



# Determination of dengue hemorrhagic fever disease factors using neural network and genetic algorithms

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## ABSTRACT

The *Aedes aegypti* mosquito and the *Aedes albopictus* mosquito are carriers of the virus that causes Dengue Hemorrhagic Fever (DHF). In Indonesia, the spread of DHF disease has taken place for 41 years. Within this period, there was an increase in the number of spreading areas by 97% and an increase in the number of cases by 99%. Based on the data from previous studies, further information is needed related to the factors that have the most influence on the level of DHF infection in a region. Based on the initial study conducted, there are 6 factors that have the potential to influence the number of DHF cases in an area, namely temperature (X1), rainfall (X2), population density (X3), altitude (X4), distribution of males (X5), and distribution of education level (X6). In this study, the problem of determination dengue disease factors was modeled using a neural network. The activation function in this neural network model then estimated using genetic algorithms. Determination of the best factor is carried out in a genetic algorithm by combining several parameters of the crossover probability (Pc) and mutation probability (Pm). This experiment show that the main factors that influence the spread of DHF in Bandung area are temperature, altitude, distribution of gender, and distribution of education levels. The best accuracy system obtained in this study using these 4 factors reached 72%.

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## 1. Introduction

The Dengue Hemorrhagic Fever (DHF) disease spread occurs because of the presence of vectors, namely *Aedes aegypti* mosquito, or *Aedes albopictus*, or *Aedes scutellaris*, which passes on the virus to humans through its infectious bite. The transmission of the virus from one person to another causes the widespread contagion of the virus. Unfortunately, so far drugs to cure dengue fever disease have not been found, and overall vaccine administration has not been carried out in Indonesia. Consequently, the DHF sufferers can only depend on their immune system.

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According to [1], over 41 years, starting from 1968 to 2009, in Indonesia there was an increase in the transmission areas of DHF by 97%. Similarly, in terms of the number of cases, there was also an increase of 99%. The number of people who died of dengue fever in 2015 was 1,229 out of 126,675 people suffering from the disease in Indonesia. This number is higher than that in 2014, in which out of 100,347 people with DHF, 907 died. The significant increase in the number of cases and the number of deaths in several regions in Indonesia shows that the prevention of DHF spread is still not optimal yet.

The above problems are confirmed by the study by [2], i.e. based on the results of the prediction of DHF spread patterns from 2016 to 2018 by using data from 2010 to 2015, the study found an increased spread of dengue disease in the city of Bandung, especially in the northern and southern parts. To prevent the spread of the dengue spreading areas as early as possible, it is very necessary to identify the factors that are thought to influence the spread, as well as the area status classification in terms of the DHF spread.

The increased number of people suffering from dengue fever can be caused by several factors such as climate, temperature, and behavior. Refer to [3], Climate change and environmental health are factors that cause the spread of dengue virus in the community. Meanwhile, we assume that the behavior factor is associated with gender and education level. According to [1], based on the gender factor, DHF tends to attack male people. As for the level of education, it is very clear that the higher the level of education earned by a person, the higher his/her awareness of a healthy lifestyle to prevent the transmission of DHF as early as possible. Based on some of the research, it cannot be concluded that the combination of factors that has the strongest influence on the level of DHF in a region.

Therefore, it is very necessary to perform a computational method to predict the factors that influence the spread of DHF. study generally seeks to determine factors that influence the increased DHF disease infection in a region. These factors are modeled using a neural network, where the prediction model used is the sigmoid function. The parameters in this sigmoid function are estimated using genetic algorithms. The genetic algorithm is the development of artificial intelligence commonly used to solve a decision-making problem involving many variables. A study on genetic algorithms conducted in 2004 by [4] discussed genetic algorithms for immunology modeling and optimization in the field of cancer chemotherapy and examined the implementation of genetic algorithms for the optimization of antigens in nucleus cells. The study managed to create an artificial immune system that biologically represents the immune system of the human body to be tested for cancer antigens and optimization of antigens against the human immune system. These results are subsequently used to develop research on anti-cancer drugs. The results of this study are expected to provide information as early as possible about the spread patterns of dengue disease along with the prediction of its spread status classification to prevent the spread of DHF outbreaks.

