, the period of the least amount of rainfall and the lightest winds is during the southwest monsoon (May–September), with rainfall dropping to a monthly low of less than 7 inches in July. April and October are intermonsoonal periods characterized by sluggish air movements and intense afternoon showers and thunderstorms. Altogether, Singapore's precipitation averages about 95 inches annually, and rain falls somewhere on the island every day of the year (Singapore | Facts, Geography, History, & Points of Interest).

4.2 Data Collection Techniques

In Singapore, the Ministry of Health (MOH) is responsible for the epidemiology and clinical management of dengue, whereas the National Environment Agency (NEA), an agency under the Ministry of Environment and Water Resources, is responsible for vector surveillance and control. Under the Infectious Diseases Act, it is mandatory for all medical practitioners and clinical laboratories to notify MOH of all clinically suspected and laboratory confirmed dengue cases within 24 hours of diagnosis. Laboratory confirmation of dengue cases is achieved through nonstructural protein 1 (NS1) antigen detection, viral RNA detection by polymerase chain reaction (PCR), or immunoglobulin Mdetection. 14,15 Imported dengue cases are defined as cases who have traveled to a dengue-endemic area outside of Singapore within 7 days before the onset of illness. National Environment Agency's epidemiologically trained officers interview the cases when necessary to obtain epidemiological and demographic data including occupation, residential and school/workplace addresses, and dates of diagnosis and onset of illness. Data on deaths from DF/DHF are obtained from the national Registry of Births and Death (Dengue in Singapore from 2004 to 2016: Cyclical Epidemic Patterns Dominated by Serotypes 1 and 2).

4.3 Data screening and Analysis

The meteorological, ecological and dengue case data were collected, analyzed and interpreted as under:

Data

Monthly dengue cases from 2000 to 2020 in Dhaka city of Bangladesh was collected from the Directorate General of Health Services (DGHS) in Bangladesh. Climatic variables such as temperature, humidity, rainfall, and sunshine hour from 2000 to 2020 in Dhaka city were collected from Bangladesh Met Office (BMD). We consulted the MOH, Singapore (https://www.moh.gov.sg/) for all dengue data about the city of Singapore from 2000 to 2020. From 2000 to 2020, Singapore's maximum temperature, humidity, precipitation, and sunlight hour data are sourced from (https://data.gov.sg/).

Dependent variable

In this study, the total number of dengue cases for each month in both Singapore and Bangladesh has been considered as the outcome variable.

Independent variables

The maximum temperature (°C), humidity (g/kg air), precipitation (mm), and sunshine hour (in (average) hours per day) are the independent variables in this study.

Statistical Analysis

To determine the basic properties (mean) of each variable for every year, descriptive statistics are first calculated for both Bangladesh and Singapore. Secondly, to ascertain whether the dengue cases varied at different month and year, a time series plot and seasonal plot was also carried out. We also used the Augmented Dickey-Fuller Test to ascertain whether there is a correlation between variables of climate and dengue incidence and prevalence, regardless of period, we employed a stationary test with R packages t series. We also observed different seasonal plots to detect the seasonality of the data. Later we utilized different Seasonal Autoregressive Integrated Moving Average (ARIMA) models using different combinations of parameters ARIMA (p, d, q) × Seasonal (P, D, Q)s (Mekparyup and Saithanu 2015). The Akaike Information Criterion (AIC) was utilized to evaluate the models' fit quality. The lowest AIC values determine which model is chosen in the end (Adams and Somto 2022). Moreover, we also used Poisson regression to estimate the parameters and compare it with the Seasonal ARIMA model (Hossain et al. 2023). Machine Learning Methods, such as Artificial neural network (ANN), Support vector machine (SVM), error, trend and seasonality model with trigonometric seasonality (ETS), Trigonometric seasonality, Box-Cox transformation, ARMA errors, Trend and Seasonal (TBATS) model, and Two-component K-H model were fitted to forecast the dengue data (Du et al. 2021; Naher et al. 2022; Polwiang 2020; Redondo-Bravo et al. 2019). We used R software (version 4.0.0) to complete the analysis part.

Seasonal ARIMA Model

ARIMA model is a time series statistical model used to explore the time series nature of the data and forecast the future series points (Kharmayana Rubaya et al. 2018). The AR parts of ARIMA indicate that the outcome variable is regressed by its own lag values. The MA parts of ARIMA indicate that the regression error terms are a linear combination of the error terms at the current time point and with its past values. When the seasonality is reported in the data sets, then the seasonal difference needs to be addressed to reduce the seasonal component. Suppose Y_t is an outcome variable at time point t and e_t is a white noise with zero mean and variance then the AR model with order p can be presented as:

$$Yt \ = \ \beta 1Yt - 1 + \ \beta 2Yt - 2 + \cdots + \ \beta 3Yt - p + \ et$$

The MA model with order q is:

$$Yt \ = \ \alpha 1et - 1 + \ \alpha 2et - 2 + \cdots + \ \alpha 3et - q + \ et$$

Then the ARIMA model can be written as:

$$Yt \ = \ \beta 1Yt - 1 + \ \beta 2Yt - 2 + \cdots + \ \beta 3Yt - p + \alpha 1et - 1 + \ \alpha 2et - 2 + \cdots + \ \alpha 3et - q + et$$

The seasonal ARIMA model with seasonal order s is (Polwiang 2020):

$$\begin{aligned} Yt = {} & \beta 1Yt - 1 + \beta 2Yt - 2 + \cdots + \beta 3Yt - p + \alpha 1et - 1 + \alpha 2et - 2 + \cdots + \alpha 3et - q \\ & + (\Phi 1Yt - s + \Phi 2Yt - 2s + \cdots + \Phi PYt - Ps) \\ & + (\Theta 1et - s + \Theta 2et - 2s + \cdots + \Theta Qet - Qs) + et \end{aligned}$$

The first part represents the non-seasonal ARIMA model described earlier. The second part represents the non-seasonal MA model. The third part captures the seasonal AR component with coefficients Φ1 to ΦP. The fourth part captures the seasonal MA component with coefficients Θ1 to ΘQ and 'et' is the white noise error term with zero mean and variance, as you mentioned.

Artificial Neural Network (ANN)

Artificial Neural Networks (ANN) can be used in time series analysis to model and forecast time series data. ANNs are particularly well-suited for capturing complex patterns and relationships within the data. However, explaining an ANN model with a single equation is challenging, as ANNs consist of multiple layers of interconnected nodes (neurons). Input Layer (layer consists of neurons that represent the input features), Hidden Layers (these intermediate layers contain hidden neurons that perform various transformations and calculations on the input data) and Output Layer (layer typically consists of a single neuron (for univariate time series) or multiple neurons (for multivariate time series). Data processing, data splitting, model training, model evaluation, and model testing steps are involved in cases of forecasting ANN time series model (Polwiang 2020).

Support Vector Machine (SVM)

Support Vector Machines (SVMs) are mechanisms learning algorithm primarily intended for classification and regression tasks. SVMs can also be applied to time series data, particularly for time series forecasting, by treating the problem as a regression task. In time series forecasting using SVM, one would typically predict future values based on historical observations. At first, Time series data need to be prepared by splitting it into input (features) and target (output) variables. Each observation is paired with its corresponding future value (e.g., lagging the time series by one or more-time steps). Then the dataset is divided into a training set and a testing set for model evaluation. Depending on the problem, one can create additional features to support in forecasting. The SVM is trained as a regression model to predict future values based on the input features. The objective is to find a regression function that minimizes the prediction error. In the case of SVM regression, the goal is to find a function that estimates the target values (Y) based on the input features (X). The SVM regression equation for a linear kernel is as follows (Co et al. 2017):

$$Y = w \times X + b$$

Here, Y represents the predicted values (the target), X represents the input features, w is the weight vector, and b is the bias term.

The SVM regression algorithm aims to find the optimal `w` and `b` that minimize the prediction error while maximizing the margin between the predicted values and the training data.

Error, Trend and Seasonality Model with Trigonometric Seasonality (ETS)

Error, trend and seasonal models are used in time series analysis which decompose the models into three components including trend, error and seasonality. The ETS model can be written as under with Yt as outcome variable (Hyndman, R.J., & Athanasopoulos 2015):

$$Yt = Tt + St + et$$

Where Tt is the trend component, St is the seasonal component and et is the error component.

Trigonometric seasonality, Box-Cox transformation, ARMA errors, Trend and Seasonal (TBATS)

The TBATS (Trigonometric, Box-Cox transformation, ARMA, Trend, Seasonal) model is a comprehensive time series forecasting approach that incorporates various elements to capture and predict patterns in time series data. It integrates trigonometric seasonality through sine and cosine functions, applies Box-Cox transformation for data normalization, incorporates ARMA (Autoregressive Moving Average) errors for handling noise, and encompasses trend and seasonal components, enabling a comprehensive and flexible framework for time series forecasting. (Pal and Prakash 2017). The TBATS can be modelled as

$$Yt = Tt + S1,t + S2,t + \ldots + Sk,t + Et$$

Where Yt is the observed value at time t, Tt represents the trend component, S1,t, S2,t, ..., Sk,t represent the seasonal components with different harmonic frequencies (e.g., yearly, quarterly, monthly), and Et is the error term.

The Box-Cox transformation is used to stabilize the variance and make the data more normally distributed. It is applied to the time series data to reduce heteroscedasticity and ensure that the model assumptions are met. The ARMA component models the autocorrelation in the error terms. It includes both Auto Regressive (AR) and Moving Average (MA) terms to capture serial correlation in the residuals. The ARMA errors model can be written as

$$Et = \varphi 1Et - 1 + \varphi 2Et - 2 + \ldots + \varphi pEt - p + \theta 1Zt - 1 + \theta 2Zt - 2 + \ldots + \theta qZt - q$$

Here, Et represents the error term at time t, φ1, φ2, ..., φp are the AR terms, θ1, θ2, ..., θq are the MA terms, and Zt-1, Zt-2, ..., Zt-q are white noise residuals. The trend component captures the long-term changes in the time series. As part of the TBATS model, the trend component is typically more complex and may include additional terms to account for multiple trend patterns.

Two-Component K-H model

The Two-Component K-H (Kuznets-Henderson) Model is a time series model used to decompose economic time series data into two primary components: a short-term (cycle) component and a long-term (trend) component. In our study we assumed both short term and long-term dengue incidence cases. The K-H model can be represented as (Earnest et al. 2012b):

$$Yt = Tt + Ct + Et$$

Where Yt represents the observed value of the time series at time t, Tt represents the trend component, which captures the changes over a long period of time in addition to gradual changes in the data, Ct represents the cyclical component, which captures the short-term fluctuations in dengue cases and Et represents the error or residual component, which includes random variations and irregularities that cannot be attributed to either the trend or cyclical component.

Chapter Five

5. Data Analysis and Research Findings in Singapore

a. Descriptive Statistics

For this study, dengue and climate data from 1990 to 2021 was used. Maximum temperature, rainfall, humidity, sunshine hour was considered in this study. This study was considered the annual mean value of the mentioned weather variables. The descriptive statistics, such as mean, standard deviation, minimum and maximum dengue incidences, and climate variables, are shown for each year (Table 1). The mean maximum temperature was increasing over the year from 1990 to 2020. The highest temperature was recorded in 2016 and 2018. It looks like an ups and downs trends over the period. The lowest temperature was observed in 1992. The reported mean rainfall depicted an ups and downs patterns over the periods. But overall, it seems to be an upward pattern over the period. The mean humidity almost constant before 2011 and the mean value has decreased after 2011. Overall, the humidity has a downward trend over the year. The mean sunshine hour increased over the period and it showed an upward trend. The highest mean sunshine hour observed in 2019. The highest dengue cases were observed in 2020. It has also an upward trend over the year (Figure 1).

Table 1: Summary statistics: N mean sd min max by(year)

Year: 1990

	N	mean	sd	min	max
max temp	12	27.592	0.787	26.2	28.6
rain	12	126.983	60.602	24.1	204.5
hum	12	82.208	2.109	77.6	86
sunshine	12	6.2	1.251	4.6	8.9
cases	12	144.417	184.484	11	608

1991

max temp	12	27.433	0.888	25.6	28.6
rain	12	156.417	127.487	37.3	492.3
hum	12	83.133	3.491	78.7	90.7
sunshine	12	5.375	1.440	3	7.1
cases	12	181.583	227.506	21	667
1992					
max temp	12	27.35	0.884	25.5	28.4
rain	12	188.4	158.155	62.4	502.7
hum	12	83.308	2.898	80.5	90.3
sunshine	12	5.525	1.351	3.4	7.7
cases	12	239.833	256.876	19	765
1993					
max temp	12	27.433	0.815	26.2	28.6
rain	12	180.725	84.862	61.7	308.5
hum	12	83.658	2.728	79.4	87.4
sunshine	12	5.883	1.171	4.2	8.5
cases	12	78.833	73.478	10	256
1994					
max temp	12	27.592	0.664	26.7	28.4
rain	12	161.817	125.749	23.7	425.4
hum	12	83.317	3.124	78.7	88.4
sunshine	12	5.417	1.207	3.5	7.6
cases	12	103.25	104.645	13	345
1995					
max temp	12	27.583	0.810	26.3	28.9
rain	12	194.383	124.747	29.5	372.8
hum	12	84.542	2.047	81.6	87.5
sunshine	12	5.05	1.026	3.1	6.6
cases	12	167.333	169.653	23	545
1996					
max temp	12	27.492	0.742	26.2	28.5
rain	12	201.5	63.410	107.5	300
hum	12	83.35	1.252	81	85.5
sunshine	12	5.558	1.097	4.3	7.7
cases	12	260.667	261.541	23	807

1997					
max temp	12	28.25	0.757	27.1	29.3
rain	12	93.242	92.452	15.4	351.9
hum	12	79.633	2.882	76.5	85.3
sunshine	12	5.708	1.455	3.2	7.7
cases	12	358.333	347.648	50	1008
1998					
max temp	12	28.3	0.852	26.6	29.5
rain	12	218.592	121.852	32.5	463.4
hum	12	82.458	2.840	77.8	88.5
sunshine	12	5.725	1.635	3.1	8.9
cases	12	438.167	430.458	75	1380
1999					
max temp	12	27.492	0.548	26.6	28.3
rain	12	177.833	75.867	67.4	340.5
hum	12	84.158	2.105	81.7	88.3
sunshine	12	5.408	1.031	3.9	6.8
cases	12	112.917	70.944	34	301
2000					
max temp	12	27.458	0.642	26.3	28.6
rain	12	197.542	97.274	81.1	385.7
hum	12	84.742	2.087	82.1	87.6
sunshine	12	5.167	1.065	3.7	6.8
cases	12	56.083	36.669	7	122
2001					
max temp	12	27.608	0.653	26.5	28.5
rain	12	231.925	150.136	86.6	609
hum	12	84.267	1.915	80.8	87.4
sunshine	12	5.217	1.146	3.7	8.1
cases	12	197.667	153.977	34	565
2002					
max temp	12	28.083	0.675	27	28.9
rain	12	145.742	99.391	10.8	307.2
hum	12	82.492	2.613	79.2	88.7

sunshine	12	6.3	0.932	4.6	7.6
cases	12	328.75	202.835	202	899
2003					
max temp	12	27.75	0.823	26.5	29.2
rain	12	199.267	110.367	50.3	444.2
hum	12	84.3	2.695	78.5	87.3
sunshine	12	5.433	0.961	3.9	7
cases	12	399	164.043	144	740
2004					
max temp	12	27.858	0.765	26.8	29
rain	12	178.033	145.948	31.9	600.9
hum	12	83.467	2.429	79.8	86.7
sunshine	12	5.967	1.091	4.2	7.7
cases	12	788.25	364.269	341	1402
2005					
max temp	12	28.017	0.678	26.6	28.8
rain	12	160.892	116.466	8.4	362.9
hum	12	83.158	2.476	77.7	86.4
sunshine	12	6.067	1.319	4.4	9.1
cases	12	1184.167	486.616	642	2178
2006					
max temp	12	27.725	0.652	26.5	28.4
rain	12	229.433	197.529	83.1	765.9
hum	12	84.592	2.831	80.9	88.5
sunshine	12	5.633	1.205	3.2	7.4
cases	12	278.083	113.454	120	502
2007					
max temp	12	27.533	0.651	26.4	28.4
rain	12	240.517	126.131	105.5	468.6
hum	12	84.5	1.582	82.5	86.8
sunshine	12	5.317	1.148	3.5	7.6
cases	12	735.5	435.989	256	1399
2008					

max temp	12	27.483	0.689	26.5	28.8
rain	12	193.758	91.041	87.2	327.3
hum	12	83.408	2.304	79.1	87.1
sunshine	12	5.242	0.782	4	6.6
cases	12	586	447.313	202	1340
2009					
max temp	12	27.917	0.751	26.8	29.1
rain	12	160.075	74.471	21.8	281.8
hum	12	82.367	2.358	79.1	86.3
sunshine	12	5.95	0.759	4.7	7
cases	12	374.833	217.866	134	767
2010					
max temp	12	28.1	0.686	26.8	29.2
rain	12	172.925	84.023	6.3	298.5
hum	12	82.875	2.422	77.3	85.9
sunshine	12	5.692	1.396	3.6	8.8
cases	12	439.917	307.832	190	1088
2011					
max temp	12	27.575	0.753	26.3	28.7
rain	12	210.35	138.021	23	513.2
hum	12	84.625	2.474	81.1	88.4
sunshine	12	5.575	1.367	3.3	7.8
cases	12	444.167	341.674	188	1134
2012					
max temp	12	27.533	0.611	26.7	28.7
rain	12	179.992	103.077	53	363.4
hum	12	83.475	3.174	79	87.3
sunshine	12	5.533	0.971	3.6	7
cases	12	386	308.778	102	946
2013					
max temp	12	27.65	0.751	26.5	29
rain	12	229.033	94.086	85.8	395.2
hum	12	81.692	3.322	74.6	86.9
sunshine	12	5.433	1.136	3.5	7.5
cases	12	1847.5	1051.561	403	3459

