Spatial-Temporal Statistics for Studying Mountain Pine Beetle Infestation of Pine Forests in Western Canada

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Joint work with
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Outline

1 Background: Mountain Pine Beetle
2 Data: Explore Spatial-Temporal Patterns
3 Regression: Link Patterns to Processes
4 GLMM: Incorporate Population Dynamics
5 Concluding Remarks

Mountain Pine Beetle

Mountain pine beetle (MPB) *Dendroctonus ponderosae* Hopkins.
- Native to western North America.
- An eruptive species of bark beetle.
- Launches pheromone-mediated mass attacks on pine trees.
- Reproduces within the stems of mature trees.
- Erupts into immense populations that kill otherwise healthy hosts over large regions.
- The predominant host is lodgepole pine; other species are ponderosa pine, western white pine, and jack pine.
Mountain Pine Beetle Outbreaks

- The northwestern part of North America experienced 4–5 major MPB outbreaks in the past century.
- An enormous outbreak took place in the past decade in the mature lodgepole pine forest of the provinces of Alberta and British Columbia, Canada.
- Exacerbated by factors such as an abundance of susceptible pine and a changing climate.
- Breached a historic geoclimatic barrier of the Rocky Mountains into northwestern Alberta in the past five years.

Mountain Pine Beetle Outbreak 1990–2003

- Study region: British Columbia, Canada
  - Southern provincial border (49°N)
  - North of Fort St. John (57°N).
  - Eastern provincial border (122°W Rocky Mountains).
  - Western provincial border (130°W Coastal Mountains).
- Total area: 53,392,412 ha.
- Time periods: 1990–1996 (incipient years) and 1999–2003 (epidemic years).
- Annual aerial survey data on a grid of 12 × 12 km cells.
- Corrected for survey bias and converted to mortality rates from categorical data.

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Research Goals

1. Investigate the spatial pattern of outbreak development.
   - Do the data suggest that the outbreak has originated from a single specific origin or multiple, coalescing point sources?
   - Are outbreak locations associated more with parks and protected lands which are areas of little to no historical management for eruptive insects (or, conservation areas)?

2. Examine the population synchrony among the buildup and the subsequent outbreak years.
   - Does population synchrony decline with distance?
   - At what distance are population fluctuations independent?
   - Does population synchrony vary by direction?

Statistical Analysis

Cluster analysis and regression.
- Compare the time series of mortality rates across space.
- Group the cells into $k$ clusters based on similarity of time-series patterns.
- Non-hierarchical algorithms (k-means and nonmetric multidimensional scaling).
- Hierarchical algorithms give similar results.
- Regression to evaluate association with conservation areas.
- Straightforward to implement, but the models are aspatial.

Spatial synchrony analysis.
- Fit by smoothed nonparametric covariance functions.
- Construct confidence intervals for the covariance function by bootstrap.
- Examine possible anisotropy in the spatial covariance functions.
Outbreak Development

- The epidemic began to intensify first in an area of west-central BC.
  - Mortality started to increase in cluster I a full year ahead of the other clusters.
  - Mortality began to decline in cluster I by 2003 but not in the other clusters.
  - The spread appears to be eastward from cluster I into the other three clusters (e.g. the local Vanderhoof and Quesnel forest districts in cluster II).
- Cluster I contained more conservation lands (62.2%) than the other clusters (<20%).
- There were isolated, localized increases (checkerboard pattern) in the southern and eastern portions.

Population Synchrony

For both the incipient years and the epidemic years, the spatial synchrony declines with increasing distance.
- In the incipient years, the average synchrony across the study region was close to zero, indicating spatial asynchrony. Local correlation was 0.53 and decayed to zero at around 200 km.
- In the epidemic years, the average synchrony across the study region was 0.38. Local correlation was 0.71 and decayed to 0.38 at around 300 km.
- Directionality was not obvious in either time period.

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Mountain Pine Beetle Outbreak 1972–1986

- Study region: Chilcotin Plateau in British Columbia, Canada
- Total area is 7,191,199 ha with an average elevation of 1,345 m.
- Annual aerial survey data on a grid of 12 × 12 km cells.
- Corrected for survey bias and converted to presence/absence of MPB colonization.

