ISSN: 0975-833X

Available online at http://www.journalcra.com

International Journal of Current Research
Vol. 7, Issue, 10, pp.21720-21724, October, 2015

INTERNATIONAL JOURNAL OF CURRENT RESEARCH

RESEARCH ARTICLE

ON PARAMETER ESTIMATION AND VALIDATION OF DENGUE EPIDEMIC IN TANZANIA

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ARTICLE INFO

Article History:
Received 24th July, 2015
Received in revised form
15th August, 2015
Accepted 07th September, 2015
Published online 31st October, 2015

Key words:
Dengue fever, Data, Outbreak, Prediction model, Forecasted, observed, Correlation, Ministry of health and social welfare in Tanzania.

ABSTRACT

Discovery of a dengue outbreak early is the major step towards implementing effective dengue interventions resulting in reduced mortality and morbidity. A dengue mathematical model is useful tool for prediction of an outbreak and evaluation of control measures. However, such a model must be carefully parameterized and validated with epidemiological data. Data obtained from the ministry of health and social welfare in Tanzania are used to analyse various parameters of dengue transmission and outbreak model. Validation of the model is done with 2010, 2011, 2012, 2013 2014 and 2015 data from ministry of health and social welfare in Tanzania, number of dengue cases obtained in the year 2010 to 2015 are used as independent variable (observed data). Accuracy of the model for predicting outbreak is assessed through coefficient of determination. A well fit model is obtained for Tanzania to be used as a predictive model to predict possible outbreak. Numerical simulations are performed to fit the model to available data for dengue fever disease in Tanzania and to determine the role played by some key parameters. From the results, it is observed that the forecasted dataagree very close to the actual data.

Citation: MassaweLaurencia Ndelamo, Massawe Estomih, S. and MakindeOluwole Daniel, 2015. "On parameter estimation and validation of dengue epidemic in Tanzania", *International Journal of Current Research*, 7, (10), 21720-21724.

INTRODUCTION

The dengue virus is the one of the arboviruses causes of classical dengue fever and dengue haemorrhagic fever primarily in the tropical and subtropical regions. Dar es Salaam city in Tanzania with the tropical climate has become an ideal region for dengue virus transmission (Karim *et al*., 2012). Dengue remains a serious threat for human health in Tanzania, as an effective dengue vaccine and anti-viral treatment are not currently available. Dengue control relies on controlling vectors of the disease, the mosquitoes Aedes aegypti. The presence of Aedes aegypti mosquito was first identified in Dar es Salaam city in Tanzania followed by few regions in the year 2014.

In July 2010 for the first time in Tanzania, an outbreak of dengue fever was reported and over 40 people were infected. From 2010 to 2015 number of infected cases has been increasing. Moreover in the year 2014 the government of Tanzania announced the danger of the disease where people were alerted about the disease and the precaution to be taken. In the year 2014 between January and December and January to April 2015, 1025 people were infected with dengue fever disease and 4 died of the disease from Dar es Salaam city. The regions which were affected with Dengue fever disease are Dar es Salaam with 1014 cases (Kinondoni-601, Temeke-144, and Ilala-269), Kigoma3, Mwanza2, Mbeya2, Kilimanjaro3, and Njombe1. Data from the ministry of health and social welfare in Tanzania are used to validate the proposed model.

Maximum likelihood estimator is used to determine the best fitting model. The idea is to have a parsimonious model that captures as much variation in the data as possible (Ngailo *et al*., 2014).The accuracy of model is judged based on explanatory capacity (coefficient of determination, R square). The number of cases that would occur (forecasted) in Tanzania in the year 2010 to 2015 will be predicted with the regression equation obtained from the best-fit model and later on compare the number of cases that are actually obtained in those years. Pearson correlation coefficient is obtained to see the strength of correlation. Coefficient of determination is used to predict the correlation between the data obtain from the ministry of health and social welfare in Tanzania and data from the literature (Karim *et al*., 2012; Rohani *et al*., 2011). In particular this paper will forecast Dengue fever infected cases using least square curve fitting method.

