

Modelling the Co-infection dynamics of HIV and Malaria

Disease Modelling, Group 2

MASAMU,
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Outline

- 1 Background
- 2 HIV-Malaria model
- 3 Mathematical Analysis
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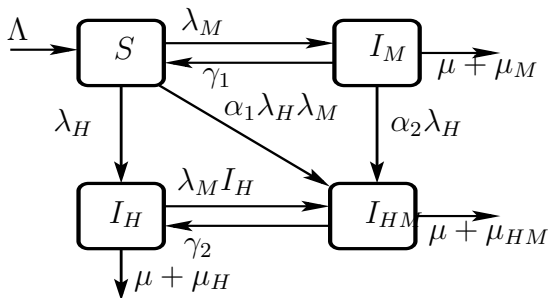
■ Malaria

- It is an infectious disease caused by the parasite genus Plasmodium.
- There are four species of this parasite causing malaria, namely, Plasmodium vivax, Plasmodium falciparum, P. ovale and P. Malariae.
- Malaria is transmitted to the human by the biting of the female Anopheles mosquito.
- Malaria disease is a major public health problem in the world.
- One of the ten killer diseases in the world.
- In each year there are estimated between 300 to 500 million children clinical episodes of malaria and 1.5 to 2.7 million deaths worldwide.

■ HIV

- HIV/AIDS has killed more than 25 million people in the world since it was first recognized in 1981.
- Its effect is most devastating in Sub-Saharan Africa, where HIV prevalence ranges between 12% to 42%.
- One of the key factors that fuels the high incidence of HIV in Sub-Saharan is the co-infection with Malaria.
- HIV has shown to increase the risk of malaria infection and accelerate the development of clinical symptoms of malaria with the greatest impact in immune suppressed persons.

Human Population



Malaria Population

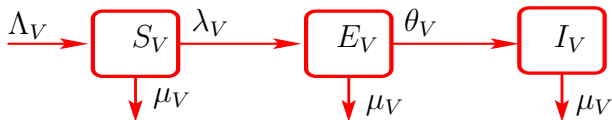


Figure: Model Diagram

$$\frac{d}{dt}S(t) = \Lambda - (\lambda_M + \lambda_H)S(t) + \gamma_1 I_M(t) - \alpha_1 \lambda_H \lambda_M S(t) - \mu S(t),$$

$$\frac{d}{dt}I_M(t) = \lambda_M S(t) - \gamma_1 I_M(t) - \alpha_2 \lambda_H I_M - (\mu + \mu_m) I_M(t),$$

$$\frac{d}{dt}I_H(t) = \lambda_H S(t) + \gamma_2 I_{HM}(t) - \lambda_M I_H(t) - (\mu + \mu_H) I_H(t),$$

$$\frac{d}{dt}I_{HM}(t) = \alpha_2 \lambda_H I_M(t) + \alpha_1 \lambda_H \lambda_M S(t) + \lambda_M I_H(t) - (\gamma_2 + \mu + \mu_H) I_{HM}(t),$$

$$\frac{d}{dt}S_V(t) = \Lambda_V - \lambda_V S_V(t) - \mu_V S_V(t),$$

$$\frac{d}{dt}E_V(t) = \lambda_V S_V(t) - \theta_V E_V(t) - \mu_V E_V(t),$$

$$\frac{d}{dt}I_V(t) = \theta_V E_V(t) - \mu_V I_V(t).$$

Force of Infection terms,

- $\lambda_H = \beta_H \frac{I_M + \epsilon I_{HM}}{N_H},$

- $\lambda_M = \beta_M b_M \frac{I_V}{N_H},$

- $\lambda_V = \beta_V b_M \frac{I_M + \eta I_{HM}}{N_H}$

Where N_H is the total human population

Objectives:

- to estimate the Malaria-notification rates as a result of HIV epidemic.
- to estimate the reduction of disease burden (morbidity, mortality) of both diseases as different treatment strategies are implemented.

Using the next generation matrix approach, the spectral radius of $\sigma(FV^{-1})$, we calculated the basic reproduction number

- $R_H = \frac{\beta_H}{\mu + \mu_H}$, HIV-only model
- $R_M = \frac{b_m}{\mu_V} \sqrt{\frac{\mu}{\lambda} \left(\frac{\theta_V}{\theta_V + \mu_V} \right) \left(\frac{\beta_m \beta_v \lambda_V}{\mu + \gamma_1 + \mu_m} \right)}$, Malaria-only model

The basic reproduction of the full system is

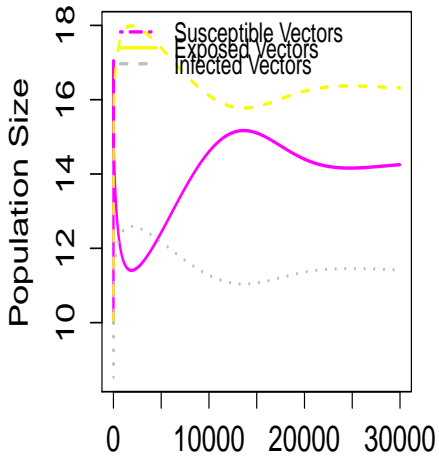
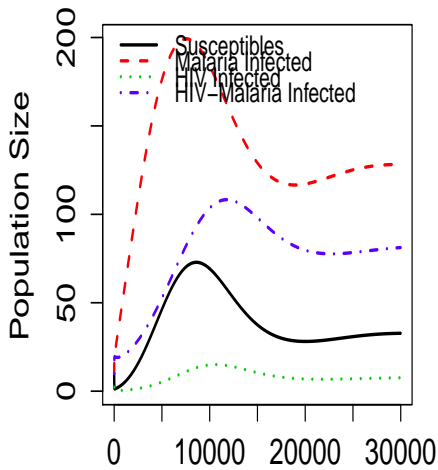
$$R_0 = \max\{R_H, R_M\}$$

- The Disease Free Equilibrium (E_0) is given by:

$$E_0 = \left(\frac{\lambda}{\mu}, 0, 0, 0, \frac{\lambda_V}{\mu_V}, 0, 0 \right)$$

It is locally asymptotically stable for $R_0 < 1$, otherwise unstable. This is an immediate result from the generation matrix or one can use also evaluate the Jacobian at E_0 and by checking for negative real eigenvalues.

- Global stability of E_0 , we plan to implement reduction method to-system (Susceptibles and Infected)
- Stability of the Endemic Equilibrium point (E^*), we plan to implement compound matrix approach



- Fitting with data from sub-saharan Africa,
- Adding exposed class for malaria and AIDS class for human population,
- This model did not consider prevention or any treatment program for HIV, we planned to incorporate this.

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- Chunky
- David
- Megan
- Nomatter

Thank You