Research Goals

- To identify environmental factors that are associated with MPB outbreak.
  - Topographic variables: Digital elevation map (DEM).
  - Temperature variables: Reflect the ecology (phenology and development) of MPB.
    - Minimum, mean, and maximum temp.
    - Cold: Number of days below -40°C.
    - Warm: Mean August temp.
    - Degree days.
    - Whether sufficient heat accumulation for hatching and flight.
  - Precipitation.
- To provide strategies for management and control of MPB.
  - Develop control methods.
  - Develop landscape level predictive models.
  - Build a general class of landscape models and identify the most appropriate components of the general model.

Climatic and Environmental Variables

<table>
<thead>
<tr>
<th>Variable type</th>
<th>Variable</th>
<th>Explanation and rationale</th>
</tr>
</thead>
<tbody>
<tr>
<td>Temporal</td>
<td>lag 1</td>
<td>Presence/absence of mountain pine beetle in a cell the previous year</td>
</tr>
<tr>
<td></td>
<td>lag 2</td>
<td>Same, two years previous</td>
</tr>
<tr>
<td></td>
<td>lag 3</td>
<td>Same, three years previous</td>
</tr>
<tr>
<td>Spatial</td>
<td>1st nbhd</td>
<td>First order neighborhood (sometimes termed “Rook’s case”)</td>
</tr>
<tr>
<td></td>
<td>2nd nbhd</td>
<td>Second order neighborhood (sometimes termed “Queen’s case”)</td>
</tr>
<tr>
<td></td>
<td>infestations</td>
<td>Number of discrete infestations in each cell. This differs from the response variable, the presence/absence of red attack in each cell.</td>
</tr>
<tr>
<td>Environmental</td>
<td>tmin</td>
<td>Minimum temperature over calendar year</td>
</tr>
<tr>
<td></td>
<td>tmax</td>
<td>Maximum temperature over calendar year</td>
</tr>
<tr>
<td></td>
<td>tmean</td>
<td>Mean temperature over calendar year</td>
</tr>
<tr>
<td></td>
<td>cold</td>
<td>Number of days below -40°C. Complete mortality occurs when larvae are exposed to these temperatures for short periods (Wygant 1940, Somme 1964).</td>
</tr>
<tr>
<td></td>
<td>warm</td>
<td>Mean August temperature. Development and emergence of new mountain pine beetle adults is closely governed by temperature. Peak flight occurs in a narrow window in summer.</td>
</tr>
<tr>
<td></td>
<td>ddeg</td>
<td>Accumulated degree days above 5.5°C from August to end of growing season</td>
</tr>
<tr>
<td></td>
<td>dd</td>
<td>Accumulated degree days above 5.5°C from August in previous year to current July</td>
</tr>
<tr>
<td></td>
<td>P1a</td>
<td>0/1 indicator variable: sufficient heat accumulation to hatch 50% of eggs before winter (306°C degree days).</td>
</tr>
<tr>
<td></td>
<td>P2a</td>
<td>0/1 indicator variable: if minimum winter temperatures were higher than -40°C</td>
</tr>
<tr>
<td></td>
<td>P3a</td>
<td>0/1 indicator variable: sufficient heat accumulation to develop to next flight (833°C degree days).</td>
</tr>
<tr>
<td></td>
<td>elevation</td>
<td>Mean elevation of cell, based on 25 sampled points (regular design) within cell. This may be a useful proxy for host tree distribution, as lodgepole pine do not grow at high elevations over our study area.</td>
</tr>
</tbody>
</table>

Table 1: Candidate variables for autologistic regressions examining the probability of an outbreaking population of mountain pine beetle in a 12×12 km cell on the Chilcotin Plateau of British Columbia, 1972-1986.

These variables were derived from pioneering work by Safranyik et al. (Safranyik et al. 1975).
Notation

- Let \( s_i \) (\( i = 1, \ldots, I \)) denote the representative sites on a spatial lattice.
  - Pixel center.
  - County seat.
- Let \( N_i \equiv \{ j : s_j \text{ is a neighbor of } s_i \} \) denote a neighborhood structure.
  - First-order, diagonal, and second-order neighbors.
  - County seats within a certain distance.
  - Let \( j \sim i \) if \( j \in N_i \).
- Time points \( t = 1, \ldots, T \).
- Let \( Y_{i,t} \) denote the binary response variables at the \( i \)th site and the \( t \)th year, where \( Y_{i,t} \equiv Y(s_i, t) = 0 \) or 1.
- Let \( X_{k,i,t} = X_k(s_i, t) \) denote the \( k \)th covariate (\( k = 1, \ldots, K \)) and \( X_{0,i,t} = 1 \).
- Let \( Y_i \equiv (Y_{1,t}, \ldots, Y_{I,t})' \) denote the binary responses at all sites and the \( t \)th year.

