

# Temperature sensitivity of dengue in Thailand

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## Abbreviations

<b>DHF</b>	Dengue Hemmorrhagic Fever
<b>ARIMA</b>	Autoregressive moving average
<b>GAM</b>	General additive model
<b>ADF</b>	Augumented Dickey Fuller test
<b>ACF</b>	Autocorrelation function
<b>pACF</b>	Partial autocorrelation function
<b>AIC</b>	Akaike's information criterion
<b>sd</b>	standard deviation

# 1 Introduction

The Dengue virus is a vector borne virus, consisting of four serotypes (DENV 1-4). It is transmitted to humans by mosquitoes, more specifically by *Aedes aegypti* and *Aedes albopictus* (Phanitchat *et al.*, 2019). The resulting infection goes asymptomatic in many cases, but can also cause Dengue Hemorrhagic Fever (DHF), characterized by symptoms like fever, headache, joint and muscle pain as well as (internal) bleeding and bruising (Gubler, 1998). Dengue is an emerging public health issue, with half of the worlds population at risk of infection. 390 million cases per year are estimated worldwide, with most of them not showing symptoms and thus not being reported. Affected areas range from sub-tropical to tropical regions, with south-east Asia, including Thailand, being one of the most seriously affected regions. Newly affected areas also include Europe (WHO, 2023). The disease control of dengue is challenging due to the absence of an effective treatment or vaccine, which leaves only the treatment of symptoms with painkillers like paracetamol (WHO, 2023). Responsible institutions in affected areas currently focus on prevention, vector and case control and prediction of possible future outbreaks (Phanitchat *et al.*, 2019).

An important factor in predicting the epidemiological dynamics of Dengue is the climate: climate fluctuations due to recurring weather phenomenons and climate change are shown to influence *Aedes* biology and infections (Descoux *et al.*, 2012; Phanitchat *et al.*, 2019). In several studies, maximal temperature has an effect on dengue transmission (Descoux *et al.*, 2012), being associated with higher incidence (Phanitchat *et al.*, 2019) between 27 °C and 29,5 °C. The temperature with the highest epidemic potential was shown to be 29,3 °C with a low temperature range throughout the day (Liu-Helmersson *et al.*, 2014). Extreme global climate events like el Niño have been shown to affect Dengue outbreaks (Anyamba *et al.*, 2019).

In Thailand, a significant climate factor is the monsoon, which can be separated into two seasons: The south-west monsoon between may and october, characterized by higher temperature and precipitation and the north-east monsoon between november and february characterized by lower temperature and low precipitation (Kripalani *et al.*, 1995). In northern districts a rise in temperature since the mid 20th century has been shown (Masud *et al.*, 2016).

In this analysis, we are going to investigate the correlation between temperature and Dengue in Thailand from 2006 to 2020 to assess the significance of climate fluctuations and extremes as well as geographical factors on Dengue infections. We concentrate on the following points: Periods of higher DHF incidence will be compared to periods of extreme weather events. It will be examined if provinces with higher temperature also show higher incidences. The observation of trends in temperature and dengue cases over the course of the given time period will be analysed and compared. Finally, two models will be generated to forecast the development of DHF cases: Autoregressive moving average (ARIMA) will be used to model the near future. Generalized Additive Model (GAM) will be generated to predict the spatial distribution of incidences over Thailand in the future.

## 2 Material and Methods

**ERA5 data (climate)** The ERA5 database is a global climate database by the European Centre for Medium-Range Weather Forecasts (ECMWF), covering the earth in a 31 km horizontal grid up to 80 km in the atmosphere in the time period from 1950 to present. It was generated from measurements of various climate variables combined with a reanalysis of existing data and past reanalysis data to accurately complete the dataset in the given resolution (Hersbach *et al.*, 2020). For this project, monthly temperature data 2 m above ground for every province in Thailand in the timeframe of 2006 - 2020 was extracted.

**Dengue data** The Dengue case numbers are retrieved from annual infectious disease reports published by the Thailand ministry of health. Monthly case numbers of DHF for every province in the timeframe of 2006 - 2020 are used in this project. The datasets are used with a resolution at province level. Thailand had 76 provinces until Bueng Kan was split from Nong Khai in 2011, and has 77 provinces to date. For better compatibility of the data before and after 2011, the two new provinces are merged into a province equivalent to Nong Khai before 2011. Only for mapping, the temperature and incidence values of Nong Khai are copied and used for Bueng Kan for compatibility with the spatial data.

**Climate forecasting data** For GAM modeling, temperature data from the CORDEX climate model is used. It includes the temperature 2 m above ground of the years 2021 - 2040 at a 22 km grid (Copernicus Climate Change Service, 2019).