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MATERIALS AND METHODS

Model formulations

In this section, we adopt the model presented in (Rodrigues *et al*., 2013).The model based on two populations, humans and mosquitoes with treatment, Human population (N_h) is divided into five groups such as S_{h_1} - Careful human Susceptibles, S_{h_2} - Careless human Susceptibles , I_h - infected human, T_h - treated infected human , R_h - recovery infected human, so that we have $N = S_{h_1} + S_{h_2} + I_h + T_h + R_h$ and the population of female mosquitoes, indexed by m is divided into three groups that is A_m -Aquatic phase (that includes the egg, larva and pupa stages), S_m -Susceptibles (mosquitoes that are able to contract the disease), I_m -Infectives (mosquitoes capable of transmitting the disease to human). In formulating the model, the following assumptions are considered:

- Total human population (N_h) is constant,
- The population is homogeneous, which means that every individual of a compartment is homogeneously mixed with the other individuals,
- Immigration and emigration are not considered,
- Each vector has an equal probability to bite any host,
- Humans and mosquitoes are assumed to be born susceptible i.e. there is no natural protection,
- The coefficient of transmission of the disease is fixed and does not vary seasonally,
- For the mosquito there is no resistant phase, due to its short lifetime,
- The possibility of careless Susceptibles contracting dengue fever disease is higher than that for careful Susceptibles.

Susceptible individuals acquire Dengue fever through the bite of female Aedes mosquito with force of infections given by $B_1\beta_{mh}\frac{I_m}{N_h}S_{h_1}$, $B_2\beta_{mh}\frac{I_m}{N_h}S_{h_2}$ and $B_3\beta_{hm}\frac{I_h}{N_h}S_{h_1}$ with $B_2 > B_1$.

Considering the above considerations and assumptions, we then have the following schematic model flow diagram for dengue fever disease with treatment, careful and careless susceptible:

From the above flow diagram, the model will be governed by the following equations:

$$
\begin{aligned}
\frac{dS_{h_1}}{dt} &= (1-\pi)\mu_h N_h - B_1\beta_{mh}\frac{I_m}{N_h}S_{h_1} - \mu_h S_{h_1} + \theta_1 R_h + \theta_2 S_{h_2}\\
\frac{dS_{h_2}}{dt} &= \pi\mu_h N_h - B_2\beta_{mh}\frac{I_m}{N_h}S_{h_2} - \mu_h S_{h_2} - \theta_2 S_{h_2}\\
\frac{dI_h}{dt} &= \left(B_1 S_{h_1} + B_2 S_{h_2}\right)\beta_{mh}\frac{I_m}{N_h} - (\mu_h + \eta_h + a)I_h\\
\frac{dT_h}{dt} &= \eta_h I_h - (\mu_h + \delta_h)T_h\\
\frac{dR_h}{dt} &= \delta_h T_h - (\mu_h + \theta_1)R_h\\
\frac{dA_m}{dt} &= \varphi\left(1 - \frac{A_m}{kN_h}\right)(S_m + I_m) - (\mu_A + \eta_A)A_m\\
\frac{dS_m}{dt} &= \eta_A A_m - \left(B_3\beta_{hm}\frac{I_h}{N_h} + \mu_m\right)S_m\\
\frac{dI_m}{dt} &= B_3\beta_{hm}\frac{I_h}{N_h}S_m - \mu_m I_m
\end{aligned}
\qquad (1)
$$

where $S_{h_1}(0) > 0$, $S_{h_2}(0) > 0$, $I_h(0) \geq 0$, $T_h(0) \geq 0$, $R_h(0) \geq 0$, $A_m(0) \geq 0$, $S_m(0) > 0$, $I_m(0) \geq 0$, for all $t \geq 0$.

