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An epidemiological compartmental model of malaria with host-vector interactions

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Extended Abstract

Malaria, a mosquito-borne disease that affects millions around the world, places a heavy health and economic toll on endemic countries with developing economies. Alleviating the burden of malaria has been a global priority for public health, and the disease is retreating in many countries. While significant reductions in malaria incidence have been reported in India over the past decade (World Health Organizaton, 2019), there are many challenges facing malaria control and elimination efforts, including varied patterns of malaria transmission in different parts of the country requiring area-specific control strategies, antimalarial drug resistance, and increasing insecticide resistance in vector populations. When faced with resource constraints, the introduction and scale-up of interventions for malaria control and elimination must be prioritized to maximize the impact for a given investment. The evaluation of strategies involving intervention combinations through large-scale field trials requires considerable amount of resources. An efficient approach to assess the effects of different strategies is to develop a general model with a parsimonious structure that reproduces malaria biology well enough to integrate the mechanisms of action of different interventions, while emulating the observed quantitative relationships between epidemiological variables in a given setting.

In this extended abstract, we present a dynamic simulation model for malaria developed in the first phase of an intervention trial using the system dynamics modelling approach and methodology. The model simulates the basic short-term malaria dynamics, tracking the transmission cycle, the course of infections, and the dynamics of morbidity and mortality as a function of transmission intensity. The model is also used to crudely simulate the short-term effects of malaria camps based on data from the literature as we wait for field data from an ongoing cluster-assigned quasi-experimental study that is currently evaluating the impact of the intervention in Odisha state, one of the high malaria burden states in India (A. Pradhan et al., 2016). The model presented in this extended abstract builds upon the established frameworks of compartmental models for malaria, using a Susceptible-Exposed-Infected-Recovered (SEIR) decomposition of populations (see Mandal et al., 2011), and includes several features unique to the dynamics of malaria in the study setting. Our model is a synthesis of existing models and, thus, it is more comprehensive. The model will be extended in the next phase of the project to capture the longer-term dynamics of malaria with aging in human population under complex policy intervention scenarios.

The model consists of three main structures which we refer to as sectors: Humans, Female Mosquitoes, and Human-Mosquito Interactions. These sectors constitute the essential backbone of the model. The Human sector consists of all key compartments and different pathways established in malaria epidemiology. The other two sectors of the model capture the seasonal fluctuations in female mosquito population, the infection dynamics within mosquitoes, and the disease transmission cycle. The parameters of the model are estimated from the published literature on malaria (see, for example, Cai et al., 2017; Mandal et al., 2011). For area-specific values, we focused primarily using data from malaria studies conducted in Odisha State (Pradhan, A. et al., 2016; Singh Parihar et al., 2019). The model outputs behave well according to expected patterns of malaria dynamics in the study area.

The human sector

Human sector has six state variables (see Figure 1); *Susceptible_h* (susceptible human population), *Exposed_h* (Exposed human population), *Asymptomatic_Infectious_h* (infectious people who have not developed symptoms or whose immune system has not yet responded in full capacity), *Symptomatic_Infectious_h* (the group has the highest death rate), *Asymptomatic_Recovering_h* (infectious people with no symptoms, who recover in time without showing any symptoms), and *Immune_h* (people with temporary immunity). There are two intervention parameters that can be used for scenario analysis, which are painted in red (Figure 1); *Fraction of symptomatic infectious receiving Rx* (i.e., symptomatic cases that are treated with antimalarials) and *Fraction of asymptomatic infectious receiving Rx* (i.e., asymptomatic cases that are treated with antimalarials). The only input to the human sector is

infection rate h, which is the fraction of the susceptible human population that gets infected per day. This input variable is calculated in the human-mosquito interaction sector and is highlighted by painting in cyan (Figure 1).

