On-lattice spatial Gillespie model of Malaria

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Introduction

Models of malaria often focus on transitions between population strata. However, agent based models (ABMs) are increasingly popular for their ability to explicitly model spatial and individual heterogeneities, as well as stochastic behaviour.
As an exploration of ABMs, we adapted the Ross-MacDonald model to an on-lattice spatial Gillespie algorithm.

Method

The Ross-Macdonald model is a system of ODEs that model transitions between population strata.

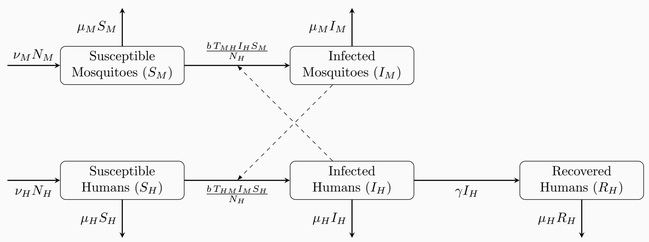

Fig. 1: Population strata and transitions in the Ross-Macdonald model.

$b = \frac{\text{bites/mosquito}}{\text{day}}$, $\nu_M = \frac{\text{births/mosquito}}{\text{day}}$, $\nu_H = \frac{\text{births/human}}{\text{day}}$, $\mu_M = \frac{\text{deaths/mosquito}}{\text{day}}$, $\mu_H = \frac{\text{deaths/human}}{\text{day}}$, $\gamma = \frac{\text{recoveries/human}}{\text{day}}$,
$T_{MH} = P(\text{transmit})_{\text{human to mosquito}}$, $T_{HM} = P(\text{transmit})_{\text{mosquito to human}}$.

The differential equation for infected humans is:
$\frac{dI_H}{dt} = \frac{bT_{HM}I_MS_H}{N_H} - \mu_H I_H - \gamma I_H \quad$ (sim. for S_H, R_H, S_M, I_M)

We adapted the Ross-Macdonal model to a Gillespie algorithm with the following events:

- human movement
- mosquito movement
- mosquito birth
- mosquito death
- human recovery
- mosquito bite

Agents were initialised on a 2D lattice, movement was on a 5-point stencil, and bites only occurred between humans and mosquitoes on the same lattice point.
Moving to spatial Gillespie, we introduced diffusion parameters (D_H, D_M) for humans and mosquitoes. We also introduced a scaled biting parameter:

$$
\begin{aligned}
B &= \frac{\text{bites attempted/mosquito}}{\text{day}} \\
&= \frac{b}{P(\text{bite successful})} \\
&= \frac{b}{P(\text{human on same lattice point as mosquito})} \\
&= \frac{b}{1-\left(1-\frac{1}{\#\text{ lattice points in domain}}\right)^{N_H}}
\end{aligned}
$$

Further Information

Code, additional details, and supplementary figures/animations at:
https://github.com/edmoC/SpatGill.git

Results

Our on-lattice spatial Gillespie model successfully recovered ODE (Ross-Macdonald) solutions.
While increasing population size improved fit, high diffusion was the most important for replicating ODE behaviour. When D_H and D_M were insufficiently large, there was no amount N_H or N_M could be increased to achieve good fit with ODE solutions.
Furthermore, Figure 4 suggested the relevant measure of diffusion was D_H+3D_M. Varying D_H and D_M while fixing this value produced similar results.
From Figure 5, we also found finer spatial resolution (more lattice points) may required higher diffusion to match ODE solutions.