## **2. Related Works**

Dengue Hemorrhagic Fever is an endemic disease commonly found in tropical and subtropical countries. It is currently spreading over all provinces in Indonesia, which initially only spread in 2 provinces in 1968 which caused 24 deaths with the mortality rate of 41.3%. After that, it continued to spread to 32 provinces by which the DHF cases increase from 58 to 158,912 [1]. The increased spread of dengue fever is caused by many factors such as the increase in population, lack of understanding of dengue fever, climate change, and other epidemiological factors.

According to [5], Climate factors such as changes in rainfall, seasonal changes, changes in temperature, humidity and wind direction, greatly affect the terrestrial and marine ecosystems, thus affecting the health of all living things, especially humans. Besides, there are also ecological factors, including the lack of sensitivity of the community to anticipate an outbreak of dengue fever.

The population of the city of Bandung continues to increase as marked by the high birth rate. The city is an endemic area of DHF with the number of cases increasing every year. Based on [6], the number of dengue fever cases in 2015 increased by 7.9% from the previous year. This was due to the density of the city's population and the high population mobility.

The study conducted by [7] of the influence of sex on the spread of disease, especially in the regions of Southeast Asia, shows that men (72%) have a higher chance of being attacked by the disease than women (23%). Such a phenomenon almost occurs in several countries such as Malaysia, Singapore, India, and Montenegro.

In the current study, the level of public education became one of the input variables with the assumption that with a higher level of education, the community would have knowledge and awareness of the prevention of the dengue fever spread. A study of the effect of public knowledge on the incidence of dengue fever was conducted in Helvetia Tengah Village, Medan by [8]. That study examined the correlation between people's behavior and the spread of dengue fever. In the study, a sample of 100 families was collected where 65 families had no knowledge of dengue fever and 35 ones had knowledge of dengue fever. Of the 65 families who did not know about dengue fever, around 79.59% of the families were affected by dengue. Meanwhile, from 35 families who had good knowledge about dengue fever, about 20.51% of them suffered from dengue fever. The test result indicated that families did not know dengue fever had an opportunity to suffer from dengue fever of 3.077 times higher than families knowing dengue fever.

A study by [9] analyzed the spatial spread patterns of dengue fever. The spatial linkages were measured by using the Moran index. The spread patterns were examined using ANN (Average Nearest Neighbor), while the mapping of the areas that had a considerable risk of the dengue fever spread was estimated with Kernel density. The results show that there are spatial autocorrelations in the spread and the occurrence patterns of dengue fever, including the clustered patterns. Also, the use of Kernel density estimation can indicate areas that have a considerable risk of dengue fever transmission.

Another related study, conducted by [10], presented data on infectious diseases in the form of a map. The map was used to determine the disease spread patterns associated with environmental conditions. The results of the study were displayed in the form of vulnerability levels where the most parameters related to the environmental conditions have no a significant correlation with the DHF deployment. Based on qualitative analysis of the vulnerability level, some areas of Semarang city were vulnerable to infectious diseases and were classified into "very vulnerable" with a percentage of 25% and "vulnerable" with a percentage of 25% as well.

A study conducted by [11] on the dengue fever deployment was carried out using several factors, namely viral location index, population density, dengue coefficient, and income level. The study results suggested that the main risk area for disease transmission is the city center where the population has the highest income. DHF disease notification is expressed using graphs and gradient maps from census data such as gender, age, population, income, and number of cases so that it can be integrated with programs for controlling vectors that transmit diseases.

Dengue fever is potentially endemic and is also a concern in Malaysia [12]. In their study, Yuhani et.al. proposed a prediction model that combines SVM with the Smallest Squares to predict future dengue outbreaks. The study used data on cases of dengue fever and rainfall from five regencies in Selangor. The data was processed using normalization before serving as the training data. The study managed to generate an SVM LS prediction model that surpasses the Artificial Neural Network model both in the predictive accuracy and the computational time. The best prediction model from the research gives an accuracy value of 91%.