**Population data** We used population data from the Statistical Yearbooks of the National Statistical Office of Thailand from 2006 - 2011. The years 2012 - 2020 were obtained from the official website (National Statistic Office of Thailand, 2021). The incidences were calculated for DHF cases per 100,000 inhabitants for every province.

**Spatial data** To associate our data with the different provinces and visualize it, we use spatial data of Thailand's provinces. The two main data types in spatial data are vector-data and raster-data. Vector-data consists of a list of points with their exact location, which can then form lines or polygons. Raster-data assigns a value to every square of a raster. In this case, maps consisting of polygons for each province are used (Pebesma and Bivand, 2023). With the `sf` package, objects associating our data for each province with its coordinates and polygons are created. The function `geom_sf` of `ggplot2` is used for mapping.

**Descriptive analysis** All missing data points were excluded for the analysis. To summarize the data, descriptive parameters like mean, standard deviation, maximum and minimum were computed and the distribution of the data was visualized in a histogram. For better comparison, a log transformation is applied to the incidence curve. The log transformed data was used for mapping. To visualize the relationship between incidence and temperature, a smoothing function is used. This function minimizes the sum of squares of the residuals, getting a smooth curve based on the data. Subsequently, the correlation between our two variables is determined via a Pearson correlation.

**ARIMA** To predict the development of the dengue cases with an ARIMA model, a time series with the total dengue cases of Thailand is created. A time series can be decomposed into the components trend, seasonality and random. A stationary time-series required for ARIMA modeling is obtained when the mean value does not change over time, the variance does not increase and the seasonality effect is minimal (Prabhakaran, 2017). Two tests were used for stationarity of the data. The Augmented Dickey-Fuller (ADF) test examines whether the time series has a unit root, indicating non-stationarity. The Kwiatkowski-Phillips-Schmidt-Shin (KPSS) test is also a unit root test but focuses on the presence of a deterministic trend in the series. If the time series is initially found to be non-stationary, the differences between consecutive observations can be calculated, and the stationarity tests can be applied again (Hyndman and Athanasopoulos, 2018). ARIMA models combine an autoregressive model AR(p) and a moving average model MA(q). The autoregressive model computes the current value from previous values and the error term:

$$y_t = c + \phi_1 y_{t-1} + \phi_2 y_{t-2} + \dots + \phi_p y_{t-p} + \epsilon_t$$

$\epsilon_t$  = white noise

$1, \dots, \phi_p$  = parameters

$y_{t-1}, \dots, y_{t-p}$  = lagged values

For the moving average the current value consists of the mean value of the time series and weighted current and past error terms:

$$y_t = c + \epsilon_t + \theta_1 \epsilon_{t-1} + \theta_2 \epsilon_{t-2} + \dots + \theta_q \epsilon_{t-q}$$

$\theta_1, \dots, \theta_q$  = parameters

I(t) is the number of times differencing is performed to make the time series stationary (Venkat, 2018). To find the optimal values for p and q, the Autocorrelation function (ACF) and partial Autocorrelation function (pACF) are evaluated. The ACF plot shows the correlations of a time-series with lags of itself. The pACF calculates the relationship between a time series and its lag, excluding the influence of linear dependencies among other lags (Prabhakaran, 2017). A second evaluation tool is the auto.arima function. The function automatically fits the best

ARIMA model by minimizing the Akaike's Information Criterion (AIC), which is a criterion for the quality of the model. The `auto.arima` function can also consider seasonal models. Optimal models will yield uncorrelated residuals with zero mean and constant variance. This can be evaluated by plotting the ACF of the residuals and by performing a portmontreau test, for example the Ljung-Box test (Hyndman and Athanasopoulos, 2018).

**GAM** GAM provides insight into the shape and direction of the relationship between temperature and dengue cases. Additionally, it was used to forecast the future dengue case development based on the temperature development prediction. A GAM is a flexible extension of Generalized Linear Models (GLMs) that allows for the modelling of non-linear relationships between the response variable and predictor variables. A linear model can be described as follows:

