Project Proposal

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EEB313 Project Proposal - DRC Malaria Modelling

Leading Question

Malaria is a deadly mosquito-borne herpesvirus caused by *Plasmodium spp* [1,2]. As a vector-borne disease, malaria is primarily transmitted by mosquitoes (*Anopheles*), whose bite allows the entry of *Plasmodium* into the bloodstream. Once in a human host, malaria presents as a set of non-specific symptoms, such as diarrhoea, fever, vomiting, and pulmonary complications [1]. In many cases, malaria leads to death - in 2021 alone, UNICEF reported more than 600,000 malaria-related fatalities [3]. Unfortunately, children under the age of 5 were the most vulnerable demographic, comprising a total of 77% of malaria-related deaths [3]. The Democratic Republic of the Congo (DRC) is among the hardest-hit countries, representing 12% of all global cases in 2021 [4]. Consequently, malaria research is a field of global interest. Besides research into the physiological, immunological, and genetic causes and consequences of malaria, many researchers focus on mathematical modeling as a measure to explain infection/death rates [5]. Such models inform institutional decisions, especially when environmental, social, economic, and migration-related variables are included [5].

Model Inspiration

For the first part of our project, we are interested in examining the predictive power of the Ross-Macdonald model for malaria transmission. Specifically, we want to test the validity of this model using pre-existing regional DRC malaria data. This model is derived from two equations, one of which observes human infections, and the other vector infections (which in this context is mosquitoes) [5,6]. More specifically, this model focuses on the susceptible population (S), and the infected population (I), and briefly considers the recovered population (R). Here is a quick summary of the different variables used within the model: * a: mosquito biting rate, * b: transmission probability from an infectious mosquito to a susceptible human per bite, * c: transmission probability from an infectious human to a susceptible mosquito per bite, * m: ratio of mosquitoes to human, * V/H: number of vectors (mosquitoes) and number of humans, * I_v/I_h: number of infectious vectors and number of infectious humans, * S_v/S_h: number of susceptible vectors and number of susceptible humans, * γ: human recovery rate, * μ: mortality rate of mosquitoes.

Furthermore, the model itself is as follows,

$$\frac{dI_h}{dt} = ab\frac{I_v}{H}S_h - \gamma I_h \quad \text{and} \quad \frac{dI_v}{dt} = ab\frac{I_h}{H}S_v - \mu I_v,$$

where $S_h = H - I_h, S_v = V - I_v$, and $R_0 = \sqrt{\frac{a^2bcm}{\gamma\mu}}$. However, the Ross-Macdonald model considers many of the parameters to be fixed (e.g., a, b, and c), which is rarely the case in actual populations. Moreover, interpreting these values as functions of time might provide greater accuracy in a malaria model. The number of mosquito bites on humans per mosquito per month is influenced by both human and environment-driven factors. Consider migration and resource allocation to combat mosquitoes for human factors, and precipitation and the temperature for environmental factors [7,8,9]. It would thus be of interest for $a(t)$ to take these values into its output. Moreover, b may be impacted by the number of infectious mosquitoes,

and the opportunities for infectious mosquitoes to feed on susceptible humans. Note that humans can be bit many times per day, however, mosquitoes may only feed a finite number of times each day. This can be perceived as there being no particular lack of resources, but that one given mosquito can only infect a finite number of individuals in a day. Moreover, c may be impacted by quarantining procedures and the virulence of the virus. As such, in the second part of our project, we will be exploring whether and how incorporating the aforementioned variables impacts the predictive value of the Ross-Macdonald model. Findings from our research have the potential to present an improved model that may better depict real-life malaria cases and perhaps even infer interactions between mechanisms. It will also be of interest to compare our model against the standard Ross-Macdonald model to verify possible discrepancies, and where certain models are more advantageous (one may be overwhelmingly better, or these may be advantageous on case-by-case conditions). Should our model prove to accurately resemble real-life data, it may also be of interest to use it for predictive purposes, to enable more insightful approaches to combatting malaria.

Citations

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