2014					
max temp	12	27.908	0.822	26.2	29
rain	12	128.2	80.121	.2	250.8
hum	12	78.525	2.568	74.5	82.6
sunshine	12	5.975	1.401	3.7	8.8
cases	12	1527.167	1057.019	230	3386
2015					
max temp	12	28.25	0.726	26.9	29.1
rain	12	105.592	73.046	18.8	302.3
hum	12	76.9	1.944	74.9	81.1
sunshine	12	6.167	1.156	4.3	7.4
cases	12	941.167	570.293	210	2033
2016					
max temp	12	28.417	0.662	27.4	29.4
rain	12	162.975	78.965	6.2	292.6
hum	12	75.95	2.456	72	79.6
sunshine	12	6	1.241	3.5	8
cases	12	1090.417	645.640	234	2053
2017					
max temp	12	27.7	0.615	26.9	28.5
rain	12	170.467	84.347	79.6	371.2
hum	12	82.625	2.156	79.6	86.3
sunshine	12	5.8	0.827	4.2	7.1
cases	12	291.667	247.593	22	669
2018					
max temp	12	27.892	0.749	26.1	28.7
rain	12	142.35	77.238	14.8	287
hum	12	79.6	2.877	77	86.6
sunshine	12	5.75	1.260	3.8	8
cases	12	273.75	165.829	39	496
2019					
max temp	12	28.425	0.706	26.7	29.3
rain	12	113.958	116.208	11.8	421.5
hum	12	76.65	3.559	72.1	83.9

sunshine	12	6.783	1.283	4.8	9.2
cases	12	1333.167	751.762	258	2543
2020					
max temp	12	28.042	0.587	27.2	28.9
rain	12	157.217	70.498	65	255.6
hum	12	78.083	2.193	75.2	81.7
sunshine	12	5.875	1.423	4	8.3
cases	12	2942.917	2145.673	802	6590
2021					
max temp	8	27.85	0.896	26	28.7
rain	8	249.4	204.818	1	692.8
hum	8	78.05	2.695	73.8	82.6
sunshine	8	6.325	1.304	4.2	8.2
cases	8	541.125	351.546	125	1178

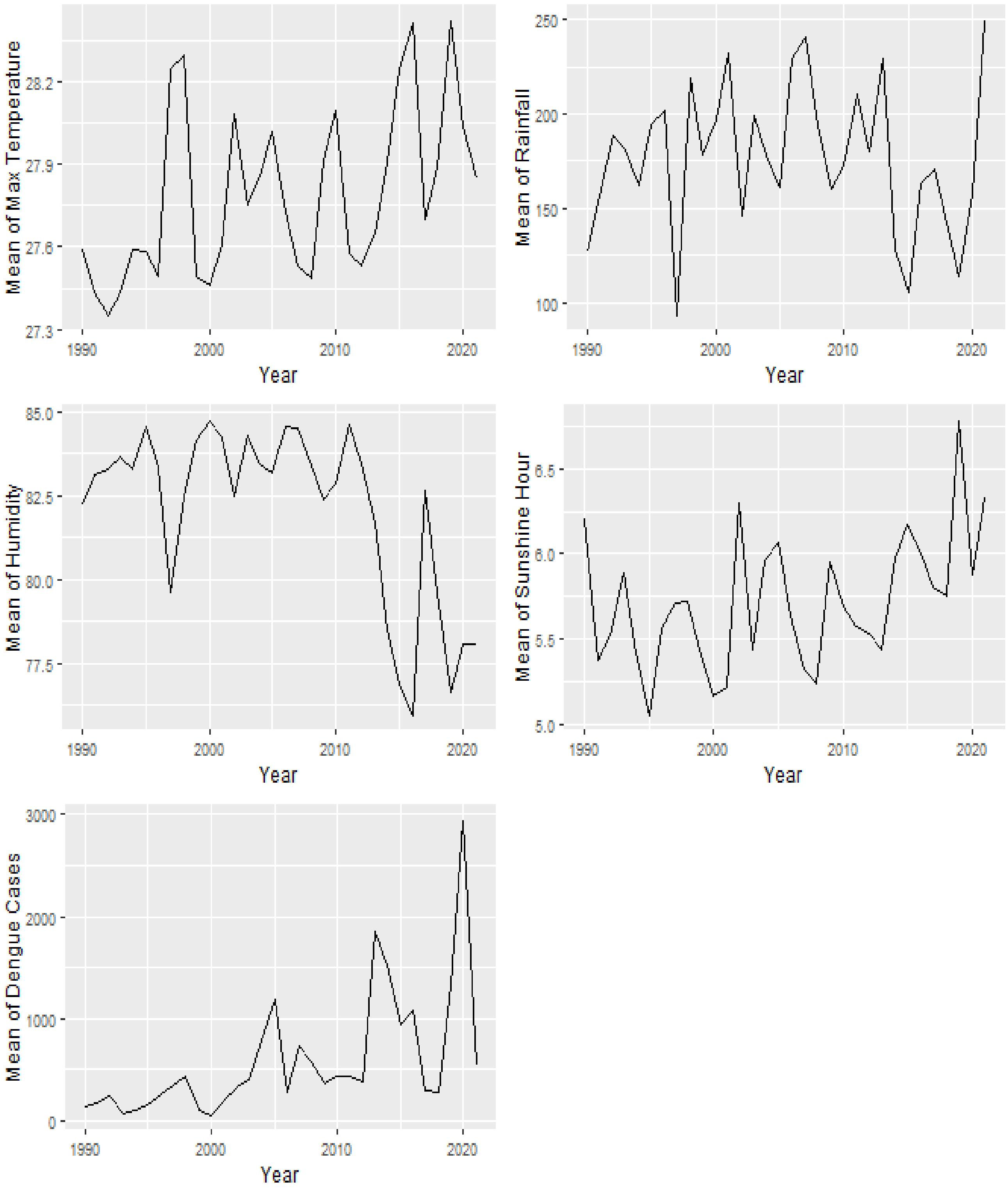


Figure 1: mean of dengue incidences and climate variables from 1990 to 2021.

b. Correlation analysis

Maximum and minimum temperature and humidity were positively correlated with dengue cases. However, rainfall and sunshine hours were negatively associated with dengue cases. Since all climate factors showed a correlation with dengue cases, we considered all climate variables as predictor variables for the outcome of dengue cases.

	Maximum temperature	Rainfall	Humidity	Sunshine hour	Dengue Cases
Maximum temperature	1.000	-0.531	-0.627	0.489	0.194
Rainfall	-0.531	1.000	0.598	-0.574	-0.051
Humidity	-0.627	0.598	1.000	-0.576	-0.361
Sunshine hour	0.489	-0.574	-0.576	1.000	-0.001
Dengue Cases	0.194	-0.051	-0.361	-0.001	1.000

Table 2: Correlation analysis with dengue cases and climate factors

c. Time series stationary test

As penned before, a stationary test was conducted which showed that, the time series process is stationary with Dickey-Fuller = -5.0617, Lag order =7, and p-value =0.01. it was , therefore, decided to conduct data analysis by-passing the time point and considering it as cross-sectional data.

d. Fitting count data model

Since the outcome was count data, the Poisson model was fitted. The results of the Poisson Regression model are as under:

Variables	Coefficient (95% CI)	P value
(Intercept)	17.260 (16.989, 17.529)	<0.000
Maximum Temperature	0.145 (0.138, 0.153)	<0.000
Rainfall	0.002 (.001, 0.002)	<0.000
Humidity	-0.171 (-0.172, -0.170)	<0.000
Sunshine hour	-0.225 (-0.229, -0.221)	<0.000

Table 3: Poisson regression model results of the association between dengue cases and climate variables.

Table 3 represents the exp (estimate), 95% confidence interval, and p-value. From the p-value, it can be interpreted, that the four climatic variables, viz, maximum temperature, rainfall, humidity, and sunshine hour were significantly associated with dengue cases. We could infer that, on the one hand, the mean number of dengue cases increased with a higher level of maximum temperature, and rainfall, while the mean number of dengue cases decreased with a higher level of sunshine hours and humidity.

Since outcome was count data, negative binomial models were also fitted. Accordingly, two models were run, model-1 (Poisson regression model) and model-2 (negative binomial regression model). AIC values were then calculated for these two models and minimum AIC values were found for model-2, thus considering this model as the final regression model for this study.

Model	**AIC**
Poisson regression model (Model-1)	204428.53
Negative binomial regression model (Model-2)	5490.90

Table 4: Two model comparisons by AIC values.

e. Final model results and interpretation

After the final screening, the selected negative binomial regression model was chosen as the final model and it was run for testing with variables. Table 5 presents the negative binomial regression model results. This table shows the exp (estimate) with 95% CI, and P value. IT was seen that, the mean number of dengue cases increases with a higher level of maximum temperature, and rainfall. On the contrary, average dengue cases decreased with two other variables-humidity and sunshine hour. Average dengue cases increase by 0.277 and 0.002 times if maximum temperature and rainfall increase by 1^{o}C and I unit respectively. On the other hand, dengue incidence decreases on average 0.277 and 0.225 times if humidity and sunshine hour increase by 1 unit.

Variables	Coefficient (95% CI)	P value
(Intercept)	15.603 (8.796, 22.412)	<0.000

Maximum Temperature	0.277 (0.097, 0.456)	0.002
Rainfall	0.002 (.001, 0.003)	0.001
Humidity	-0.277 (-0.391, -0.163)	<0.000
Sunshine hour	-0.225 (-0.229, -0.221)	<0.000

Table 5: Negative binomial regression model results of the association between dengue and climate factors.

Numerous studies [40-41] indicate that ecological and climate factors play an important role in the seasonal occurrence of dengue virus. Certain climate variables have a direct impact on the reproduction and proliferation of mosquito vectors, which are closely associated with these factors. In regions characterized by subtropical and tropical climates, which have historically been conducive to the breeding of dengue vectors, such as Singapore and neighboring South East Asian countries, climate change is of paramount significance as to the containment of health maladies. This is caused predominantly by the spread of dengue fever in these regions. In 2020, a total of 35,315 confirmed dengue cases were reported in Singapore [42]; this represented a significant increase from the previous year.

This study examines the connection between climate factors and the incidence of dengue fever outbreaks in Singapore. There has been observed to be a correlation between the incidence of dengue and climate factors. Statistical analysis of the correlation between dengue incidence and climatic variables is difficult, however, due to the complexity of the vector and host life cycles.

This complexity is a result of the sensitivity of the life cycles of Aedes aegypti and Aedes albopictus to climate conditions.

Singapore does not exhibit traditional seasons as typically experienced in temperate regions. The local population experiences a period of reduced precipitation, commonly referred to as the dry season, which spans from March to August. During this time, temperatures reach their peak. Conversely, a period of increased rainfall, known as the rainy season, occurs from September to February, coinciding with lower temperatures. However, the magnitude of the change is rather small. In the arid season, precipitation occurs nearly on a daily basis [43]. This study presents a computational model that evaluates the impact of various climatic conditions on the incidence of dengue cases, which are predominantly observed in the Indian Subcontinent during the monsoon season. Several investigations [43-47] have been undertaken in the South Asia and ASEAN regions to examine the impact of changing climate on dengue transmission. Dengue has emerged as a significant public health concern in these regions, according to these studies. Temperature and precipitation are the primary climate factors that have a significant impact on dengue outbreaks, according to these studies. In addition, these studies have revealed a previously unaccounted-for impact of particular climate factors over time. This study finds the impact of a comprehensive set of climate variables with the inclusion of humidity and sunshine hours along with the traditional temperature and rain fall, on dengue incidence. The result is fascinating as the two added variables negated the impact while the previous two factors positively factored in dengue incidence. Thus, a complete scenario of dengue-climate relationship got unleased. It would now comprehensively address the exact incidence picture of dengue and would help reduce and contain (the hitherto untamed) havoc of dengue incidence in Singapore, allowing time, resources and administrative measures for preparedness.

The goal of this study is to identify the climatic factors that may influence the occurrence of dengue cases and the specific pattern in which they affect the number of cases. According to the findings of this study, there is a positive correlation between maximum temperatures and the occurrence of dengue cases. A rise in global temperature is likely to increase the occurrence of vector-borne diseases [48]. A recent scientific investigation discovered that the ideal temperature range for Aedes aegypti vector multiplication is between 21.3 and 34 C [49]. Once again, the findings of our investigation show a significant inverse association between relative humidity and the prevalence of dengue cases. There was a drop of reported dengue cases during the monsoon seasons which correlated with an increase in relative humidity levels.

Several studies have also found a continuous positive relationship between rainfall and the frequency of dengue cases [44-46]. Rainfall and dengue cases had a negative link during the winter season, whereas a positive correlation was seen during the summer months, notably April and June. Rainfall has an impact on mosquito growth that is both beneficial and destructive. Rainfall has the ability to create standing water, which mosquitoes use as a hatching site. However, it is crucial to highlight that excessive or unwise rainfall might have a negative impact on mosquito populations [50].

Furthermore, there was a significant correlation between the duration of sunshine exposure and a decrease in the incidence of dengue cases. According to a recent study, there exists a correlation between the duration of sunshine and a reduced incidence of dengue fever [51]. The transmission of dengue is more probable in conditions of reduced sunlight, as mosquitoes exhibit increased activity during nighttime hours and tend to engage in more frequent biting behavior in darkness [48]. When considering both positive and negative elements, a comprehensive statistical outcome is derived.

This study's main focus is to address the relationship gap between the two traditionally used climate factors-temperature and rainfall and dengue incidence in Singapore. The two new variables-humidity and sunshine hours were added to fil the gap, thus addressing the association of climate and dengue holistically. Dengue incidence has been observed to be positively impacted by maximum temperature and rainfall, but negatively impacted by humidity and daylight hours. By simulating dengue outbreaks using all four of these climate factors, this research discovered a potential alarm system. This is necessary to devise a thorough correlation scenario that will enhance public health and disease management systems. Policymakers in Singapore will find the study's conclusions useful in creating a climate-based warning system that takes into account all potential variables, which were not taken into account up until now. As a result, this study will serve as a trailblazer for all subsequent attempts to develop an all-encompassing model to predict the overall incidence of dengue, taking into account vector and human factors, demographic, and climatic data. Additionally, community-based observation will be utilized to develop more useful dengue prevention strategies in Singapore in order to avert an epidemic. Based on Singapore model and experience, all other countries could also develop respective dengue prevention and containment strategy nationally and locally. International organizations, particularly World Health Organization (WHO) could also venture to device regional and global dengue prevention plan and preparedness in light with the new model.