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p + \epsilon$$

GAMs are now a nonparametric form of regression where the linear predictors ( $\beta_i x_i$ ) of the regression are replaced by smooth functions of the explanatory variables,  $f(x_i)$ . The model can be defined as:  $y_i = f(x_i) + \epsilon_i$  where  $y_i$  is the response variable,  $x_i$  is the predictor variable, and  $f$  is the smooth function (Wood, 2006). It is called an additive model, because all the  $f(x_i)$  functions and therefore their predictor variables contribute individually to the response variable and are added up. The advantage is that the different smooth functions can capture complex relationships by flexibly fitting curves to the data. There are two different ways to interpolate the functions of the predictor values. Finding a polynomial with a specific degree that passes through all the data points is a polynomial interpolation approach. Because high-degree polynomials may result into wide oscillation or overfitting, piece-wise interpolation is sometimes more accurate. Here, the data is divided into smaller intervals. Each one is described by an individual function. Defining the number of knots determines into how many segments the model is divided. All polynomials together are called splines with a degree of  $k$ , connecting the knots one by one. The spline can be differentiated  $k-1$  times. A smaller number of knots makes the response smoother, while a higher  $k$  value results in a curve that closely follows the individual data points. Choosing from various types of splines, smoothing splines were used, which try to fit the data closely while maintaining smoothness (Peri, 2021). The obtained model includes the relationship between incidence and temperature. Such GAMs can be used to forecast the development of the response variable (incidence of dengue fever) based on the predictor variables (temperature). The predicted values can then be plotted on a map of Thailand. The prediction is based on the average temperature over the time period of 2021 until 2040 in Thailand.

### 3 Results

#### 3.1 Descriptive Analysis

In the given time period, the maximum temperature of Thailand was 31.07°C in April 2016, while the minimum temperature was 22.05°C December 2013. Over the years, the yearly average temperature rose slightly, as Figure 8 (see Appendix) shows. The average temperature for all years, for the whole country of Thailand is 27.04°C. The mean and the median temperatures over Thailand have similar behaviours, as can be seen in Figure 9 (see Appendix). However, the median-temperature is on average 0.09°C higher than the mean-temperature.

The maximum number of dengue cases with a value of 8324 were reported in Bangkok, November 2015. The standard deviation of dengue cases is 203.6. The mean over all years and regions is 99.1. The resulting incidences were in a range of 0 to 370, with the maximum being reported in June 2013 in Nong Bua Lam Phu. The mean is 11.4 and the standard deviation is 15.7.

The temperature histogram is shaped similarly to a normal distribution with the mean of 27.04°C and a standard deviation (sd) of 2.12°C. Figure 7 (see Appendix) shows the distributions of temperature and incidences. The incidence shows an exponential decay for higher values, whereas the values are compressed and more distinguishable after log transformation.

The fitted curve based on the relationship of temperature and incidence shows us two maximums at around 25°C and 28°C. 60.72% of the dengue cases happen in between 27°C and 29.5°C. At lower and higher temperatures less dengue fever infections happen (see Figure 1).

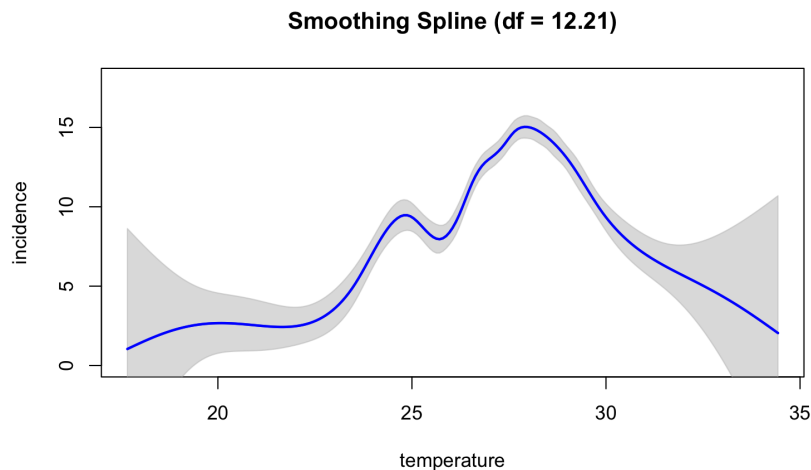


Figure 1: Smoothing spline of incidences over temperature

The Pearson correlation value between average annual dengue cases and average annual temperature of Thailand is 0.43. This suggests a moderate positive linear relationship.

On average over the years, the temperature in north-eastern thailand is low in comparison to the rest of the country. The central region shows higher than average temperatures. Some regions with high average temperature do have high incidences, but others do not match this relationship. There is no consistent pattern. The highest contrast can be observed in the northwest where high incidences occur, despite low temperatures.

### 3.2 Time series decomposition

The additive decomposition of the time series shows a seasonal pattern with a frequency of 12 months <sup>5</sup>. The trend shows fluctuation over time with two periods of comparatively high dengue cases in 2013/14 and 2015/16.