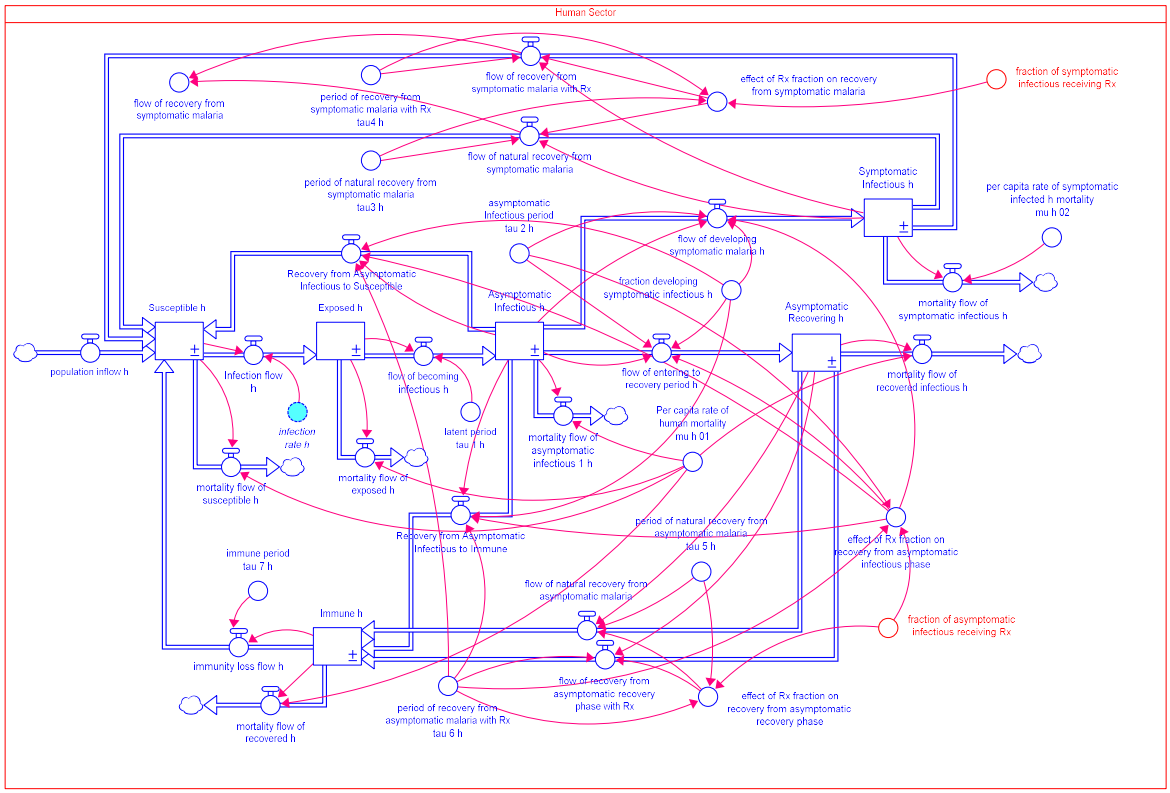

Figure 1. The structure of the human sector

The female mosquito sector

The female mosquito sector has four state variables (see Figure 2); *Juvenile_fm_egg_larva_pupa* (standing for female mosquito's egg, larva, and pupa phases), *Susceptible_fm* (susceptible female mosquito population), *Exposed_fm* (exposed female mosquito population), and *Infectious_fm* (infectious female mosquito population). There are two inputs to the female mosquito sector: The first one is *infection rate fm*, which is the fraction of the susceptible female mosquito population that gets infected per day. The second one is *total biting rate fm*, which is the total number of effective biting rate per female mosquito per day that results in a successful blood meal from the perspective of the mosquitos. These input variables are calculated in the human-mosquito interaction sector and are highlighted by coloring in cyan (Figure 2).

