TIME SERIES ANALYSIS OF DENGUE FEVER IN NORTHEASTERN THAILAND

Present by: Siriwan Wongkoon

Advisors:
Assoc. Prof. Dr. Mullica Jaroensutasinee
Asst. Prof. Dr. Krisanadej Jaroensutasinee

Center of Excellence for Ecoinformatics
Computational Science Graduate Program, School of Science, Walailak University, Nakhon Si Thammarat, Thailand

Outline

- Dengue fever in Northeastern Thailand
- Proposed Techniques
  - Data Collection
  - Time Series Analysis
- Results
- Conclusion

Dengue Fever

- Dengue Fever is caused by dengue virus.
- Dengue virus are transmitted to humans through the bites of infected *Aedes* mosquitoes, principally *Ae. aegypti*.
- This mosquito is a tropical and subtropical species widely distributed around the world.

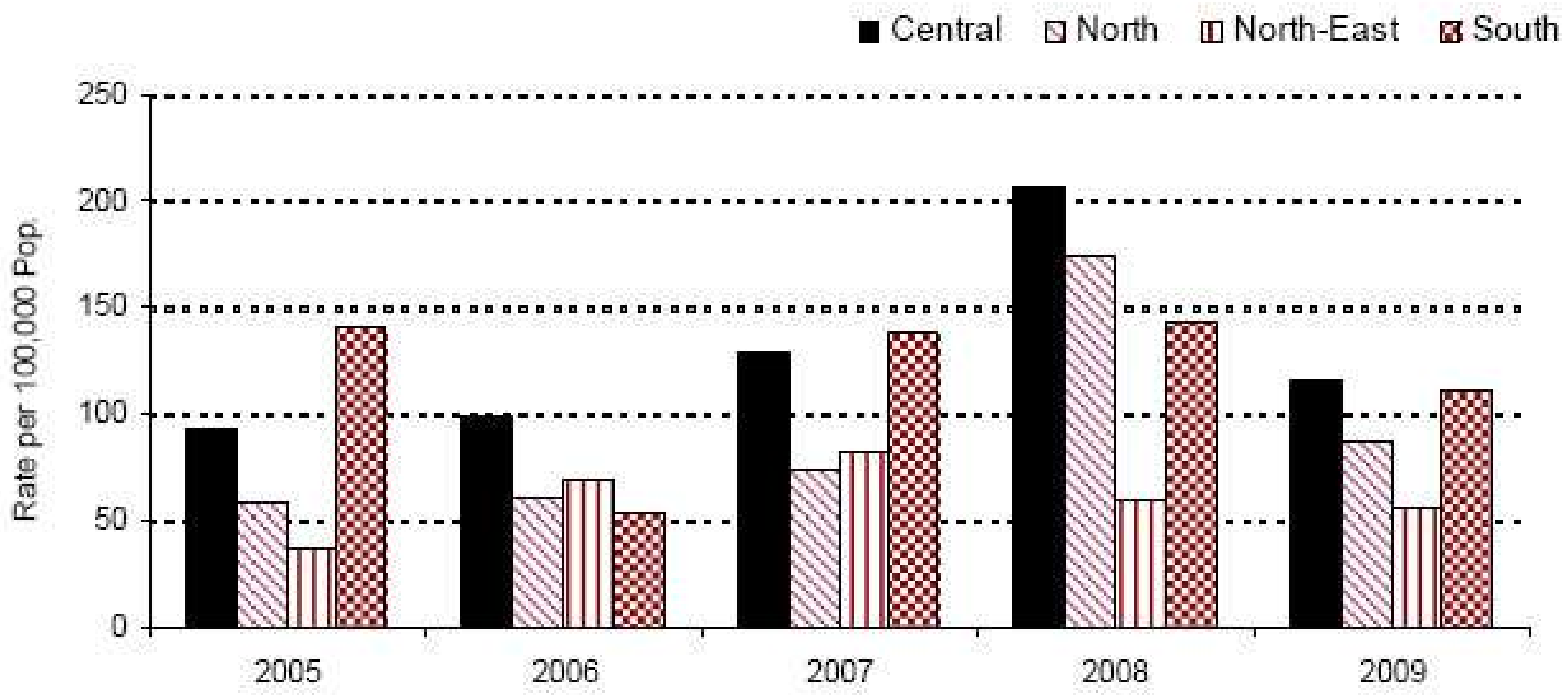
The contour lines of the January and July isotherms indicate the potential geographical limits of the northern and southern hemispheres for year-round survival of *Adeas aegypti*, the principal mosquito vector of dengue viruses.

