Spatial Modeling of Whitebark Pine in Three Rocky Mountain Ecosystems
FEScUE Program, Summer 2009

Whitebark Pine
- Whitebark pine (Pinus albicaulis) is a keystone subalpine species of the family Pinaceae, subgenus Strobus.

White Pine Blister Rust?
- Pathogen: Cronartium ribicola
- Originated in Asia, infected seedlings were shipped over
- Infection spread across the Northern Rocky Mountain region
- Kills cone-bearing branches and trees
- Mortality reaches 90% or higher
- Rust-resistant alleles: 1 to 5%
- Main areas of interest: Bitterroot Mountain Ecosystem, the Northern Divide, the Greater Yellowstone Ecosystem

Symptoms
- Initially yellow spots on needles
- Yellow to orange swellings on branches and trunk
- Rupture and produce orange-yellow spores
- Symptoms appear in late summer, early fall
- Swellings rupture in early or mid spring and disappear until the next year

What and Why in WPBR?
- WPBR affects mutualism between the Clark’s Nutcracker and the White Pine
- How does density affect WPBR?
- What are the effects of genetics?
- What would a model based on individuals look like?
- What is the variance?
- Does restoration really make a big enough difference?

Our plan of action... ABMs
ABM: Agent Based Models
Tracks specific trees through time
See total population structure as a result.

3 existing models.
1 working with genetics
1 ‘in the shop’ with genetics and density
1 working with genetics, dd, Visio-spatial
Why ABMs?

**Pros**
- Statistical approach
- Gives multiple samples
- Motivates more questions
- Cooler graphs

**Cons**
- Takes time to run
- Not as intuitive as good ol’ Leslie
- Harder to code
- Hard to debug

S&D: How it works

- Tracking the first seedling

<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
<th>Probability</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1st seedling</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>2nd seedling</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Seedling</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>Young Adult</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>Mature Adult</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>Infection</td>
<td></td>
</tr>
</tbody>
</table>

S&D: How it works

- Tracking event
  - Survives?
  - Grows?
  - Becomes infected?
  - Probabilities derived from SUT’s data
  - Independent events: 
    \[ P(A \cap B) = P(A)P(B) \]

S&D: How it works

- Let’s do this for an entire forest!
  Luckily, Matlab has 3D matrices

S&D: How it works

Bringin’ it all back Home,
We sum the z components...

<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1st seedling</td>
<td>81</td>
</tr>
<tr>
<td>2</td>
<td>2nd seedling</td>
<td>70</td>
</tr>
<tr>
<td>3</td>
<td>Seedling</td>
<td>66</td>
</tr>
<tr>
<td>4</td>
<td>Young Adult</td>
<td>99</td>
</tr>
<tr>
<td>5</td>
<td>Mature Adult</td>
<td>197</td>
</tr>
<tr>
<td>6</td>
<td>Infection</td>
<td>0</td>
</tr>
<tr>
<td>7</td>
<td>Infected Seedling</td>
<td>0</td>
</tr>
<tr>
<td>8</td>
<td>Grows</td>
<td>3</td>
</tr>
<tr>
<td>9</td>
<td>Dies</td>
<td>4</td>
</tr>
<tr>
<td>10</td>
<td>Infected Young Adult</td>
<td>3</td>
</tr>
<tr>
<td>11</td>
<td>Infected Mature Adult</td>
<td>2</td>
</tr>
</tbody>
</table>

S&D: the Results

- Graph showing model outcomes
• Why incorporate genetics?
  – to monitor resistance in the population
  – to see the effects of infection on resistance
  – vice versa

The How

Made one 36x36 projection matrix with a 12x12 portion for each genotype.

Altered the projection matrix for resistance triplicate condense multiply By M

Similarly changed the state vector to a 36x1

Allele Frequency

Spatially Explicit Modeling

• A 1-ha square within a research site

Whitebark Pine Range

• Multiple research sites were established within three distinct ecosystems in the Central and Northern Rocky Mountains, USA:
  – The Northern Divide Ecosystem in northwestern Montana
  – The Bitterroot Mountain Ecosystem in west-central Montana and east-central Idaho
  – The Greater Yellowstone Ecosystem in southwestern Montana and northwestern Wyoming

The Northern Divide Ecosystem

• Among ecosystems, cone production and nutcracker occurrence were lowest in the Northern Divide.
• Nutcrackers failed to be observed in 80% of the Northern Divide site-years.
The Bitterroot Mountains Ecosystem

• Nutcrackers failed to be observed in 40% of site-years in the Bitterroot Mountains.

The Greater Yellowstone Ecosystem

• Among ecosystems, cone production and nutcracker occurrence were highest in the Greater Yellowstone.
• Nutcrackers were present and dispersing seeds in all years in the Greater Yellowstone Ecosystem.