A Metapopulation Model for Predicting the Success of Genetic Control Measures for Malaria

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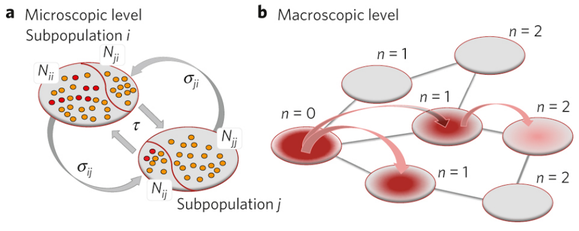
Problem

Scientists are working on new malaria control measures – genetically modified mosquitoes that are refractory to malaria parasites. However, little is known about whether the refractoriness will propagate throughout the mosquito population and how this will impact on the dynamics of malaria.

Modelling Approach

Metapopulation approach – multiple subpopulations, possibility of mixing.
Subpopulations – human settlements.
Actors – mosquitoes and mosquito larvae with various genotypes, humans.
Microscopic level – processes within populations.
Macroscopic level – mobility between populations.



Metapopulation approach. Illustration from [1]

This work proposes a metapopulation model with three main components:

Epidemiological – malaria dynamics: human and mosquito infection, progression, transmission.
Population Biology – mosquito fertility and death rate, population capping, genotype fitness.
Mobility – mosquito short- and long-distance mobility, human mobility.

Contributions

- A model that combines epidemiological, population biology, and mobility components.
- An approach for creating mobility networks based on cartographic data.
- Evaluation of refractory mosquitoes as a malaria control measure.

Genotype Fitness

$$w_{f,ss} = d \cdot (1 - exp(-\gamma \cdot k)) \cdot \alpha$$

$$w_{f,rs} = d \cdot (1 - exp(-\gamma \cdot k \cdot (1 - h \cdot s))) \cdot \alpha$$

$$w_{f,rr} = d \cdot (1 - exp(-\gamma \cdot k \cdot (1 - s))) \cdot \alpha$$

In the equations above, w is fitness, d is larval death rate, γ is prevalence of malaria in the human population, k is the daily rate of mosquitoes biting humans, s is the efficacy of refractoriness, h is dominance, and α is parasite virulence [2].

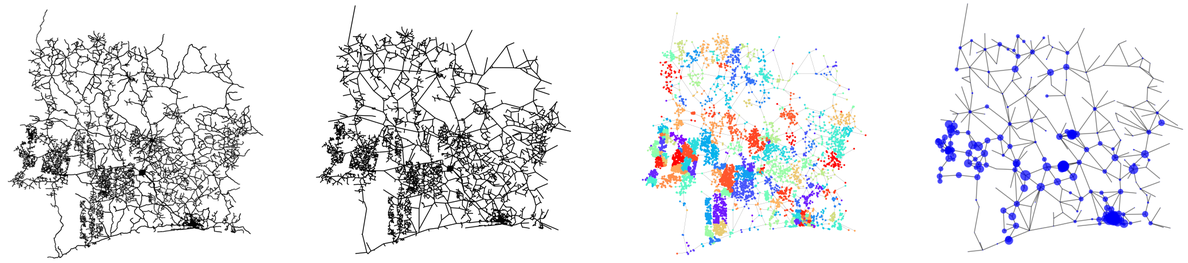
Implementation

Platform Python 3
Network analysis and handling NetworkX, NetworKit
Data processing Pandas
Interactive computing IPython Notebook
Cartography geopy, PyProj, OSM.py
Distributed computing IPython Parallel
Cloud infrastructure Microsoft Azure

Future Work

- Additional model and parameter verification.
- Comparison of predicted malaria dynamics to the data collected in the field.
- Alternative mosquito genotype fitness mechanisms.
- Improved models of human and mosquito mobility.

Mobility Network Creation



1. Road network 2. Simplify 3. Find settlements 4. Mobility network

- Possibility of migration between human settlements.
- No datasets for the regions of interest.
- Build networks using OpenStreetMap data.
- Three network layers – mosquito short-distance (proximity), mosquito long-distance (road connectivity), and human (road connectivity).

Predictive Modelling

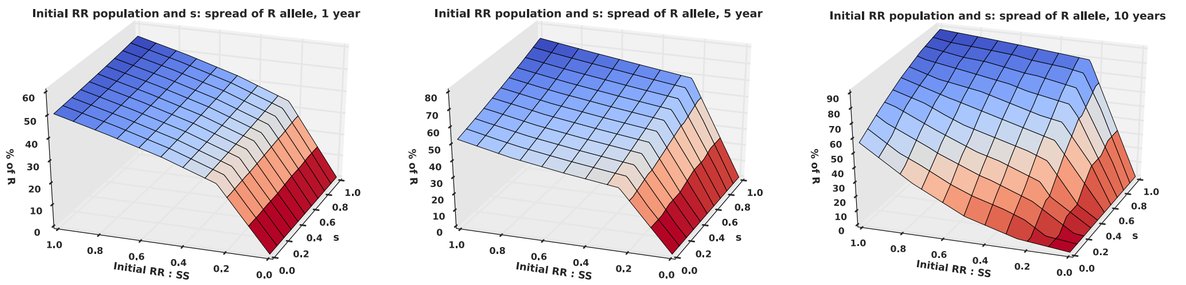


Figure 1: Fraction of R (refractory) allele – 1, 5, 10 years after deployment

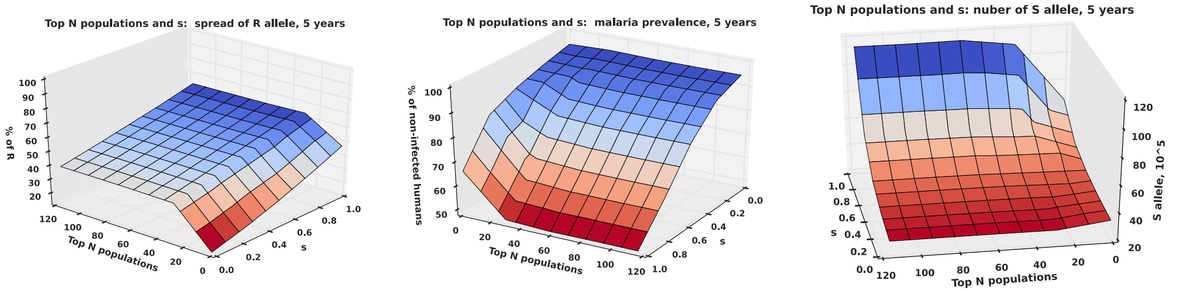


Figure 2: Selective deployment: R allele prevalence, impact on the human population, S allele prevalence

Main results:

- Refractoriness (R allele) can propagate throughout the populations (Fig. 1).
- Efficacy of refractoriness has a major impact given a longer period of time (Fig. 1).
- Graph centrality measures allow selection of optimal locations for deployment (Fig. 2a).
- Human malaria prevalence is not always reduced, due to heterozygous mosquitoes (Fig. 2b,c).

References

[1] D. Balcan and A. Vespignani. Phase Transitions in Contagion Processes Mediated by Recurrent Mobility Patterns. In Nature Physics

[2] C. Boëte and J. C. Koella. A Theoretical Approach to Predicting the Success of Genetic Manipulation of Malaria Mosquitoes in Malaria Control. In Malaria Journal, vol. 1, 2002

Acknowledgements

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