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# Development of temporal modeling for prediction of dengue infection in Northeastern Thailand

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## ABSTRACT

**Objective:** To model the monthly number of dengue fever cases in northeastern Thailand using time series analysis. **Methods:** Autoregressive Integrated Moving Average (ARIMA) models have been developed on the monthly data collected from January 1981 to December 2006 and validated using the data from January 2007 to April 2010. **Results:** The ARIMA(3,1,4) model has been found as the most suitable model with the least Akaike Information Criterion (AIC) of 14.060 and Mean Absolute Percent Error (MAPE) of 7.000. The model was further validated by the Portmanteau test with no significant autocorrelation between residuals at different lag times. **Conclusions:** Early warning based on the data in the previous months could assist in improving vector control, community intervention, and personal protection.

## 1. Introduction

Dengue virus is transmitted to humans through the bites of infected *Aedes* mosquitos, principally *Aedes aegypti* (*Ae. aegypti*) and possibly *Aedes albopictus* (*Ae. albopictus*)<sup>[1–3]</sup>. These mosquitoes are tropical and subtropical species widely distributed around the world, mostly between latitudes 35 ° N and 35 ° S<sup>[3,4]</sup>. They are well adapted to the urban environment and successfully breed in containers where water is allowed to accumulate, such as discarded cans, bottles, plastic containers, and tires<sup>[5,6]</sup>. In recent decades, *Ae. albopictus* has spread from Asia to Africa, the Americas and Europe, notably aided by the international trade in used tires in which eggs are deposited when the tires contain rainwater. The eggs can remain viable there for many months in the absence of water<sup>[7]</sup>.

Dengue is the most rapidly spreading mosquito-borne viral disease in the world. An estimated 50 million dengue infections occur annually and approximately 2.5 billion people live in dengue endemic countries<sup>[3,8,9]</sup>. In the last 50 years, incidences have increased 30-folds with increasing geographic expansion to new countries, particularly in

rapidly expanding urban and semi-urban areas in middle and low income countries where water storage and waste disposal services are limited<sup>[3,10]</sup>. Some 1.8 billion (more than 70%) of the population at risk of dengue worldwide live in member states of the World Health Organization (WHO) South-East Asia Region and Western Pacific Region, which bears nearly 75% of the current global disease burden due to dengue<sup>[7]</sup>.

In Thailand, dengue occurred first only in Bangkok in 1958, but soon spread to all regions of Thailand<sup>[11,12]</sup>. The northeastern region has the high dengue transmission intensity in Thailand, mainly due to the highest prevalence of public water wells<sup>[13]</sup>. The residents who obtain water from public wells store the water in household containers, which provide suitable breeding sites of vector, *Aedes*<sup>[13]</sup>.

Without a vaccine or specific treatment available<sup>[7,14]</sup>, dengue infection is a great burden on Thai public health. Vector control by using a predictive model is the only way to prevent the disease. In northeastern Thailand, few studies have been done on biological, entomological aspects and forecasting models<sup>[15–17]</sup>. However, the forecasting models for dengue, which were constructed on data collected over a short period of time (*i.e.* 10 years, might be unreliable<sup>[17]</sup>).

This study proposes a forecasting model for dengue incidences in northeastern Thailand with a 30-year data set. It offers the potential for improved contingency planning of public health intervention in northeastern Thailand.

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## 2. Materials and methods

The northeastern region of Thailand occupies a large land area of 172 500 km<sup>2</sup> situated in a strategic location bordering on Laos and Cambodia to the east. The region is comprised of 19 provinces with a local population of 21 442 693 and a density of 124.31 people/km<sup>2</sup>[18] (Figure 1). The region usually conjures up the image of an arid land area. The major income of the people there is mainly derived from agriculture, especially the cultivation of rice. Northeastern Thailand has in recent years become a significant starting point for adventurous journeys to the Mekong countries. The climate is dominated by two tropical monsoons: southwest and northeast monsoons. Southwest monsoon starts in May whereas northeast monsoon begins in November. Seasonal weather of northeastern Thailand is characterized by three distinct seasons: summer (February–May), rainy (May–October) and winter (October–February)[19].



**Figure 1.** Map of Northeastern (shaded area) Thailand.

### 2.1. Data collection

We obtained monthly-notified dengue fever cases in northeastern Thailand for the period of January 1981 to April 2010 from the Bureau of Epidemiology, Department of Disease Control (DDC), Ministry of Public Health (MOPH)[20].