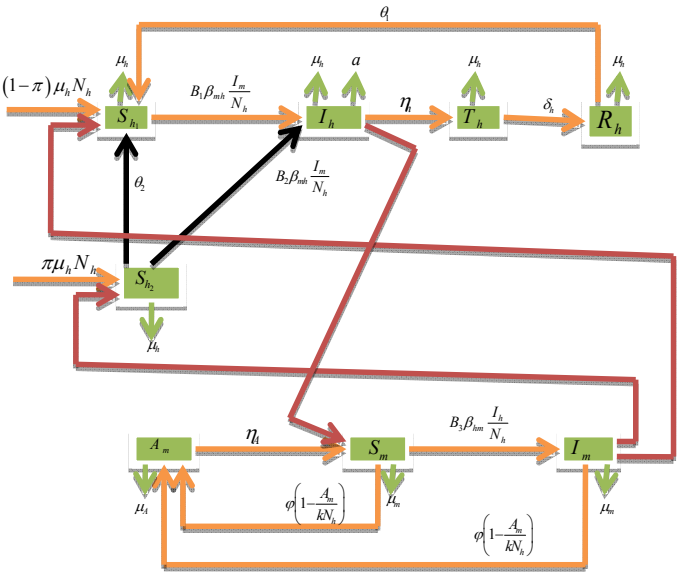


Figure 1. Model flow diagram for dengue fever disease with treatment, careful and careless susceptible

Data Analysis

In this subsection, we adopt the idea of Ngailo *et al*. (2014) where the work is dedicated to fitting the predicted data of the models to the Tanzania data obtained from the ministry of health and social welfare in Tanzania and (http://www.wavuti.com/2014/05/wizara – ya –afya -kitengo- cha.html).

Parameters values were estimated by using maximum likelihood estimator so as to get the best fit between the computed and observed data. Statistical test is carried out in order to establish the relationship between forecasted and observed data using SPSS.

RESULTS

The original data set consist of 5years observations of the Tanzania dengue fever disease cases from January 2010 to April 2015 in six month interval as shown in Table 1.

Table 1. Dengue fever cases which occurred between 2010-2014, semi-annually

Period	Number of cases
2010 (Jan-June)	11
2010 (July-December)	29
2011 (Jan-June)	25
2011 (July-December)	20
2012 (Jan-June)	35
2012 (July-December)	15
2013 (Jan-June)	45
2013 (July-December)	32
2014 (Jan-June)	399
2014 (July-December)	624
2015 (Jan-Mei)	626

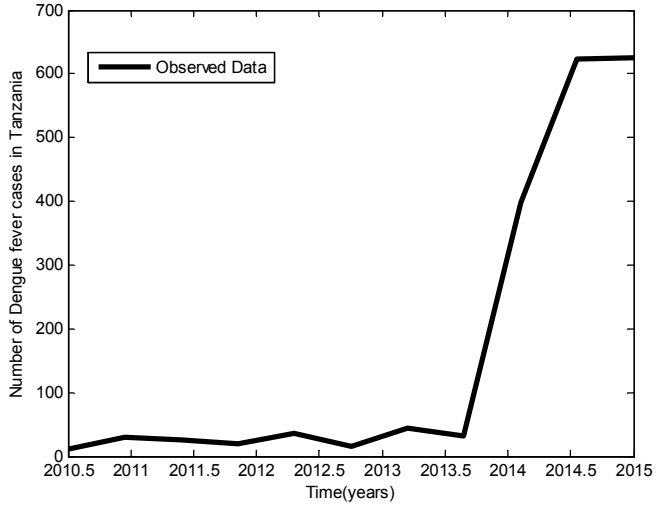


Figure 2. Raw data of dengue fever disease cases in Tanzania

From Figure 2, it is observed that the number of infected population is increasing as time goes.