Chapter Six

6. Data Analysis and Research Findings in Bangladesh

Like other Southeast Asian (SE) nations, Bangladesh is located in the tropical and subtropical regions and like them, has developed into a favorable habitat for the dengue vector and its increased transmission. Before 2000, Dhaka and other areas of the country only sometimes reported dengue cases. Following an extreme epidemic in 2000 that resulted in 5,551 cases and 93 fatalities across the country, dengue became a significant public health concern. Both types of the vectors (Aedes aegypti and Aedes albopictus) were identified in Bangladesh during the dengue outbreaks between 2000 and 2017. According to the findings of the Bangladesh National Health Accounts study, the current dengue situation in Bangladesh causes an economic burden on our health sector as funding for health care decreases gradually each year while out-of-pocket expenses are rising (67%, which is highest in the Southeast Asia Region) [Health Economics Unit, Bangladesh National Health Accounts (BNHA-V), 1997-2015, Ministry of Health & Family Welfare, Dhaka, Bangladesh, 2015]. In Bangladesh, dengue is a major source of disease and mortality (Ahsan et al. 2021; Sharmin et al. 2015). The two Aedes mosquito species that are the major vectors of the dengue virus in the environment are Aedes aegypti (Ae. aegypti) and Aedes albopictus (Ae. albopictus) [Lambrechts, Scott, and Gubler 2010]. A study estimates that by 2080 there will be 2.25 billion dengue cases globally (Messina et al. 2019). Local climate factors including rainfall, temperature, relative humidity, and unplanned rapid urbanization influence the risk of dengue fever significantly (WHO 2021). In both tropical and subtropical regions of the world, it has become recognized as a major global public health concern (Gubler 2011). When bitten by an infected mosquito, people become infected with the virus that causes dengue fever. In South-East Asia, Pacific Asia and Latin America, dengue fever is the most devastating. But South

Asian countries like Pakistan, India and Bangladesh have also noted a significant increase in infections which has had a significant impact on public health (Anders and Hay 2012; Bhatt et al. 2013; Stanaway et al. 2016). Unexpectedly it has been shown that the local climatic variables, such as temperature, rainfall, sunshine and humidity affect dynamics of the vector population, viral circulation and the probability of dengue fever transmission (Correia Filho 2017a; Ruzman and Rahman 2017; Xiang et al. 2017). Additional studies have been carried out regarding the correlations amongst climatic conditions and surge of dengue. The majority earlier studies (Adnan et al. 2020; S. C. Chen et al. 2010; Y. Li et al. 2020; Malik et al. 2017; Ruzman and Rahman 2017; Shaheen 2020; Singh et al. 2022) found that there is a significant association between climatic variables and dengue incidence. In addition to average temperature, diurnal temperature range (DTR, the difference between daily maximum and minimum temperature) has an impact on dengue fever transmission. Aedes aegypti, the primary mosquito that transmits dengue fever, is affected by temperature change in terms of biting rate, dengue fever transmission possibility, extrinsic incubation duration and vector mortality rate according to temperature-dependent empirical and mathematical research. Vectorial capacity rises with narrow daily temperature difference at high mean temperatures. Adult Ae. aegypti had a reduced rate of survival in temperatures above 30°C as rainfall can be either light or very heavy. Rainfall and dengue incidence are positively correlated, as has been seen in multiple locations. Inter-annual weather variability around the world has been associated with large-scale climatic events such as the El Nino phenomenon- Southern Oscillation, which is caused by the combination of large-scale ocean and atmospheric circulation processes in the equatorial Pacific Ocean. Local temperature and rainfall as well as year-to-year variations in dengue occurrence are known to be determined by the warm and cold phases of the Southern Oscillation, El Nino and La Nina respectively. The incidence of dengue is also influenced by socio economic variables. Economic development is expected to decrease risk even though the number of people at risk for dengue will probably increase as a result of increases in population. Bangladesh is a member of the World Health Organization (WHO). After over three decades of occasionally dengue, the South-East Asia region experienced its first pandemic in 2000. In Bangladesh, dengue is a very seasonal disease with a monsoon-related surge in their frequency. From 2000 to 2009, scenarios were reported from 29 of Bangladesh's 64 districts with the capital city Dhaka, accounting for 91% of the total number of instances (Disease Control Directorate, Directorate General of Health Services. Dengue Register. Dhaka, Bangladesh). Since 2010, very few instances from regions other than Dhaka have been identified (Disease Control Directorate, Directorate General of Health Services. Dengue Register. Dhaka, Bangladesh) most likely as a result of a change in reporting requirements that currently require for providing laboratory diagnosis. Aedes mosquitoes are sensitive to changes in the weather. It acts as the main host for dengue and yellow fever virus amplification and transmission. Climate plays a significant role when determining the Aedes mosquito's geographic range. Multiple studies have found an important and accurate correlation between the number of dengue cases and the climate in a specific region of the world. The capability of Aedes mosquitoes to survive and reproduce is significantly impacted by differences in mean temperature. Since they consume all over the day, it is most effective for mosquitoes to transmit dengue when the diurnal temperature range (DTR) is near to 29.3°C. As Aedes mosquitoes prefer to lay their eggs in man-made containers which are more frequently found in urban areas. Rainfall and human population density are also significant factors. As a result, dengue cases in Bangladesh reflect significant year-to-year variability and seasonality. This indicates that dengue is a highly climate-wise sensitive disease. In Bangladesh, there are four distinct seasons- the dry winter season (December to

February), the hot pre-monsoon summer season (March to May), the rainy monsoon season (June to September) and the post-monsoon autumn season (October to November). The monsoon and post-monsoon seasons are when dengue cases are most common (Mordecai E A et al 2019 Thermal biology of mosquito-borne disease Ecol. Lett. 22 1690–708). For a milieu with a high emission of green house gases, projected increases in Bangladesh's mean temperature relative to the pre-industrial period (1861-1880) range from 3.2°C to 5.8°C by the end of the 21st century. In this regard, figuring out the future quantity, timing and spatial distribution of dengue burden in Bangladesh requires an understanding of the correlations between dengue and climatic factors. In order to encourage appropriate public health responses and the establishment of an official policy for adaptation and risk mitigation, country-specific evidence is necessary. In Bangladesh, dengue or "Dacca Fever" was first noted in the 1960s. But during the 2000 monsoon, Bangladesh noticed its first known dengue fever pandemic, with a reported 5521 officially recorded cases and having a death toll of 93. Due to urbanization and the increasing number of the Aedes aegypti mosquito, dengue has become widespread in Bangladesh. The rise in dengue incidence since 2010 has been linked with a heavier regional precipitation scenario (May to September) and a rise in ambient temperatures. Bangladesh's climatic environment are becoming more conducive for the propagation of dengue as well as other vector-borne diseases like malaria, leishmania, yellow fever and chikungunya due to excessive rainfall, water logging, flood, high temperature and erratic changes in the country's normal seasons (Dengue-Bangladesh, World Health Organization, 2022). The estimated annual frequency of dengue incidence decreased between 2000 and 2010. The number of annual dengue cases has however sharply increased in Bangladesh since that period. The second-biggest incident occurred in 2018, while the largest outbreak the country has witnessed in 2019.

Bangladesh is located in South Asia between latitude of 20-27 °N and longitude of 88- 93 °E. It is a low-lying, riverine country with a large marshy jungle coastline of 710 km on the Northern littoral of the Bay of Bengal. It is one of the most densely populated countries (density 964/km²) in the world and covers 147,570 km². Bangladesh is divided into eight administrative divisions and these are subdivided into districts. There are 64 districts in Bangladesh, each further subdivided into Upazila or Thana. A subtropical humid climate prevails in Bangladesh which is distinguished by significant seasonal changes in rainfall, temperatures and high relative humidity.

Figure: Dhaka City GIS Map. Source: (Google)

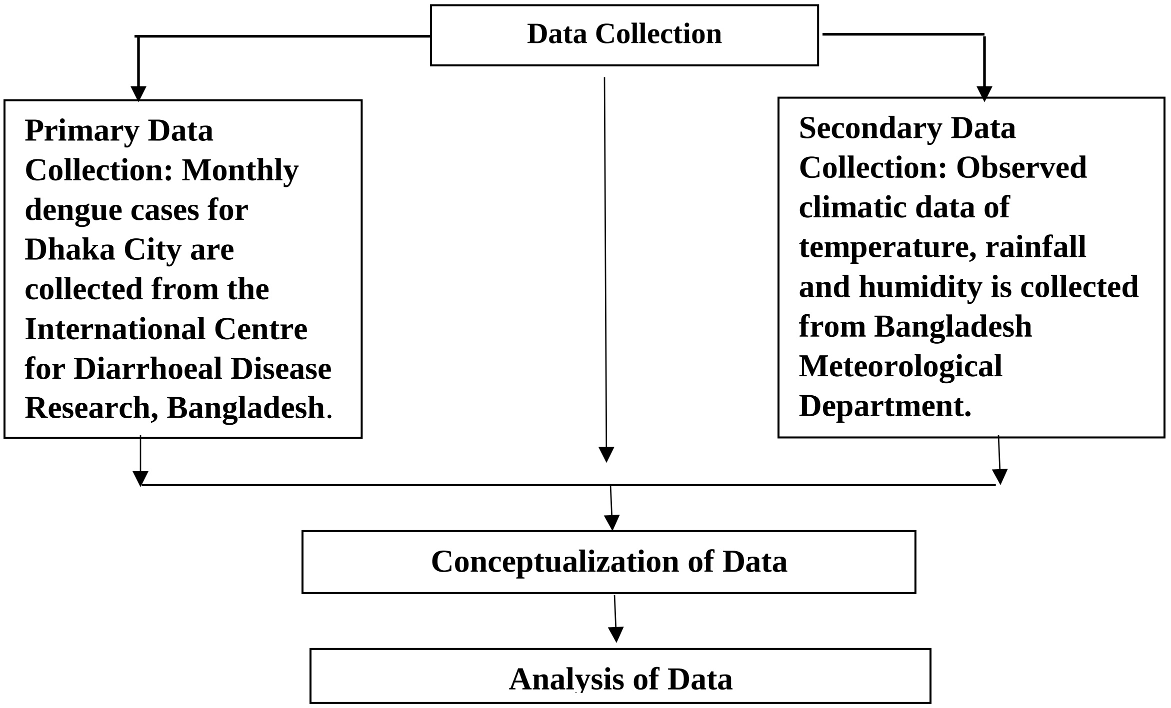
Dhaka is the capital of Bangladesh. Dhaka is located in central Bangladesh at 23°42′ North latitude and 90°22′ East longitude or almost in the geographical center of Bangladesh, on the eastern bank of Buriganga River with an area of 1464 km². Dhaka is currently the center of population concentration and economic activity in the nation as a result of its geographic location and historical, economic and political dynamics (Source: Google).

According to the Dhaka City Corporation Urban Area Plan, the total population of the city as a whole in the twenty-first century is estimated to reach close to 25 million. This statistic indicates the rise in population density and the pronounced impact of humans on the environment. The physical environment is defined by diverse physiographic zones including lowlands, rivers, plain lands and ponds and it is always changing as a result of social interactions between people. The Dhaka City Corporation has seen a number of environmental system consequences as a result of historical societal development including air temperature and highest decrease in vegetation and rainfall (Source: Google).

Year wise monthly dengue cases for Dhaka City Area (**2008 - 2022**) are collected from the **International Centre for Diarrheal Disease Research, Bangladesh (icddr,b).** ICDDR, B is an international health research organization located in Mohakhali, Dhaka, Bangladesh. Dedicated to saving lives through research and treatment, ICDDR, B addresses some of the most critical health concerns facing the world today, ranging from improving neonatal survival to HIV/AIDS. In collaboration with academic and research institutions over the world, ICDDR, B conducts research, training and extension activities, as well as programmed-based activities to develop and share knowledge for global lifesaving solutions. ICDDR, B has a mix of national and international staff including public health scientists, laboratory scientists, clinicians, nutritionists, epidemiologists, demographers, social and behavioral scientists, IT professionals and experts in emerging and re-emerging infectious diseases and vaccine sciences.

Observed climatic data of temperature, rainfall, wind speed and humidity are collected from **Bangladesh Meteorological Department (BMD)**. The Bangladesh Meteorological Department is the national meteorological organization of Bangladesh, working under Ministry of Defense of the Government of Bangladesh. It is responsible for maintaining the network of surface and upper air observatories, radar and satellite stations, agrometeorological observatories, geomagnetic and seismological observatories and meteorological telecommunication system of Bangladesh. However, for this study purpose, data of temperature, precipitation, wind speed and humidity are being collected for Dhaka Station of BMD during the period **2008 - 2022.**

This chapter explains the methodology adopted to attain the objectives as analyze study area selection and data collection procedure, data analysis etc. Flow chart of the research methodology is presented in the bellow-



Primary Data Collection: Monthly dengue cases for Dhaka City are collected from the International Centre for Diarrhoeal Disease Research, Bangladesh.

Secondary Data Collection: Observed climatic data of temperature, rainfall and humidity is collected from Bangladesh Meteorological Department.

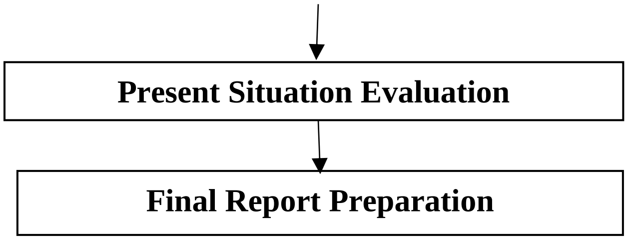


Figure: Flow Chart of the Research Methodology.

a. Descriptive Statistics

For this study, dengue and climate data from 2008 to 2022 was used. Average temperature, average maximum temperature and minimum temperature, average rainfall, average relative humidity, average wind speed and dengue cases were considered in this study. This study was considered the annual mean value of the mentioned weather variables. The descriptive statistics, such as mean, standard deviation, high and low picks of dengue incidences, and climate variables are shown for each year (Table 1). The mean maximum temperature was increasing over the year from 2008 to 2022. The highest maximum temperature was found in 2014 and 2021. It looks like an ups and downs trends over the period. The lowest maximum temperature was observed in 2011. The mean rainfall also showcased an ups and downs trend over the periods. But overall, it seems to be an upward pattern over the period. The mean humidity almost constant between 2009-2015 and the mean value has variations after 2016-2022. Overall, the humidity has a downward trend over the year. The mean wind speed increased over the period and it showed an upward trend. The highest mean wind speed observed in 2019. The highest dengue cases were observed in 2022. It has also an upward trend over the year (Figure 1).

Table 1: Summary Statistics: N mean sd min max by (Year)

Year: 2008

	N	mean	sd	min	max
Av. Temperature	12	25.875	3.936	19	29.3
Av. Max Temperature	12	30.566	3.416	24.46	34.67
Av. Min Temperature	12	22.171	4.580	14.48	26.49
Av. Rainfall	12	152.917	149.958	0	461
Av. Relative Humidity	12	73.417	7.561	61	83
Av. Wind Speed	12	3.068	0.497	2.25	3.91
Dengue Cases	12	95.917	160.777	0	473
2009					
Av. Temperature	12	26.525	3.748	19.7	30.2
Av. Max Temperature	12	31.604	3.133	25.91	35.56
Av. Min Temperature	12	22.534	4.566	14.84	26.72
Av. Rainfall	12	132.46	180.448	0	553
Av. Relative Humidity	12	70.25	9.265	53	82
Av. Wind Speed	12	3.056	1.011	1.6	4.58
Dengue Cases	12	39.333	71.438	0	188
2010					
Av. Temperature	12	26.575	4.314	17.6	30.4
Av. Max Temperature	12	31.401	3.538	23.82	35.52
Av. Min Temperature	12	22.828	5.209	12.8	27.43
Av. Rainfall	12	105	95.291	0	278
Av. Relative Humidity	12	70.417	7.609	56	79
Av. Wind Speed	12	2.722	0.593	2.01	4.11
Dengue Cases	12	34.083	60.072	0	183
2011					
Av. Temperature	12	25.817	4.122	17.3	29.2
Av. Max Temperature	12	30.575	3.305	23.44	33.46
Av. Min Temperature	12	21.942	4.999	12.2	26.71
Av. Rainfall	12	122.417	125.822	0	335
Av. Relative Humidity	12	70.917	8.989	54	82

Av. Wind Speed	12	2.185	0.498	1.25	2.81
Dengue Cases	12	113.25	200.894	0	691
2012					
Av. Temperature	12	26.092	4.244	18.4	30.1
Av. Max Temperature	12	30.826	3.658	23.96	34.62
Av. Min Temperature	12	22.249	4.930	14.49	26.91
Av. Rainfall	12	91.647	86.375	.76	230
Av. Relative Humidity	12	70.25	8.730	52	79
Av. Wind Speed	12	2.183	0.430	1.43	2.71
Dengue Cases	12	55.917	81.707	0	262
2013					
Av. Temperature	12	26.092	4.037	17.6	30.1
Av. Max Temperature	12	30.951	3.077	24.22	34.21
Av. Min Temperature	12	22.188	5.001	12.25	27.16
Av. Rainfall	12	107	117.061	0	309
Av. Relative Humidity	12	70.5	9.415	55	81
Av. Wind Speed	12	2.163	0.477	1.55	2.97
Dengue Cases	12	145.75	177.135	0	495
2014					
Av. Temperature	12	26.233	4.489	18.3	30.7
Av. Max Temperature	12	31.127	3.885	24.29	36.44
Av. Min Temperature	12	22.219	5.051	13.66	26.87
Av. Rainfall	12	96.583	113.613	0	320
Av. Relative Humidity	12	69.833	9.311	52	82
Av. Wind Speed	12	2.043	0.445	1.26	2.83
Dengue Cases	12	31.25	33.273	0	82
2015					
Av. Temperature	12	26.175	3.711	19.1	29.9
Av. Max Temperature	12	30.887	2.970	24.77	34.07
Av. Min Temperature	12	22.267	4.427	14.6	26.9
Av. Rainfall	12	149.563	172.171	0	510
Av. Relative Humidity	12	70.75	7.979	52	81
Av. Wind Speed	12	2.067	0.467	1.39	2.79
Dengue Cases	12	263.5	375.095	0	965

2016					
Av. Temperature	12	26.733	3.688	18.9	30.4
Av. Max Temperature	12	31.609	2.997	24.87	35.13
Av. Min Temperature	12	23.091	4.451	14.15	27.02
Av. Rainfall	12	93.667	98.852	0	331
Av. Relative Humidity	12	72.583	6.775	59	82
Av. Wind Speed	12	2.13	0.456	1.41	2.84
Dengue Cases	12	505	588.625	3	1544
2017					
Av. Temperature	12	26.375	3.391	20.1	29.9
Av. Max Temperature	12	31.107	2.535	26.36	34.5
Av. Min Temperature	12	22.643	4.350	14.86	26.88
Av. Rainfall	12	199.25	180.347	0	478
Av. Relative Humidity	12	73.417	8.649	57	83
Av. Wind Speed	12	1.924	0.434	.96	2.82
Dengue Cases	12	230.75	165.272	36	512
2018					
Av. Temperature	12	26.083	3.985	17.5	29.8
Av. Max Temperature	12	31.177	3.320	23.59	34.12
Av. Min Temperature	12	22.184	4.662	12.64	27.14
Av. Rainfall	12	119.583	134.065	0	321
Av. Relative Humidity	12	71.583	7.609	59	81
Av. Wind Speed	12	2.983	0.610	2	3.77
Dengue Cases	12	845.667	1064.104	7	3087
2019					
Av. Temperature	12	26.358	3.901	19.3	29.9
Av. Max Temperature	12	31.337	3.084	24.76	34.58
Av. Min Temperature	12	22.465	4.648	14.6	27.15
Av. Rainfall	12	127.23	95.765	.76	313
Av. Relative Humidity	12	72.5	7.810	59	82
Av. Wind Speed	12	3.315	0.584	2.48	4.01
Dengue Cases	12	8446.167	15226.544	17	52636