Model Specification

- The conditional distribution of \( Y_{t} \) given the past depends on the most recent \( S \) time points \( t−1, \ldots, t−S \):
  \[
  p(Y_{t} | Y_{t'} : t' = t−1, t−2, \ldots) = p(Y_{t} | Y_{t'} : t' = t−1, \ldots, t−S)
  \]
  for \( t = S+1, \ldots, T \).
- For a given time point \( t \), the response variable \( Y_{i,t} \) follows a MRF under a preselected spatial neighborhood structure:
  \[
  p(Y_{i,t} | Y_{t'} : j \neq i, Y_{t'} : t' = t−1, \ldots, t−S) = p(Y_{i,t} | Y_{t'} : j \in N_i, Y_{t'} : t' = t−1, \ldots, t−S)
  \]
  where \( N_i \) consists of the indexes of the neighbors of the \( i \)th site.

Neighborhood Structure

- On a regular grid, the neighbors of the \( i \)th site can be ordered according to their distance to the \( i \)th site.

Conditional Logistic Regression

- Model the conditional distribution of \( Y_{i,t} \) by Bernoulli:
  \[
  [Y_{i,t} | Y_{t'} : j \in N_i, Y_{t'} : t' = t−1, \ldots, t−S] \sim \text{Bernoulli}(\pi_{i,t}).
  \]
- Consider a logit link function for the conditional probability of outbreak \( \pi_{i,t} \):
  \[
  \logit(\pi_{i,t}) = \sum_{k=0}^{K} \theta_{k} X_{k,i,t} + \frac{1}{2} \sum_{l=1}^{L} \theta_{K+l} \sum_{j \in N_{i}^{(l)}} Y_{j,t} + \sum_{s=1}^{S} \theta_{K+L+s} Y_{i,t-s}.
  \]
Data Analysis of MPB Outbreak

- Spatial-temporal autologistic models.
  - Maximum pseudo-likelihood estimation.
  - Monte Carlo maximum likelihood.
  - Bayesian hierarchical modeling.
- Model selection:
  - Determine an appropriate spatial-temporal dependence structure.
  - Select covariates using a stepwise procedure.

Model Selection

Table: AIC for the first-order and second-order neighborhood combined with up to one-year, two-year, and three-year time lags.

<table>
<thead>
<tr>
<th>Neighborhood</th>
<th>Without covariates</th>
<th>With covariates</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Temporal lag</td>
<td>Temporal lag</td>
</tr>
<tr>
<td></td>
<td>1 year</td>
<td>1-2 years</td>
</tr>
<tr>
<td>First order</td>
<td>3357.79</td>
<td>3260.47</td>
</tr>
<tr>
<td>First and second</td>
<td>3367.85</td>
<td>3309.89</td>
</tr>
</tbody>
</table>

Parameter Estimation

Table: Monte Carlo MLE and standard errors (SE) based on the model with one- and two-year time lags, and first-order neighborhood.

<table>
<thead>
<tr>
<th>Term</th>
<th>Parameter</th>
<th>MLE</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>$\theta_0$</td>
<td>-3.35</td>
<td>0.21</td>
</tr>
<tr>
<td>$X_1$ Cold days</td>
<td>$\theta_1$</td>
<td>-0.013</td>
<td>0.0071</td>
</tr>
<tr>
<td>$X_2$ August temp</td>
<td>$\theta_2$</td>
<td>0.019</td>
<td>0.0071</td>
</tr>
<tr>
<td>$X_3$ Elevation</td>
<td>$\theta_3$</td>
<td>-0.00020</td>
<td>0.000072</td>
</tr>
<tr>
<td>Spatial</td>
<td>$\theta_4$</td>
<td>1.45</td>
<td>0.38</td>
</tr>
<tr>
<td>Temporal 1-year lag</td>
<td>$\theta_5$</td>
<td>0.75</td>
<td>0.072</td>
</tr>
<tr>
<td>Temporal 2-year lag</td>
<td>$\theta_6$</td>
<td>0.47</td>
<td>0.080</td>
</tr>
</tbody>
</table>