### 2.2. Time series analysis

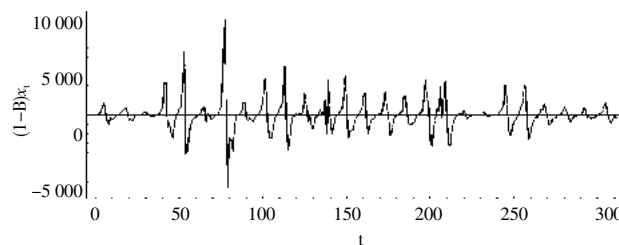
This study used the Box–Jenkins approach. The first step was to determine whether the time series was stationary or non-stationary. If non-stationary, it was transformed into a stationary time series by applying suitable degree of differencing to it. This gave value of  $d$ . Then appropriate values of  $p$ , and  $q$  were found by examining auto-correlation function (ACF) and partial auto-correlation function (Partial ACF) of the time series. Having determined  $p$ ,  $q$  and  $d$ , the coefficients of autoregressive and moving average terms were estimated using the nonlinear least squares method[21,22].

The relating of a model of this kind to data was best achieved by a three-stage iterative procedure based on: (1) identification: the use of the data and of any information on how the series was generated to suggest a subclass

of parsimonious models worthy to be entertained; (2) estimation: the efficient use of the data to make inferences about the parameters conditional on the adequacy of the model entertained; and (3) diagnostic checking: checking the fitted model in its relation to the data with intent to reveal model inadequacies and so to achieve model improvement.

The most suitable models were chosen based on their adequate predictions. In order to evaluate the models, data were split into two groups: training and validation. The training group was used to build the time series model, and the validation group was used to evaluate the time series model. Two measures, namely, Akaike Information Criterion (AIC) and Mean Absolute Percent Error (MAPE), based on information theory, were used to achieve a trade-off between an adequate prediction and a few number of parameters[23]. Lower values of AIC and MAPE were preferable. We used the Portmanteau test to test the hypothesis of model adequacy.

We transformed monthly dengue fever cases by using one-differenced dengue fever cases in northeastern Thailand from January 1981 and December 2006 (Figure 2). The transformed data were used to construct the Autoregressive Integrated Moving Average (ARIMA) model. The forecasting accuracy of this model was verified using the data between January 2007 and April 2010. All statistical analyses were conducted using Mathematica Software with Time Series package.

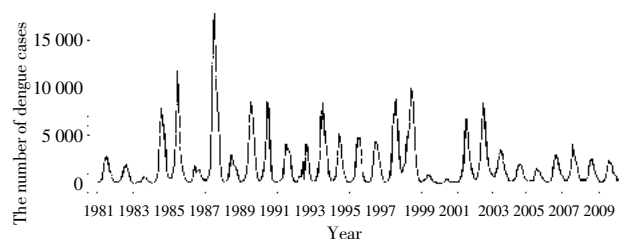


**Figure 2.** One-differenced dengue fever cases in northeastern Thailand from January 1981 to December 2006.

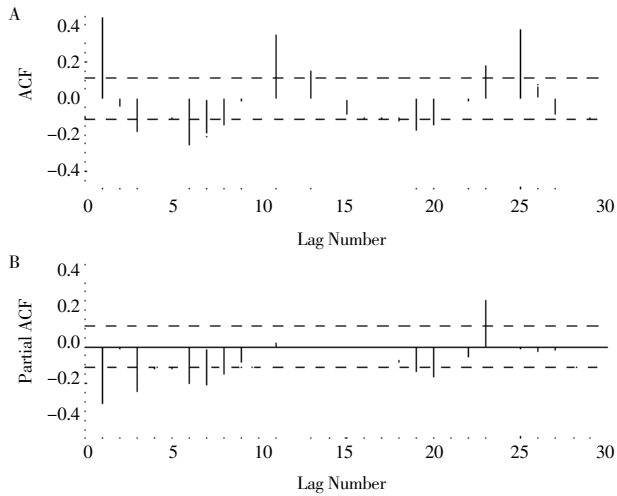
## 3. Results

There were 634 075 dengue fever cases reported in northeastern Thailand over the study period with the major incidence peak in July, 1987 of 17 990 dengue fever cases (Figure 3). Several minor peaks occurred mainly before the year 2000 followed by a decreasing trend (Figure 3). There was a yearly seasonal distribution of the disease occurring in the rainy season from June to September (Figure 3).

The ACF and Partial ACF were analyzed from dengue fever cases in northeastern Thailand (Figure 4A, B). The ACF and Partial ACF instigated to explore a set of models based on the training data from January 1981 to December 2006 (Table 1). Among these models, ARIMA(3,1,4) had both lowest AIC (14.060) and MAPE (7.000) values and appeared to be the best model (Table 1).



