A metapopulation model for malaria transmission

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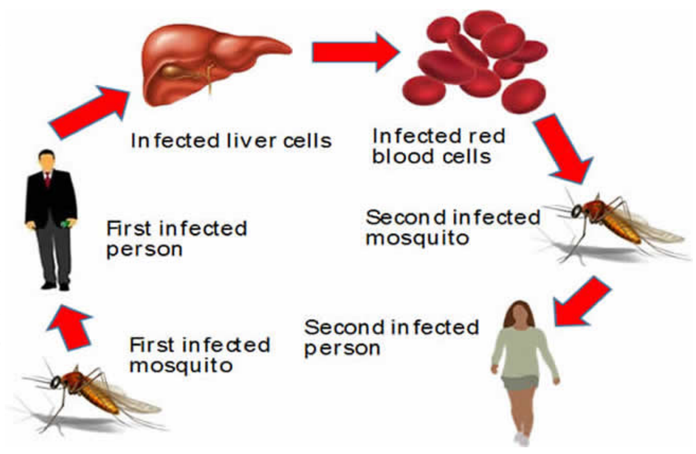
Abstract

The main purpose of our work is to develop and study a mathematical model based on ordinary differential equations to describe the dynamics of malaria transmission. In the first part, we formulate a model for a single isolated patch to describe the transmission process. In the second part we are interested in a generalization, a meta-population model type to study the spatial and temporal spread of malaria. Thus, we subdivide the space into n small geographical areas said patches. Such that in each patch $i, i = 1, \cdots, n$; we have a similar model of an isolated patch plus the movement of humans from one patch to another, we obtain a system of $5n$ differential equations.
Keywords Malaria, Basic reproduction number $\mathcal{R}_0$, The backward bifurcation, Meta-population, Global stability.

Life cycle of Malaria

Usually, people get malaria by being bitten by an infective female *Anopheles* mosquito. Only *Anopheles* mosquitoes can transmit malaria and they must have been infected through a previous blood meal taken from an infected person.When a mosquito bites an infected person, a small amount of blood which contains microscopic malaria parasites is taken. About 1 week later, when the mosquito takes its next blood meal, these parasites mix with the mosquito's saliva and are injected into the person being bitten. [4]



Schematic representation of our the model in each patch

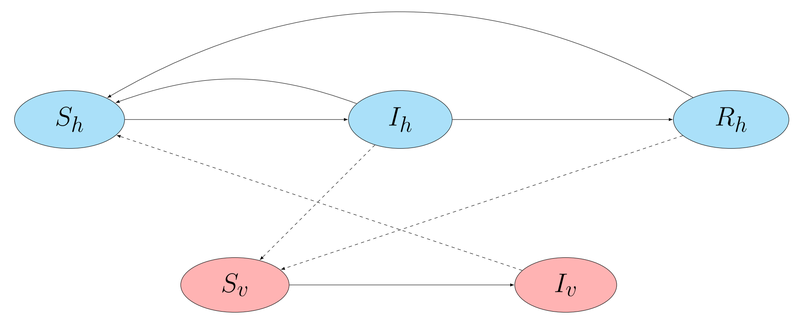
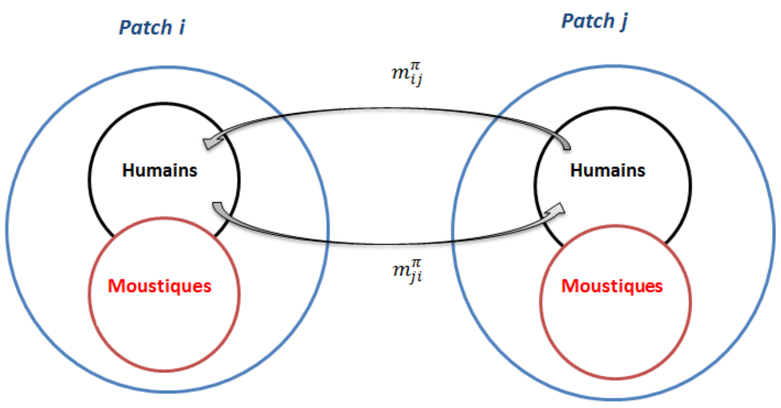


