— Project and Code Status (last updated June 15, 2021) —

This document details the current state of the project and code, covers what I see as the main use of the model in its current state, and highlights what I see as the most important next steps

If you have any questions please email me at morganpkain@gmail.com

Project Overview

The goal of this project was to construct a general, mechanistic, and spatially-explicit vector-borne disease transmission model. The model is of a "bottom-up" construction in that it uses (among other components)—host and mosquito physiological responses to infection; mosquito biting preferences and survival; host and mosquito movement—to model the spread of infectious diseases on a landscape. The model can simulate landscapes or take in "real" landscapes. In both cases, the model requires a measure of tree cover and a measure of urban intensity.

For further background details on the model see the preprint at: https://www.biorxiv.org/content/10.1101/2021.06.09.447801v1

What the model CAN do + Suggested Model Use

— Small scale (for computational reasons approximately 20x20 km +/- a bit) estimates for:
    — Average disease transmission potential on a landscape
    — Identifying the highest risk locations on the landscape
    — Comparison of risk between Malaria, Dengue, and Yellow Fever
— Compare relative risk among alternative scenarios of land-use (as long as those scenarios involve forest and urban area)
— Form hypotheses for absolute risk for future testing (see "model weaknesses" below)

What the model CAN'T do (as is)

— Any large scale estimates (don't bother with county level analyses for example)
    — WHY: too computationally intensive (but see **"Next Steps"** below)
— Estimates for the risk of these three diseases in other parts of the world (e.g., Sub Saharan Africa)
    — WHY: too ecologically distinct (but see **"What the model COULD do"** below)

What the model COULD do (with a bit of modification)

— Capture the transmission of any vector borne disease or the transmission of these diseases (Dengue, Malaria, Yellow Fever) in another part of the world given disease- and region-specific parameter values

Model Strengths

— Large synthesis of empirical data and current knowledge for Dengue, Malaria, and YF
— Built from mechanism at all steps in a piece-wise (component by component) way so any model component/assumption can be altered without too much hassle
— Can be used to forecast or for scenario analysis given that it is built on mechanism

Model Weaknesses

— Not yet validated with health data or mosquito trapping data
— Computationally intensive (can really only be used for a relatively small region and for a smallish-suite of parameter values and alternative scenarios)
— Extremely parameter heavy. Modeling even the transmission of these three well studied diseases took a lot of literature searching and manual data extraction from old graphs

Future work

— Reframe: adjust the model and rewrite the code to use continuous distributions / convolutions with analytic forms to get around the huge computational cost of looping over discrete spatial distributions of host movement and two levels of mosquito movement (both the susceptible and the infected mosquitoes)
— Validate: predict disease hotspots on a given landscape and compare to where people are getting sick using fine-scale health records
— Forecast: use the model to predict current risk and risk after/under a known landscape change (will require both a known scenario and fine-scale health data)

Code

— The model code is split into a series of R scripts. To use the code, first open "top_level_script.R". That script is heavily commented and will walk you through all of the code. All other scripts are sourced from within that primary script. All files in the GitHub repo are detailed in the readme file.

— The model code was written first without host movement and then host movement was added afterwards. For this reason, the code is a bit less streamlined than it could be—some of the loops over the cells that hosts and mosquitoes enter can be a bit hard to follow (I have done my best to comment clearly, but I imagine they are still probably confusing)

— The majority of the mechanics of the model don't need to change to accommodate a different mosquito or a different disease. However, all of the parameters will need to get updated. I have done my best to make sure that all of the downstream mechanics are dynamic and just rely upon the updated parameters, but there is always a chance that some array size or some other minor thing[s] would also need to get tweaked