

# Modeling the influence of beech bark disease on root sprout regeneration in hardwood forests of northeastern North America

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## THE PROBLEM

- Despite sustained elevated adult mortality<sup>1</sup>, reduced annual growth rate<sup>2</sup>, and models and empirical data predicting replacement by competitor species<sup>3,4</sup>, American beech (*Fagus grandifolia* Ehrl.) remains an important forest component 116 years since the introduction of the beech bark disease complex.
- Positive feedback between the disease and root sprout regeneration could resolve this apparent paradox, though this relationship has been historically difficult to test.

## HYPOTHESES AND FRAMEWORK:

- Beech bark disease promotes the growth and survival of root sprouts facilitating the persistence of beech, beech dominance in the mid- and understory, and a structural shift toward high densities of smaller stems of more uniform age.
- Spatial modeling of adult tree and sprout distribution within a stand allows for probabilistic assignment of sprouts and seedlings to present and past adult trees, facilitating fine-scale analysis of the role of disease in sprout production and demography.

## APPROACH

We began by adapting a seed rain model, which we found to be conceptually parallel to modeling root sprout regeneration in a closed canopy. Equations and parameter estimation procedures come from Clark *et al.*<sup>5</sup>

## MODEL AND THEORETICAL ASSUMPTIONS:

- Some function  $f(x)$  describes the shape of a "sprout shadow" around each adult beech
- The contribution of sprouts by a beech individual depends in part on its basal area
- The likelihood of a root sprout at a given point in the understory is the product of the probabilistic contributions of the all adults within a given distance

## TESTING HYPOTHESES

- Once constructed, we will compare all possible models using Bayesian Information Criteria values.
- A significant model containing a disease term will be interpreted as support for the hypothesized relationship between disease and sprout demographics

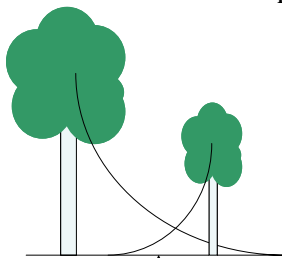


Fig. 1 – Theoretical "sprout shadow" of root sprouts around each adult beech

## SAMPLING DESIGN

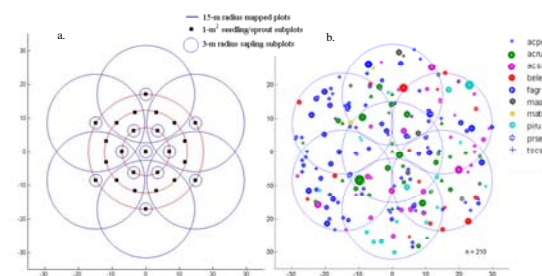


Fig. 2 – Plot design schematic (a); mapped site example, Monongahela N.F. (b)

- To date, we have revisited 8 of 30 plots historically monitored (1979-92) by Dave Houston and others for beech bark disease.
- Mapped all stems (>10cm dbh); measured regeneration and recruitment for all seedlings/sprouts and poles in systematically located subplots.
- Measured *Cryptococcus fagisuga* and *Neonectria* populations after Burns and Houston (1987)<sup>6</sup>, along with measures of bark defect, bole necrosis and tree vigor.

## MODEL FORM AND FUNCTION

$$\hat{s}(d_{ij}; b_i; \mathbf{p}) = \prod_{i=1}^{n \text{ trees}} b_i * \exp \left[ - \left( \frac{d_{ij}}{\alpha_i} \right)^c \right]$$

- $\hat{s}$  = "sprout shadow"
- $d_{ij}$  = distance matrix
- $b_i$  = basal area tree  $i$
- $\alpha_i$  = dispersion parameter of sprouts around tree  $i$
- $c$  = shape parameter (e.g.  $c=1$  exponential;  $c=2$  Gaussian)
- $\mathbf{p}$  = vector of fitted parameters (estimates  $\alpha_i$ )

- We used Maximum Likelihood Estimation to fit the mean dispersion parameter ( $\alpha$ ) for each tree, describing the probability of root sprouting as a function of distance.
- Future models will fit and compare distributions beyond the exponential and Gaussian functions tested to date.

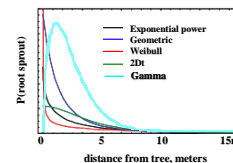


Fig. 3 – Potential sprout shadow distribution functions (adapted from Austerlitz *et al.*<sup>7</sup>)

## RESULTS AND DISCUSSION

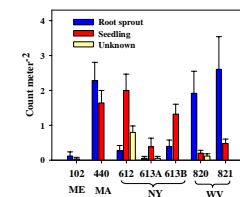


Fig. 4 – Root sprout and seedling densities at six historically monitored sites, 2005. Error bars represent SE.

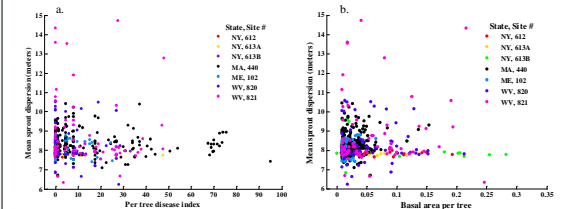


Fig. 5 – Estimated mean dispersion parameter ( $\alpha_i$ ) as a function of disease index (a) and basal area (b).

- Fitting the model using an exponential distribution yielded a mean dispersion of sprouts around each tree of  $8.62 \pm 0.82$  SD.
- Currently there is observable relationship between dispersion distance and basal area or disease index.

## NEXT STEPS

- Evaluate alternative probability distribution functions that may improve model fit.
- Directly incorporate disease indices; compare resulting models
- Estimate per tree sprout production and survival; calculate a "clumping" parameter ( $\theta$ ) to represent degree of spatial autocorrelation in sprout distribution

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