Figure 1: A schematic representation of the mathematical model. *The dotted arrows* show the direction of the transmission from infectious human to susceptible mosquito or from infected or infectious mosquitoes to susceptible human

General presentation of the model



Travellers, whatever their destination, are frequently victims of health problems, one of these problems is Travellers, whatever their destination, are frequently victims of health problems, one of these problems is malaria. There are currently several countries affected by this disease, which are visited annually by more than 125 million travellers [5].

In this work we study the system descibing the spread of this disease between several regions called patches, with humans who can move from a patch i to a patch j for all $i = 1, \cdot, n$, but we neglect the movement of mosquitoes.

The mathematical model for one patch

The model for one patch is given as follow

$$\begin{cases} \frac{dS_h}{dt} = \Lambda_h + \rho_h R_h + \alpha_h I_h - \beta_{vh}\frac{S_h}{H} I_v - \mu_h S_h \\ \frac{dI_h}{dt} = \beta_{vh}\frac{S_h}{H} I_v - \alpha_h I_h - \gamma_h I_h - \mu_h I_h - \delta_h I_h \\ \frac{dR_h}{dt} = \gamma_h I_h - \rho_h R_h - \mu_h R_h \\ \frac{dS_v}{dt} = \Lambda_v - \left(\beta_{hv}\frac{I_h}{H} + \hat{\beta}_{hv}\frac{R_h}{H}\right) S_v - \mu_v S_v \\ \frac{dI_v}{dt} = \left(\beta_{hv}\frac{I_h}{H} + \hat{\beta}_{hv}\frac{R_h}{H}\right) S_v - \mu_v I_v \end{cases} \quad \text{(II)}$$

ith initial conditions $S_h(0), S_v(0) > 0; I_h(0), I_v(0), R_h(0) \geq 0$.

The general mathematical model

Suppose that space is subdivided into n regions called patches. In each patch $i = 1, \cdots, n$, we have the following model:

$$\begin{cases} \frac{dS_{H,i}}{dt} = \Lambda_{H,i} + \rho_{H,i} R_{H,i} + \alpha_{H,i} I_{H,i} - \beta_{V_i,H_i}\frac{I_{V,i}}{H_i} S_{H,i} - \mu_{H,i} S_{H,i} + \sum_{j=1}^{n} m_{ij}^{S} S_{H,j} - \sum_{j=1}^{n} m_{ji}^{S} S_{H,i} \\ \frac{dI_{H,i}}{dt} = \beta_{V_i,H_i}\frac{I_{V,i}}{H_i} S_{H,i} - \alpha_{H,i} I_{H,i} - \gamma_{H,i} I_{H,i} - \mu_{H,i} I_{H,i} - \delta_{H,i} I_{H,i} + \sum_{j=1}^{n} m_{ij}^{I} I_{H,j} - \sum_{j=1}^{n} m_{ji}^{I} I_{H,i} \\ \frac{dR_{H,i}}{dt} = \gamma_{H,i} I_{H,i} - \rho_{H,i} R_{H,i} - \mu_{H,i} R_{H,i} + \sum_{j=1}^{n} m_{ij}^{R} R_{H,j} - \sum_{j=1}^{n} m_{ji}^{R} R_{H,i} \\ \frac{dS_{V,i}}{dt} = \Lambda_{V,i} - \left(\beta_{H_i,V_i}\frac{I_{H,i}}{H_i} + \hat{\beta}_{H_i,V_i}\frac{R_{H,i}}{H_i}\right) S_V V, i - \mu_{V,i} S_{V,i} \\ \frac{dI_{V,i}}{dt} = \left(\beta_{H_i,V_i}\frac{I_{V,i}}{H_i} + \hat{\beta}_{H_i,V_i}\frac{R_{H,i}}{H_i}\right) S_{V,i} - \mu_{V,i} I_{V,i} \end{cases} \quad \text{(I)}$$

with initials conditions: $S_{H,i}(0) > 0; S_{V,i}(0) > 0$ et $I_{H,i}(0), R_{H,i}(0), I_{V,i}(0) \geqslant 0$, for all $i = 1, n$.
All parametres are positive expet of $\delta_{H,i} \geq 0$.