Dengue fever is an endemic disease to most tropical regions. [13] examined the correlation of climate factors and the tendency of dengue fever cases to conceptualize more effective measures of pre-emptive control against dengue outbreaks. The study proposed pre-processing data method using the wavelet transformation and combined by the Support Vector Machines (SVM) as classifier and based genetic algorithms and linear regression to select the most prominent features. The use of genetic algorithms in the study only serves to select the influential factors, and then it was used as an input factor to SVM regression. The regression method and SVM were used for forecasting the model. The experimental results indicate a strong correlation between the seasonal rainy season and the transmission of the dengue virus. This also confirms that monthly temperature and season have a minimum contribution to the disease outbreak.

The research conducted by [14] tried to develop a visualization model and a predictive model of the pattern of the spread of DHF. This study contribute a new approach of probabilistic functions that represent CA transmission rules using the Hidden Markov Model (HMM) and the Von Neumann environment. The data used is the number of DHF cases in West Bogor in 2013, which have not taken into consideration the factors that have the potential to influence their spread and pay special attention only to the spatial distribution of the infected area. This study also has not considered human behavior and the population of Aedes Aegypti mosquitoes. The infected data is divided into four categories and affect to cell definition as an area. Testing is done by comparing the proposed model with the Susceptible Infected Recovered (SIR) model. The test results show that the CA model can produce a pattern similar to the pattern produced by the SIR model with a similarity value of 0.95.

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While [15] develop Model-Based Agents (ABM) which a model for simulation, behavior representation, and autonomous agents interaction. The creation of dynamic models of dengue fever by considering the behavior and interaction agents is the main problem of this study. This study develop agents of interactive behavior and simulation models associated with the spread of a dynamic dengue fever epidemic. In the model building, there are two agents, namely human agents as hosts and mosquitoes as vectors. Besides, temperature and humidity are also used as environmental parameters. The conclusions obtained showed that the model results agent-based significant downward trend occurs with the actual data pattern.

Based on the discussion presented above, it can be concluded that the previous studies are still limited to population scenarios and crossover opportunities. There is no prediction model in the form of factor functions, thus not being able to generate a map displaying the dengue fever spread status per sub-district. Similarly, for studies using genetic algorithms, there is a tendency towards decreasing the level of accuracy. Also, another study that can present a map of the vulnerability level of dengue fever spread does not consider the influence of dengue fever spread factors. Therefore, the current study sought to predict the main factors of the dengue fever case in each sub-district in Bandung City.

The use of ANN in this study is based on the fact that the level of classification accuracy obtained by this method is classified as good in various fields, such as the health field according to [9], in the field of psychology according to [16], the financial field according to [17], and also in other fields according to [18]. This method has a good learning ability which adapts the learning ability of the human brain. The ANN method has 3 layers, namely the input, hidden and output layer. This method can also solve problems by using a complex mathematical model by increasing the number of hidden layers. The use of Genetic algorithms in this research is used to obtain the optimal network weight replacing the Back Propagation method which is commonly used in ANN. It is expected that by using the Genetic algorithm, the network weight value obtained will be more optimal so that the level of accuracy obtained will also increase. As is well known, Genetic algorithms are algorithms that are quite popular and are widely used in solving various complex research problems. For example, [19] use of Genetic algorithms to solve Traveling Salesman Problem, [20] use this algorithm to solve Facility Layout Problem, and [18] use the same algorithm to solve multi-objective optimization problems. Genetic Algorithm has several parameters such as Population, Generation, Probability of Crossover (Pc) and Probability of Mutation (Pm) which can affect the level of accuracy obtained.

### **3. Methodology**

#### **3.1 Data**

This study required data on causes of dengue fever based on literature reviews such as rainfall, temperature, population density, distribution of males, distribution of education level, the altitude of residential areas, and the number of dengue fever cases. The data is obtained from 30 sub-districts in the Bandung. The data served as the input for training data and system test data to be built with the output of the prediction of the number cases of dengue fever.