Dengue Fever

- Dengue is the most rapidly spreading mosquito-borne viral disease in the world.
- An estimated 50 million dengue infections occur annually.
- Some 1.8 billion (more than 70%) of the population at risk for dengue worldwide live in South-East Asia Region and Western Pacific Region.

Dengue Fever in Thailand

Fig. 2 Reported Cases of D.H.F, Total(26,27,66) per 100,000 Population, by Region, Thailand, 2005 - 2009



Ref: Annual Epidemiological Surveillance Report 2009, pp. 32.

Dengue Fever in Northeastern

- Few studies in Northeastern region found that:
  - Rural area in Khon Kaen, common breeding sites were
    - small earthen jars
    - large earthen jars
    - cement jars storing water for drinking
  - Overall 26% of water containers were infested with larvae.

Time series Technique

- Time series methodology has a long history of application in econometrics, particularly in the domain of forecasting.
- Recently it has been increasingly used in epidemiologic researches on infectious diseases.

Objective of this study

- The purpose of this study is to determine the forecasting model on the number of dengue fever cases in Northeastern Thailand using the time series analysis technique.
- This forecasting model offers the potential for improved contingency planning of public health intervention in Northeastern Thailand.

Data Collection

- We obtained monthly-dengue fever cases in Northeastern Thailand for the period of January 1981 to April 2010 from the Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health.

Figure 1. Study site: Northeastern Thailand

Time Series Analysis: Model Building

- Identification:
  - 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.
- Estimation:
  - use of the data to make inferences about the parameters conditional on the adequacy of the model entertained.
- Diagnostic checking:
  - checking the fitted model in its relation to the data with intent to reveal model inadequacies and so to achieve model improvement.

Time Series Analysis

- The most suitable models were chosen based on their adequate predictions.
- In order to evaluate models, data were split into two groups:
  - Training: build the time series model
  - Validation: evaluate the time series model
- Akaike Information Criterion (AIC) based on information theory was used to achieve a trade-off between an adequate prediction and a few number of parameters.

ARIMA Model

- Autoregressive Integrated Moving Average process of orders *p*, *d*, *q* or ARIMA(*p*, *d*, *q*).
  - p: degree of AR process
  - q: degree of MA process
  - d: times to difference the time series

Time Series Analysis

- We transformed monthly dengue fever cases by using one-differenced dengue fever cases in Northeastern Thailand from January 1981 and December 2006.
- The transformed data were used to construct the ARIMA model.
- The forecasting accuracy of this model was verified using the data between January 2007 and April 2010.
- We used the *Portmanteau* test to test the hypothesis of model adequacy.
- All statistical analyses were conducted using Mathematica Software with Time Series package.

