Spatial Clustering of Aedes Aegypti in Coastal Ecuador: Covariate Selection and a Hierarchical Bayesian Model

Group 2

MBI at Ohio State University

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Background

- Dengue is a viral infection caused by any of 4 viruses transmitted mostly by the adult female Aedes aegypti mosquito bites.
- As there are no commercial vaccines available for Dengue, the primary method of control is the management of the Aedes aegypti mosquito.
- Disease management requires finding out the spatial patterns of the mosquito and analysing the specific factors that causes this kind of pattern.
Questions of Interest

- Can the spatial clustering of adult female Aedes aegypti mosquitoes be completely explained by characteristics of the neighboring homes?

- What covariates can help explain the variability in the cluster pattern?

- Is there a maximum radius around a house to where the presence of a mosquito has no effect?
Data

The city of Borbón spans a geographic area of 1.3 sq km with 5,000 residents living in 1,175 houses. 199 sampled houses.
Model Introduction

\[
Y(s_i) = \begin{cases} 
1 & \text{if at least 1 mosquito at } s_i \\
0 & \text{otherwise} 
\end{cases}
\]

- If we were to assume independence between spatial locations, we can define \( Y(s_i)^{ind} \sim \text{bernoulli}(p_i) \quad i = 1, 2, \ldots n \)

and use logistic model

\[
\log\left(\frac{p_i}{1 - p_i}\right) = X_i \beta
\]

with some covariates \( X_i \)
But, we know we have spatial dependency! Then we can define \( Y(s_i)|w(s_i) \overset{ind}{\sim} \text{Bernoulli}(p_i) \), and

\[
\log\left( \frac{p_i}{1 - p_i} \right) = X_i \beta^* + w(s_i)
\]

where \( w(s_i) \overset{ind}{\sim} \text{MVN}(0, \Sigma_w(\theta)) \) is a spatial process with covariance structure \( \Sigma_w(\theta) \).

Note: The interpretation of \( \beta^* \) differs from \( \beta \) since our interest is in \( Y(s_i)|w(s_i) \).
Defining Covariates

Characteristics by Grid Cell
Defining Covariates

How can we define covariates in our logistic model?

- number of houses within each grid cell (density)
- proportion of houses with mosquitos among sampled houses in each cell
- proportion of houses with mosquitos among all houses
- minimum distance to a house with mosquitos
- number of houses with mosquitos within a radius $k$
Bayesian Hierarchical Models

1. **Data Model** \( Y(s_i) | w(s_i) \overset{ind}{\sim} \text{bernoulli}(p_i) \)

   \[
   \log\left( \frac{p_i}{1-p_i} \right) = X_i \beta^* + w(s_i)
   \]

2. **Process Model** \( w(s_i) \overset{ind}{\sim} \text{MVN}(0, \Sigma_w(\theta)) \), \( \Sigma_w = \sigma^2 \exp(-\phi h) \)
   (exponential covariance structure)

3. **Parameter Model**

   \( \beta^* \sim \text{Normal}(0, \Sigma_{\beta}) \), \( \sigma^2 \sim \text{Inverse Gaussian}(a_\sigma, b_\sigma) \), \( \phi \sim \text{Uniform}(a_\phi, b_\phi) \).
Results

Ignoring the spatial dependence

\[ \log\left( \frac{p_i}{1 - p_i} \right) = \beta_0 + \beta_1 \times \text{density} \]
Ignoring Spatial Dependence

\[ \log\left(\frac{p_i}{1 - p_i}\right) = \beta_0 + \beta_1 \times \text{density} \]
Results (Bayesian Hierarchical Model)

Model 0: Assume there is no other predictors, i.e., $X\beta^*$ just represents the intercepts.

$$\hat{\beta}_0^* = -1.41(-1.76, -1.04),$$
$$\hat{\sigma}^2 = 0.37(0.13, 0.99), \quad \hat{\phi} = 2.07(0.66, 4.72)$$
Model 1: Model with the predictor “minimum distance to a house with mosquitos”.

\[
\hat{\beta}_0^* = -1.20 (-1.81, -0.66), \quad \hat{\beta}_1^* = -0.003 (-0.012, 0.005)
\]
\[
\hat{\sigma}^2 = 0.40 (0.16, 1.36), \quad \hat{\phi} = 0.88 (0.17, 3.33)
\]
Results (Bayesian Hierarchical Model)

Model 2: Model with the predictor “proportion of houses with mosquitos among sampled houses in each cell”.

\[ \hat{\beta}_0^* = -1.82(-2.88, -0.92), \quad \hat{\beta}_1^* = 2.64(-1.92, 7.68), \]
\[ \hat{\sigma}^2 = 0.50(0.18, 1.9), \quad \hat{\phi} = 2.60(0.39, 4.7) \]