The decomposition of the time series of the dengue cases was compared to the decomposition of the time series of temperatures. Both time series have an annual seasonal pattern. The trends show similar patterns with differences in the amplitudes and slight shifts on the time axis, as shown in Figure 2. In 2010 and 2012/13, there were temperature peaks, followed by peaking

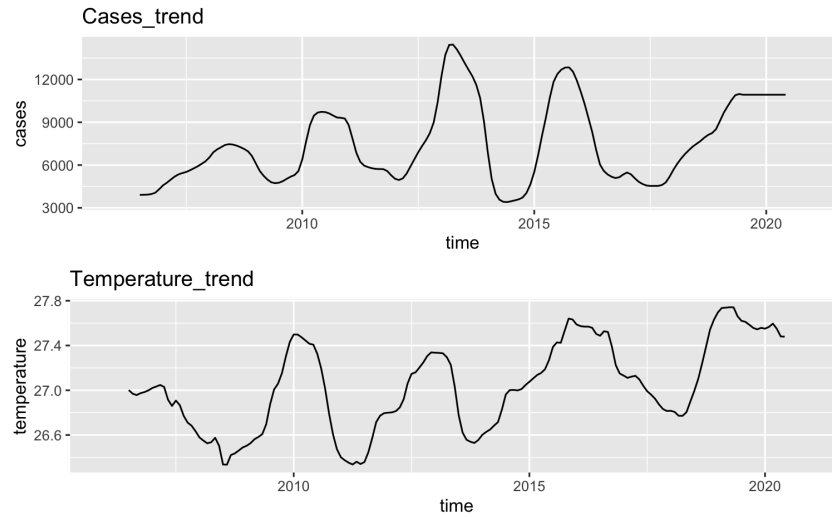


Figure 2: Trend of the total dengue cases in Thailand compared to the trend of the average temperature in Thailand for the years 2006 till 2020.

dengue cases a few months after. In 2015/16, rising temperatures were accompanied by rising dengue cases.

### 3.3 ARIMA model and forecast

ARIMA modeling was performed to forecast the dengue case development in Thailand. ADF and KPSS test both indicate stationarity of the time series, therefore differencing is not necessary. Observation of the time series ACF showed oscillations which suggests the presence of seasonality



in the data. The pACF exhibits a notable pattern with an initial positive peak followed by a significant negative peak. This pattern indicates the need to consider both autoregressive and moving average components in the model. To test for the optimal ARIMA model, models with different combinations of  $p$ ,  $d$  and  $q$  values were generated and the best model was selected by comparing the AICs. The best model was found to be (2,2,2) with an AIC of 3319.732. Because this method could not account for seasonality in the data, the `auto.arima` function was used. “ARIMA(1,0,2)(1,1,0)[12] with drift” was found to be the best model. This model consists of an autoregressive term and two moving average terms. No differencing was performed. The model also has seasonal compounds with a period of 12. “With drift” means that a constant is included in the model. As the AIC of 3108.35 is lower and thus more accurate than the AIC of the former model, the `auto.arima` model was used for further analysis. The evaluation of the histogram of the residuals revealed that the residuals were distributed similar to a normal distribution. The ACF plot indicates some significant autocorrelation at lag 1, while the remaining lags show no significant autocorrelation. The p-value of the Ljung-Box test was 0.41. Thus, the residuals are not distinguishable from white noise and the model has adequately captured the information in the data. Based on the model, a forecast was made for the next four years, which extends beyond the data (see Figure 3).

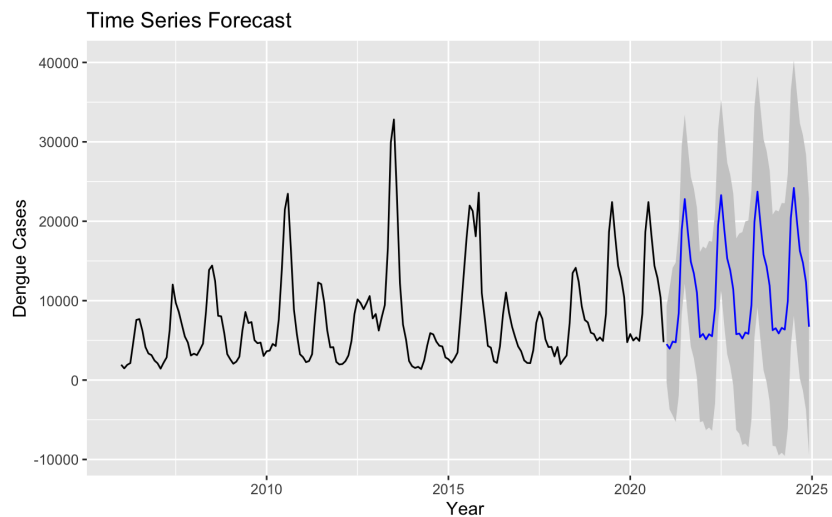


Figure 3: ARIMA forecast of the dengue cases in Thailand for 2021-2024.

To compare the accuracy of the forecast, the time series was cropped after December 2016 and the years 2017 till 2020 were forecasted, as shown in Figure 6.

Although the forecast is more uniform than the actual cases in the years 2017 to 2020, the reported cases are in the range of deviation shown in grey.

