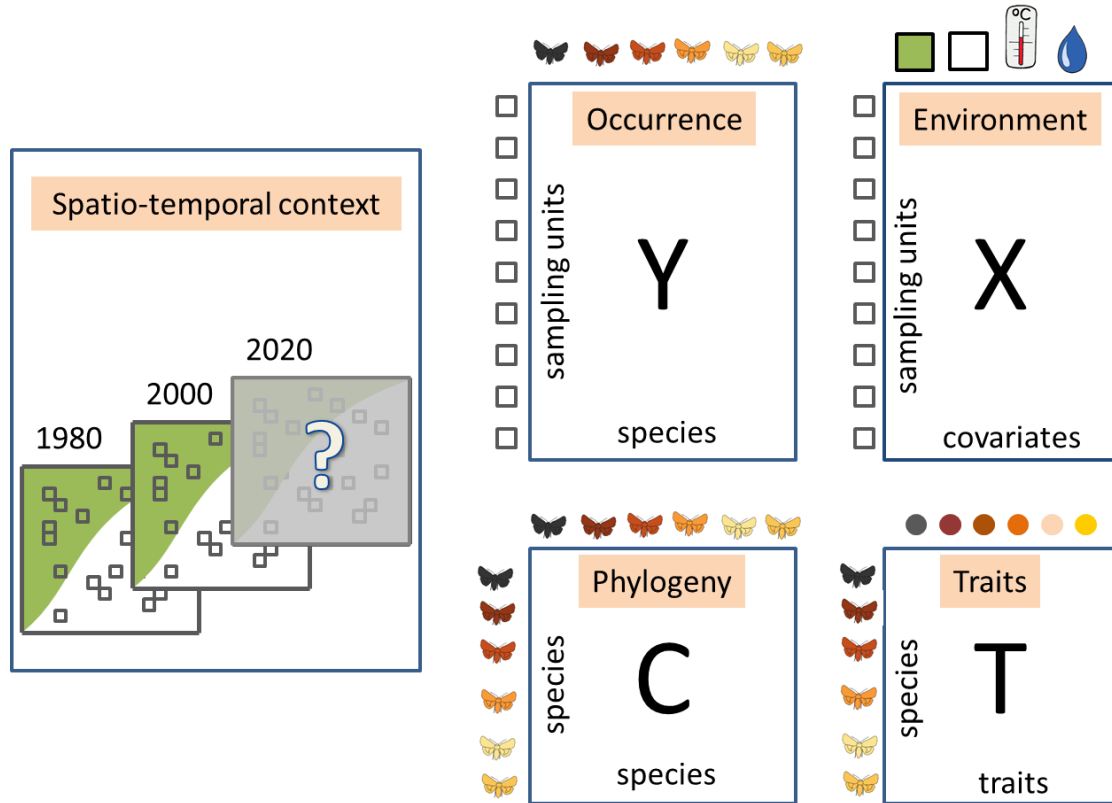


Building HMSC step by step: variation in species niches

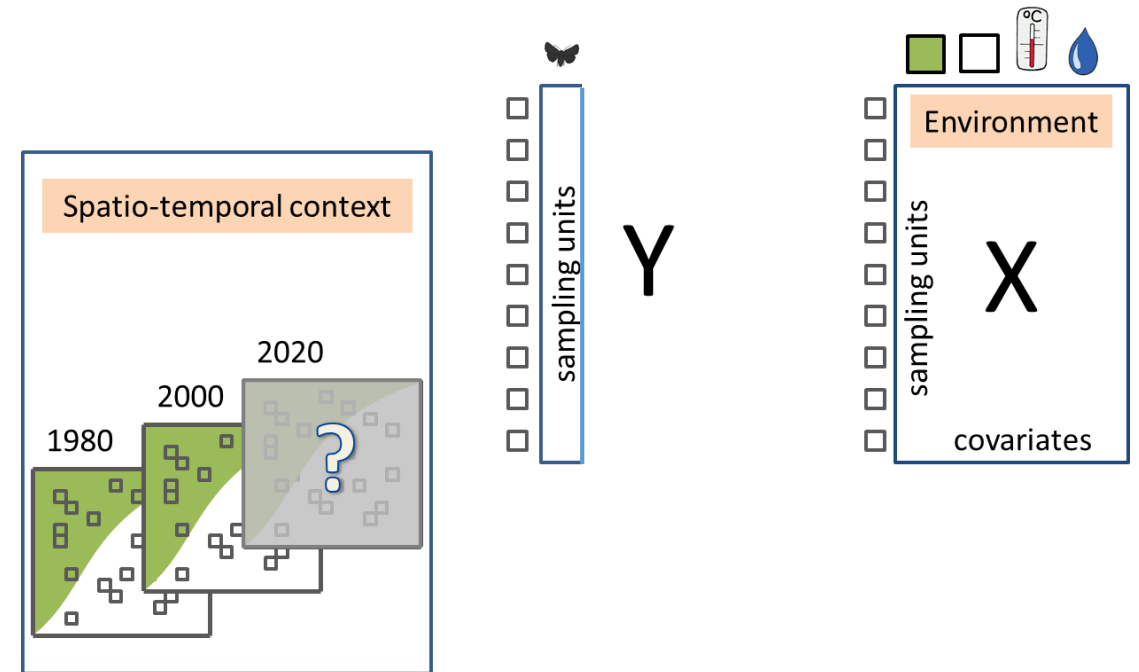
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Full HMSC



