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**Appendix A. Derivation of  $\sigma^2_{\text{repulse}}\Sigma_{\text{repulse}}$ .**

Model III in the main text assumes that phylogenetically related species are less likely to co-occur in the same site, that is, they show phylogenetic repulsion. To incorporate phylogenetic repulsion in the model, we assume the covariance matrix  $\sigma^2_{\text{repulse}}\Sigma_{\text{repulse}} = (\sigma^2_{\text{spp}}\Sigma_{\text{spp}})^{-1}$ , where  $\sigma^2_{\text{spp}}\Sigma_{\text{spp}}$  is the covariance matrix for a hypothetical trait that evolves up a phylogenetic tree according to a Brownian motion model of evolution. To demonstrate that this is a reasonable choice, suppose that species undergo interspecific competition so that their dynamics are given by the Lotka-Volterra-like set of equations

$$d\mathbf{N}/dt = \mathbf{N}(t)\mathbf{F}[(\mathbf{R} - \mathbf{A}\mathbf{N}(t))] \quad (\text{A.1})$$

where  $\mathbf{N}(t)$  is the vector of densities of species at time  $t$ ,  $\mathbf{A}$  is a competition “community matrix” (e.g., May 1974) whose elements  $\alpha_{jl}$  give the competitive effect of species  $l$  on species  $j$ ,  $\mathbf{R}$  is a  $n \times 1$  vector of independent Gaussian random variables  $r_j$  with common variance  $\sigma^2_r$ , that give the intrinsic rate of increase of species  $j$ , and  $\mathbf{F}[\cdot]$  is a vector function that translates competition into the per capita population growth rate of each species, with  $\mathbf{F}[\mathbf{0}] = \mathbf{0}$ . A particular form of  $\mathbf{F}[\cdot]$  could be simply  $(\mathbf{R} - \mathbf{A}\mathbf{N}(t))$ , which gives a version of the linear Lotka-Volterra model. Regular matrix multiplication is denoted  $\mathbf{A}\mathbf{N}$ , while  $\mathbf{N}\mathbf{F}$  represents the element-by-element (Schur) product. Equation A.1 assumes that the population dynamics of the  $n$  species are deterministic, but each of the  $n$  species has a different intrinsic rate of increase that is a realization from the random variable  $\mathbf{R}$ .

From Eq. A.1, the equilibrium densities of species are given by the  $n \times 1$  random variable

$$\mathbf{N}_{\text{equil}} = \mathbf{A}^{-1}\mathbf{R} \quad (\text{A.2})$$

Note that even if  $\mathbf{R}$  is constrained to take positive values, values of  $\mathbf{N}_{\text{equil}}$  may be negative. Because  $\mathbf{R}$  is a set of independent Gaussian random variables,  $\mathbf{N}_{\text{equil}}$  has a multivariate Gaussian distribution with covariance matrix  $E[(\mathbf{N}_{\text{equil}} - \bar{\mathbf{N}})(\mathbf{N}_{\text{equil}} - \bar{\mathbf{N}})'] = E[(\mathbf{A}^{-1}\mathbf{R})(\mathbf{A}^{-1}\mathbf{R})'] - \bar{\mathbf{N}}^2 = E[\mathbf{A}^{-1}(\mathbf{R}\mathbf{R}')(\mathbf{A}^{-1})'] - \bar{\mathbf{N}}^2 = \sigma^2_r \mathbf{A}^{-1}(\mathbf{A}^{-1})'$ , which is a square, symmetric matrix. If we let the probability of species occurring in a site be determined by  $\mathbf{N}_{\text{equil}}$ , then we can set  $\sigma^2_{\text{repulse}}\mathbf{\Sigma}_{\text{repulse}} = \mathbf{A}^{-1}(\mathbf{A}^{-1})'$ . Finally, to impose the condition that competition is more likely between closely related species, we let  $\mathbf{A}'\mathbf{A} = \sigma^2_{\text{spp}}\mathbf{\Sigma}_{\text{spp}}$ , thereby giving  $\sigma^2_{\text{repulse}}\mathbf{\Sigma}_{\text{repulse}} = (\sigma^2_{\text{spp}}\mathbf{\Sigma}_{\text{spp}})^{-1}$ . We acknowledge that there are numerous ways to envision processes giving phylogenetic repulsion and to derive  $\mathbf{\Sigma}_{\text{repulse}}$ . However, the approach we took is simple and produces a biological plausible form of  $\mathbf{\Sigma}_{\text{repulse}}$  which decreases the probability that closely related species co-occur in the same site.