### 3.4 GAM model

A GAM model is generated based on the monthly temperature and incidence of all provinces of Thailand over the years 2006 - 2020. The predictor value (temperature) is passed into a

smoothing function to create a smoothed spline curve. For the response variable (incidence) a quasi-Poisson distribution was chosen. The link function is a log transformation.

To figure out the optimal model, the degrees of freedom of the smoothing function were alternated. The effective degrees of freedom, which were found to be 13.82, resemble the complexity of the smooth curve. This value is relatively high, which indicates a “wigglier” spline. F-value and p-value indicate the statistical significance of the smooth function. In this case, the smooth function of temperature is highly significant (p-value  $< 2e-16$ ). The computed R-squared value of 0.0465 indicates how well the model explains the variance in the dependent variable. Here, the model explains approximately 4,7% of the variance in the data. A low GCV (Generalized Cross Validation) value suggests a good fit of the model. The generated model has a GCV of 11.77. Additionally, the AIC value of the smooth model (112947.1) was compared with that of a linear model (113361.2). The smooth model had a lower value, which indicates a better fit. Taking all these parameters into account, the GAM was computed with a k of 16. Subsequently the model was used to predict the average dengue case incidences over the period of 2021 - 2040, based on forecasted average temperature. You can see the average incidences of the past and future in Figure 4.

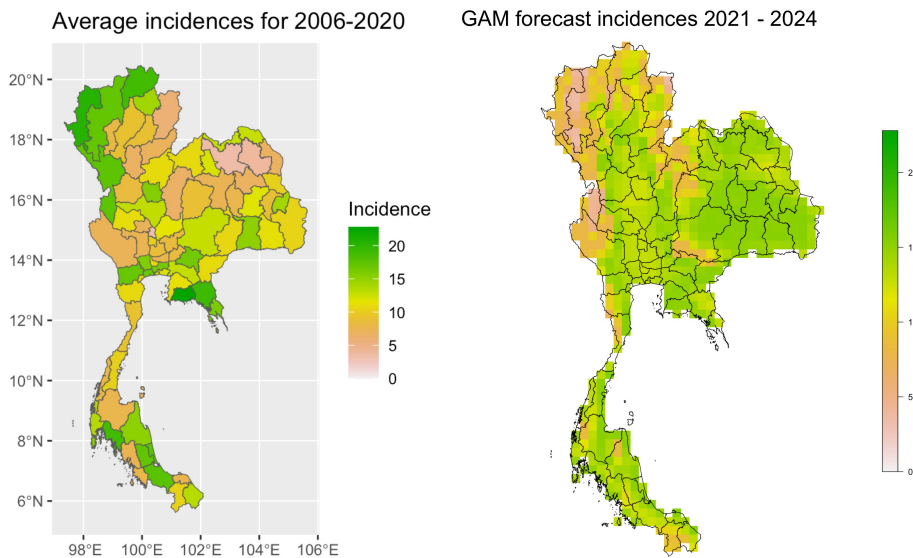


Figure 4: Comparison of average incidence (2006 - 2020)to incidence in GAM forecast (2021 - 2024)

## 4 Discussion

It was shown that increasing temperatures, resulting from climate change as well as recurrent weather phenomena, are significantly associated with increasing DHF cases. The relationship between temperature and DHF did not show a significant correlation, but a non-linear pattern was identified. DHF cases exhibited an increase with temperature up to 28°C, followed by a subsequent decrease. Similar temporal patterns were observed, indicating that high temperatures align with high case numbers. By comparing the spatial distribution of temperature and DHF, certain areas with similar patterns were identified. However, it cannot be concluded that provinces experiencing high temperatures also exhibit high case numbers. The characterized relationship could be observed in predictions as well.

It was shown that DHF cases and temperature have a similar seasonal pattern and general trend: Time periods with high temperatures correspond to periods with high case numbers. The trends in Figure 2 show the second highest DHF case numbers in 2015-16, which is the period of one of the strongest El Niño events since 1950. El Niño increased the temperature in Thailand in that timeframe, leading to higher DHF cases due to effects of temperature on Dengue infections elaborated above (Anyamba *et al.*, 2019), which our analysis confirms. Previous studies have also found this effect by applying an autoregressive model: Similar effects of El Niño on Dengue incidences occurred between 1996 and 2005 (Tipayamongkhogul *et al.*, 2009). Another El Niño event took place in 2018-19, which was another period with high DHF cases. In 2019, El Niño led to early monsoon onset (Hu *et al.*, 2020), a possible contributing factor to Dengue transmission.