Prediction

Maps of the predicted risk (i.e. probability) of MPB outbreak in 1985 and 1986.
- Along with maps of the corresponding standard error of the predicted risk.
- The prediction error rates are 0.29 and 0.56 for 1985 and 1986, respectively.
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**Alternative Modeling Approaches**

- Consider generalized linear mixed models (GLMM) with spatial-temporal random effects.
- Spatial-temporal GLMM is a flexible alternative to spatial-temporal autologistic models.
  - Develop spatial-temporal GLMM for spatial-temporal binary responses.
  - Embed population dynamic models in the latent process.
  - Capture complicated spatial and temporal dependence and interactions.
  - A three-stage Bayesian hierarchical framework.

\[
\text{[Process, Parameters|Data]} \propto \text{[Data|Process, Parameters]} \\
\quad \times \text{[Process|Parameters]} \\
\quad \times \text{[Parameters]}
\]

---

**Data Model**

- Let \( \pi_{i,t} \) denote the probability of outbreak in the \( i \)th cell and at the \( t \)th time point.
- Let \( \pi_t = (\pi_{1,t}, \ldots, \pi_{I,t})' \).
- Conditional on the spatial-temporal process \( \{\pi_t : t = 1, \ldots, T\} \), for \( i = 1, \ldots, I \) and \( t = 1, \ldots, T \), let
  \[
  [Y_{i,t}|\pi_{i,t}] \sim \text{Bernoulli}(\pi_{i,t})
  \]
  follow a Bernoulli distribution.
- Assume that \( Y_{i,t}'s \) are conditionally independent across space and over time.

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**Process Model**

- Under a logit link function, let
  \[
  \text{logit}(\pi_t) = \sum_{k=0}^{K} \theta_k X_{k,t} + u_t + \epsilon_t,
  \]
  follow a linear mixed model.
- \( \sum_{k=0}^{K} \theta_k X_{k,t} \) denotes a regression on the covariates
  \( X_{k,t} = (X_{k,1,t}, \ldots, X_{k,I,t})' \).
- \( u_t = (u_{1,t}, \ldots, u_{I,t})' \) denotes a latent process (or, random effects) explaining the remainder spatial-temporal variation after regression and reflecting dispersal.
- \( \epsilon_t = (\epsilon_{1,t}, \ldots, \epsilon_{I,t})' \) denotes an error process that accounts for any measurement error and is assumed to be independent across space and over time with
  \[
  [\epsilon_t] \sim \text{Normal}(0, \sigma^2 \epsilon I).
  \]
To feature spatial and temporal dependence, impose a spatial dynamic model on $u_t$:

$$u_t = Hu_{t-1} + \eta_t,$$

for $t = 1, \ldots, T$.

- $H$ is a transition matrix and controls the dynamics of $u_t$.
- Let $u_t$ start at at $u_0$ with

$$u_0 \sim \text{Normal}(\mu_0, \Sigma_0),$$

where $\mu_0 = 0$ and $\Sigma_0 = \sigma_0^2 I$ for some large $\sigma_0^2$.

- $\eta_t = (\eta_{1,t}, \ldots, \eta_{l,t})'$ models the small-scale variation and is assumed to be independent across space and over time, but can be extended to have a spatial covariance structure.

### Latent Process $u_t$

- Model insect dispersal by partial differential equations (PDE) such as diffusion and advective transport.

- Consider a diffusion-convection equation for the parametrization of $H$:

$$\frac{\partial u}{\partial t} = D \left( \frac{\partial^2 u}{\partial x^2} + \frac{\partial^2 u}{\partial y^2} \right) - w_x \frac{\partial u}{\partial x} - w_y \frac{\partial u}{\partial y}. $$

- $D$ is a diffusion coefficient representing the rate of diffusion.

- $w_x$ and $w_y$ are convection coefficients representing convection rates in the $x$ and $y$ directions.

- The dispersal of insects is thus a combination of random motion (diffusion) and directed motion (convexion or advection).

- Convection occurs when, for example, insects orient toward external stimuli or are carried by the wind.