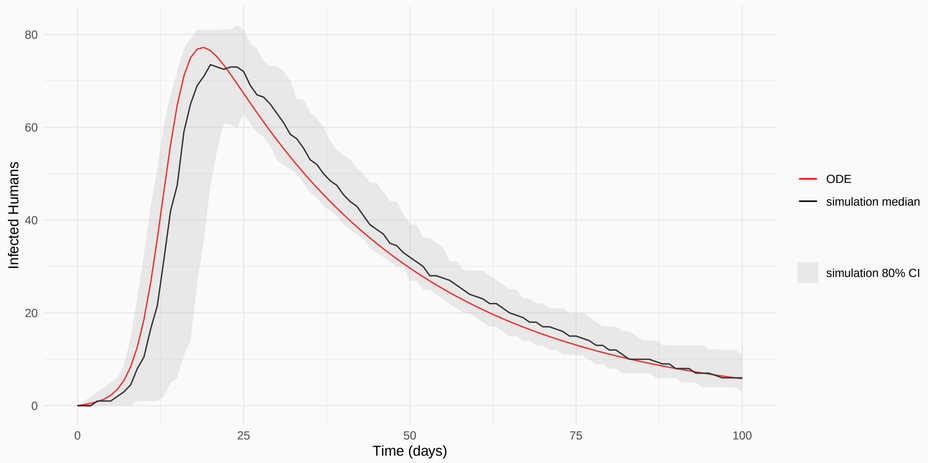

Fig. 2: 50 on-lattice spatial Gillespie simulations against ODE (Ross-Macdonald) solutions.
For each simulation, 100 susceptible humans, 299 susceptible mosquitoes, and 1 infected mosquito were randomly initialised on a 10 point by 10 point domain.
$b = 0.5$, $\mu_M = \nu_M = 0.143$ (1wk mosquito lifespan), $\gamma = 0.033$ (1mth infectious period), $T_{HM} = 0.5$, $T_{MH} = 0.8$, $D_H = 10\,\frac{\text{compartments}}{\text{day}}$, $D_M = 1\,\frac{\text{compartments}}{\text{day}}$.

Fig. 3: Snapshots of humans in the spatial domain for a single simulation. Each square is a compartment corresponding to a lattice point. Parameter values same as in Figure 2.

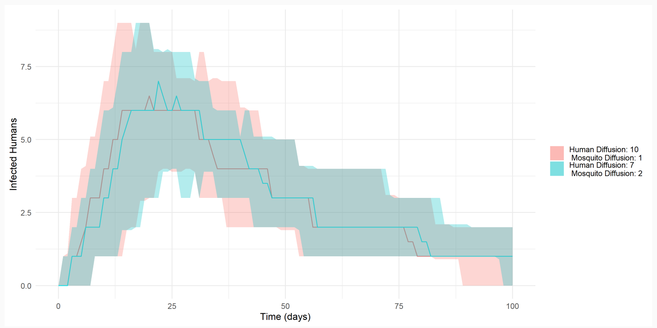

Fig. 4: Comparing different combinations of D_H and D_M.

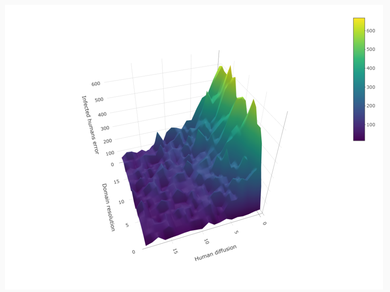

Fig. 5: Error surface (simulated I_H against ODE I_H) over domain resolution (# lattice points) and D_H.

Conclusions

With sufficient diffusion for a well mixed system, our on-lattice spatial Gillespie model replicated dynamics of the Ross-Macdonald model. That is, our simple ABM can at least model systems where the Ross-Macdonald model is applicable.
The sensitivity of fit on diffusion was also not unexpected. For one, the Ross-Macdonald model assumes a well mixed system and mixing increases with diffusion. Additionally, our formulation for B assumes sufficient movement occurs between bite events such that the spatial configurations of humans are independent.

Now while our model successfully replicated a well mixed system, AMBs are primarily for capturing dynamics outside of well mixed systems, where population strata based models do not apply. The Gillespie algorithm is relatively modular and additional events can be easily added. Thus, we can introduce meal-seeking or commuting behaviours to extend our model beyond well mixed systems.
It was beyond the scope of this project to fit these behaviours to real world data and verify their implementation. Nonetheless, our results on the sensitivity of fit on diffusion suggest our current model may be best suited for extension into systems that are not well mixed due to spatial heterogeneities.

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Citations

1. Keeling, M.J. and Rohani, P. (2007) *Modelling Infectious Diseases in Humans and Animals.* Princeton University Press. pg 135-141.
2. Lev Lafayette, Greg Sauter, Linh Vu, Bernard Meade, "Spartan Performance and Flexibility: An HPC-Cloud Chimera", OpenStack Summit, Barcelona, October 27, 2016. doi.org/10.4225/49/58ead90dceaaa