Transformed data

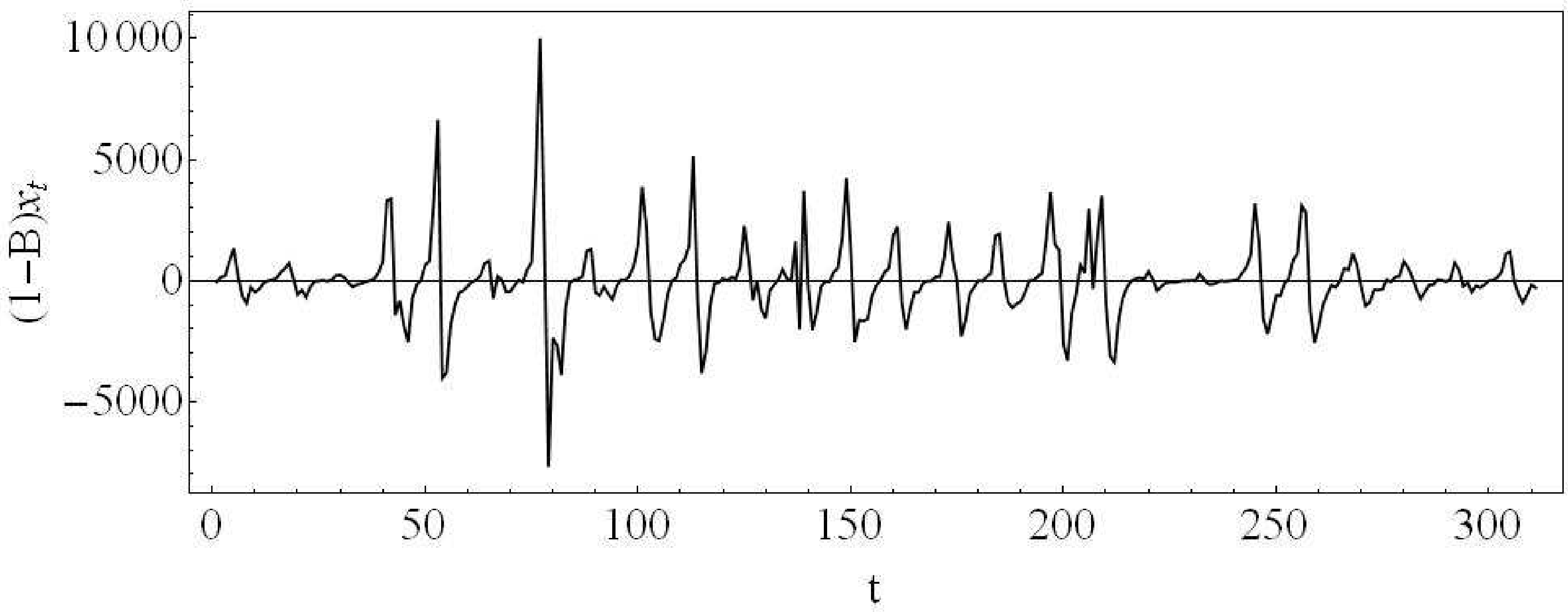


Figure 2. One-differenced dengue fever cases in Northeastern Thailand from January 1981 to December 2006.

