A novel technique to estimate biological parameters in an epidemiology problem

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A novel technique to estimate biological parameters in an epidemiology problem

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1. Abstract

In this work we describe a study of parameters estimation technique [1] to estimate a set of unknown biological parameters of a nonlinear dynamic model of dengue. We also explore a **Levenberg-Marquardt** (**LM**) algorithm to minimize the cost function [2, 3, 4, 5]. A classical model describes the dynamics of dengue mosquitoes in water and winged phases, where the data are availables. The main interest is fit the model to the data taking into account the parameters estimated. Numerical simulation was performed to show the the robustness of **LM** in estimating parameters.

2. Objectives

Develop a new technique to estimate the biological parameters in a ODE model of dengue and fit the data of male and females mosquito populations.

3. Model

Let the state variables and the biological parameters in Tables (1) and (2) respectively. The ode system used in this work is given below, We define $\mathbf{X}(t) = [A(t), I(t), F(t), M(t)]$ representing the continuous solution vector of the system (1) at time t.

$$\begin{cases} \dfrac{dA}{dt} = \phi\left(1-\dfrac{A}{C}\right)F - (\gamma+\mu_A)A \\ \dfrac{dI}{dt} = r\gamma A - (\beta+\mu_I)I \\ \dfrac{dF}{dt} = \beta I - \mu_F F \\ \dfrac{dM}{dt} = (1-r)\gamma A - \mu_M M \end{cases} \tag{1}$$

Table 1: State variables at the time t.

$A(t)$	aquatic phase (immature forms)
$I(t)$	no-fertilized females (before mating)
$F(t)$	fertilized females (after mating)
$M(t)$	males insects (natural male)

Table 2: Parameters to the model (1).

Parameter	Description	Value [6]	Unit
γ	Ratio of transition to winged form	0.121	$days^{-1}$
β	The effective mating rate	0.7	$days^{-1}$
r	The proportions of females	0.5	–
$(1-r)$	The proportions of males	0.5	–
μ_A	Aquatic phase mortality rate	0.0583	$days^{-1}$
μ_I	Unmating female mortality rate	0.0337	$days^{-1}$
μ_F	Mating fertilized mortality rate	0.0337	$days^{-1}$
μ_M	Male mortality rate	0.06	$days^{-1}$
ϕ	Intrinsic oviposition rate	6,353	$days^{-1}$
C	Carrying capacity	3	$mosquito^{-1}$

4. Cost function

Let $i \in \mathbb{D} := \{0, \cdots, N\}$, where N is the maximmum data observed in $[0, T]$, T is the total experimental time.
Let $E = \{\mathbf{X}_{iobs}\}$: the data from the experimental observation, for $i = 0, \cdots, N$.
Let $\mathbf{b} = [b_{iobs}]$: the vector of known parameters (observed data), $\forall i = 1, \cdots, m$.
Let $\mathbf{p} = (p_1, \cdots, p_n)$, where n is the number of parameters to be estimated.
Cost function: Let the cost function W be defined as:

$$W(\mathbf{p}) = \frac{1}{2}\parallel w(\mathbf{p}) \parallel^2 = \frac{1}{2}\sum_{i=1}^{m} w_i(\mathbf{p})^2 = \frac{1}{2}\sum_{i=1}^{m}\sum_{l=1}^{k}(\mathbf{X}_i^l(\mathbf{p},\mathbf{b}) - \mathbf{X}_{iobs}^l)^2, \tag{2}$$

The main problem involving parameter estimation consists of:

Minimize W**:** Determine $\mathbf{p}$ that minimizes the cost function W, subject to $p_k \geq 0, \forall k = 1, \cdots, n$.

5. Algorithms

5.1 Parameters Estimation

Step 1 - **Input** the observed data;
Step 2 - **Set** initial parameter guess $\mathbf{p}^0 = [p_1^0, \cdots, p_n^0]$ for $\mathbf{p}$;
Step 3 - **Build** a function to calculate $\mathbf{X}$ from a mathematical model;
Step 4 - **Calculate** the cost function W from Eq. (2);
Step 5 - **Build** a routine to minimize W;
Step 6 - **Return** $\mathbf{p}$.

5.2 Levenberg-Marquardt (LM)

Step 1 - Define $\mathbf{p} = \mathbf{p}_0$ and $\nu = 2$;
Step 2 - Calculate $B = J(\mathbf{p})^{\mathbf{T}}J(\mathbf{p})$ and $\mathbf{g} = J(\mathbf{p})^{\mathbf{T}}w(\mathbf{p})$;
Step 3 - Do $\lambda = \tau * max\{b_{ii}\}$;
Step 4 - If $\parallel \mathbf{g} \parallel_\infty \leq \varepsilon_1$, go to **Step 8**;
Step 5 - Solve $(J^{\mathbf{T}}J + \lambda I)\mathbf{h}_{lm} = -\mathbf{g}$, in $\mathbf{h}_{lm}$, with $\lambda \geq 0$;
Step 6 - If $\parallel \mathbf{h}_{lm} \parallel \leq \varepsilon_2(\parallel \mathbf{p} \parallel + \varepsilon_2)$, go to **Step 8**;
Otherwise, Do $\mathbf{p}_{new} = \mathbf{p} + \mathbf{h}_{lm}$;
Calculate $\varrho = (W(\mathbf{p}) - W(\mathbf{p}_{new}))/(L(\mathbf{0}) - L(\mathbf{h}_{lm}))$;
Step 7 - If $\varrho > 0$, do $\mathbf{p} = \mathbf{p}_{new}$, up to date B and $\mathbf{g}$, and Do $\lambda = \lambda * max\{\frac{1}{3}, 1-(2\varrho-1)^3\}$ and $\nu = 2$;
Otherwise, Do $\lambda = \lambda * \nu$ and $\nu = 2 * \nu$;
$it = it + 1$; Back to **Step 4**;
Step 8 - Return $\mathbf{p}$.

