

Sensitivity of metapopulation models of infectious disease dynamics to underlying host mobility networks

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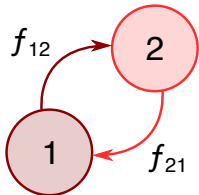
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PREMISE

- Our goal is to infer transmission parameters like R_0 based on prevalence estimates, census data, and host movement data
- Use a network metapopulation compartmental model of infectious disease dynamics; parameterize the strengths of interactions between metapopulations using host movement data
- There are different candidate models for describing host movement. We investigate how infectious disease model outcomes are affected by the choice of host movement models.

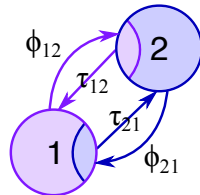
TWO MOVEMENT MODELS

Flux Model



- "Eulerian"
- Nomadism; migration; planktonic
- Requires 1 time scale per location pair
- Describes memoryless, 1-step frequency f_{ab} of movement $a \rightarrow b$

Time at Risk Model



- "Lagrangian"
- Commuting; tourism; home ranges
- Requires 2 time scales per location pair
- Describes frequency of traveling to another location (ϕ_{ab}) and the rate of returning home (τ_{ab}): $a \rightarrow b \rightarrow a$

The Time at Risk model gives a more detailed description of host movement, specifying **how much time a host spends exposed while traveling** before returning home. As a way of directly comparing the two movement models, we parameterize them based on the same data by **matching volumes of travelers** moving between each location pair.

MOVEMENT MODEL DATA REQUIREMENTS

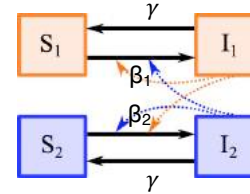
The Time at Risk model has twice as many free parameters as the Flux model, which also means it requires more detailed data sets to parameterize. The Time at Risk model requires knowing the rates at which people leave home and return home, meaning that it requires GPS trip loggers, travel surveys, disaggregated cell phone call data records, or similarly detailed information on human travel. The Flux model only requires knowing the volume of travelers moving between two locations, as in aggregated flux data. Time at Risk model data are sufficient for parameterizing a Flux model, but not vice-versa.

CONCLUSIONS

- Comparing the two movement models directly, we find that the disease model's outcome does depend on one's choice of movement model in certain parameter regimes. This is true even if the two models are calibrated to the same data set.
- Failing to account for movement model sensitivity can lead to erroneous or even nonsensical results. Specifically, the flux model may fail to accurately reflect the time spent exposed while traveling and produce inaccurate or unrealistic predictions.
- Travel data sets that enable detailed parameterization of movement models are necessary both for model accuracy and for model sensitivity analysis.

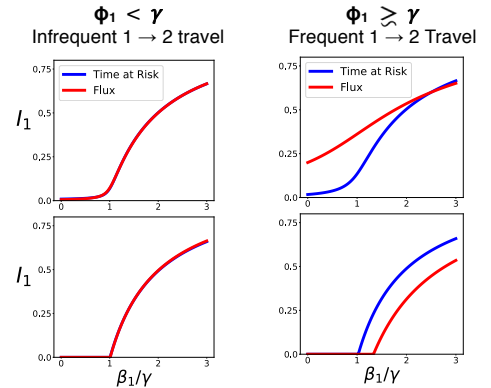
MOVEMENT MODEL DIRECT COMPARISON

Metapopulation SIS Model



$\beta_2 > \gamma$
Travel to high transmission area

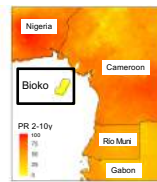
$\beta_2 < \gamma$
Travel to low transmission area



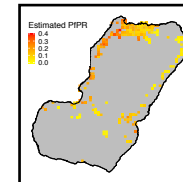
- Calibrate movement models to the same movement data
- Use movement models to parameterize the interactions between location 1 and location 2
- Holding β_2 fixed, how does prevalence I_1 vary with β_1 ?
- Given prevalence I_1 , what can we infer about β_1 ?**
- SIS model inference sensitive to movement model**

APPLICATION: MALARIA TRANSMISSION ON BIOKO ISLAND

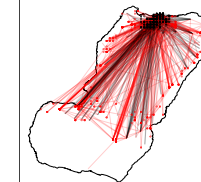
Bioiko Island, Equatorial Guinea



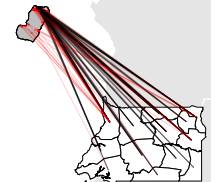
Estimated Malaria Prevalence



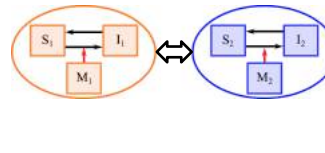
Within-Island Travel Data



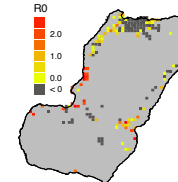
Off-Island Travel Data



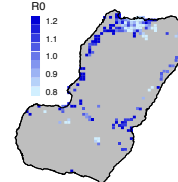
Spatially-Explicit Malaria Transmission Model



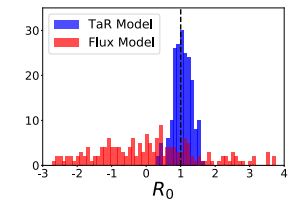
Flux Model R_0 Estimates



Time at Risk Model R_0 Estimates



R_0 Distribution Comparison



- Construct spatially-explicit transmission model describing malaria transmission on Bioiko Island, Equatorial Guinea
- Goal is to **estimate spatially heterogeneous transmission intensity in each area on the island**
- Calibrate movement model(s) to **travel survey data**
- Calibrate transmission model(s) to **estimates of malaria prevalence**
- Find realistic R_0 estimates using the Time at Risk movement model; unrealistic R_0 estimates using the Flux movement model

REFERENCES

- Cosner, C., et al. (2009). The effects of human movement on the persistence of vector-borne diseases. *J. of Theo. Bio.*, 258(4), 550-560
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- Guerra, C.A.G., et al. (2019). Human Mobility Patterns and Malaria Importation on Bioko Island. *Nature Communications*, (in press)

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