ACF and PACF

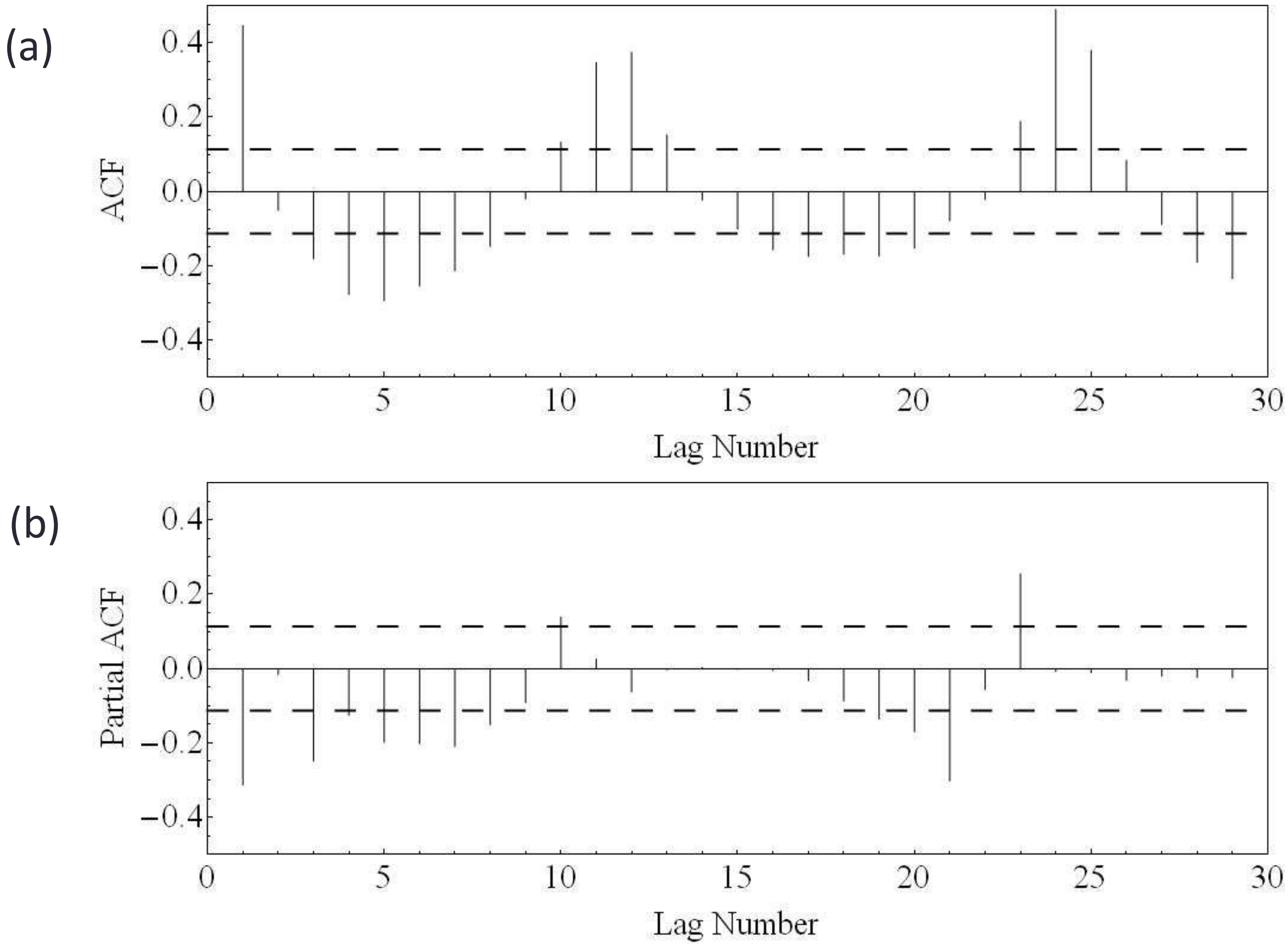


Figure 3. The ACF (a) and PACF (b) of one-differenced dengue fever cases.

Results: ARIMA(4,0,4)