2020					
Av. Temperature	12	26.242	4.011	18.5	29.6
Av. Max Temperature	12	31.143	3.390	24.02	33.83
Av. Min Temperature	12	22.518	4.829	14.35	27.25
Av. Rainfall	12	131.897	118.605	0	330
Av. Relative Humidity	12	74.833	9.262	57	85
Av. Wind Speed	12	2.517	0.510	1.44	3.29
Dengue Cases	12	117.083	155.128	10	546
2021					
Av. Temperature	12	26.775	3.846	19.4	30.4
Av. Max Temperature	12	31.929	3.326	25.58	36.12
Av. Min Temperature	12	22.871	4.462	14.83	26.71
Av. Rainfall	12	129.083	137.923	0	462
Av. Relative Humidity	12	71.917	9.385	57	83
Av. Wind Speed	12	2.387	0.340	1.68	2.93
Dengue Cases	12	2369.083	3054.993	3	7841
2022					
Av. Temperature	12	26.85	3.917	19.6	30.5
Av. Max Temperature	12	31.664	3.239	25.14	34.26
Av. Min Temperature	12	23.128	4.614	15.33	27.72
Av. Rainfall	12	110.333	81.864	9	243
Av. Relative Humidity	12	70.667	7.353	55	80
Av. Wind Speed	12	2.593	0.531	1.8	3.35
Dengue Cases	12	5198.5	7801.190	20	21932

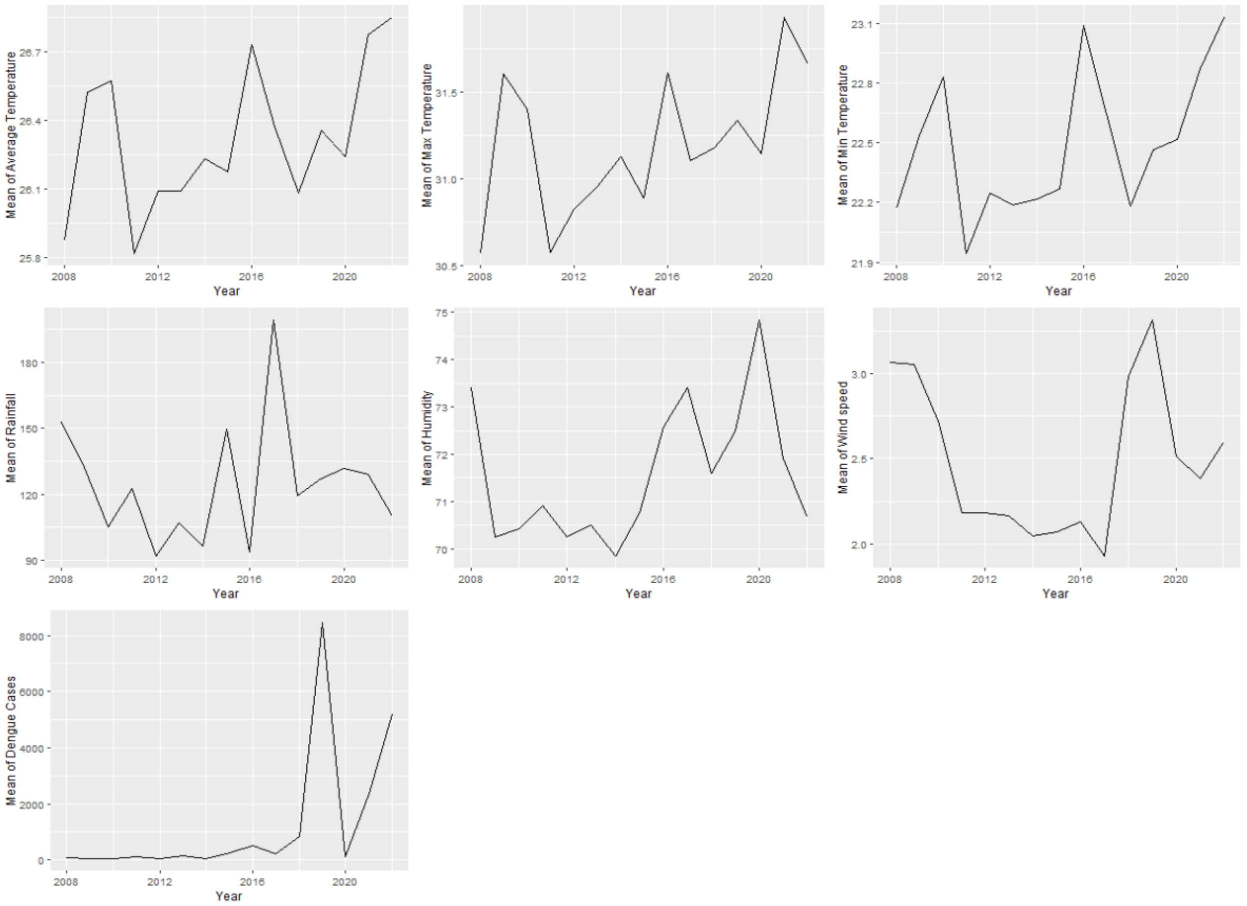


Figure 1: Mean of Climate Factors and Dengue Cases from 2008 – 2022.

b. Correlation Analysis

Average temperature, average maximum temperature, average minimum temperature, average rainfall, average relative humidity average wind speed was positively correlated with dengue incidence. However, there was no negative association with dengue cases. Since all climate factors showed a positive correlation with dengue cases, we considered all climate variables as predictor variables for the outcome of dengue cases.

Table 2: Correlation Analysis with Dengue Cases and Climate Factors.

Variables	(1)	(2)	(3)	(4)	(5)	(6)	(7)
(1) Av. Temperature	1.000						
(2) Av. Max Temperature	0.973	1.000					
(3) Av. Min Temperature	0.981	0.914	1.000				
(4) Av. Rainfall	0.594	0.459	0.673	1.000			
(5) Av. Relative Humidity	0.394	0.207	0.550	0.692	1.000		
(6) Av. Wind Speed	0.336	0.372	0.291	0.190	-0.014	1.000	
(7) Dengue Cases	0.131	0.116	0.151	0.099	0.149	0.112	1.000

c. Poisson Regression

Since the outcome was count data, Poisson model was fitted. Table 3 represents the expected estimation of 95% confidence interval and p-value. From the p-value, it can be inferred that average temperature, average maximum temperature, average minimum temperature, average rainfall, average relative humidity, average wind speed had a significant positive correlation with dengue cases. It could also be postulated that, on the one hand, the mean value of dengue incidence increased with a higher degree of average maximum temperature, average minimum temperature, average relative humidity, average wind speed, while the mean number of dengue cases decreased with a higher level of average temperature and average rainfall. The results of the Poisson Regression model are depicted underneath-

Table 3: Poisson Regression Model Results of the Association between Dengue Cases and Climate Variables.

Dengue Cases	Coef.	St. Err.	t-value	p-value	[95% Conf	Interval]	Sig
Av. Temperature	-3.249	.016	-197.43	0	-3.281	-3.216	***
Av. Max Temperature	1.546	.008	193.82	0	1.53	1.561	***

Av. Min Temperature	1.826	.01	187.92	0	1.807	1.845	***
Av. Rainfall	-.001	0	-29.17	0	-.001	-.001	***
Av. Relative Humidity	.029	.001	31.70	0	.027	.031	***
Av. Wind Speed	.517	.003	157.14	0	.51	.523	***
Constant	-.48	.105	-4.59	0	-.684	-.275	***

Mean dependent var	1232.750	SD dependent var	4918.385
Pseudo r-squared	0.215	Number of obs.	180
Chi-square	204337.645	Prob > chi2	0.000
Akaike crit. (AIC)	746437.461	Bayesian crit. (BIC)	746459.811

**** p<.01, ** p<.05, * p<.1*

d. Negative Binomial Regression

As elaborated earlier, after the final screening, the negative binomial regression model was selected as the final model and the variables were fit into it to run the model. Table 4 presents the negative binomial regression model results. This table shows the exp (estimate) with 95% CI, and P value. It clearly showcases that, the mean number of dengue cases increases with a higher degree of average maximum temperature, average minimum temperature, average rainfall and average wind speed. Analysis shows that 1°C increase of average maximum and minimum temperature will increase 3.844 and 4.23 times of dengue cases. Again, 1mm increase of average rainfall will increase .006 times of dengue cases. On the contrary, the mean number of dengue cases decreases with average temperature and average relative humidity. Analysis shows that 1°C increase of average temperature will decrease 7.783 times of dengue cases. Again, 1% increase of average relative humidity will decrease .081 times of dengue cases.

Table 4: Negative Binomial Regression Model Results of the Association between Dengue and Climate Factors

Dengue Cases	Coef.	St. Err.	t-value	p-value	[95% Conf	Interval]	Sig
Av. Temperature	-7.783	1.332	-5.84	0	-10.394	-5.173	***
Av. Max	3.844	.758	5.07	0	2.357	5.33	***

Temperature							
Av. Min Temperature	4.23	.818	5.17	0	2.627	5.833	***
Av. Rainfall	.006	.003	1.74	.082	-.001	.012	*
Av. Relative Humidity	-.081	.079	-1.02	.31	-.236	.075	
Av. Wind Speed	.102	.336	0.30	.762	-.557	.76	
Constant	.978	10.576	0.09	.926	-19.75	21.705	
ln alpha	1.614	.095	. b	. b	1.427	1.8	

Mean dependent var	1232.750	SD dependent var	4918.385
Pseudo r-squared	0.023	Number of obs.	180
Chi-square	51.163	Prob > chi2	0.000
Akaike crit. (AIC)	2189.034	Bayesian crit. (BIC)	2214.577

**** p<.01, ** p<.05, * p<.1*

e. Discussion

Our research results indicate that the dengue incidence in Dhaka City Area had a positive correlation with the monthly average maximum and minimum temperature, rainfall, and humidity. These results are in contrast to the findings of other studies and might assist in anticipate dengue outbreaks in different locations. (Descloux et al., 2012; Hii et al., 2009; Hsieh and Chen, 2009; Johansson et al., 2009). The most significant weather variables for mosquito vector growth and dispersal as well as possible indicators of dengue epidemics are temperature and humidity (Chen et al., 2010; Wu et al., 2007). ***Aedes*** mosquitoes' life cycle, including growth rate, larval survival, and the length of the reproductive cycle, is influenced by temperature (Hopp and Foley, 2001; Patz et al., 2005). A maximum mosquito survival rate of 88-93% between 20-30 °C was observed (Tun-Lin et al., 2000). The virus's ability to replicate, mature, and have an infectious phase are all impacted by temperature. Higher temperatures reduce the period of viral incubation within the vector, increasing the likelihood that mosquitoes will get an infection during the span of their lifetime (Hopp and Foley, 2001; Patz et al., 1998; Yang et al., 2009). Humidity is also necessary for adult mosquito survival (Hopp and Foley, 2001; Patz et al., 1998). Given the association between temperature and dengue, the anticipated temperature alter as a result of climate change may make it easier for diseases to spread in Dhaka City Area. By the end of the 21st century, the annual mean temperature in Dhaka City will have increased by 3.3 °C, according to the IPCC. Both the summer and the winter will experience the anticipated warming (IPCC, 2007). Since summer will be warmer than usual, it is anticipated that the warmer weather may facilitate disease transmission and raise the incidence of dengue. Few dengue cases were previously reported in Dhaka throughout the winter. If the winter temperature rises as predicted, dengue transmission conditions may improve, extending the outbreak season. Therefore, if climate change occurs, dengue outbreaks may become more severe in the future. In several succeeding months, temperature and humidity have an impact on the occurrence of dengue (IPCC, 2007).

The biology of mosquitoes, the viruses they spread, and more broadly, the cycles of dengue transmission, are all significantly influenced by climatic variables. Higher temperatures hasten the growth of mosquito larvae and adult mosquitoes, increase mosquito biting rates, and shorten the time needed for virus replication inside the insect. Extremely high temperatures may shorten the period that mosquitoes may survive, which might counteract the beneficial effect on insect abundance. These studies have made use of a variety of statistical techniques while taking into account various temperature indices, such as mean, maximum, and lowest temperatures. The findings are typically similar, demonstrating that the dengue outbreaks are partially influenced by the climate.

Another important element that has an impact on different stages of the life cycle of mosquitoes is relative humidity. The combined effects of temperature and humidity have a substantial impact on the frequency of blood meals. They can also have an impact on the vector's survival rate and the likelihood that it will become infected and spread dengue. Temperature and relative humidity are two of the most significant factors that could affect dengue transmission, according to the literature. Temperature and rainfall both have an impact on relative humidity, which in turn affects mosquito lifetime and the likelihood of viral transmission. According to research by Hales et al., the most significant meteorological predictor of the occurrence of dengue worldwide was yearly average relative humidity. Therefore, by effecting the vector of dengue- the aedes egypti mosquito, temperature, rainfall, and relative humidity will significantly factor in determining the geographic boundaries within which dengue propagation can be anticipated to continue. Seasonal variations in these variables will also play a significant role in determining the duration and possibly the intensity of transmission within places where the lowest optimum limits of these climate parameters are sufficient to maintain dengue transmission.

f. Conclusion:

The objective of this study was to determine how the impacts of climate change factors on the occurrence of dengue in Dhaka, Bangladesh. The results show that average temperature, average maximum and minimum temperature, average rainfall, average relative humidity, average wind speed was positively associated with dengue incidence. However, there was no negative association with dengue cases. Analysis shows that 1°C increase of average maximum and minimum temperature will increase 3.844 and 4.23 times of dengue cases. Again, 1mm increase of average rainfall will increase .006 times of dengue cases in Dhaka City. Dengue, an emerging disease, will remain in Bangladesh and will continue to constitute a serious public health problem as is happening worldwide. Addressing changing epidemiology is important, as is constant monitoring, resulting in the need for increasing the surveillance areas and addressing the problems that mitigate the disease's effects on the nation's economic and public health. It may be challenging to totally eradicate the disease from the supply side, and an ongoing effort is needed to alter urban citizens' behavior so that they can join the fight against Aedes mosquitoes. In order to devise a more effective prevention strategy in Dhaka, Bangladesh, additional efforts should be made to build a model to predict dengue incidences, taking into account immunological and entomological data, demographic and climate variables. To determine the primary causes of dengue infection, future study will also need to take into account additional unmeasured confounders, such as deteriorating water quality, air pollution, waste management, etc. Bangladesh therefore needs to put in place a very strong action to stop the rising trend of dengue transmission in Bangladesh. Based on Bangladesh's seasonal climate change, the study's findings will assist policymakers and public health officials in taking the appropriate dengue preventative measures.

Chapter Seven

7. Comparison between Singapore and Bangladesh Cases

There has been a consistent increase in monthly dengue cases over the years, with a notably higher occurrence in 2019 compared to other years (Figure 1). Dengue cases in Singapore exhibited fluctuations from 1990 to 2020 (Figure 1). Meanwhile, the mean temperature has shown a continuous upward trend during this period, with Bangladesh consistently having higher mean temperatures than Singapore. Both Bangladesh and Singapore experienced fluctuations in average precipitation levels until 2014, after which Singapore's levels began to decrease while Bangladesh's increased. In terms of mean sunshine hours, there was no significant difference between Bangladesh and Singapore until 2010, but after that, Singapore's mean sunshine hours increased while Bangladesh's decreased. Additionally, Singapore had higher mean humidity levels than Bangladesh throughout the entire period (Figure 2). Although Singapore had higher mean dengue cases from 2003 to 2007, it's noteworthy that after that period, Bangladesh had higher mean dengue cases. Likewise, the incidence rate of dengue cases has been consistently higher in Singapore compared to Bangladesh over the years, with the highest rate reaching 51.7 in Singapore in 2020 and 41.6 in Bangladesh in 2019

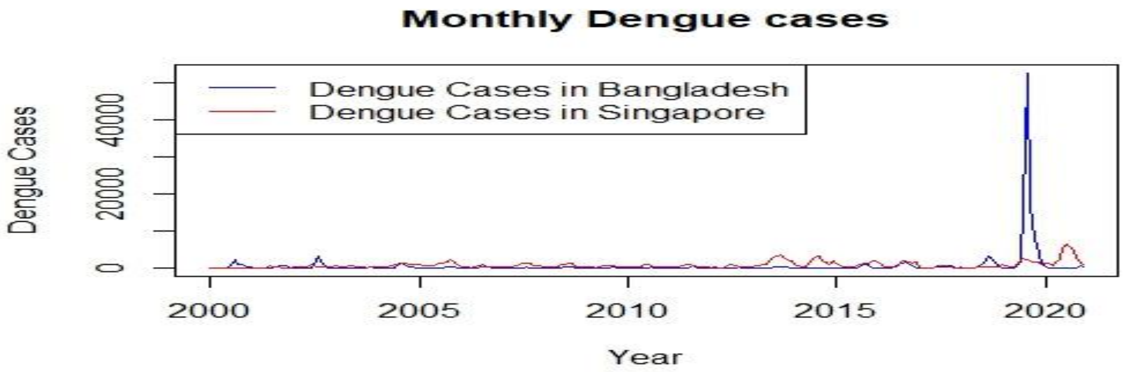


Figure 1: Month Dengue cases in both Bangladesh and Singapore from 2000 to 2020.