The existence and uniqueness of the solution

Let $\Omega = \mathbb{R}_{+}^{*2n} \times \mathbb{R}_{+}^{3n}$; The points in Ω are denoted by $Let(S, I)^T$, with $S = (S_{H,i}, S_{V,i})$ and $I = (I_{H_i}, R_{H,i}, I_{V,i})$ for $i = 1, \cdots, n$.

Theorem 1. *For any initial condition $(S(0), I(0))$ in Ω, our system has a unique globally defined solution $(S(t), I(t))$ which remains in Ω for all $t \geq 0$*

Principal results

The disease-free equilibrium DFE

Denote by: $\Lambda_H = (\Lambda_{H,1}, \cdots, \Lambda_{H,n})^T$; $\Lambda_V = (\Lambda_{V,1}, \cdots, \Lambda_{V,n})^T$; $S_H^* = (S_{H,1}^*, \cdots, S_{H,n}^*)^T$; $S_V^* = (S_{V,1}^*, \cdots, S_{V,n}^*)^T$; $L_H = diag(\mu_{H,i} + \sum_{j=1}^{n} m_{ji}^{S}) - M^S$; $L_V = diag(\mu_{V,i})$ for all $i = 1 \cdots, n$.

Theorem 2. *Our system has a unique disease-free equilibrium DFE in Ω for the all system, given by $S_H^* = L_H^{-1}\Lambda_H \quad S_V^* = L_V^{-1}\Lambda_V$*

- *The DFE is locally asymptotically stable if $\mathcal{R}_0 \leq 1$. In the case of one patch we proved:*
- *If $\mathcal{R}_0 < 1$ then the DFE is asymptotically stable.*
- *The DFE is globally asymptotically stable when $\mathcal{R}_0^2 < \frac{\mu_h}{\mu_h + \delta_h}$.*

Existence of Backward bifurcation when $\delta_h \neq 0$

Theorem 3. *Our system may have up to three biologically plausible equilibria.*

1) The disease free equilibrium is always a boundary equilibrium.

2) When $\mathcal{R}_0 > 1$ the system has a unique positive equilibrium.

3) When $\mathcal{R}_0 < 1$ then system has two positive equilibria under some conditions depending on the parameters of the system.

The endemic equilibrium EE

Let $\Phi_t(S, I)$ be the flow corresponding to system (II).
$\Phi_t(S, I)$ denote the solution of System (II) that starts at $S(0)$, $E(0)$, $I(0)$, $R(0) \geq 0$. Then $\Phi_t(S_0, I_0) = (S(t), I(t))$ where $S = (S_h, S_v)$ and $I = (I_h, R_h, I_v)$. The flow property follows from the uniqueness of solution that we had already proved.

Theorem 4. *If $\mathcal{R}_0 > 1$ then system (II) is uniformly persistent.*

Theorem 5. *In the case of one patch we have the following results:*

1. *The EE is locally asymptotically stable if $\mathcal{R}_0 > 1$*
2. *Under the following conditions $\delta_h = 0$, $\hat{\beta}_{hv} = 0$ and $\rho_h - \alpha_h \leq \frac{\gamma_h}{2}$ the EE is globally asymptotically stable if $\mathcal{R}_0 > 1$. We used the geometric approach for the proof [3].*

The disease control using a pesticide induce death rate for mosquitoes

We study the effect of pesticide for the control of malaria transmission by introducing an other death rate (induced by the pesticide) for mosquitoes in order to make the DFE globally asymptotically stable.

Bibliography

References

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[4] `https://www.cdc.gov/malaria/about/disease.html`

[5] `https://www.who.int/`