The rainfall and temperature data were obtained from the Meteorological, Climatological, and Geophysical Agency (BMKG). Meanwhile, data on population density, distribution of males, and distribution of education level were collected from the Population and Civil Registration Office of the City of Bandung. The amount of rainfall and temperature data was 150, while data on the population density, distribution of males and education level, and altitude of residential areas with a period from 2010 to 2014 were used as training data and test data.

#### **3.2 Definition of input and target**

The variables served as the input included temperature (X1), rainfall (X2), population density (X3), altitude (X4), distribution of males (X5), and distribution of education level (X6). The cases number of dengue fever in an area served as the target. The input and target data were normalized with a range (0.1) so that 150 training data and test data were obtained.

The used data was divided into 30 data based on sub-districts in Bandung city. Based on the span time of 2010 to 2014, the variables causing dengue fever were divided based on the sub-district location, the number of cases per sub-district, the density of each sub-district, the sub-district

altitude. Meanwhile, in terms of the temperature and rainfall data, the average temperature and rainfall in Bandung City were taken. All data were then normalized so that data variations become similar.

### 3.3 Parameters in Experiment

System testing used the most influential factor search scenario. It was performed in the same way by testing all variables with a combination of different input variables, thus resulting in MAPE values to determine the relationship of variables with the target. The higher the MAPE value, the lower the relationship between the variables and the target, and vice versa. The following is the first testing scenario from which the Crossover Probability (Pc) 0.7, 0.8, 0.9, and mutation probability (Pm) 0.1, 0.2, 0.3, the population size of 100, and generation size of 100 is performed. While the combination of factors carried out is 4 factors, 5 factors and overall factors with a tolerance of MAPE of 20. The parameters in the Genetic algorithm used in the experiment can be seen in detail in Table 2.

Table 2. The Parameters Used in The Experiment

Combination of Factors	Population	Generation	MAPE tolerance	Pc	Pm
X1, X2, X3, X4, X5, X6	100	100	20	0.7	0.1
X2, X3, X4, X5, X6					
X1, X3, X4, X5, X6					
X1, X2, X4, X5, X6					
X, X2, X3, X5, X6					
X1, X2, X3, X4, X6	150	500	20	0.8	0.2
X1, X2, X3, X4, X5	200	1000		0.9	0.3
X1, X2, X3, X4					
X2, X3, X4, X5					
X3, X4, X5, X6					
X1, X4, X5, X6					
X1, X2, X5, X6					
X1, X2, X3, X6					

## 4. Modeling of System

### 4.1 Architecture of ANN

In this study, the single-layer perceptron model architecture was used to implement the feedforward method. This model is the simplest model of artificial neural networks where there are only 6 values of weight to be determined. In Figure 1, X1, ..., X6 states the factors that influence the rate of spread of DHF.