- The magnitudes of the coefficients identify the relative strengths for the two processes.

### Compute the numerical solution to the PDEs by a first-order forward finite differencing in time:

$$\frac{\partial u}{\partial t} = \frac{u_t(x, y) - u_{t-\Delta t}(x, y)}{\Delta t},$$

and also apply centered differences in space:

$$\frac{\partial u}{\partial x} = \frac{u_t(x + \Delta x, y) - u_t(x - \Delta x, y)}{2\Delta x},$$

$$\frac{\partial u}{\partial y} = \frac{u_t(x, y + \Delta y) - u_t(x, y - \Delta y)}{2\Delta y},$$

$$\frac{\partial^2 u}{\partial x^2} = \frac{u_t(x + \Delta x, y) - 2u_t(x, y) + u_t(x - \Delta x, y)}{\Delta_x^2},$$

$$\frac{\partial^2 u}{\partial y^2} = \frac{u_t(x, y + \Delta y) - 2u_t(x, y) + u_t(x, y - \Delta y)}{\Delta_y^2},$$

where centered differences are valid for any time $t$.

Thus,

$$u_t(x, y) = u_{t-\Delta t}(x, y) \left\{ 1 - 2D \left( \frac{\Delta_t}{\Delta_x^2} + \frac{\Delta_t}{\Delta_y^2} \right) \right\} + u_{t-\Delta t}(x + \Delta x, y) \left( -w_x \frac{\Delta_t}{2\Delta_x} + D \frac{\Delta_t}{\Delta_x^2} \right) + u_{t-\Delta t}(x, y - \Delta y) \left( w_y \frac{\Delta_t}{2\Delta_y} + D \frac{\Delta_t}{\Delta_y^2} \right) + u_{t-\Delta t}(x, y + \Delta y) \left( -w_y \frac{\Delta_t}{2\Delta_y} + D \frac{\Delta_t}{\Delta_y^2} \right) + \eta_t(x, y).$$

Assume unit spatial/temporal increment: $\Delta x = \Delta y = \Delta t = 1$.

Assume that $u_t(x, y) = 0$ if cell $(x, y)$ is not in the study domain.

Thus,

$$u_t = H(D, w_x, w_y)u_{t-1} + \eta_t.$$
Bayesian Inference

- For statistical inference, use Bayesian hierarchical modeling.
- The posterior distribution is
  \[ p(\pi_1, \ldots, \pi_i, u_0, \ldots, u_T, \sigma_0^2, D, w_x, w_y, \sigma_2^2 | Y_1, \ldots, Y_T) \]
  \[ \propto \left\{ \prod_{t=1}^{T} p(Y_t | \pi_t) p(\pi_t | \theta, u_t, \sigma_1^2) \right\} \left\{ \prod_{t=1}^{T} p(u_t | u_{t-1}, D, w_x, w_y, \sigma_0^2) p(u_0) \right\} \]
  \[ \times p(\theta) p(D) p(w_x) p(w_y) p(\sigma_1^2) p(\sigma_2^2), \]

  where \( \theta = (\theta_0, \ldots, \theta_K)' \).

- Conjugate normal priors for \( \theta, D, w_x \) and \( w_y \) and conjugate inverse-gamma priors for \( \sigma_1^2 \) and \( \sigma_2^2 \).

- To sample from the posterior, use a Gibbs sampler and update the parameters component-wise.

- Transform \( \pi_i,t \) to \( \nu_i,t = \logit(\pi_i,t) \) for \( i = 1, \ldots, l \) and \( t = 1, \ldots, T \), and sample from a full conditional by Metropolis-Hastings (MH).

- Transform \( \nu_i,t \) back to \( \pi_i,t = \exp(\nu_i,t)/(1 + \exp(\nu_i,t)) \).

- Sample the latent process \( u_t \) with \( t = 0, \ldots, T \) and the model parameters from full conditionals directly.