The observation that rising temperatures preceded the rise of dengue cases by a few months suggests an influence of high temperatures on *Aedes* biology and virus transmission. Higher temperature can indeed positively influence Dengue transmission, as it alters *Aedes* biology: It makes reproduction of the mosquitoes more efficient by shortening the maturation period of larvae. Virus transmission is promoted as well, as the virus needs less time to spread in its host and make it infectious. These two effects lead to increasing numbers of infectious mosquitoes (Anyamba *et al.*, 2019). The optimal temperature has been observed to lie at 29.3 °C with a small daily range of deviation (Liu-Helmersson *et al.*, 2014). Another study also proved 29°C to be the temperature of maximal dengue transmission (Phanitchat *et al.*, 2019). They found 80% of dengue cases occurring at a mean temperature of between 27.0 and 29.5 °C. Our analysis proved 61% of infections to occur between 27 and 29.5 °C, aligning with both sources 1.

In the maps showing mean DHF cases in the different provinces, the northwestern provinces have comparatively high incidences, although the temperatures are lower 10. Regional patterns are probably more outbreak specific and may be influenced by extreme weather events. The sd of the average temperature per region is 1.1 °C, which indicates that temperature values are relatively stable over Thailand. A possible cause for the unexpected observation could be frequent floods during south-west monsoon, associated with high incidences in that region (e.g. Mae Hong Son)

(Chaithong, 2022). The connection of floods and incidences could result from increased water sources for mosquito breeding grounds and loss of preventive actions and healthcare resources.

To evaluate the further development of DHF cases in Thailand in the future, two different models were applied for forecasting. The ARIMA model projected a seasonal pattern with a slight upward trend in Thailand from 2021 to 2024, capturing the fundamental characteristics of case development in the country. However, a comparison of the model's predictions for 2017 to 2020 with the reported cases during that period revealed discrepancies in the amplitudes of the model. Since the model only relies on past cases and does not consider nonlinear trends, it cannot accurately predict complex relationships influenced by various factors. Nevertheless, the actual cases still lie in the deviation range, proving the general validity of the model.

Secondly, the GAM was used to predict future DHF cases based on the temperature. The edf value is 13.82 and very close to  $k$  with 16, which indicates that the model is using most of the available flexibility to capture the underlying relationship. The edf value is far from 1, therefore a linear correlation can be eliminated. It was shown that the smooth function of the temperature has a highly significant impact on the predicting incidence, but the model only explains 4.7% of the variance in the data. This underlines the point that temperature is one significant of many parameters which will influence the development of dengue. In the future, the east of Thailand will be the main origin of dengue fever outbreaks. This could be very critical, because of the low coverage of health care establishments (Witthayapipopsakul *et al.*, 2019). Although the east will be a hotspot, the model suggests that the average incidence in Thailand will increase compared to the period of 2006 to 2020. This prediction should be viewed with caution. One reason is that there is a high fluctuation in the incidence values ( $sd = 15.7$ ) and stable temperature values ( $sd = 2.1$  °C). This suggests, like mentioned before, that there is a great part of incidence variance which can't be forecast on the basis of temperature.

Despite many of the findings suggesting a causal relationship between temperature and Dengue infections, it cannot be assumed that temperature is the main factor leading to the observed epidemiology. Humidity and precipitation are two climatic factors that can be assumed to strongly influence *Aedes* reproduction, as water sources are crucial for mosquito breeding (Abdullah *et al.*, 2022) (Li *et al.*, 1985). Those factors were not recognized in this analysis, but will possibly provide valuable context to the findings, as Thailand's monsoon seasons significantly differ in humidity and precipitation (Kripalani *et al.*, 1995).

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## 5 Appendix

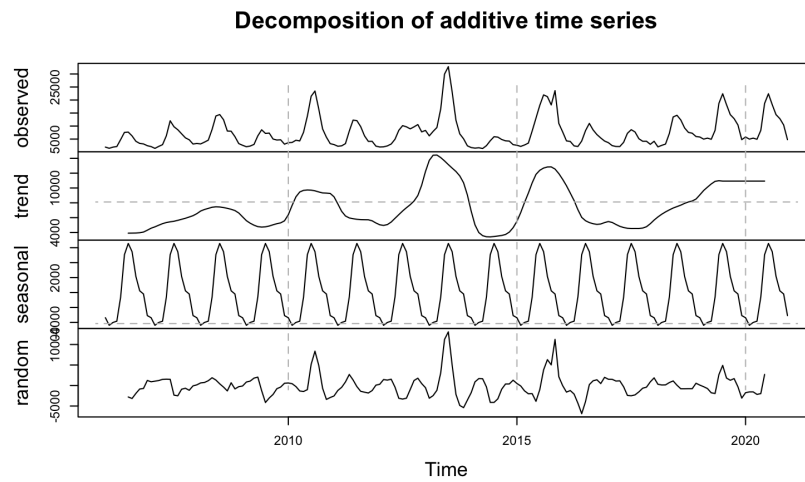


Figure 5: Decomposition of the additive time series of the total dengue cases in Thailand