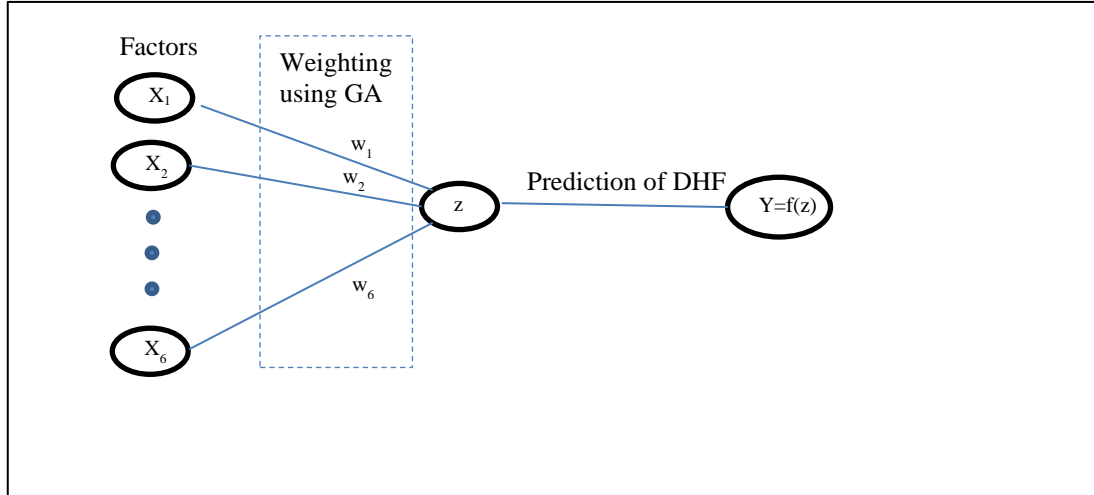


Figure 1. ANN Architecture of DHF Prediction

#### 4.2 Prediction Model of ANN

The prediction model is a mathematical equation model used to predict the number of dengue fever cases in the city of Bandung. This study employed the sigmoid function [21] as a prediction model obtained within 5 years. The sigmoid function can be seen in equation (1).

$$f(z) = \frac{1}{1+e^{-z}} \quad (1)$$

where

$$z = bias + \sum_{i=1}^6 w_i x_i$$

$w_i$  : weight of  $x_i$   
 $x_i$  : factor i

#### 4.3 Determination of weights using Genetic Algorithms (GA)

There are several stages in the Genetic algorithm in determining weights:  $w_i$ , i.e. Parameter Initialization, Weight Initialization, Parent Selection Process, Crossover Process, and Mutation Process.

##### 4.3.1 Parameter Initialization

The initial stage of designing the system in this study was the parameter initialization performed by specifying several values such as the probability of crossover (Pc), probability of mutation (Pm), number of hidden layers, MAPE tolerance, the maximum number of generations, number of population, and threshold value. The threshold value was determined by trial and error until the value that best fitted the model was obtained.

##### 4.3.2 Weight Initialization

At the initial weight initialization stage, 100 random numbers were generated in a real form (0.1) for each data/population. One input data had 100 populations that would be potential solutions. The initial weight calculation was made using the feedforward technique. In the feedforward process, there was a binary sigmoid activation function which is the same as the equation that the prediction model has.

#### 4.3.3 Parent Selection Process

In the selection process, there are two steps to be done, i.e. calculating *Linear Fitness Ranking* (LFR) and making the selection using the *Roulette Wheel method*. After all, individuals were arranged in order by the LFR value, the next process was to select individuals based on the LFR value using the Roulette Wheel method. Individuals who had a larger LFR value would have a higher chance of being selected. The LFR formula can be seen in equation 2[22].

$$f_{LR} = f_{max} (f_{max} - f_{min}) \left( \frac{R(i) - 1}{N - 1} \right) \quad (2)$$

where:  $f_{max}$  : maximum fitness

$f_{min}$  : minimum fitness

$R(i)$  : the i-th individual rank

$N$  : Number of chromosomes in the population

#### 4.3.4 Crossover Process

The *crossover process* means a process of producing a new chromosome as a result of the combination of two parents who have been selected at random. The result indicated new individuals implying a new route. The ultimate goal was to bring out individuals with better fitness. The crossover rate used was 0.8. The *crossover mechanism* used the PPX (Precedence Preservative Crossover).

#### 4.3.5 Mutation Process

The process of mutation in the formation of routes here was done by replacing or switching genes or points of intersection with each other in the hope of making the fitness value better than before. The mutation probability used in this study was 0.1. The mutation probability value was chosen not too high so that the chromosome of the new offspring did not change in the extreme. The optimal value of mutation probability is different for each case handled. In some cases of non-transportation fields, the optimal value of mutation probability is obtained from a higher value [20], [23]. While in the field of transportation research, the used mutation probability value is relatively low [24]–[26].

### 5. Result and Discussion

#### 5.1 Determination of the Most Influential Factors

The testing was performed by applying a scenario for determining the most influential factors. the results of the scenario testing can be seen in Table 3. Based on Table 3, the lowest MAPE value of 28.03 is generated by a combination of genetic algorithm parameters of 200 populations, 1000 generations,  $P_c$  0.9, and  $P_m$  0.1 in scenario 3. This indicates that the temperature, altitude, distribution of males, and distribution of education level result in the best system accuracy with an accuracy of 71.97%.