Model Estimation and Evaluation

Maximum likelihood estimation is used to determine the best fitting of the model. The idea is to have a parsimonious model that captures as much variation in the data as possible. Usually the simple graph model captures most of the variability in most stabilized data (Ngailo *et al*., 2014). We use model system (1) to the observed data on dengue fever disease in Tanzania. The model system (1) is fitted to the data for infected individuals in Tanzania. Parameter values were obtained from the different literatures like (Rodrigue *et al.,* 2013; Massawe *et al*., 2015; Dumont *et al*., 2008). Other parameter values are estimated to vary within realistic means and given as shown below:

$\beta_{hm} = 0.375$, $\beta_{mh} = 0.39$, $\pi = 0.96$, $B_1 = 0.09$,

$B_2 = 0.9$, $B_3 = 0.7$, $\mu_m = \frac{1}{11}$, $k = 3$, $\eta_A = 0.35$,

$\mu_A = 0.25$, $\mu_h = \frac{1}{60 \times 365}$, $\eta_h = 1/3$, $\varphi = 4$, $\theta_1 = 0.01$,

$\theta_2 = 0.6$, $a = 0.005$, $\delta_h = 0.9$.

Figure 3 shows the dynamic behaviour of predicted and observed data using model system (1) and actual data respectively

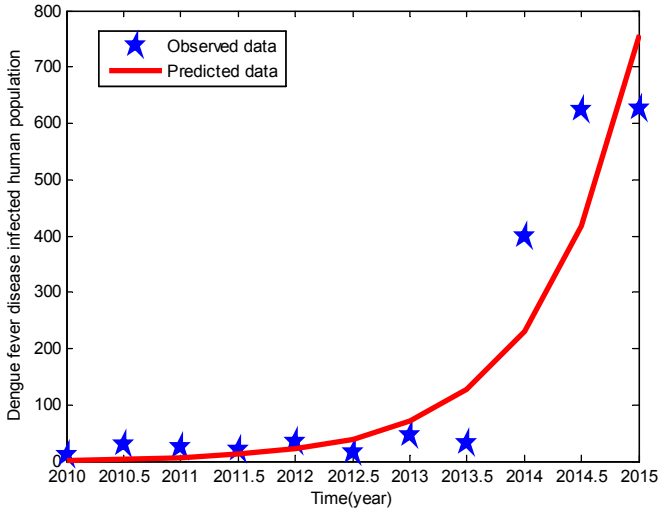


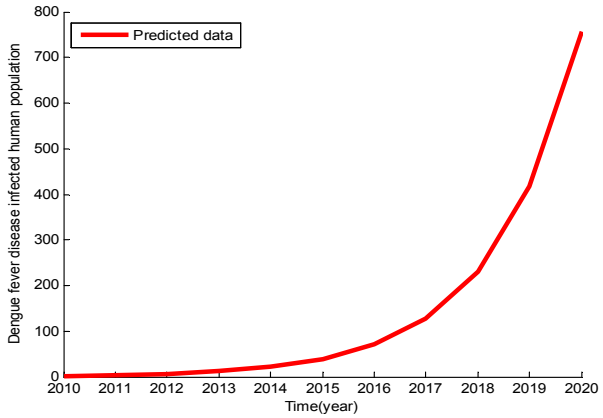
Figure 3. The dynamic behaviour of predicted and observed data using model system (1) and actual data respectively

From Figure 3 it is observed that, many actual data values lie within the limits. Few lie exactly, meaning that the predicted data is agree very closely to the actual data.

Parameters values were estimated by using maximum likelihood estimator so as to get the best fit between the computed and observed data and obtain the following parameter values as shown in Table 2.

For the purpose of management and planning of dengue fever disease in Tanzania it is important to project of prevalence of the disease in five years to come of the model. The model projects that there will be an increase on prevalence of dengue fever diseasein Tanzania. The same parameter values are used from Table 2.

Figures 4 show the projection of Dengue fever disease infected population in the society of Tanzania up to 2020.