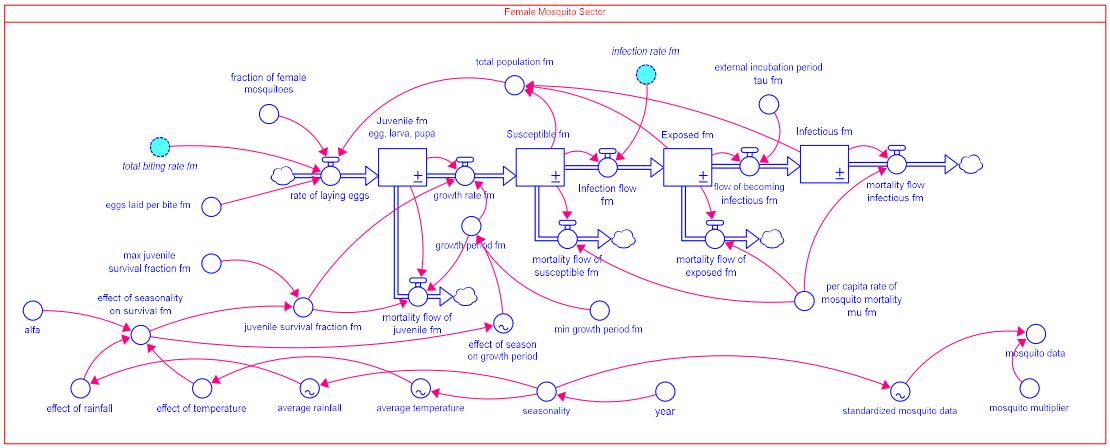

Figure 2. The structure of the female mosquito sector

The human-mosquito interaction sector

The human-mosquito interaction sector does not have new state variables, but it uses the state variables of the other two sectors to calculate the spread of the disease. The input variables are highlighted in cyan (Figure 3).

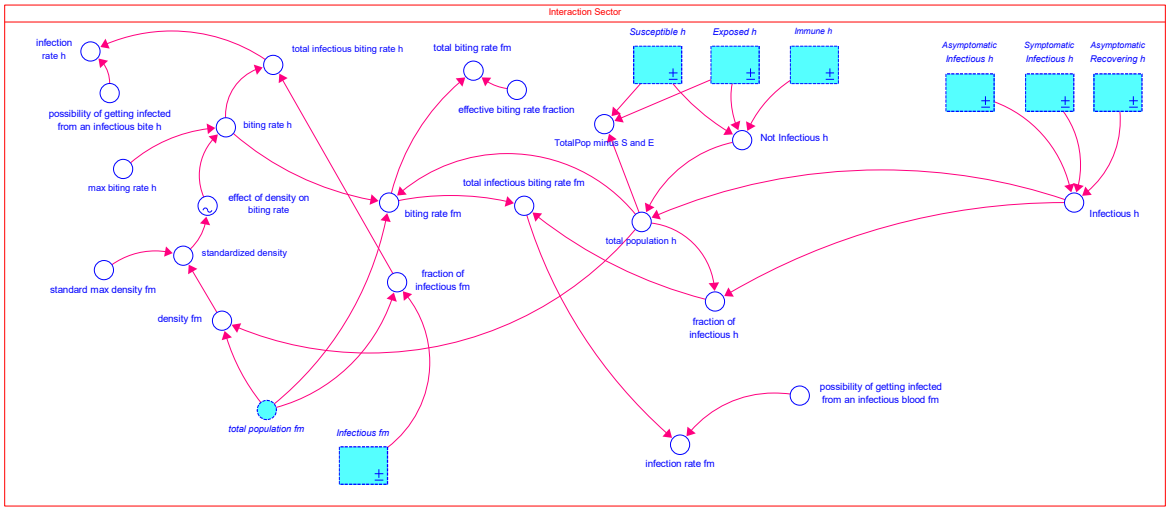

Figure 3. The structure of the human-mosquito interaction sector

Simulation results (base run)

The model outputs display two main dynamics: endogenous disease dynamics (as a result of host-vector interactions) and seasonal variation in female mosquito population. Figures 4, 5, and 6 present the base run results where 25% of symptomatic cases are treated with antimalarials and there is no treatment of asymptomatic cases (no mass test and treat intervention); *Fraction of symptomatic infectious receiving Rx* is 0.25 and *Fraction of asymptomatic infectious receiving Rx* is 0. The model outputs behave well according to the available data and expected patterns of malaria in the study area.