#### 5.2 Experiment Result

The testing was performed by applying a scenario for determining the most influential factors. The results of the scenario testing can be seen in Table 3. Based on Table 3, the lowest MAPE value of 28.03 and the best accuracy value obtained around 72% is generated by a combination of genetic algorithm parameters of 200 populations, 1000 generations,  $P_c$  0.9, and  $P_m$  0.1 in scenario 3. This indicates that the temperature, altitude, distribution of males, and distribution of education level result accounted for 72% of the DHF cases that occurred. The accuracy results obtained are comparable to the results of similar studies from [27]. The results obtained are also complementary to the results obtained by [27], where the factors used are disease surveillance, meteorological and socio - economic data. However, the use of different datasets and different factors makes objective comparisons difficult to do.

The testing results as shown in Table 3 indicate that the best combination is shown by X1, X4, X5, and X6 with the best accuracy values in scenarios 2, 3, and 5. The weight values that correspond to these factors are  $w_1 = 0.4139$ ,  $w_4 = 0.7592$ ,  $w_5 = 1.3254$ ,  $w_6 = 0.4311$  and bias =2. The combination of genetic algorithm parameters affects the value of system accuracy. For example, as illustrated in Table 3 scenario 1, which are parameter combinations of 100 populations, 100

generations,  $P_c$  0.9, and  $P_m$  0.1, only produces an accuracy of 71.09%. The accuracy value increases in scenario 3 in which parameters combination of 200 populations, 1000 generations,  $P_c$  0.9, and  $P_m$  0.1 results in an accuracy of 71.97% which is the best accuracy of the system.

Table 3. The factor combinations testing for various parameters of the Genetic algorithm model

Scenario	Population	Generation	Combination	$P_c$	$P_m$	MAPE	Accuracy
1	100	100	X1, X3, X4, X5	0,9	0.3	28,91	71.09
2	150	500	X1, X4, X5, X6	0,9	0.1	28,17	71.83
3	200	1000	<b>X1, X4, X5, X6</b>	0,9	0.1	28.03	71.97
4	100	100	X1,X2,X3,X4,X5	0,8	0.1	28.30	71.70
5	150	500	X1,X4,X5,X6	0,8	0.1	28.07	71.93
6	200	1000	X1,X2,X3,X4,X5	0,8	0.1	28.09	71.91
7	100	100	X1,X2,X4,X5,X6	0,7	0.1	28.41	71.59
8	150	500	X1,X2,X3,X4,X5,X6	0,7	0.1	28.05	71.95
9	200	1000	X1,X2,X3,X4,X5	0,7	0,1	28.11	71.89

The mutation probability value of 0.1 produces the most accurate value for each scenario. This suggests that the smaller the mutation probability, the higher the accuracy. Meanwhile, the combination of population parameters with a small number of generations produces the lowest accuracy compared to scenarios with a more number of population and generation. In conclusion, the more individuals in a generation can improve system accuracy because it will enlarge the search space for optimal solutions.

## 6. Conclusion

Based on the previous discussion, the following conclusions are drawn, that the application of genetic algorithms can increase the value of accuracy, e.g. the testing scenarios of 200 populations and 1000 generations can produce an accuracy around 72%. The accuracy results obtained are comparable to the results of similar studies from [12]. But the use of different datasets and other conditions makes objective comparisons difficult to do.

This study also shows that the factors that greatly influence the increasing number of DHF patients are temperature ( $X_1$ ), altitude ( $X_4$ ), distribution of males ( $X_5$ ), and distribution of education level ( $X_6$ ). The best prediction model obtained in this study based on the sigmoid function has the following parameters:  $w_1 = 0.4139$ ,  $w_4 = 0.7592$ ,  $w_5 = 1.3254$ ,  $w_6 = 0.4311$  and bias = 2. The best system accuracy obtained with this model is 71.97% with a MAPE value of 28.03.

The interesting things obtained from this study are that the rainy season has a smaller effect than the height of the area and the education level of the population. This means that education on environmental hygiene programs has a significant influence on reducing the rate of spread of dengue disease. Locations with a certain altitude also affect the increasing number of DHF patients in the area. The future work of this research is to add new factors and the development of new models for future predictions. These additional factors are expected to be factors that can be retrieved automatically via the web so that the data update process can be done more easily and periodically.

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