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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 α_{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 σ^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 $E[(\mathbf{N}_{\text{equil}} - \bar{\mathbf{N}})(\mathbf{N}_{\text{equil}} - \bar{\mathbf{N}})'] = E[(\mathbf{A}^{-1}\mathbf{R})(\mathbf{A}^{-1}\mathbf{R})'] - \bar{\mathbf{N}}^2 = E[\mathbf{A}^{-1}(\mathbf{R}\mathbf{R}')(\mathbf{A}^{-1})'] - \bar{\mathbf{N}}^2 = \sigma_r^2 \mathbf{A}^{-1}(\mathbf{A}^{-1})'$, 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 $\sigma_{\text{repulse}}^2 \Sigma_{\text{repulse}} = \mathbf{A}^{-1}(\mathbf{A}^{-1})'$. Finally, to impose the condition that competition is more likely between closely related species, we let $\mathbf{A}'\mathbf{A} = \sigma_{\text{spp}}^2 \Sigma_{\text{spp}}$, thereby giving $\sigma_{\text{repulse}}^2 \Sigma_{\text{repulse}} = (\sigma_{\text{spp}}^2 \Sigma_{\text{spp}})^{-1}$. We acknowledge that there are numerous ways to envision processes giving phylogenetic repulsion and to derive Σ_{repulse} . However, the approach we took is simple and produces a biological plausible form of Σ_{repulse} which decreases the probability that closely related species co-occur in the same site.