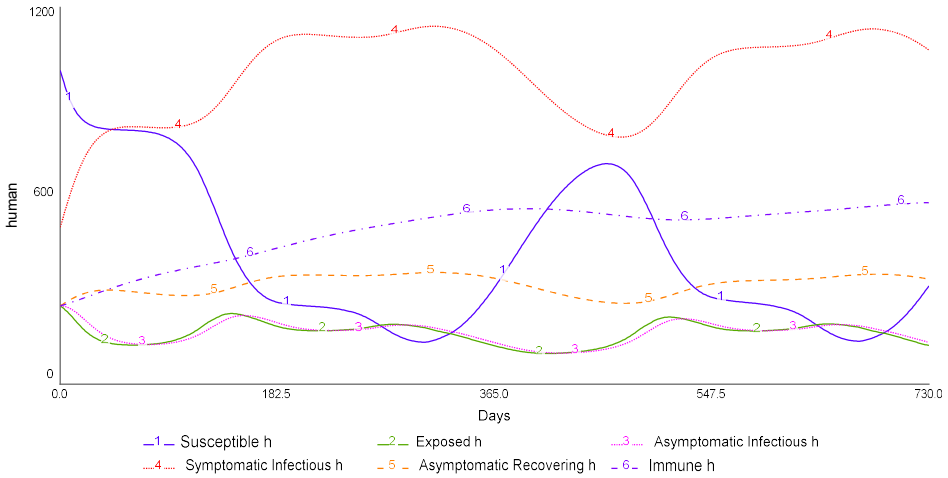

Figure 4. The dynamics of the human population

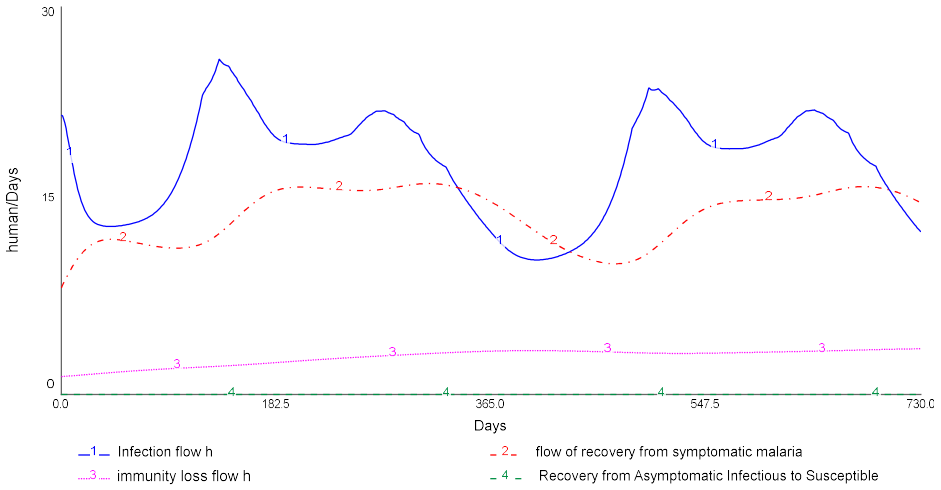

Figure 5. The dynamics of the important flows of the human sector

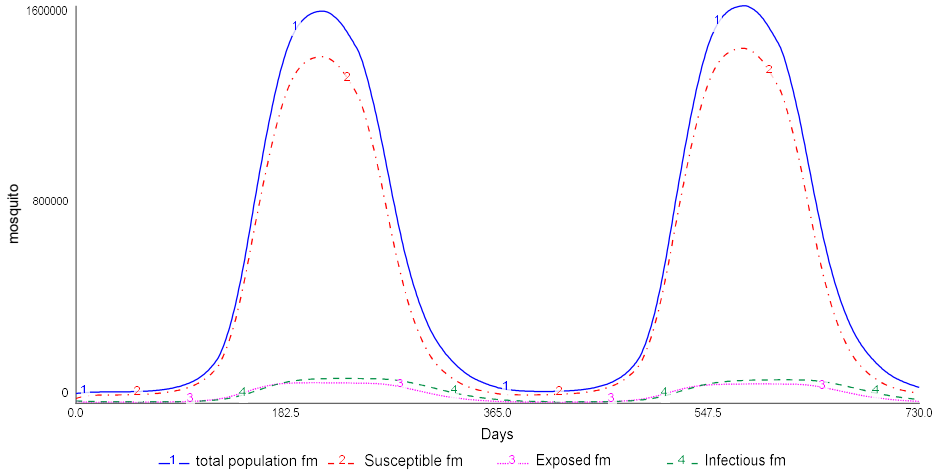

Figure 6. The dynamics of the female-mosquito population

The validity of the model structure is tested by numerous extreme condition and sensitivity tests throughout the model development process. We are convinced that the model, given its purpose, is structurally and behaviourally valid. The model can be used as an experimental laboratory in which alternative treatment strategies and future scenarios can be tested.

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