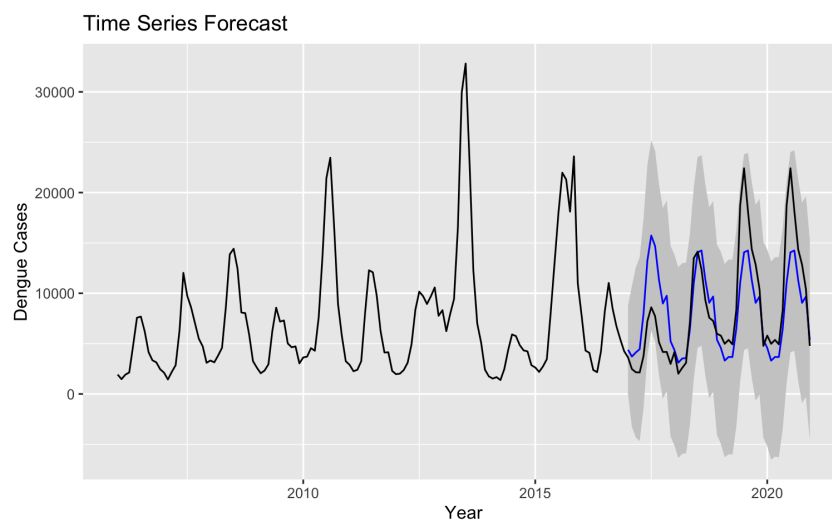


Figure 6: ARIMA forecast of the dengue cases in Thailand for the years 2017-2020 (blue) compared to the actual dengue cases (black).



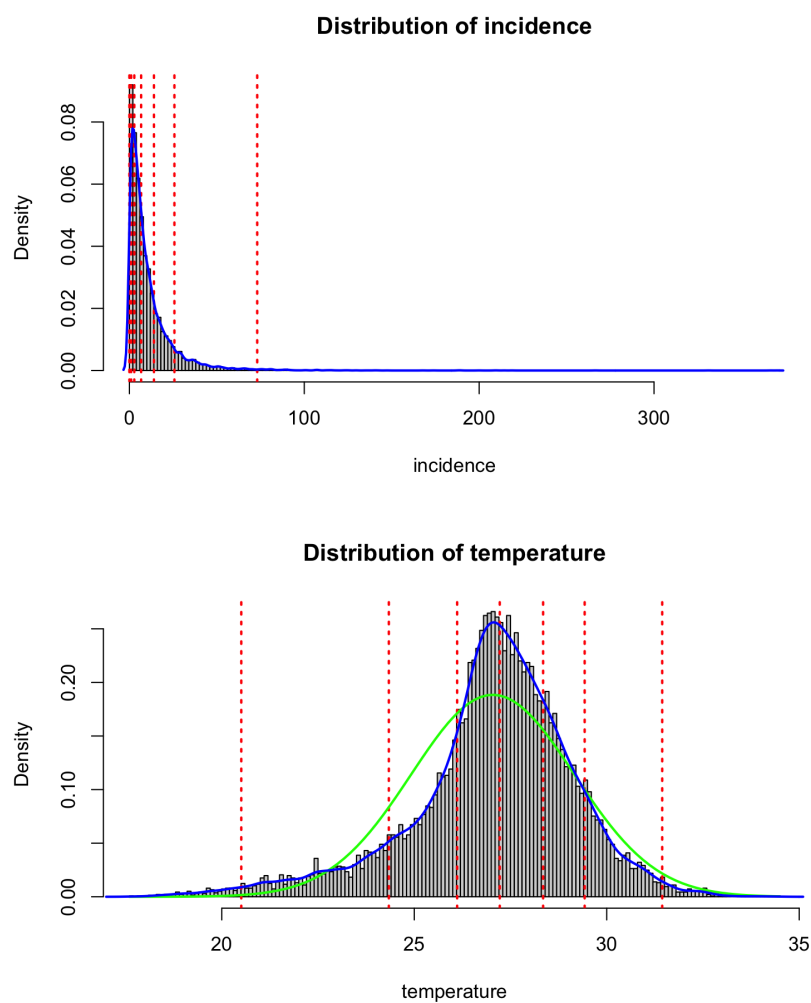


Figure 7: Distribution of incidence (top) and distribution of temperature: blue = density, green = normal distribution (bottom)

