IDK

Peter D. Smits[1,*]

1. University of Chicago, Chicago, Illinois 60637.

* Corresponding author; e-mail: psmits@uchicago.edu.

Manuscript elements:

Keywords:

Manuscript type: Article

Prepared using the suggested LaTeX template for *Am. Nat.*

Materials and Methods

Taxon occurrence information

Supertree inference

Model specification

Define y as a $N \times T$ matrix of the observed 0/1 occurrence of species i at time t, and z as a $N \times T$ matrix of the "true" 0/1 occurrence of species i at time t. The observation presence of a taxon $y_{i,t}$ is modeled as following a Bernoulli distribution defined

$$y_{i,t} \sim \text{Bernoulli}(\rho_t z_{i,t}) \tag{1}$$

where ρ is a length T vector of the probability that a species is observed at time t given that it is present at time t ($\rho_t = \Pr(y_{\_t} = 1 | x_{\_t} = 1)$).

Observation probability ρ_t is modeled as Bernoulli distributed variable with probability equal to the inverse logit transformed length T vector ρ' (Eq. 2). The elements of ρ' are modeled as exchangeable draws from a Normal distribution with location $\rho^{''}$ and scale $\sigma_{\rho'}$; these are given weakly informative Normal and half-Cauchy priors, respectively.

$$\begin{aligned}
\rho_t &\sim \text{Bernoulli}\left(\text{logit}^{-1}(\rho'_t)\right) \\
\rho'_t &\sim \mathcal{N}(\rho^{''}, \sigma_{\rho'}) \\
\rho^{''} &\sim \mathcal{N}(0, 1) \\
\sigma_{\rho'} &\sim \text{C}^{+}(1)
\end{aligned} \tag{2}$$

The "true" presence/absence states of taxa z are modeled as a logistic regression (Eq. 3) where the probability of being present ($z = 1$) is a function of individual-level and group-level effects. The intercept of this regression α is a length T vector which varies by time t (Eq. 4). Individual-level covariates are a $N \times D$ matrix x whose regression coefficients are the length D column vector β.

These regression coefficients are given independent weakly informative Normally distributed priors.

$$
\begin{aligned}
z_{i,1} &\sim \text{Bernoulli}(\alpha_1 + x_i \beta) \\
z_{i,t} &\sim \text{Bernoulli}\left(\text{logit}^{-1}(z_{i,t-1}(\alpha_t + x_i \beta) + \left(\prod_{k=1}^{t-1} 1 - z_{i,k}\right)(\alpha_t + x_i \beta)\right) \\
\beta &\sim \mathcal{N}(0, 1).
\end{aligned}
\tag{3}
$$

Note that the product term ensures that loss is an absorbing state so that once a species has left the system it cannot return (i.e. extinction) (**?**).

The value of α_t is itself defined as a regression (Eq. 4). The intercept of the this group-level regression is defined as μ. The effect of plant regime p is modeled as the length P vector ϕ whose elemnts are draws from a Normal distribution with a location of 0 and scale of σ_{ϕ}. The group-level covariates corresponding to global climate values of interest is defined as the $T \times U$ matrix u where γ is a length U column vector of regression coefficients. Finally σ_{μ} is positive real value. μ, the elements of γ, σ_{μ}, and σ_{ϕ} are all given weakly informative independent priors (Eq. 4).

$$
\begin{aligned}
\alpha_t &\sim \mathcal{N}(\mu + \phi_{p[t]} + u_t \gamma, \sigma_{\mu}) \\
\mu &\sim \mathcal{N}(0, 5) \\
\sigma_{\mu} &\sim \text{C}^{+}(1) \\
\phi_p &\sim \mathcal{N}(0, \sigma_{\phi}) \\
\sigma_{\phi} &\sim \text{C}^{+}(1) \\
\gamma &\sim \mathcal{N}(0, 1)
\end{aligned}
\tag{4}
$$

Posterior inference and model adequacy

Acknowledgements

I would like to thank K. Angielzcyk, M. Foote, P. D. Polly, and R. Ree for helpful discussion and advice. This entire study would would not have been possible without the Herculean effort of the many contributors to the Paleobiology Database. In particular, I would like to thank J. Alroy and M. Uhen for curating most of the mammal occurrences recorded in the PBDB. This is Paleobiology Database publication XXX.