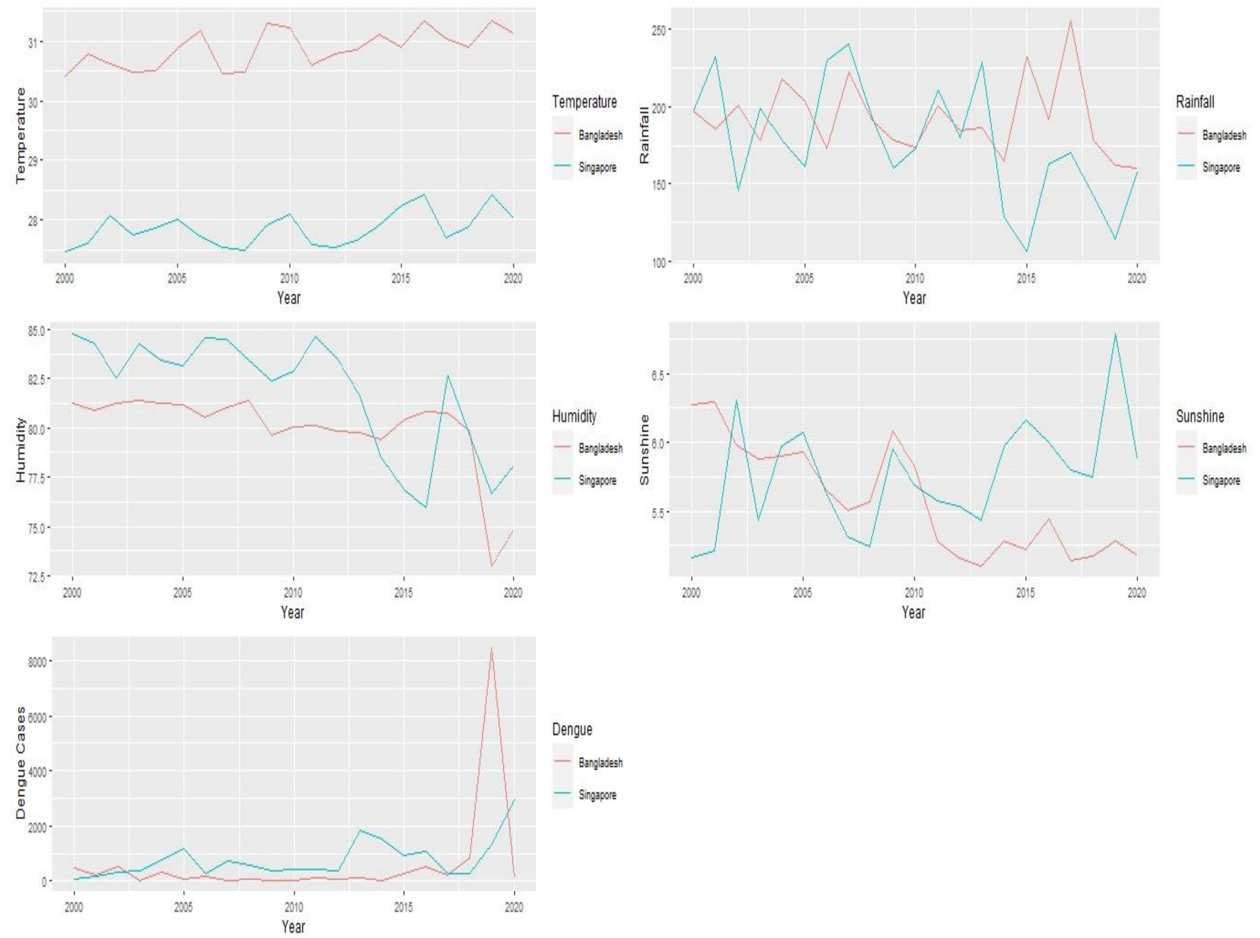


Figure 2: Mean temperature, rainfall. humidity, sunshine and dengue cases in both Bangladesh and Singapore from 2000 to 2020.

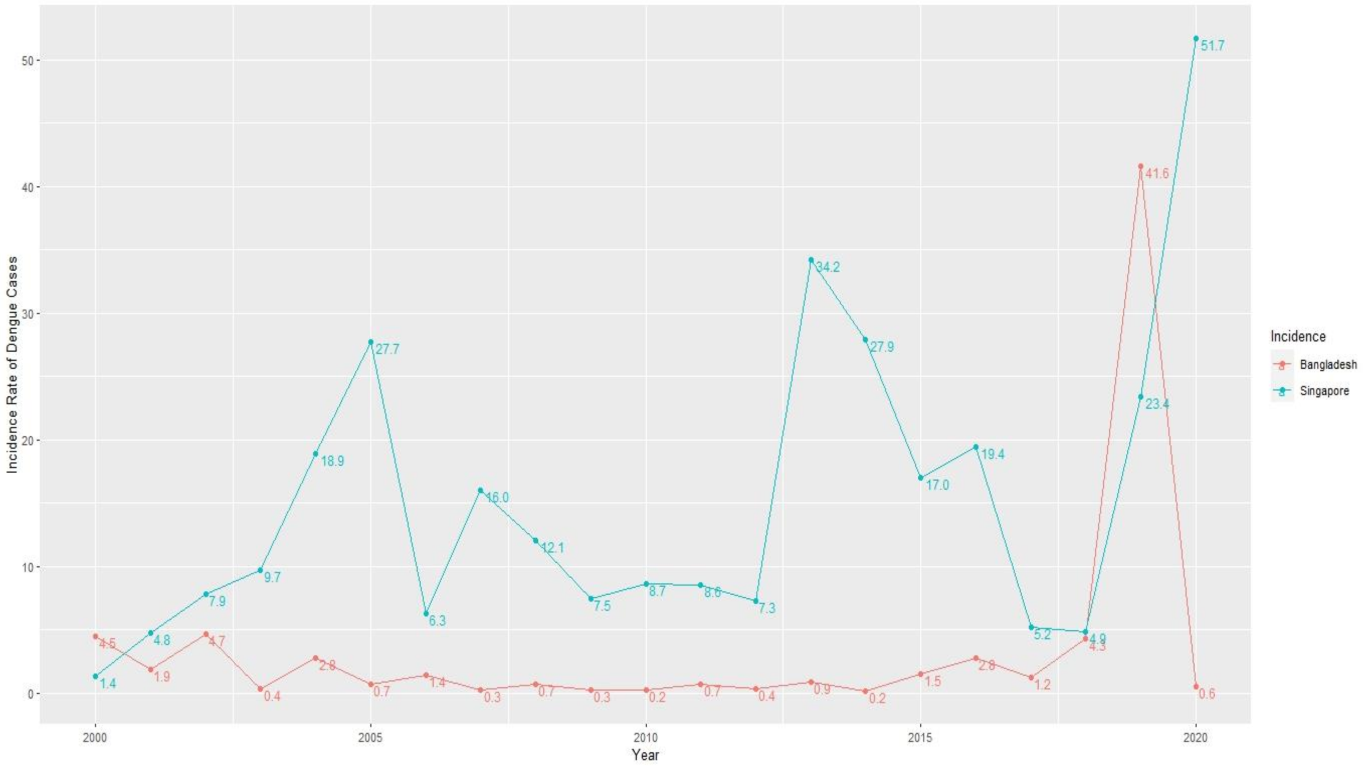


Figure 3: Incidence rate of dengue cases (per 100,000 people) in both Bangladesh and Singapore from 2000 to 2020.

a. Time series stationary test

As previously mentioned, a stationary test was conducted and it was found that the time series process displayed stationary results. The Dickey-Fuller test statistic yielded a value of -5.2952, with a lag order of 7 and a p-value of 0.01 for Bangladesh. Moreover, the Dickey-Fuller test statistic yielded a value of -3.5813, with a lag order 6 and a p-value of 0.036 for Singapore. These p-value from the Dickey-Fuller test confirmed the stationary of the time series process for dengue cases in both Bangladesh and Singapore.

b. Seasonality Test

Based on the analysis of Figure 4, it was evident that dengue cases exhibit seasonality throughout the year. While a minor trend effect was observable, it had been disregarded in our time series modeling. Our decision to exclude this trend was based on the Autocorrelation (ACF) and partial autocorrelation (PACF) analyses, which favor the adoption of an ARIMA (1,0,0) model for Bangladesh and ARIMA (2,0,1) for Singapore, as illustrated in Figures 4 and 5. Nevertheless, in our study, we pursued a comprehensive approach by running multiple models. The final model selection was determined by evaluating each model's feat against the Akaike Information Criterion (AIC) (Figure 7).

c. Spearman Correlation Test

From the spearman correlation test, it is observed that rainfall, humidity and sunshine hour is significantly associated with dengue cases in Bangladesh. Temperature, rainfall, and humidity is significantly associated with dengue cases in Singapore. Therefore, only significant variables are considered for the final model fitting.

Table 1: Spearman Correlation test between climate variables and Dengue cases

Variables	**Bangladesh**		**Singapore**	
	Rho	**P value**	**Rho**	**P value**
Temperature	0.20	0.11	0.26	<0.001
Rainfall	0.39	<0.001	-0.12	0.04
Humidity	0.50	<0.001	-0.42	<0.001
Sunshine	-0.45	<0.001	0.05	0.43

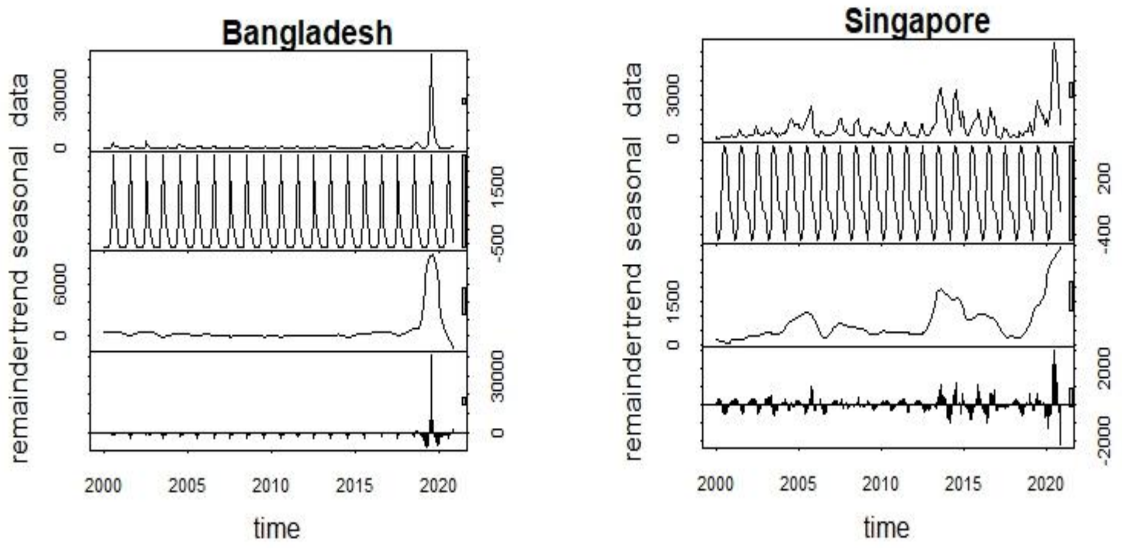


Figure 4: Decompose of Time series data of Dengue Cases using Seasonal and Trend decomposition using Loess. Left panel (Bangladesh), and right panel (Singapore).

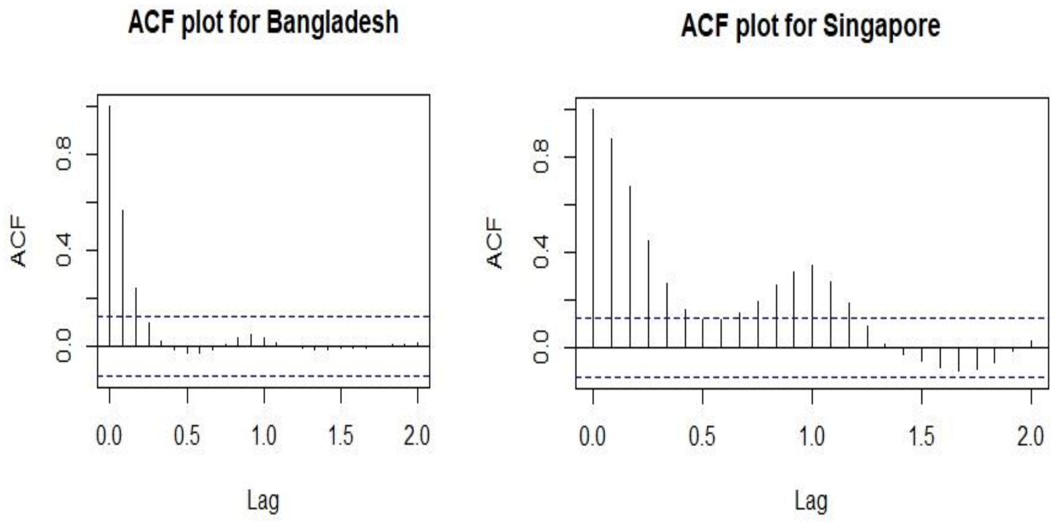
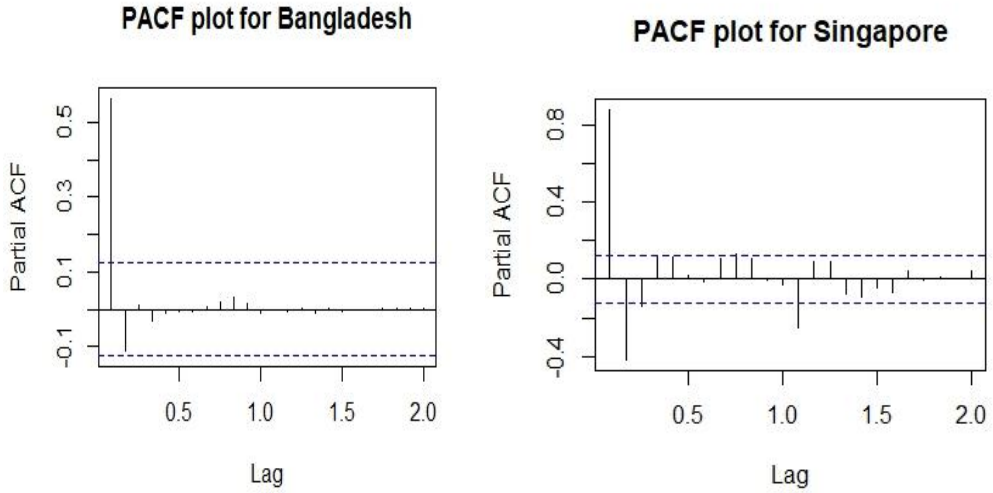


Figure 5: ACF plot for time series data of dengue cases


PACF plot for Bangladesh

PACF plot for Singapore

Figure 6: PACF plot for time series data of dengue cases

d. Sensitivity analysis and Final time series model selection

In the case of modelling dengue time series data, we primarily started with an ARIMA (1,0,0) and ARIMA (2,0,1) model for Bangladesh and Singapore, respectively. Since we identified the presence of seasonality in our data, we conducted different types of Seasonal ARIMA models which capture the seasonality in the model.

We considered different types of ARIMA (p,d,q) × Sesonal (P,D,Q)s models. Parameters of ARIMA model such as p, d, and q, determine the autoregressive order, differencing, and moving average order in the ARIMA model. The parameters P, D, and Q indicate the autoregressive order, seasonal differencing, and moving average order in the Seasonal ARIMA model. Moreover, we explored two different seasonal periods, S=12, representing monthly seasonal influence, and S=4, indicating quarterly seasonal patterns.

After conducting this analysis and comparing various model configurations, we identified the model with the best fit to the data, based on the evaluation of statistical criteria AIC values. This model, denoted as ARIMA (1,1,2) × Seasonal (0,1,2) with S=12, emerged as the most suitable choice for Bangladesh with AIC values 4543.63. Furthermore, the ARIMA (3,1,1) × Seasonal (0,1,2) with S=12 got selected as the best model for Singapore with AIC values 3506.13.

AR1 (Auto Regressive coefficient for lag 1) signifies the impact of a 1-unit increase in the prior month's Dengue cases, denoted as a lag of 1 (one-time step back). An increase of approximately 0.41 units in the current Dengue cases in Bangladesh is associated with such an increment. MA1 (Moving Average coefficient for lag 1) implies the consequence of a 1-unit increase in the prior month's error term at lag 1. This change is related to a decrease of roughly 0.79 units in the current Dengue cases. MA2 (Moving Average coefficient for lag 2) suggests the outcome of a 1-unit increase in the prior month's error term at lag 2. This is associated with an increase of approximately 0.19 units in the current Dengue cases. SMA1 (Seasonal Auto Regressive coefficient for lag 12) denotes the effect of a 1-unit increase in the value of Dengue cases at a seasonal lag of 12, representing the same month in the previous year. Such an increase is associated with a decrease of roughly 0.96 units in the current Dengue cases. SMA2 (Seasonal Auto Regressive coefficient for lag 24) signifies the influence of a 1-unit increase in the value of Dengue cases at a seasonal lag of 24, equivalent to the same month in the two years prior. It is associated with an increase of approximately 0.35 units in the current Dengue cases (Table 2).

An increase of approximately 0.92 units in the current Dengue cases in Singapore is associated with such an increment. AR2 is linked to a decrease of approximately 0.04 units in the current Dengue cases (Table 2). Similarly, AR3 is also associated with a decrease of 0.32 units in the current dengue cases. MA1 change is related to a decrease of roughly 0.78 units in the current Dengue cases. SMA1 reports a decrease associated with a decrease of roughly 0.53 units in the current Dengue cases. SMA2 is associated with a decrease of approximately 0.29 units in the current Dengue cases.

