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IMPACT OF AGE-DEPENDENT RELAPSE
AND IMMUNITY ON MALARIA DYNAMICS

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An age-structured mathematical model for malaria is presented. The model explicitly includes the human and mosquito populations, structured by chronological age of humans. The infected human population is divided into symptomatic infectious, asymptomatic infectious and asymptomatic chronic infected individuals. The original partial differential equation (PDE) model is reduced to an ordinary differential equation (ODE) model with multiple age groups coupled by aging. The basic reproduction number $\mathcal{R}_0$ is derived for the PDE model and the age group model in the case of general n age groups. We assume that infectiousness of chronic infected individuals gets triggered by bites of even susceptible mosquitoes. Our analysis points out that this assumption contributes greatly to the $\mathcal{R}_0$ expression and therefore needs to be further studied and understood. Numerical simulations for $n = 2$ age groups and a sensitivity/uncertainty analysis are presented. Results suggest that it is important not only to consider asymptomatic infectious individuals as a hidden cause for malaria transmission, but also asymptomatic chronic infections (>60%), which often get neglected due to undetectable parasite loads. These individuals represent an important reservoir for future human infectiousness. By considering age-dependent immunity types, the model helps generate insight into effective control measures, by targeting age groups in an optimal way.

Keywords: Malaria; Endemic Model; Age-structure; Reproductive Number; Uncertainty and Sensitivity Analysis.

1. Introduction

Malaria is a vector-borne infectious disease caused by parasites of the genus *Plasmodium*. Malaria is a major international health problem, with an annual estimate of 216 million documented cases and around 1 million deaths.[1] The disease is mostly common in tropical and subtropical regions including much of Sub-Saharan Africa,

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