Figures 4. The projection of Dengue fever disease infected population in the society

Table 2. Parameter values that give the best fit to the data in the model

Parameters	Descriptions	Estimated parameter Value
B_1	Average daily biting for careful susceptible (perday)with $B_2 > B_1$	0.2477
B_2	Average daily biting for careless susceptible	0.8956
B_3	Average daily biting for mosquito	0.6909
β_{mh}	Transmission probability from I_m (per bite)	0.4792
β_{hm}	Transmission probability from I_h (per bite)	0.1431
$\frac{1}{\mu_h}$	Average lifespan of humans (in days)	1/(60*365)
$\frac{1}{\eta_h}$	Mean viremic period (in days)	1.1976
$\frac{1}{\mu_m}$	Average lifespan of adult mosquitoes (in days)	0.0599
φ	Number of eggs at each deposit per capita (per day)	5.5920
$\frac{1}{\mu_A}$	Natural mortality of larvae (per day)	0.3964
δ_h	Rate at which dengue fever infected individualsprogress for treatment.	0.2502
η_A	Maturation rate from larvae to adult (per day)	0.8076
K	Number of larvae per human	3.8009
π	Fraction of subpopulation recruited into the population.	0.5349
θ_1	Rate at which recovery individuals lose immunity	0.0137
θ_2	Positive change in behaviour of Careless individuals	0.7532
a	Per capita disease induced death rate for humans	0.0105

From Figure 4, it is observed that the disease increase slightly at the beginning and increase sharply. This indicates that the application of treatment only is not enough. There is a need to educate society on how to get rid of the disease by using mosquito nets, mosquito repellent, removing vector breeding areas, insecticide application and control maturation rate to adult mosquito. Statistical test is carried out in order to establish the relationship between forecasted and observed data using SPSS.

Summary for statistics for Tanzania's semiannually observed data is as shown in Table 3 and 4.

Table 3. Summary for statistics for Tanzania's semiannually observed data

Model	R	R Square	Adjusted R Square	Std. Error of the Estimate
1	0.921[a]	0.848	0.831	97.789

a. Predictors: (Constant), Observed Data

From Table 3 it is observed that coefficient of correlation (R) is +0.921 indicate that there is strong relationship between predicted and observed data as it takes the value between +1 and -1 so +0.921 is close to +1. Coefficient of determination (R Square) is +0.848 showing that there is strong relationship between Predicted and Observed data as it takes the value between 0 and +1 so +0.848 is close to +1. Therefore 85% of the total variability of the predicted data supports the observed data of the model.

Table 4. Coefficients[a]

Model	Unstandardized Coefficients		Standardized Coefficients	t	P-value
	B	Std. Error	Beta		
1	6.195	36.088		0.172	0.868
(Constant)	0.870	0.123	0.921	7.075	0.000
Observed Data					

a. Dependent Variable: Predicted Data

From Table 4, $p<0.05$ and then the coefficients in column B which help to predict the model, we have $\text{Predicted data} = 6.195 + 0.870 * \text{Observed data}$ .This implies that the predicted data increases by 0.870 for every unit increase in the observed data.

DISCUSSION

In this paper, A compartmental model for Dengue fever disease was presented; based on two populations, humans (with temporary immunity, careful and careless susceptible) and mosquitoes with treatment. Modelling was examined with a special application to modelling dengue fever disease data in Tanzania. In particular, the least squire curve fitting analysis was explored and applied to the data from January 2010 to April 2015. The best fitting model based on how well the model captures the data. From the results, it is observed that the forecasted data agree very closely to the actual data.

Moreover statistical test is carried out in order to establish the relationship of forecasted and observed data. A statistical test showed significant correlation between predicted and observed number of cases in 2010-2015 (R =0.921, R square=0.848). Furthermore the correlation was significant. $\text{Predicted data} = 6.195 + 0.870 * \text{Observed data}$, meaning that if observed data is increases by one, the model predict that, the predicted data increases by 0.870, so model was found to be valid since the statistic assumption is satisfied.

Conflict of interest

None.

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