Table 2: Estimated values from model ARIMA (p,d,q) × Seasonal (P,D,Q) with S=12

	Bangladesh ARIMA (1,1,2) × Seasonal (0,1,2)	Singapore ARIMA (1,1,2) × Seasonal (0,1,2)
Model Coefficient	Estimate (SE)	Estimate (SE)
AR1	0.41*** (0.11)	0.92*** (0.09)
AR2		-0.04*** (0.09)
AR3		-0.32*** (0.07)
MA1	-0.79*** (0.12)	-0.78*** (0.07)
MA2	-0.19*** (0.11)	
MA3		
SMA1	-0.96*** (0.06)	-0.53*** (0.07)
SMA2	0.35*** (0.13)	-0.29*** (0.07)
Rainfall	-0.08 (2.30)	0.09 (0.17)
Humidity	-38.46 (89.76)	-19.38 (11.79)
Temperature		-34.09 (61.98)
Sunshine	161 (250)	

<0.001***, 0.01 <p<0.05**, 0.05<p<0.10*

Table 3: Poisson regression estimates

	Bangladesh	Singapore
Model Coefficient	Estimate (SE)	Estimate (SE)
Rainfall	0.0027*** (0.00173)	-0.005*** (0.00046)
Humidity	-0.124*** (0.00587)	-0.316*** (0.00934)
Temperature		0.665*** (0.184)
Sunshine	-0.487*** (0.00263)	

e. Poisson regression estimates

Table 3 reports that a 1-unit increment in rainfall is positively correlated with a modest rise of approximately 0.027 units in the incidence of Dengue cases in Bangladesh. Conversely, a 1-unit elevation in relative humidity and sunshine hour demonstrates a notable negative association, resulting in a substantial reduction of about -0.124 and -0.487 units in Dengue cases, respectively. Rainfall (-0.005) and humidity (-0.316) reports negative association with dengue cases in case of Singapore whereas temperature (0.665) showed positive association the dengue incidence.

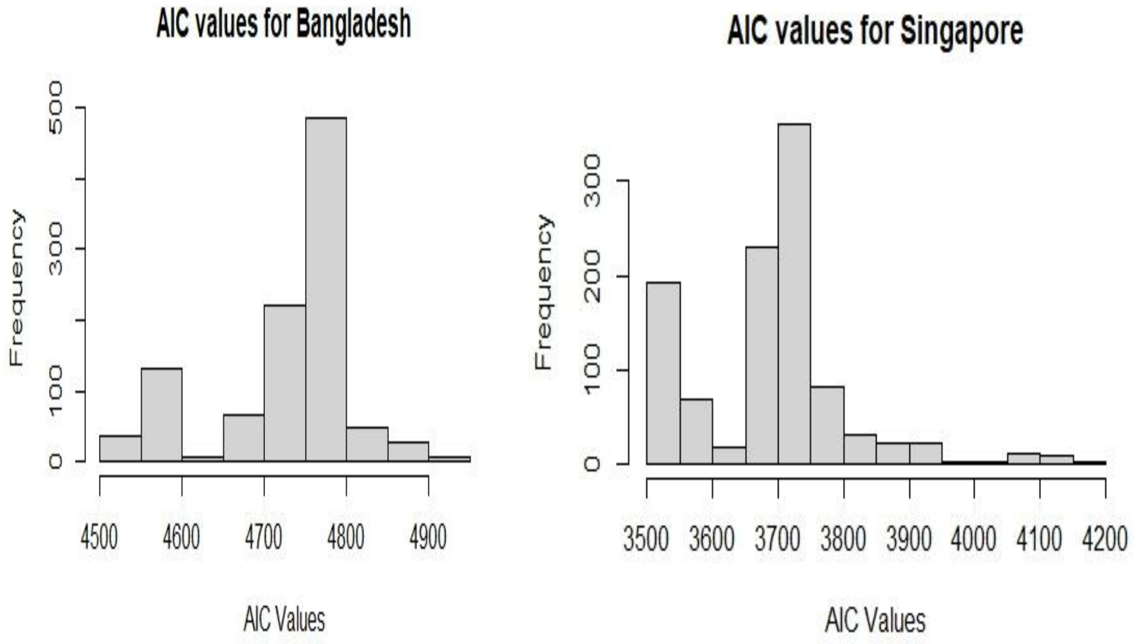


Figure 7: AIC values for different Seasonal ARIMA models for Bangladesh (left panel), and Singapore (right panel).

Forecasting of Dengue cases in Bangladesh and Singapore using different forecasting models'

Information obtained from various forecasting models and corresponding plots indicates that dengue cases in Bangladesh are projected to increase over the next 10 years, spanning from 2021 to 2030 (Figure 8-11). Notably, ARIMA models predict the highest number of dengue cases in Singapore will occur in 2023, surpassing the cases in Bangladesh (Figure 8). Other forecasting models show fluctuations in total dengue cases projections from 2021 to 2030 in Singapore. Based on the Root Mean Square Error (RMSE) analysis, it is evident that the TBATS model is the most accurate forecasting model for predicting dengue cases in Bangladesh, with an RMSE of 2904.48. In the case of Singapore's dengue cases, both the ARIMA model (RMSE = 341.55) and the TBATS model (RMSE = 341.92) performed well. In conclusion, the TBATS model is considered the superior choice for forecasting dengue cases in both Bangladesh and Singapore (Table 4).

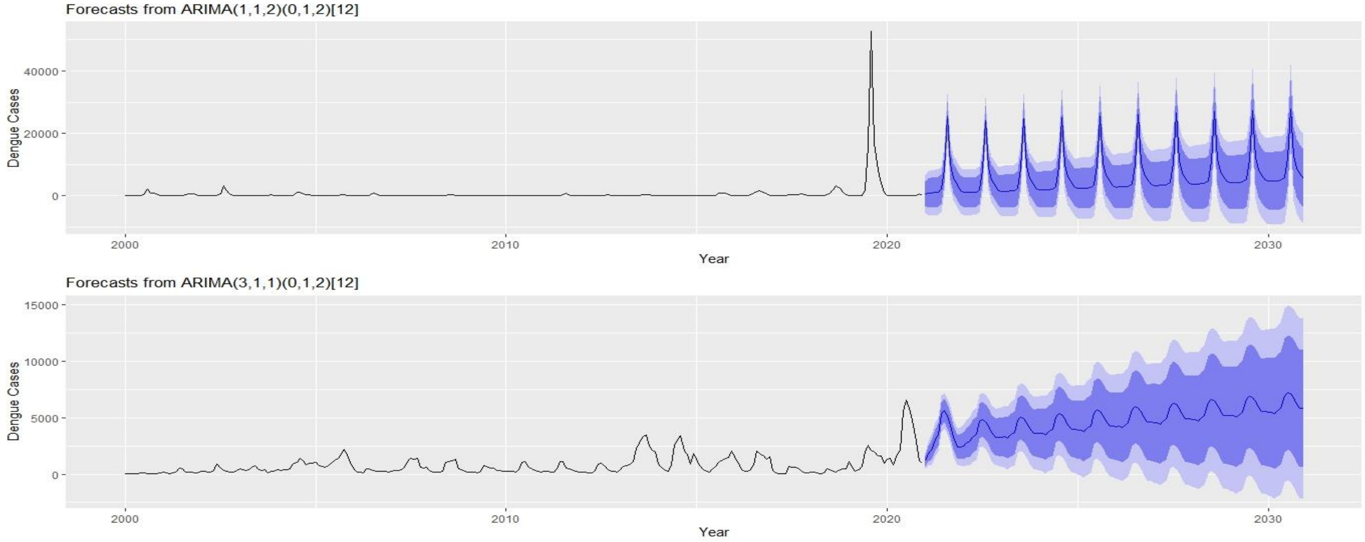


Figure 8: Forecasting of Dengue cases for next 10 years using Seasonal ARIMA model for both Bangladesh and Singapore

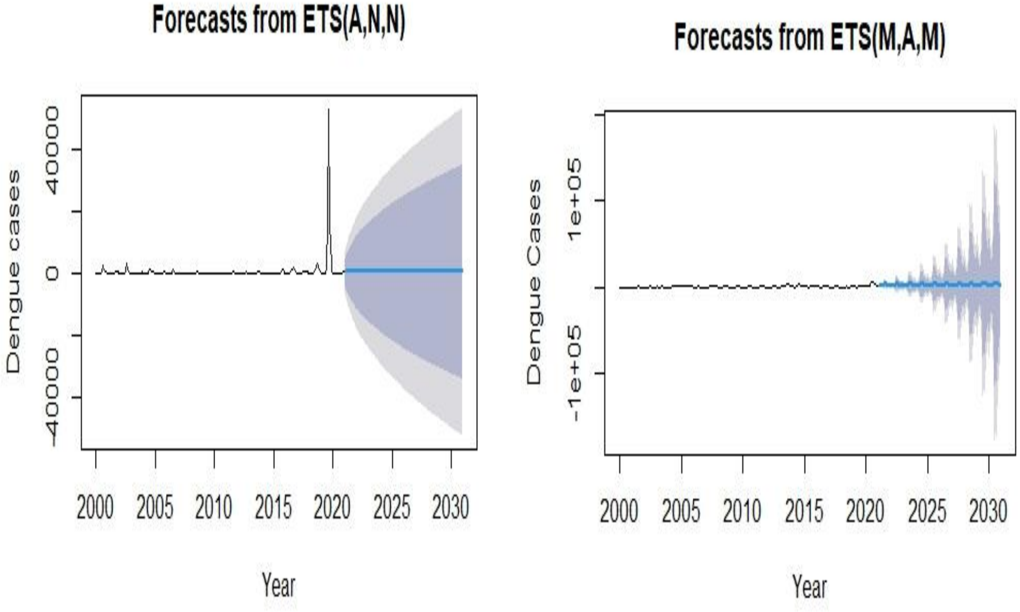


Figure 9: Forecasting of Dengue cases for next 10 years using ETS model for both Bangladesh (left panel) and Singapore (right panel)

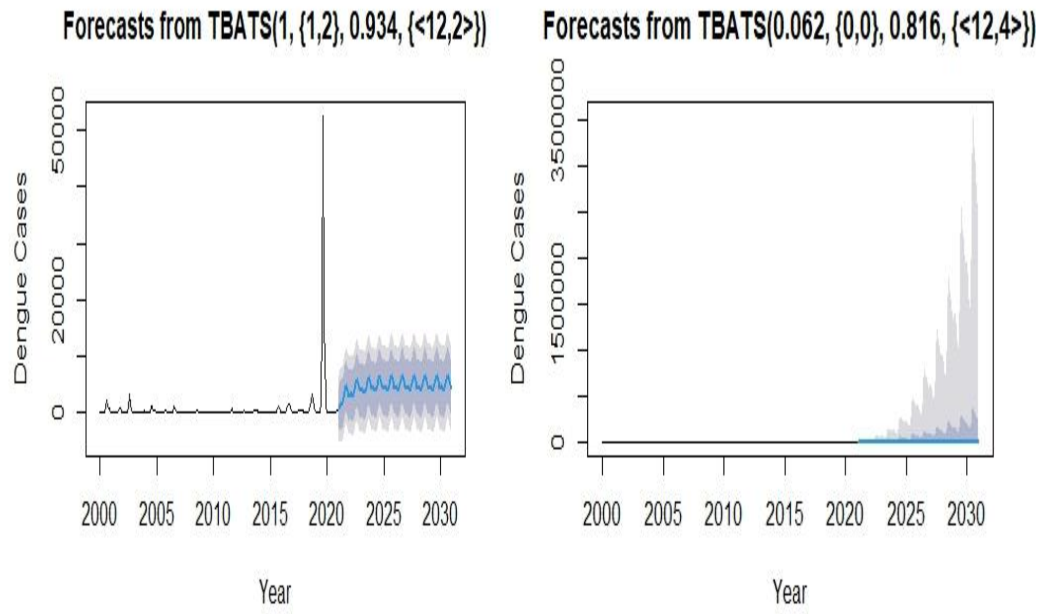


Figure 10: Forecasting of Dengue cases for next 10 years using TBATS model for both Bangladesh (left panel) and Singapore (right panel)

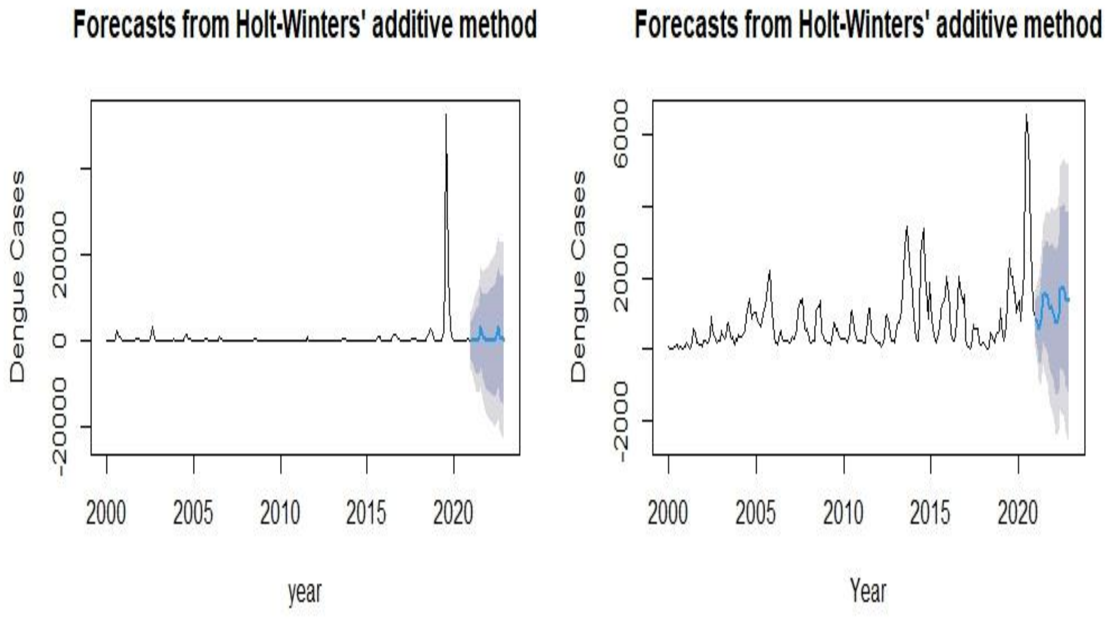


Figure 11: Forecasting of Dengue cases for next 10 years using Two component K-H model for both Bangladesh (left panel) and Singapore (right panel)

Table 4: Forecasting accuracy for different models.

Model Names	Bangladesh	Singapore
	Root Mean square error (RMSE)	Root Mean square error (RMSE)
Seasonal ARIMA	2985.70	341.55
ANN	8035.34	1601.25
SVM	8204.64	1448.26
ETS	3360.15	402.08
TBATS	2904.48	341.92
Two component KH Model	3241.45	393.59

f. Discussion:

The relationship between environmental change and disease causation is a much-talked about issue in epidemiology. Higher temperatures can lead to increased rates of proliferation and reproduction of vectors, as well as an extended transmission season for diseases. Furthermore, these changes can disrupt ecological balances and contribute to climate-related migrations of disease vectors, reservoir hosts, and human populations. To analyze the agents of disease causation, various environmental variables such as temperature, humidity, rainfall, and sunshine hours have been considered (Butler 2012; Weiss and McMichael 2004). This study examined the connection between climate factors and the incidence of dengue fever outbreaks in Singapore and Bangladesh. Statistical analysis of the correlation between dengue incidence and climatic variables is difficult due to the complexity of the vector and host life cycles. In this research, we found the impact of a comprehensive set of climate variables with the inclusion of humidity and sunshine hours along with the traditional temperature and rainfall, on dengue incidence.

This study found a significant positive correlation between temperature and dengue incidence in Singapore. Pinto et al. (2011) also found that for every 2-10°C of variation of the maximum temperature, there was an average increase of 22.2-184.6% in the number of dengue cases (Pinto et al. 2011). Gharbi et al. (2011) showed that minimum temperature at lag-5 weeks and average temperature at lag-11 weeks were variables the most positively correlated to dengue incidence (Gharbi et al. 2011). Temperature has been established as the most important weather variable in the growth and transmission of aedes mosquito vector and potential predictor of dengue surge according to a study in 2010 (Campbell-Lendrum et al. 2015; Chen et al. 2010) . Temperature influences the life cycle of Aedes mosquitoes including growth rate and larval survival and the length of reproductive cycle (Patz et al. 1998). Several studies also found strong relation between temperature and dengue cases (Cazelles et al. 2005; Descloux et al. 2012; Earnest et al. 2012a; Hossain et al. 2023; Hu et al. 2012; Johansson et al. 2009) which is similar to our study.

