

**Supplemental materials for:**

**Title:** Inferring controls on the epidemiology of beech bark disease from spatial patterning of disease organisms

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**Journal:** Agricultural and Forest Entomology

**This PDF contains:**

Table S1

Figures S1-S3

Table S1. Description of numerical codes for quantifying scale insect and *Neonectria* level on living beech trees. All codes are derived from Houston *et al.*, 1979, adopted in part to facilitate comparison between current and past infestation levels in historically monitored plots (Garnas *et al.*, 2011b). Field training was provided by David R. Houston to ensure consistent classification.

<b>Level</b>	<b>Scale insects</b>	<b>Neonectria</b>
0	absent	absent
1	trace; one to a few lightly scattered colonies (one or two larger colonies may be present)	sparse; few localised perithecia [fruiting structures], or perithecia in a few scattered circular infection sites
2	light; moderate scattered colonies present; some larger colonies may be present	light; scattered, moderate fruiting
3	moderate; many colonies visible; substantial number of larger colonies may be present	moderate; many isolated infections with abundant perithecia
4	heavy; many large colonies present; some colonies coalescing.	heavy; large areas covered with perithecia; bark conspicuously red/brownish
5	very heavy; much of bark conspicuously white due to scale wax	Code for past years' infections. Not used in our analyses.

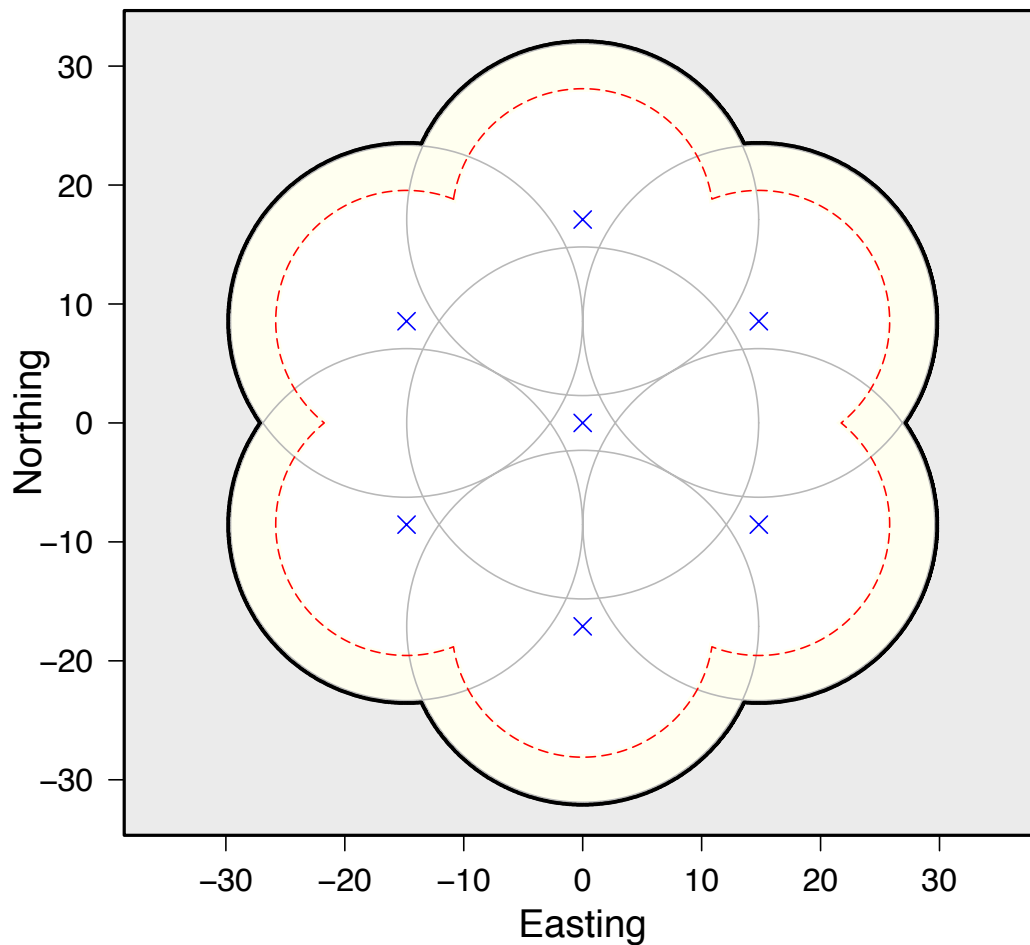


Figure S1. Plot design for spatially mapped sites ( $n=7$ ). A Haglof DME 360 ultrasound distance transponder was placed consecutively at the centre of each circular subplot (marked with a blue 'x'), and distance readings were taken with a handheld receiver placed alongside each tree (at DBH), aiming toward subplot centre. A second fieldworker, standing at subplot centre, recorded azimuth for each tree using a compass. Together, distance and azimuth values were combined to accurately definite each tree's location within the total plot area (0.28 ha.). Edge trees (outside the dotted red line, 6 m from the plot border) were excluded as focal trees in our analyses of spatial aggregation.