**Figure 3.** The number of dengue cases in northeastern Thailand from January 1981 to April 2010.

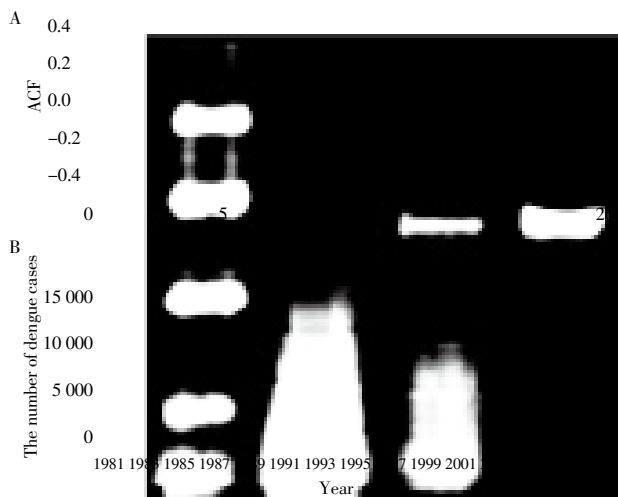


**Figure 4.** (A) ACF and (B) Partial ACF of dengue fever cases in northeastern Thailand from January 1981 to December 2006 (--- represents 95% upper and lower confidence intervals).

$$X_t = 2.399X_{t-1} - 2.153X_{t-2} + 0.666X_{t-3} - 2.10186Z_{t-1} + 1.035Z_{t-2} + 0.634Z_{t-3} - 0.557Z_{t-4} + Z_t \quad (1)$$

Where  $X_t$ : the dengue fever cases at time  $t$ ;  $Z_t$ : white noise process at time  $t$ .

A plot of the residual autocorrelation function died out after one lag and the residual autocorrelations fell within 95% confidence limit (Figure 5a). This suggested that autocorrelation function of residuals at different lag times in the ARIMA(3,1,4) model did not differ from zero (Portmanteau statistic  $Q_{18} = 18.46$ ,  $\chi^2_{0.95,13} = 22.36$ ,  $P > 0.05$ , Figure 5A). The observed and predicted dengue fever cases in northeastern Thailand from January 1981 to April 2010 matched reasonably well (Figure 5B).



**Figure 5.** (A) ACF of residuals from ARIMA(3,1,4) model (--- represented 95% upper and lower confidence intervals) and (B) the number of dengue cases in northeastern Thailand from January 1981 to April 2010. — represents actual data, --- represents predicted data from ARIMA(3,1,4) model.

**Table 1**

MAPE and AIC of Time series models.

Models	MAPE	AIC
ARIMA(4,1,1)	27.763	14.160
ARIMA(2,1,3)	23.721	14.156
ARIMA(4,1,2)	27.622	14.144
ARIMA(2,1,2)	25.752	14.179
ARIMA(2,1,4)	22.586	14.156
ARIMA(3,1,3)	22.560	14.162
ARIMA(4,1,3)	21.979	14.131
ARIMA(3,1,2)	25.215	14.168
ARIMA(1,1,2)	25.355	14.225
ARIMA(3,1,4)	7.000	14.060

#### 4. Discussion

The dengue incidence varies widely from year to year, showing as much as a tenfold difference between years but no specific temporal pattern. This finding contradicts the previous study<sup>[17]</sup> which reported that the dengue epidemic occurred every two years with approximately three-year epidemic periods. This might be because we used the 30-year dengue dataset whereas they only used the 10-year dataset from 1996 to 2005.

The ARIMA models have been used successfully in epidemiology to monitor and predict dengue fever cases<sup>[17,24–27]</sup>. Our results show that the ARIMA(3,1,4) model gives a good prediction of dengue incidence in northeastern Thailand from January 2007 to April 2010 (*i.e.* 40 months). This prediction covers a much longer period compared with those of other studies (*e.g.*<sup>[17,25,26,28]</sup>) that reported a predictive period of up to 24 months.

Our results indicate that the predicted values could follow the upturn and downturn of the observed data reasonably well, especially during the high peaks in July, 2007, July, 2008 and June, 2009. The sharp seasonal peaks, observed in June or July in northeastern Thailand, might be attributed to patterns of vector occurrence and the high rates of dengue transmission in May and June<sup>[17,29]</sup>.

Increasing attention has been focused on the use of the ARIMA model for dengue incidence<sup>[17,24,25,28]</sup>. Our modeling approach can be used to monitor and predict dengue incidence in northeastern Thailand. This indicates that the ARIMA model could be used to optimize dengue prevention and early warning system by providing estimates on dengue incidence trends. Early warning based on forecasts could assist in improving vector control, community intervention and personal protection. However, in this study we focused only on the dengue fever cases. Other factors that are reported to have significant impact on the transmission of dengue fever include climatic<sup>[27,30,31]</sup>, social<sup>[5,32]</sup>, biological<sup>[29,33–35]</sup>, and economic factors such as population immunity, housing conditions, mosquito control measures, local ecological environments (vegetation, irrigation system), and drug resistance<sup>[16,36–38]</sup>.

#### Conflict of interest statement

We declare that we have no conflict of interest.

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