This study also ventured to determine the association between rainfall and dengue cases both in Bangladesh and Singapore. A positive correlation was found in Bangladesh, but a negative relation was noticeable for Singapore. Several studies have also found an association between rainfall and dengue cases (Cazelles et al. 2005; Chen et al. 2010; Descloux et al. 2012; Hu et al. 2012; Johansson et al. 2009). Among these studies, some studies had found strong positive correlation and other negative correlation between rainfall and dengue cases. Rainfall is affects agents of diseases, particularly vectors of infectious diseases. It has been demonstrated that increased precipitation increases the number of reproductive sites, which in turn increases the mosquito population. Insects, mites, and parasites survive longer in humid environments. Tropical and subtropical regions with high levels of urbanization and expanding deforestation are frequently the most vulnerable because vector-borne diseases flourish in hot, humid climates and can exploit recently damaged ecosystems (Wu et al. 2016). It was observed that the incidence of Dengue was reduced during the winter months of April and June, when precipitation was abundant, but increased during the summer months of winter. Rain is believed to have both positive and negative impacts on the development of mosquitoes. An excess of precipitation can harm mosquitoes that may be present and produce standing water in which they can deposit their eggs (Lindsay and Birley 1996). This study found a significant negative association between dengue cases and relative humidity in both Bangladesh and Singapore. The findings of our investigation show a significant inverse association between relative humidity and the prevalence of dengue cases. But some researchers found positive association between relative humidity and dengue cases (Descloux et al. 2012; Hossain et al. 2023).

Also, there was a significant adverse correlation between sunshine hour and dengue cases in Bangladesh. This study finds the impact of a comprehensive set of climate variables with the inclusion of humidity and sunshine hours along with the traditional temperature and rainfall, on dengue incidence. An earlier study also recorded a negative correlation between dengue incidence and average sunshine hours (Pham et al. 2011). Fewer sunshine hours for shorter periods is good for spreading dengue because mosquitoes are more active when it's dark, which means more times they will bite (Pham et al. 2011).

Predicting the rise in dengue cases is becoming increasingly critical for the coming decades due to the growing incidence of this disease in both Bangladesh and Singapore. Developing effective forecasting models is essential to assist policymakers in mitigating the disease's impact. Our research revealed that machine learning models, such as Artificial Neural Networks (ANN) and Support Vector Machines (SVM), did not perform well in this context. In contrast, both the ARIMA and TBATS models proved to be suitable for accurately forecasting dengue cases in both Bangladesh and Singapore. A study conducted in 2022 specifically found that the TBATS model provided precise forecasts for dengue cases in Bangladesh (Naher et al. 2022) which is similar to our study. Previous research, including studies conducted by Co et al. in 2017, Du et al. in 2021, Polwiang in 2020, and Zhao et al. in 2020 (Co et al. 2017; Du et al. 2021; Polwiang 2020; Zhao et al. 2020), employed a variety of forecasting models, such as ANN, SVM, ETS, TBATS, and ARIMA, to predict dengue cases in various countries. In our investigation, we comprehensively assessed all these models and discovered that the TBATS model outperformed the others in forecasting dengue cases in both the countries. So, it emerged as the Model of choice.

g. Limitations

This research has some limitations also. Initially, the government repository lacks continuous time-series data pertaining to dengue cases and vectors. Furthermore, the correlation between climate and environmental factors and vector reproduction was insufficiently investigated in this study due to financial, time, and resource constraints. Furthermore, longitudinal surveillance statistics pertaining to vectors and dengue diseases are absent in Bangladesh. Administrative officials in Bangladesh lack a strategy for data exchange, resulting in the dispersion of the limited data at their disposal. Fourth, an exhaustive survey on institutional (government and NGO) control methods was not conducted because it was unnecessary for the model's construction. However, additional research and effort on the part of private sector entities and individuals to prevent and control dengue vectors would strengthen the disease control program.

h. Conclusion

Understanding the historical trends of dengue cases and predicting future scenarios is crucial for policymakers to formulate effective preventive measures. In light of this, the authors have developed a model to analyze the current dengue situation and project future cases over the next decades in both Bangladesh and Singapore. This study investigates the correlation between climate factors and the incidence of dengue fever outbreaks in the two countries. The findings suggest that maximum temperature and rainfall positively impact on dengue incidence, while humidity and daylight hours have a negative impact on the disease occurrence. Model selection criteria indicate that the seasonal ARIMA model and TBATS model perform well, showing lower Root Mean Square Error (RMSE) and proving to be the most suitable models for forecasting dengue cases in both Bangladesh and Singapore.

The study's findings indicate a projected increase in the incidence of dengue cases in Bangladesh in the coming years. In response, it is imperative for both government and non-government organizations, as well as policymakers, to launch nationwide initiatives aimed at enhancing public awareness on these issues. Anticipating future dengue cases, effective preventive measures is crucial. Additionally, policymakers in both Singapore and Bangladesh can use this study as a roadmap to formulate a comprehensive model for forecasting overall dengue cases, considering factors such as immunological, entomological, demographic, and climatic data. Drawing from the experiences of Singapore and Bangladesh, other countries can develop their own tailored dengue prevention and containment strategies at both national and local levels. Furthermore, international organizations, particularly the World Health Organization (WHO), could take the lead in creating regional and global dengue prevention plans and preparedness based on the insights provided by this new model.

Chapter Eight

8. Novelty and Findings of the study: Narratives and Summary

Theory interpretation in context:

The germination, transmission, and propagation of dengue depends on the prevailing climate scenario of a given region. Dengue is transmitted by vectors, specifically Aedes aegypti and Aedes albopictus, two species of mosquitoes. The density and presence of these vectors have the greatest impact on the spread of dengue. Numerous studies [40-41] indicate that ecological and climate factors play an important role in the seasonal occurrence of dengue virus. Certain climate variables have a direct impact on the reproduction and proliferation of mosquito vectors, which are closely associated with these factors. In regions characterized by subtropical and tropical climates, which have historically been conducive to the breeding of dengue vectors, erratic climatic change poses a significant bad impact on human health. This is caused predominantly by the spread of dengue fever in these regions. In 2020, a total of 35,315 confirmed dengue cases were reported in Singapore [42]; this represented a significant increase from the previous year.

This study presents a computational model that evaluates the impact of various climatic conditions on the incidence of dengue cases, which are predominantly observed in the Indian Subcontinent during the monsoon season. Several experiments [43-47] have been carried out in the South Asia and ASEAN region to examine the impact of climate change on all the epidemiological dimensions of dengue. Dengue fever has emerged as a significant public health concern in these regions, according to these studies. Temperature and precipitation are the primary climate factors that have a significant impact on dengue outbreaks, according to these studies. In addition, these studies have revealed a previously unaccounted-for impact of particular climate factors over time. This study finds the impact of a comprehensive set of climate variables with the inclusion of humidity and sunshine hours along with the traditional temperature and rain fall, on dengue incidence. The result is fascinating as the two added variables negated the impact while the previous two factors positively factored in dengue incidence. Thus, a complete scenario of dengue-climate relationship got unleased. It would now comprehensively address the exact incidence picture of dengue and would help reduce and contain (the hitherto untamed) any prospective dengue outbreak in Singapore, allowing sufficient time for preparedness.

In sum, this study was driven by the objective that, it would identify the climate variables that may influence the occurrence of dengue cases and the specific pattern in which they affect the number of cases. According to the findings of this study, there is a positive correlation between maximum temperatures and the dengue incidence. A rise in global temperature may increase the vector-borne disease cases, dengue being no exception [48]. A recent scientific investigation discovered that the ideal temperature range for Aedes aegypti vector multiplication is between 21.3 and 34 C [49]. Once again, the findings of our investigation show a significant inverse association between relative humidity and the prevalence of dengue cases. There was a reduction in the tally of reported dengue cases during the monsoon season, which correlated with an increase in relative humidity levels.

Furthermore, there was a significant correlation between the duration of sunshine exposure and a decrease in the incidence of dengue cases. According to a recent study, there exists a correlation between the duration of sunshine and a reduced incidence of dengue fever [51]. The transmission of dengue is more probable in conditions of reduced sunlight, as mosquitoes exhibit increased activity during nighttime hours and tend to engage in more frequent biting behavior in darkness [48]. When considering both positive and negative elements, a comprehensive statistical outcome is derived.

Case study in perspective:

- In theory, establishing the causal relations of any disease or health event is crucial as to its prediction and protection is concerned. Taking dengue as a model case in Bangladesh and Singapore, this study has ventured to apply an innovative step-wise approach to determine the causal associations within the epidemiological triad of climate-vector-disease relationships as well as ecological and human factors in the cities of Dhaka and Singapore. The study established a significant correlation between climatic variables and vector abundance, ecological factors and vector population and between vector population and dengue occurrence in temporal and spatial dimensions. Again, the study investigated the relationship between seasonal variation and dengue incidence accounted for 20 years and long-term climate trends of climatic factors and dengue incidence over a 10-year period. In this study, the study was able to generate a useful data set for future researches in the field of impact of climate change as well as ecology on dengue transmission in Dhaka and Singapore, in the regions of the South and South East Asia at large.
- Based on the findings, a model mapping system was envisioned to predict the future incidence of dengue and thereby, to predict any such disease or health event and devising prevention guidelines thereto at local, national, regional and global level.
- In one hand, differences of variables in different cities and regions have been proved as to applying one regional model for another region, on the other hand, incorporating crucial variables in one model through a compare and contrast study enabled to frame a relatively common model mapping system applicable for any given entity of a region. It is a huge enabler on global and regional scale to address the outbreak of any given disease in entities with different economic setting. Devising this technique of **Mapping and modelling by addressing Spatial variations is an important novelty of this study.**

- **Finding out temporal variations of variables over time, particularly decadal impact of variables is another crucial attribute of the Model to apply it effectively in preventive medicine and urban planning.**
- This research also found that city areas with more paved roads, highways and concrete building had the highest level of aedes mosquito concentrations. These results showcase that, the rapidly changing urban and suburban landscape of developing world is one of the major reasons leading to a fortified incidence of dengue in metropolitan areas. This is a crucial inference as to the dengue prediction and prevention mapping is concerned that, unplanned urbanization, particularly development of shanty slum area is crucial to dengue fever spread.
- Again, the mapping results of this study have important contributory function to aide in developing apt and differentiated policies for containing vectors and preventing the propagation of dengue disease in Dhaka, Bangladesh and Singapore and other vulnerable areas of the regions and the globe at large.

Conclusive Interpretation and findings of the Study:

For both the study areas-Dhaka, Bangladesh and Singapore, the 10 years comprehensive data of the four determined variables are placed and interpreted against the chosen two models as under:

- **After incorporating 10 years data of Bangladesh**

Poisson regression

Dengue_Cases_B	Coef.	St.Err.	t-value	p-value	[95% Conf	Interval]	Sig
Max_T_B	.594	.002	278.36	0	.59	.599	***
Rainfall_B	-0.003	0	-17.51	0	0	0	***
Humidity_B	-.145	.001	-199.93	0	-.146	-.143	***
Sunshinehour_B	-.865	.003	-312.37	0	-.871	-.86	***
Constant	3.538	.092	38.64	0	3.358	3.717	***

Mean dependent var	608.869	SD dependent var	3667.187
Pseudo r-squared	0.275	Number of obs	252
Chi-square	214048.815	Prob > chi2	0.000
Akaike crit. (AIC)	563308.235	Bayesian crit. (BIC)	563325.883

**** p<.01, ** p<.05, * p<.1*

Interpretation: The estimated coefficient 0.594 means that for a one-degree Celsius change in the maximum temperature, the difference in the logs of expected counts is expected to change by 0.594, given the other predictor variables in the model are held constant which is statistically significant at 1% level.

The estimated coefficient -0.003 means that for a one mm change in rainfall, the difference in the logs of expected counts is expected to change by 0.003, given the other predictor variables in the model are held constant which is statistically significant at 1% level.

The estimated coefficient -0.145 means that for a one percentage change in the relative humidity, the difference in the logs of expected counts is expected to change by 0.145, given the other predictor variables in the model are held constant which is statistically significant at 1% level.

The estimated coefficient -.865 means that for a one-hour change in the sunshine hour, the difference in the logs of expected counts is expected to change by 0.865, given the other predictor variables in the model are held constant which is statistically significant at 1% level.

After incorporating 10 years data of Bangladesh
Negative binomial regression

Dengue_Cases_B	Coef.	St.Err.	t-value	p-value	[95% Conf	Interval]	Sig
Max_T_B	.44	.083	5.27	0	.276	.603	***
Rainfall_B	-.003	.002	-1.89	.059	-.007	0	*
Humidity_B	.035	.043	0.81	.419	-.05	.119	
Sunshinehour_B	-.763	.152	-5.03	0	-1.06	-.465	***
Constant	-5.81	3.996	-1.45	.146	-13.642	2.022	
lnalpha	1.836	.087	.b	.b	1.666	2.005	

Mean dependent var	608.869	SD dependent var	3667.187
Pseudo r-squared	0.020	Number of obs	252
Chi-square	53.361	Prob > chi2	0.000
Akaike crit. (AIC)	2613.755	Bayesian crit. (BIC)	2634.932

**** p<.01, ** p<.05, * p<.1*

- **Interpretation:** The estimated coefficient 0.44 means that for a one-degree Celsius change in the maximum temperature, the difference in the logs of expected counts is expected to change by 0.44, given the other predictor variables in the model are held constant which is statistically significant at 1% level.
- The estimated coefficient -0.003 means that for a one mm change in rainfall, the difference in the logs of expected counts is expected to change by 0.003, given the other predictor variables in the model are held constant which is statistically significant at 10% level.
- The estimated coefficient 0.35 means that for a one percentage change in the relative humidity, the difference in the logs of expected counts is expected to change by 0.35, given the other predictor variables in the model are held constant which is not statistically significant.
- The estimated coefficient -.763 means that for a one-hour change in the sunshine hour, the difference in the logs of expected counts is expected to change by 0.763, given the other predictor variables in the model are held constant which is statistically significant at 1% level.

After incorporating 10 years data of Singapore

- **Poisson regression**

Dengue_Case_S	Coef.	St.Err.	t-value	p-value	[95% Conf	Interval]	Sig
Max_T_S	.047	.004	11.15	0	.039	.055	***
Rainfall_S	.001	0	29.94	0	.001	.001	***
Humidity_S	-.149	.001	-211.59	0	-.151	-.148	***
Sunshine_Hour_	-.249	.002	-	0	-.254	-.244	***

S			104.84				
Constant	18.724	.149	125.89	0	18.432	19.015	***

Mean dependent var	783.151	SD dependent var	932.025
Pseudo r-squared	0.269	Number of obs	252
Chi-square	52971.788	Prob > chi2	0.000
Akaike crit. (AIC)	144076.349	Bayesian crit. (BIC)	144093.996

**** p<.01, ** p<.05, * p<.1*

- **Interpretation:** The estimated coefficient 0.047 means that for a one-degree Celsius change in the maximum temperature, the difference in the logs of expected counts is expected to change by 0.047, given the other predictor variables in the model are held constant which is statistically significant at 1% level.
- The estimated coefficient 0.001 means that for a one mm change in rainfall, the difference in the logs of expected counts is expected to change by 0.001, given the other predictor variables in the model are held constant which is statistically significant at 1% level.
- The estimated coefficient -0.149 means that for a one percentage change in the relative humidity, the difference in the logs of expected counts is expected to change by 0.1459 given the other predictor variables in the model are held constant which is statistically significant at 1% level.
- The estimated coefficient -.249 means that for a one-hour change in the sunshine hour, the difference in the logs of expected counts is expected to change by 0.249, given the other predictor variables in the model are held constant which is statistically significant at 1% level.

After incorporating 10 years data of Singapore

- **Negative binomial regression**

Dengue_Case_S	Coef.	St.Err.	t-value	p-value	[95% Conf	Interval]	Sig
Max_T_S	.106	.104	1.02	.308	-.098	.309	
Rainfall_S	.001	.001	1.55	.122	0	.003	
Humidity_S	-.176	.021	-8.45	0	-.216	-.135	***
Sunshine_Hour_	-.285	.062	-4.58	0	-.406	-.163	***

S							
Constant	19.39	3.817	5.08	0	11.908	26.871	***
lnalpha	-.323	.081	.b	.b	-.482	-.164	

Mean dependent var	783.151	SD dependent var	932.025
Pseudo r-squared	0.023	Number of obs	252
Chi-square	87.154	Prob > chi2	0.000
Akaike crit. (AIC)	3787.163	Bayesian crit. (BIC)	3808.340

**** p<.01, ** p<.05, * p<.1*

- **Interpretation:** The estimated coefficient 0.106 means that for a one-degree Celsius change in the maximum temperature, the difference in the logs of expected counts is expected to change by 0.106, given the other predictor variables in the model are held constant which is not statistically significant.
- The estimated coefficient 0.001 means that for a one mm change in rainfall, the difference in the logs of expected counts is expected to change by 0.001, given the other predictor variables in the model are held constant which is not statistically significant.
- The estimated coefficient -0.176 means that for a one percentage change in the relative humidity, the difference in the logs of expected counts is expected to change by 0.176, given the other predictor variables in the model are held constant which is statistically significant at 1% level.

Novelty of the Research:

Summary Point-One: Data Interpretation for variable determination in city/zone: The germination, transmission, and spread of dengue depend on the prevailing enviroment. Dengue is transmitted by vectors, specifically Aedes aegypti and Aedes albopictus, two species of mosquitoes. The density and presence of these vectors have the greatest impact on the spread of dengue. Numerous studies [40-41] indicate that ecological and climate factors play an important role in the seasonal occurrence of dengue virus as certain climate variables have a direct impact on the reproduction and proliferation of mosquito vectors, which are closely associated with these factors. In regions characterized by subtropical and tropical climates, which have historically been conducive to the breeding of dengue vectors, climate variables pose a discernible vulnerability to human health. This is caused predominantly by the spread of dengue fever in these regions. This study is driven by the objective to identify the climate variables in Space and Time that may influence the occurrence of dengue cases and the specific pattern in which they affect the number of cases.

