

Victor Johansson, Thomas Ranius, and Tord Snäll. Year. Epiphyte metapopulation dynamics are explained by species traits, connectivity, and patch dynamics. *Ecology* VOL:pp–pp.

Appendix B. Modeling colonization probability and connectivity.

We modeled the colonization probability (C_i) as a function of connectivity (S_i) as

$$C_i = 1 - e^{-S_i}. \quad (\text{B.1})$$

This relationship assumes independent colonization success among propagules, which is biologically reasonable for our study species. The original IFM used a sigmoid relationship, which is a way to model Allee effects (Hanski 1994). Our connectivity measure (S_i) assumes that propagules are dispersed from unknown background sources at long distance, or from local surrounding occupied patches according to a dispersal kernel. Specifically,

$$S_i = \Xi + \Phi \sum_{j \neq i} f(r_{ij}), \quad (\text{B.2})$$

where Φ is the colonization parameter that includes the rate of emigration of dispersal propagules from occupied patches, and the propagules establishment ability (“the force of infection” using epidemiological terminology). The parameter Ξ denotes the rate of background deposition of dispersal propagules, which essentially models long-distance dispersal. The function $f(r_{ij})$ is the dispersal kernel, where r_{ij} is the distance in meters between trees i and j . Specifically, $f(r)$ is the probability density that a propagules settles at a location (x, y) with distance $r = \sqrt{x^2 + y^2}$ from its point of release. The variable $p_j = 1$ if tree j is occupied by the species; otherwise $p_j = 0$. We use the dispersal kernel:

$$f(r) = \frac{\alpha^2}{2\pi} e^{-\alpha * r}, \quad (\text{B.3})$$

where α is a parameter regulating the dispersal range. The kernel has been normalized so that it represents a two-dimensional probability density, i.e., $\int_0^\infty f(r) * 2\pi r dr = 1$.

LITERATURE CITED

Hanski, I. 1994. A practical model of metapopulation dynamics. *Journal of Animal Ecology* 63:151–162.