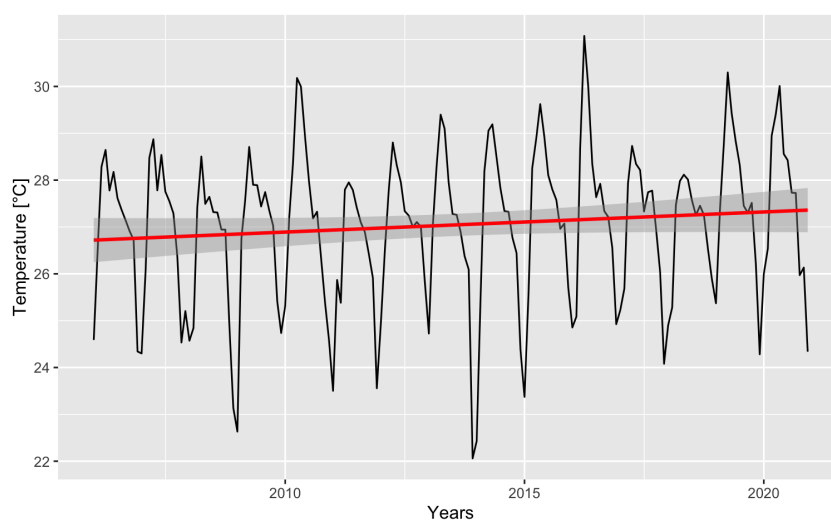


Figure 8: Monthly mean temperature of Thailand over the analyzed timeframe (black), linear regression of temperature (red).

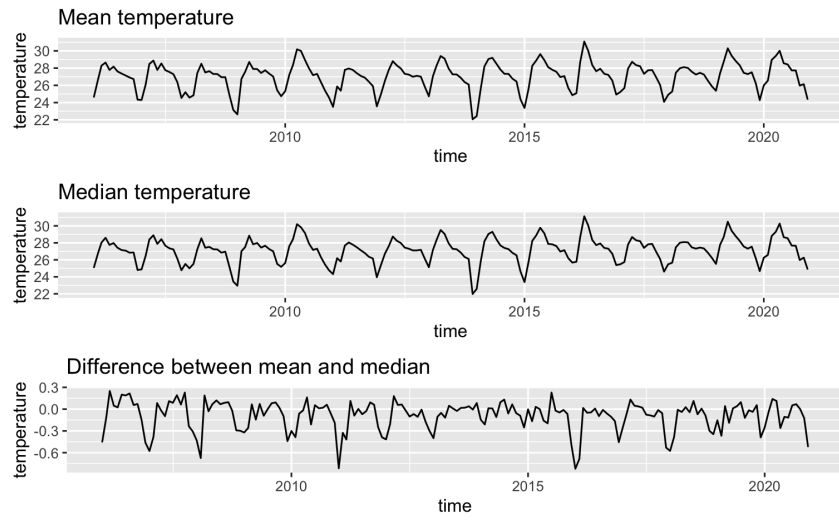


Figure 9: Temperature mean, median and difference between mean and median (Thailand average)

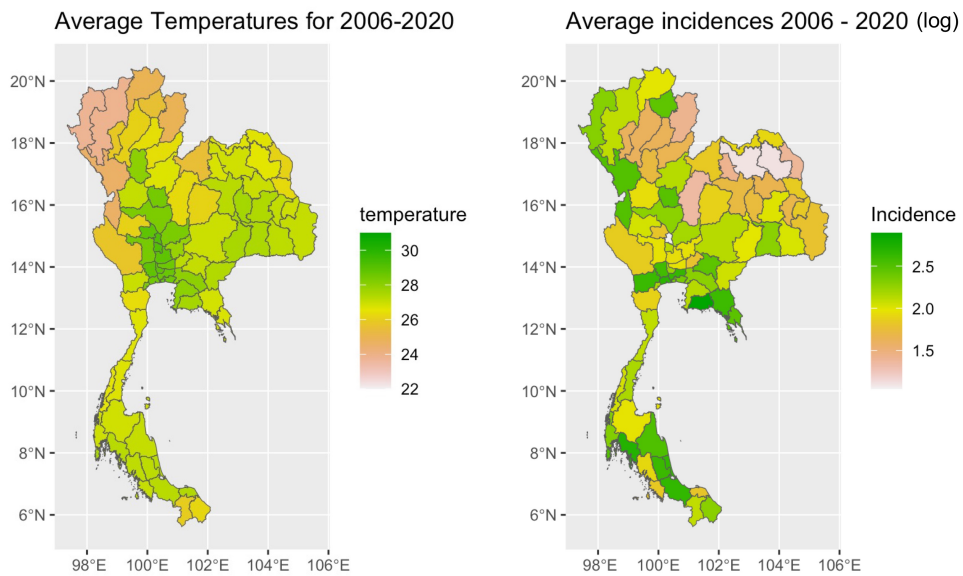


Figure 10: Comparison of average temperature and average incidence (log-transformed) in thailand provinces