Temperature:

a. Warm temperatures are conducive to the growth of Aedes aegypti mosquitoes, which have been implicated for transmitting the dengue virus between host and vectors. Elevated temperatures expedite the maturation process of mosquitoes and the dengue virus they harbor, thereby precipitating a surge in the rate of transmission. The replication of the dengue virus within mosquitoes may be facilitated by higher temperatures, which may result in a reduction of the incubation period and an increase in transmission efficacy.
b. According to the findings of this study, there is a positive correlations between maximum temperatures and dengue incidence. A rise in temperature may increase the occurrence of vector-borne disease cases, such as dengue [48]. A recent scientific investigation discovered that the ideal temperature range for Aedes aegypti vector multiplication is between 21.3 and 34 degree celcius [49].
c. Rainfall;
d. Plasmids of the species Aedes aegypti proliferate in bodies of standing water. As precipitation can generate and restock breeding grounds, including pools, containers, and other water-retentive structures, mosquito populations can increase. Transmission Variations: Although heightened precipitation facilitates the establishment of additional

breeding grounds, an overabundance of precipitation can effectively flush away these breeding sites. Hence, a multifaceted correlation may exist between precipitation patterns and the transmission of dengue, whereby inadequate or excessive precipitation can have an impact on mosquito populations.

b. Several studies have also found a continuous positive relationship between rainfall and the frequency of dengue cases [44-46]. Rainfall and dengue cases had a negative link during the winter season, whereas a positive correlation was seen during the summer months, notably April and June. Rainfall has an impact on mosquito growth that is both beneficial and destructive. Rainfall has the ability to create standing water, which mosquitoes use as a hatching site. However, it is crucial to highlight that excessive or unwise rainfall might have a negative impact on mosquito populations [50].

Humidity:

Again, the findings of our investigation show a significant inverse association between relative humidity and the prevalence of dengue cases. There was a decrease in dengue incidence during the monsoon season, which correlated with an increase in relative humidity levels.

Sunshine:

Furthermore, there was a significant correlation between the duration of sunshine exposure and a decrease in the incidence of dengue cases. According to a recent study, there exists a correlation between the duration of sunshine and a reduced incidence of dengue fever [51]. The transmission of dengue is more probable in conditions of reduced sunlight, as mosquitoes exhibit increased activity during nighttime hours and tend to engage in more frequent biting behavior in darkness [48].

Summaries of variables:

When considering above positive and negative elements together, a comprehensive statistical outcome is derived. This study finds the impact of a comprehensive set of climate variables with the inclusion of humidity and sunshine hours along with the traditional temperature and rain fall, on dengue incidence. The result is fascinating as the two added variables negated the impact while the previous two factors positively factored in dengue incidence. Thus, a complete scenario of dengue-climate relationship got unleashed. It would now comprehensively address the exact incidence picture of dengue and would help reduce and contain (the hitherto untamed) any prospective dengue outbreak in Dhaka, Bangladesh and Singapore, allowing sufficient time, administrative measures and resources for preparedness.

Summary Point-Two: Comparative Model Study: model determination of spatial variation (regions and national level versus city/zone)

It's common in epidemiological and environmental studies to use a variety of statistical methods to analyze the relationship between variables and predict outcomes. In this case, the study employed multiple linear regression, Poisson regression, negative binomial regression, and a machine learning approach to assess the impact of temperature and rainfall on dengue cases. Here is the summary of each of these methods and why machine learning was proved advantageous over others while selecting a model applicable across a region or nationwide in lieu of a model feasible for a specific city or zone.

Multiple Linear Regression:

Used when there is a linear relationship between the dependent variable (e.g., dengue cases) and multiple independent variables (e.g., temperature, rainfall). Assumes a linear and additive relationship between the variables.

Poisson Regression:

Appropriate when the dependent variable represents counts, such as the number of dengue cases, and follows a Poisson distribution. This model is useful for modeling the relationship between independent variables and the occurrence of rare events.

Negative Binomial Regression:

Similar to Poisson regression but more flexible in handling over dispersion, which occurs when the variance of the dependent variable is greater than the mean. It is suitable for count data with excess zeros or variability.

Machine Learning Approach:

Offers a more flexible and complex modeling technique that can capture nonlinear relationships and interactions among variables. Can handle large datasets and complex patterns that may be challenging for traditional statistical methods. Common machine learning algorithms for regression tasks include decision trees, random forests, support vector machines, and neural networks. Choosing the best model depends on the characteristics of the data, the assumptions of each method, and the specific goals of the analysis. Machine learning approaches are particularly powerful when dealing with complex, nonlinear relationships or when there are interactions between variables that traditional regression models might not capture as effectively.

When comparing the results, researchers typically evaluate the models based on criteria such as accuracy, precision, recall, and F1 score, depending on whether the problem involves classification or regression. The choice of the "best" model also depends on the interpretability of the results and the specific requirements of the study.

Summaries of the Models:

It's positive that the machine learning approach yielded the best results in our study, as this suggests that it can capture the complexity of the relationship between temperature, rainfall, and dengue cases more effectively than traditional regression models in this context.

Summary Point Three: Data Interpretation for the determination of temporal variation (year versus decade):

Table: Bangladesh Decadal Scenario

Year	Dengue Cases	Temperature	Rainfall	Humidity	Sunshine
2000	**462.5833333**	**30.40333**	**197.0517**	**81.2575**	**6.270833**
2001	202.5	30.785	185.1258	80.86833	6.298333
2002	519.3333333	30.63167	200.5892	81.25583	5.975833
2003	40.5	30.48167	178.5883	81.37583	5.880833
2004	327.8333333	30.51	217.8233	81.225	5.9
2005	87.33333333	30.8725	203.3633	81.165	5.930833
2006	183.3333333	31.1825	172.6258	80.56083	5.66
2007	38.83333333	30.46833	222.31	81.03083	5.51
2008	96.08333333	30.48417	191.9775	81.41083	5.5625
2009	39.5	31.30417	178.5783	79.5975	6.086667

2010	**34.08333333**	**31.22167**	**173.8117**	**80.06417**	**5.830833**
2011	113.25	30.59833	200.5042	80.15167	5.285
2012	55.91666667	30.79417	184.1225	79.8475	5.160833
2013	145.75	30.86083	186.0175	79.77917	5.100833
2014	31.25	31.125	164.3808	79.39583	5.285833
2015	263.5	30.89667	232.0467	80.40917	5.223333
2016	505	31.35083	191.3283	80.85333	5.444167
2017	230.75	31.0325	255.9258	80.7775	5.145833
2018	845.6666667	30.905	178.2167	79.85167	5.1775
2019	8446.166667	31.34	161.555	72.98167	5.286667
2020	**117.0833333**	**31.14667**	**160**	**74.83333**	**5.1875**

Table: Singapore Decadal Scenario

Year	Dengue Cases	Temperature	Rainfall	Humidity	Sunshine
2000	**56.08333**	**27.45833**	**197.5417**	**84.74167**	**5.166667**
2001	197.6667	27.60833	231.925	84.26667	5.216667
2002	328.75	28.08333	145.7417	82.49167	6.3
2003	399	27.75	199.2667	84.3	5.433333
2004	788.25	27.85833	178.0333	83.46667	5.966667
2005	1184.167	28.01667	160.8917	83.15833	6.066667
2006	278.0833	27.725	229.4333	84.59167	5.633333
2007	735.5	27.53333	240.5167	84.5	5.316667
2008	586	27.48333	193.7583	83.40833	5.241667
2009	374.8333	27.91667	160.075	82.36667	5.95

2010	**439.9167**	**28.1**	**172.925**	**82.875**	**5.691667**
2011	444.1667	27.575	210.35	84.625	5.575
2012	386	27.53333	179.9917	83.475	5.533333
2013	1847.5	27.65	229.0333	81.69167	5.433333
2014	1527.167	27.90833	128.2	78.525	5.975
2015	941.1667	28.25	105.5917	76.9	6.166667
2016	1090.417	28.41667	162.975	75.95	6
2017	291.6667	27.7	170.4667	82.625	5.8
2018	273.75	27.89167	142.35	79.6	5.75
2019	1333.167	28.425	113.9583	76.65	6.783333
2020	**2942.917**	**28.04167**	**157.2167**	**78.08333**	**5.875**

Accruing data from both the study areas and interpreting them through varied models, it has become clear that, the impacts of the variables do not become evident by one year or two. It is rather a decadal phenomenon, i.e., the results of the changing variables are felt at a gap of 10 years. This is a very interesting finding of the research. The most plausible cause behind this finding might lie in the fact that the epidemiological variables, particularly those that are directly influenced by anthropogenic factors such as human mobility and urbanization, take a time gap to impart their visible impacts on nature. Admittedly, it might not be necessarily 10 years in all epidemiological settings, but the findings of this research have stirred our understanding that the variables silently impart their effects to a fully bloomed climate event(s) at a later time. This warrants a policy planning a priori.

Preventive measure taken by Singapore and Bangladesh:

When it comes to combating dengue disease, Singapore and Bangladesh demonstrate the contrasting nature of their preventive measures. Singapore exemplifies meticulous and proactive planning, while Bangladesh faces challenges that hinder its ability to achieve the same level of preparedness as Singapore.

Singapore: Pioneering the Movement

Singapore, known for its careful organisation and resolute resolve, has become a world leader in the fight against dengue disease. The country's all-encompassing strategy include a diverse vector control programme coordinated by the National Environment Agency (NEA). Singapore effectively controls mosquito populations and reduces the transmission of the dengue virus by conducting frequent inspections, implementing focused fumigation measures, and utilizing advanced technical solutions.

In addition to vector control measures, Singapore is dedicated to preventing dengue by conducting intensive public awareness programmes among its population. These activities serve the purpose of educating residents about the significance of eradicating mosquito breeding areas, while also promoting a culture of attentiveness and accountability. Remarkably, this principle is well ingrained in communities, where engaging in proactive measures to prevent dengue has become the standard practice. Residents actively identify potential breeding areas and work together to keep their surroundings clean, so strengthening the nation's defences against dengue outbreaks.

Bangladesh: Confronting Different Obstacles

Unlike Singapore's proactive strategy, Bangladesh faces numerous hurdles in its efforts to prevent dengue fever. Despite sincere endeavours, the country faces limitations in resources, insufficient infrastructure, and social inequalities that hinder the execution of effective preventive measures. Vector control attempts face substantial obstacles, especially in rural and highly inhabited regions where breeding grounds multiply in unhygienic settings, intensifying the risk of dengue transmission.

In addition, the effectiveness of health education initiatives is hindered by low levels of literacy and communication obstacles, which restrict their scope and influence. Resistance to community mobilisation initiatives arises from conflicting priorities and deeply rooted socio-cultural norms, impeding collective action in the control of dengue. In addition, Bangladesh's surveillance systems, while in place, suffer from deficiencies in reporting and delays in responding, which diminishes their efficacy in controlling outbreaks and minimising the disease's impact on public health.

Summary: Closing the Divide

Singapore serves as a shining example in the worldwide battle against dengue fever, showcasing the effectiveness of proactive policies and comprehensive interventions. The comprehensive strategy, which includes strict vector control measures, substantial public education programmes, and active community involvement, sets an example for dengue prevention globally. On the other hand, the difficulties faced by Bangladesh highlight the urgent need for specific actions, more funding, and improved cooperation among all groups involved, in order to strengthen its ability to protect against dengue.

By closing the divide between ambition and execution, both countries may together work towards a future when dengue fever no longer poses a significant danger to public health. By leveraging the experiences of Singapore and Bangladesh, we can make a determined and focused effort to achieve a dengue-free world, safeguarding the health and prosperity of current and future generations.

Limitations of the Research Findings

Some limitations have been encountered during the study period to complete this research work. Those are given below-

- Both quantitative and qualitative methodologies are used in this research. However, quantitative data relates to secondary data for dengue cases, and climate variables such as, temperature, rainfall, sunshine and humidity are gathered from the Met offices of Dhaka, Bangladesh and Singapore and the International Centre for Diarrheal Disease Research, Bangladesh (ICDDR, B). ICDDR, B collected this data, particularly the dengue data, however it is just intended for reporting purposes. As a result, age, sex, and other socioeconomic characteristics were not taken into consideration when analyzing the data for this study. Only a few clinical settings used computers to record and retain data at the time of data collection; the majority of data record keeping systems were manual.
- This study is based on accessible, regularly gathered data. We were unable to account for a variety of environmental factors, such as urbanization, mosquito species and densities, and population immunity, that may have an impact on the link between anthropological factors of climate and the transmission of dengue fever. For Dhaka City, specific information on these factors is not available. However, in the case of Singapore, there were no paucity of such data.

- Data on temperature, rainfall, sunshine, and humidity were gathered for Dhaka Station from BMD between 2008 and 2022 for the sake of this study. Prior to 2008, we were unable to access data on the climate and dengue. Between 2000 and 2007, there were no particular data records at BMD and ICDDR, B. These data were gathered by the field workers from the office and hospital records. It was a huge undertaking, as most of the data were hand written. Again, the data of Singapore were handy.
- Since disease diagnosis and monitoring methods are customized based on time and place, the quality of dengue fever notification data may also change. While dengue non-prevalent countries (such as Australia) have the luxury to use more accurate molecular methods to identify and record dengue fever cases, nations in the Asia-Pacific area, such as Bangladesh and Singapore, only use symptomatic assessment to confirm a dengue fever case. Although, we developed the working definition of dengue in this research, the variation in dengue fever reporting could introduce bias into our analysis.
- In Bangladesh, a small number of dengue-infected persons do not seek treatment or a diagnosis at a hospital. This leads to an under-enumeration issue because these patient types were not accurately counted by DGHS, Bangladesh. The study result would be more accurate and consistent if we could account for all the factors mentioned.
- Insufficient financial support also posed a big constraint while conducting the research work.

Recommendations for Improving the Adaptive Response for Climate Change and Health, Focusing on Dengue Fever in Bangladesh

This study recommends the following to address dengue fever and its relation to climate change that takes into account the research and key needs. These are:

- Hospitals and Health offices should be properly equipped with data collection and analysis procedures to study temporal and spatial variations of diseases and variables.
- Based on the differences of disease incidence and variables, R and D wings of the concerned health departments should be specialized for adaptation responses.
- Awareness raising and capacity building with community and other sectors relating to health and climate change.
- Integration of climate change into health policies within the health sector and system.
- Integration of public health issues into climate change adaptation and mitigation policies of UN member states and UN itself.

It also recommends-

- By using a mechanism like the creation of a national research agenda, strengthening the body of knowledge already available about the hitherto unaccounted for factors of climate change on human health,
- Finding susceptible areas, or "hotspots," prioritizing health concerns that require intervention, and then creating a set of suitable short-, medium-, and long-term measures within an implementation framework. Principles and illustrations from worldwide guidance could be applied to this recommendation.
- Adapting current health and basic service infrastructure to anticipated changes, as well as developing methods and strategies to incorporate climate resilience into future infrastructure and system design.
- Creating a framework for monitoring, evaluation, and review that takes into account the iterative nature of adaptation as well as the continuously evolving body of knowledge regarding the effects and efficiency of adaptation.

- Aiding local governments with resources and support so they can take part in and, if necessary, take the lead in health-related climate change adaptation, mitigation and reversal projects.
- Increasing the ability of health professionals to promote, direct, organize, plan, or carry out activities related to health adaptation to climate change.

Future Research Directions:

One of the most significant global public health issues is dengue disease. It is evident that more research in this area is necessary given how complex the connection between climate change and dengue disease is. The following suggestions for further research may be made on the basis of the key results of this study-

Better Understanding of the Ecology of Dengue Fever: Continuous changes in socio-demographic characteristics and the climate have been proposed as potential causes for the dengue fever outbreak in the cities of Singapore and Dhaka. On this topic, more study is warranted. To evaluate the effects of rapidly changing climate on dengue fever, it is also useful to integrate varied meteorological data with long-term dengue data in various regions. More information on essential factors like mosquito species and densities, population immunity and mosquito control efforts and anthropogenic variables such as urbanization rate, housing and habitats data are needed to be gathered.

Evaluation of the Effectiveness of the Public Health Interventions: Using spatiotemporal analysis approach, which enables the identification and monitoring of high-risk areas for disease transmission and the targeting of education campaigns and vector control at specific sites, can increase the effectiveness of public health interventions. Controlling dengue fever epidemics can also be addressed by training medical staff and public health experts in high-risk locations. As a result, it's important to assess the efficiency of public health interventions for dengue fever while taking spatiotemporal approaches into account.

Policy Development:

Guidelines, methods, and carefully planned and controlled activities are needed for dengue management. The cooperation of individuals, families, and the larger society is necessary for dengue prevention and management. Effective control, prevention, and management of dengue could be based on a dengue management strategy that includes recommendations and activities.

There are some key broad elements that need to be incorporated for better dengue management. These are-

- Increasing understanding of climate change, vulnerability, and adaptability as well as dengue fever dynamics.
- National responses should take into account the variety of local challenges and seek to prioritize action based on methodical assessments of vulnerability and risk.
- Maintaining institutions and capacities at all levels; institutions at the national and sectoral levels must be able to create integrative policy frameworks that ensure efficient coordination and implementation, and institutions below the national level must be able to recognize their local vulnerability and adaptation requirements and take appropriate action using the direction provided by national and sectoral policy.
- Establishing and maintaining political will is a difficult task, especially in nations of the Asia Pacific regions where changing administrations may have different priorities and strategies for treating dengue fever and climate change that are at least partly motivated by political views. So, policy stability, if not political stability, lies at the core of the dengue

management plan, based on ecological and epidemiological realities. This was the call of this research, not to speak.

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