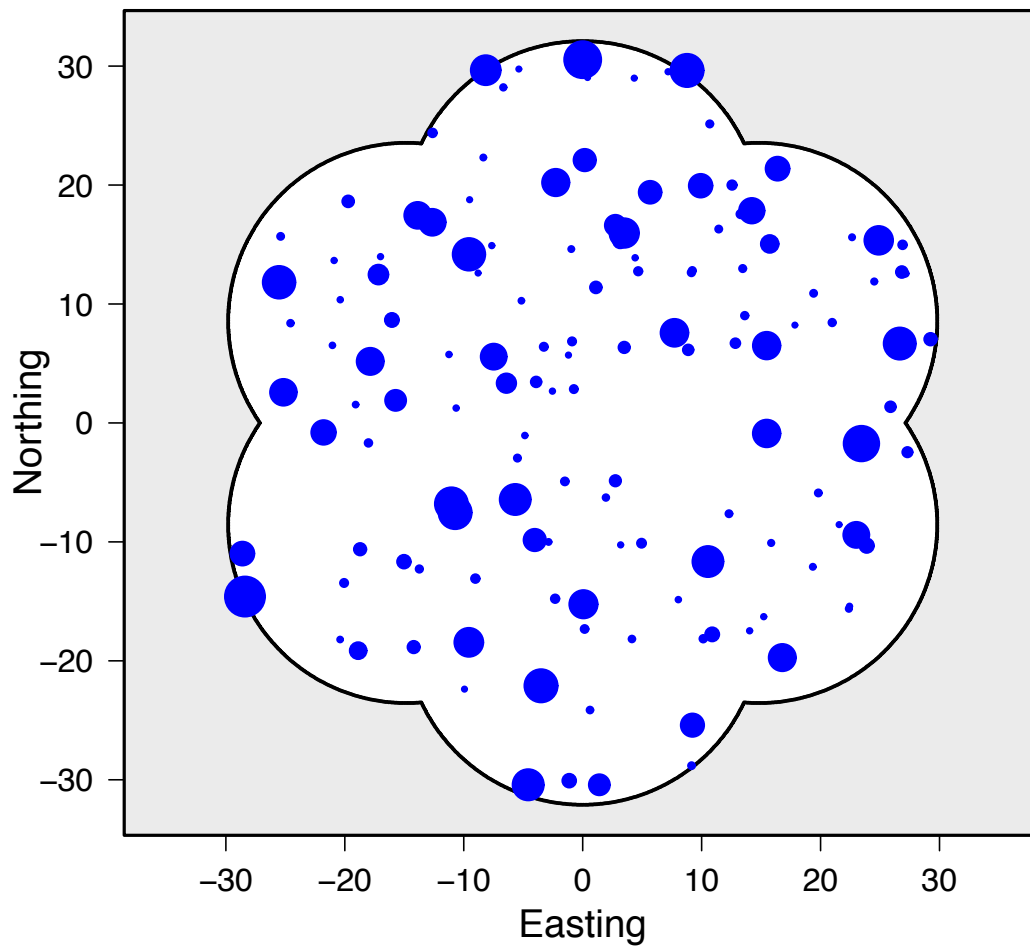


Figure S2. Sample spatially mapped plot (NY site 613B). Blue dots represent living beech trees; circle size is proportional to diameter at breast height. Each tree was scored for a host of disease characters, as well as crown class, crown colour and fullness, and apparent overall health (see Methods for details).

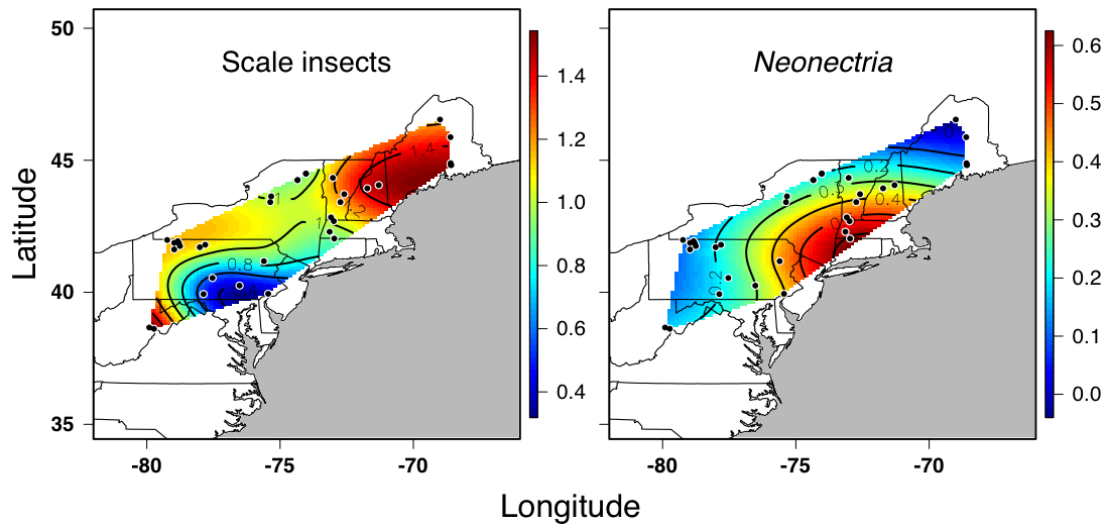


Figure S3. Surface contour plots drawn from 35 sites (black circles) showing spatially interpolated densities of scale insects (left) and *Neonectria* (right) across northeastern United States, 2005-2007. Population estimates for Bartlett and Hubbard Brook Experimental Forests (New Hampshire) represent mean value values derived from intensive sampling at these sites ( $n = 22$  and  $n = 25$  plots respectively).