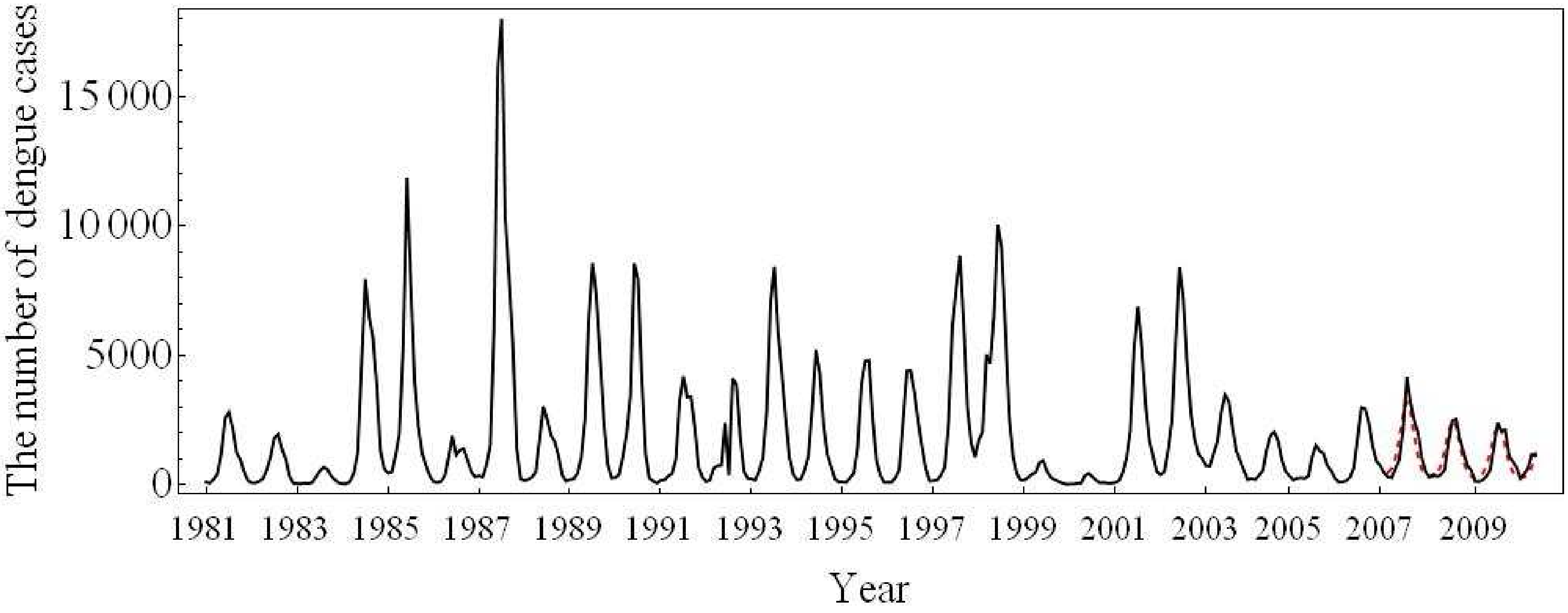


Figure 3. (c) The number of dengue cases in Northeastern Thailand from January 1981 to April 2010. – represents actual data, --- represents predicted data from ARIMA(4,0,4) model.

Results

- However, when we tested the Portmanteau test for the model adequacy, ACF of residuals at different lag times in ARIMA(4,0,4) model was differed from zero.

Results: ARIMA(3,1,4)

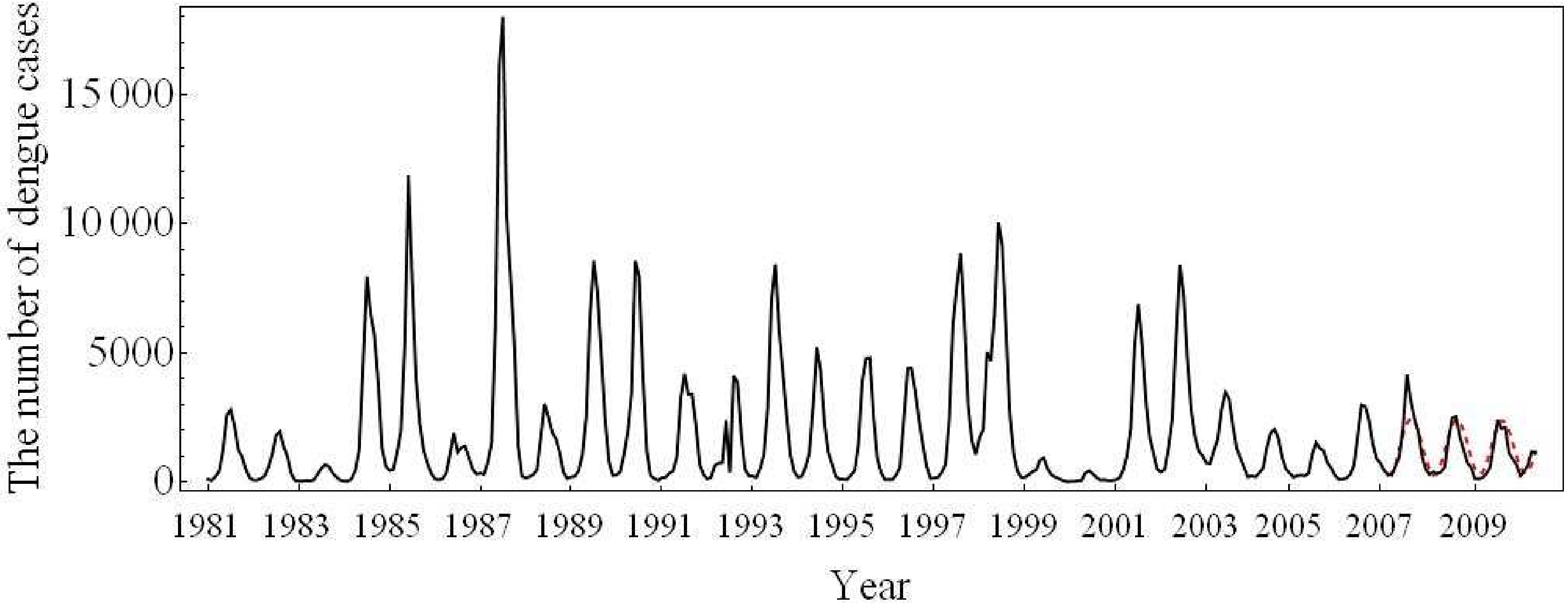


Figure 4. (a) The number of dengue cases in Northeastern Thailand from January 1981 to April 2010. – represents actual data, --- represents predicted data from ARIMA(3,1,4) model.