6. Results

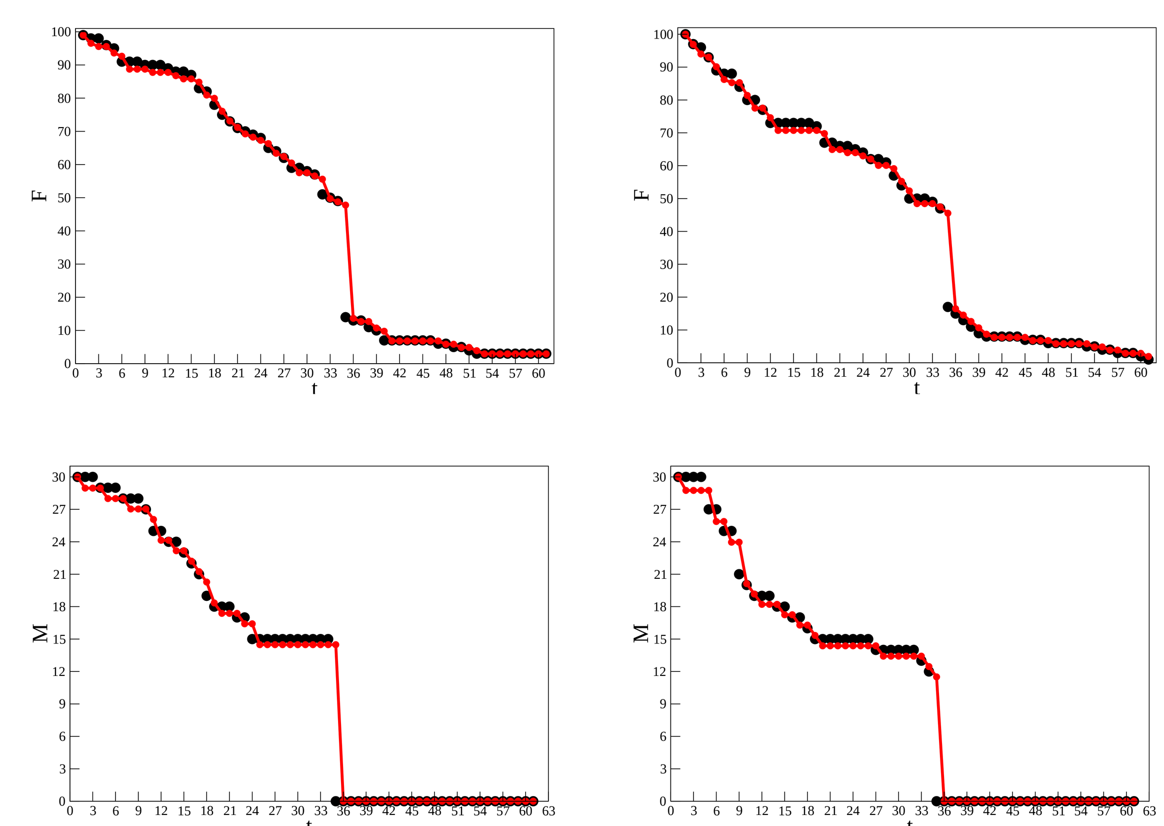
We present here the results of the estimations.

1. Parameters to be estimated: $\mathbf{p} = (\mu_F, C, \mu_M)$;
2. Available data: $\mathbf{X}_{iobs} = [A_{iobs}, F_{iobs}, M_{iobs}]$;
3. Observed parameters: $\mathbf{b} = [\phi_{iobs}]$;
4. Initial conditions $(A_0, F_0, M_0) = (0, 100, 30)$;
5. Parameters of simulations: Time-step $dt = 1$, $\tau = 10^{-3}$ and $\varepsilon_1 = \varepsilon_2 = 10^{-8}$.

Table 3 shows the Comparisons μ_F and μ_M estimations at 25°C). Figures (1) shown the numerical solution of the model 1 fitting the data of female and male mosquitoes, respectively. Table 4 shows *Pearson correlation coefficient* ρ [9] values for cities A and B (30°C), indicating the strong linear correlation between the parameters estimated and the real data.

Table 3: Comparisons μ_F and μ_M estimations (25°C).

(Thomé, 2010) [8]		**Present work**			
μ_F	μ_M	μ_F - City A	μ_F - City B	μ_M - City A	μ_M - City B
0.0337	0.06	0.0249	0.0311	0.0666	0.0416



(c) (d)

Figure 1: Dynamic of dengue mosquito populations $F(t)$ and $M(t)$ (from top to bottom) for the cities A (left) and B (right) in 25°C. Red line means predictions of the model and black dots depict the observed data of the aquatic phase, fertilized females and males of dengue mosquitoes.

Table 4: ρ values (30°C).

	A	F	M
City A	0.999989726	0.998431825	0.996482096
City B	0.999976721	0.999048742	0.995447591

7. Conclusions

1. The model was able to fit the dengue data in all tests performed;
2. The numerical solutions comparison with data show the robustness of the code to fit the dengue data available.
3. There are agreement between the estimated parameters and values from the literature;
4. The results show that this technique can be an important data analysis tool to be applied in dynamic population systems;
5. The novel technique presented here improved the application of the *LM* algorithm as an optimization alternative to analyze the dengue disease with real data.

8. Acknowledgments

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9. References

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