Parameter Estimation

- Let \( Y = (Y'_1, \ldots, Y'_T)' \).
- For prediction at future time points \( T + 1, \ldots, T + \Delta T \), consider the posterior predictive distribution:
  \[ p(Y_{T+1}, \ldots, Y_{T+\Delta T} | Y) \]
  \[ = \int \left( \prod_{\Delta t=1}^{\Delta T} p(Y_{T+\Delta t} | \pi_{T+\Delta t}) \right) p(\pi_{T+1}, \ldots, \pi_{T+\Delta T} | Y) d\pi_{T+1} \cdots d\pi_{T+\Delta T} \]

  To sample from the posterior prediction distribution, first sample \( u_T, \theta, D, w_x, w_y, \sigma_0^2, \) and \( \sigma_2^2 \) from their posteriors and then sample \( u_{T+1}, \ldots, u_{T+\Delta T} \) in turn according to transition probabilities.

- Let \( \nu_{i,T+\Delta t} = \logit(\pi_{i,T+\Delta t}) \) for \( i = 1, \ldots, l \) and \( \Delta t = 1, \ldots, \Delta T \).

- Sample \( \nu_{T+\Delta t} \) from \( p(\nu_{T+\Delta t} | \theta, u_{T+\Delta t}, \sigma_2^2) \) and let \( \pi_{i,T+\Delta t} = \exp(\nu_{i,T+\Delta t})/(1 + \exp(\nu_{i,T+\Delta t})) \).

- Last, sample \( Y_{i,T+\Delta t} \) from the conditional distribution \( p(Y_{i,T+\Delta t} | \pi_{i,T+\Delta t}) \).

### Dana Analysis of MPB Outbreak

- Noninformative priors.
- MCMC: 20,000 iterations with a burn-in length of 2,000.

### Parameter Estimation

<table>
<thead>
<tr>
<th>Term</th>
<th>Parameter</th>
<th>GLMM</th>
<th>Autologistic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>( \theta_0 )</td>
<td>3.639 (3.003, 3.887)</td>
<td>-3.35 (-3.76, -2.94)</td>
</tr>
<tr>
<td>X1 Cold days</td>
<td>( \theta_1 )</td>
<td>-0.002 (-0.006, 0.001)</td>
<td>-0.013 (-0.027, 0.001)</td>
</tr>
<tr>
<td>X2 August temp</td>
<td>( \theta_2 )</td>
<td>-0.025 (-0.036, -0.005)</td>
<td>0.019 (0.006, 0.033)</td>
</tr>
<tr>
<td>X3 Elevation</td>
<td>( \theta_3 )</td>
<td>-0.0012 (-0.0013, -0.0010)</td>
<td>-0.0002 (-0.0003, -0.0001)</td>
</tr>
<tr>
<td>Diffusion</td>
<td>( D )</td>
<td>0.183 (0.177, 0.190)</td>
<td>0.019 (0.006, 0.033)</td>
</tr>
<tr>
<td>Convection</td>
<td>( w_x )</td>
<td>-0.068 (-0.100, -0.031)</td>
<td>-0.013 (-0.027, 0.001)</td>
</tr>
<tr>
<td>Convection</td>
<td>( w_y )</td>
<td>0.076 (0.045, 0.100)</td>
<td>0.019 (0.006, 0.033)</td>
</tr>
<tr>
<td>Spatial</td>
<td></td>
<td>1.45 (0.71, 2.19)</td>
<td>0.47 (0.31, 0.63)</td>
</tr>
<tr>
<td>Temporal 1-yr</td>
<td></td>
<td>0.75 (0.61, 0.89)</td>
<td>0.47 (0.31, 0.63)</td>
</tr>
<tr>
<td>Temporal 2-yr</td>
<td></td>
<td>0.47 (0.31, 0.63)</td>
<td>0.47 (0.31, 0.63)</td>
</tr>
</tbody>
</table>
Maps of the predicted risk of MPB outbreak in 1985 and 1986. The prediction error rates are 0.30 and 0.54 for 1985 and 1986, respectively.
I would like to thank...

**Collaborators**
- Dr. Brian Aukema, University of Minnesota
- Dr. Allan Carroll, University of British Columbia
- Dr. Perla Reyes, University of California
- Dr. Kishan Sambaraju, Canadian Forest Service
- Dr. Yanbing Zheng, University of Kentucky

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- United States Department of Agriculture CSREES

**References**
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- Aukema et al. (2006, 2008)
- Reyes et al. (2011+)
- Sambarju et al. (2011+)
- Zheng and Aukema (2010)
- Zhu et al. (2008, 2010)
- ...and the references therein.

Thank you / Merci!