Results: ACF of residuals

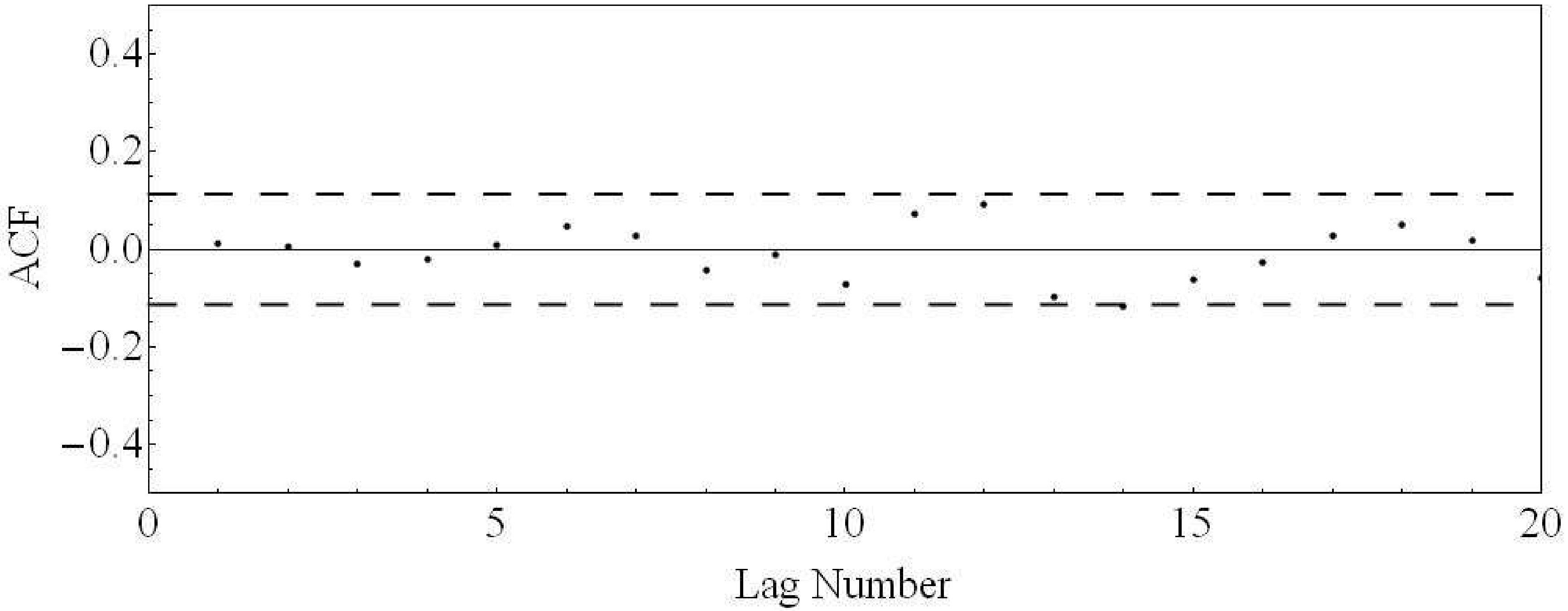


Figure 4. (b) the correlation function of residuals from ARIMA(3,1,4) model (--- represented 95% upper and lower confidence intervals).

Conclusion

- In this study, ARIMA(3,1,4) model is the most suitable model in predicting dengue fever cases in Northeastern Thailand.
- Such a finding could be applied to assist in establishing a early warning system based on the data in the previous months.
- It can make a decision on public health prevention program such as timing for executing programs on vector control, other environmental intervention, and personal protection promotion in the region.

Acknowledgements

- This work was supported in part by the Thailand Research Fund through the Royal Golden Jubilee Ph.D. Program (Grant No. PHD/0201/2548), Walailak University Fund 06/2552, and Center of Excellence for Ecoinformatics, NECTEC/Walailak University.
- We also thank the Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health for data collection.

THANK YOU FOR YOUR ATTENTION