

Project Proposal: Exploring Temperature Effects on Mosquito Biting Rate with MCMC

Yusi Yao

Rahul Rengan Ramakrishnan

Mar 27, 2025

Scientific Paper

“Understanding uncertainty in temperature effects on vector-borne disease: a Bayesian approach” by Leah R. Johnson et al. (2015). **Link to Paper:** <https://doi.org/10.1098/rsif.2014.1038>

Description of the Study

This study investigates how temperature influences malaria transmission through the basic reproductive number, R_0 , which measures disease spread potential. The paper decomposes R_0 into components such as mosquito biting rate, egg-laying rate, and lifespan, modeling their temperature-dependent responses. Using a Bayesian framework, the authors employ Markov Chain Monte Carlo (MCMC) to sample posterior distributions of model parameters, quantifying uncertainty in how temperature affects malaria transmission. The analysis highlights temperature thresholds where transmission either ceases (too cold) or diminishes (too hot), providing insights into vector-borne disease dynamics.

Project Goals

For this stochastic simulation project, we will focus on the mosquito biting rate, $a(T)$, a temperature-dependent component of R_0 identified as critical, particularly at lower temperatures. Our goal is to develop a custom MCMC algorithm to estimate the posterior distributions of the parameters in the Brière function used to model $a(T)$, capturing uncertainty in how temperature affects mosquito biting behavior.

By isolating this component, we aim to understand the range of likely biting rates across different temperatures and assess how sensitive the function is to parameter variation. This focused scope keeps the project computationally feasible while still contributing meaningful insight into vector-borne disease modeling under climate variability.

- **Component Selection:** Target $a(T)$, the biting rate, due to its significance and feasibility for analysis. Among the components of R_0 , $a(T)$ is particularly influential at lower temperatures where transmission thresholds are most sensitive. This makes it a strong candidate for isolated study within a manageable simulation scope.
- **Model Specification:** Use the Brière function, $a(T) = cT(T - T_0)(T_m - T)^{1/2}$, with parameters c (scaling factor), T_0 (minimum temperature), and T_m (maximum temperature) to be estimated. This form captures the unimodal, asymmetrical shape observed in temperature-dependent biological traits, with clear biological interpretations for each parameter.

- **Likelihood:** Assume a truncated normal distribution for observed biting rates, reflecting their non-negative nature, and compare these to Brière function predictions. This choice accommodates natural variability in observations while enforcing realistic bounds, ensuring biologically plausible model behavior.
- **Priors:** Start with simple uniform priors (e.g., $T_0 \in [0, 20]$, $T_m \in [30, 50]$, $c > 0$) to reflect plausible biological ranges without imposing strong assumptions. These priors can be adapted based on preliminary simulation results or literature-reported values if necessary.
- **MCMC Implementation:** Code a Metropolis-Hastings algorithm to sample posteriors for c , T_0 , and T_m , building it from scratch. Proposal distributions will be tuned manually, and diagnostics such as trace plots and acceptance rates will be used to evaluate convergence and mixing quality.
- **Output:** Generate plots of $a(T)$ across temperatures, showing mean estimates and uncertainty intervals from the posterior samples. These visualizations will help identify the range of likely biting rates at different temperatures and quantify uncertainty around critical thresholds.

This scope keeps the project manageable, with potential expansion to explore $a(T)$'s impact on R_0 if time allows.

Data and Code

- **Data:** Biting rate data presumably are available through the VectorByte project or supplementary materials from the original study. As these data have been previously published, we assume they are accessible for academic use, but we will confirm data availability and any usage restrictions prior to download. If the original dataset is unavailable, we will either locate a comparable published dataset or generate synthetic data consistent with the paper's assumptions for validation purposes.
- **Code:** We will write the MCMC algorithm entirely from scratch without relying on pre-built packages such as `rstan` or `PyMC`. The core Metropolis-Hastings logic—including proposal generation, acceptance criteria, and sampling—will be implemented manually to demonstrate a full understanding of the algorithm's mechanics and flexibility in modifying it as needed.

Additional Details

Given the project's timeline, we will begin with a basic MCMC setup (e.g., 10,000 iterations with a single chain) and increase complexity based on performance. Diagnostics such as trace plots, acceptance rates, and posterior summaries will be used to evaluate convergence and guide tuning of the proposal distributions. We will also explore the impact of initial values and step sizes on the stability of the chain. If convergence issues arise, we will apply adjustments informed by course materials and external resources. All simulations and plots will be reproducible and well-documented in a single, annotated script.