$$L_{ij} = \sum_{k=1}^{n_c} \beta_{kj} x_{ik}$$

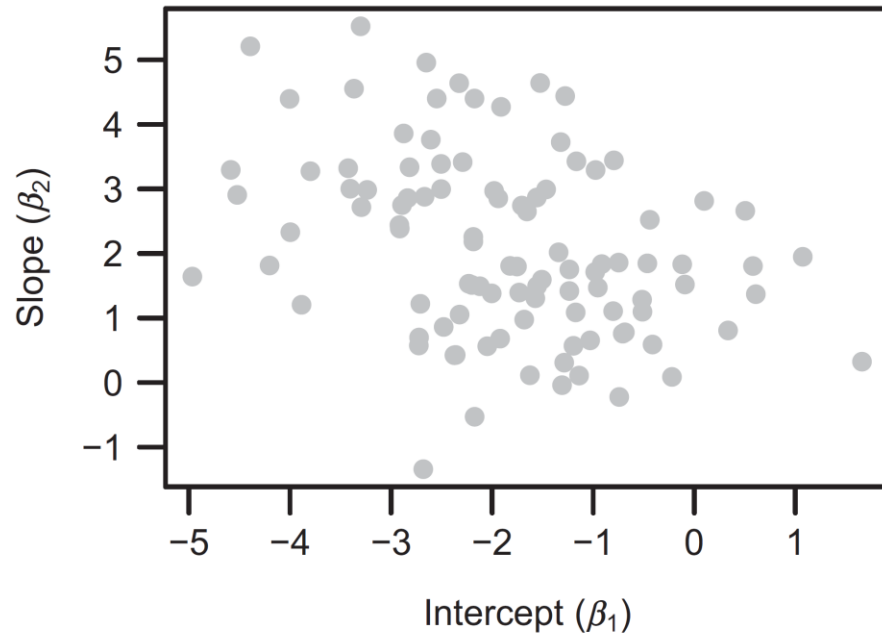
Single-species HMSC



$$L_i = \sum_{k=1}^{n_c} \beta_k x_{ik}$$

Variation in species niches among the species

(A)



(B)

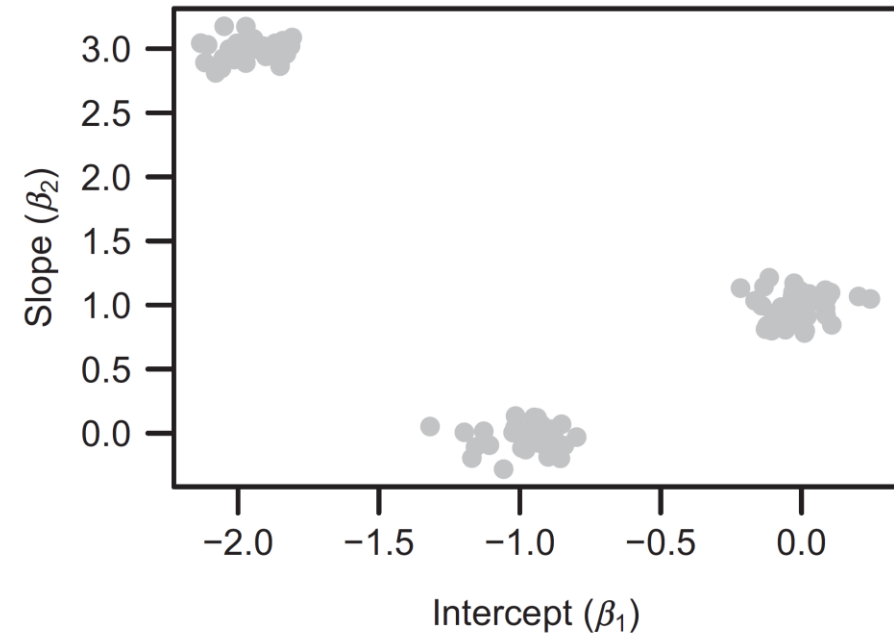
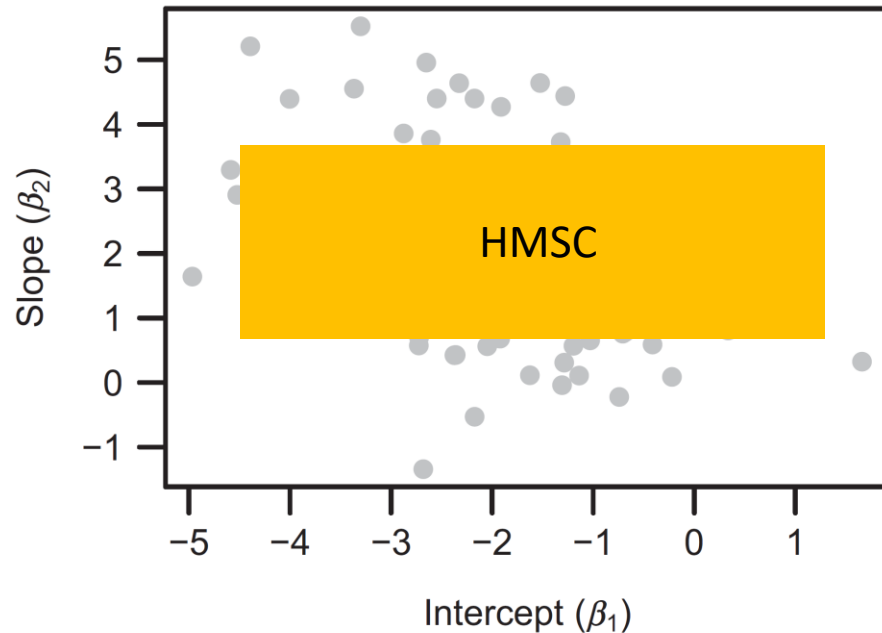


Figure 6.1 Illustration of variation in species niches. In both panels, each dot corresponds to one species in a community of 100 species. In panel A, there is continuous variation among species niches, whereas in panel B the species niches form three clusters.

Variation in species niches among the species

(A)



(B)

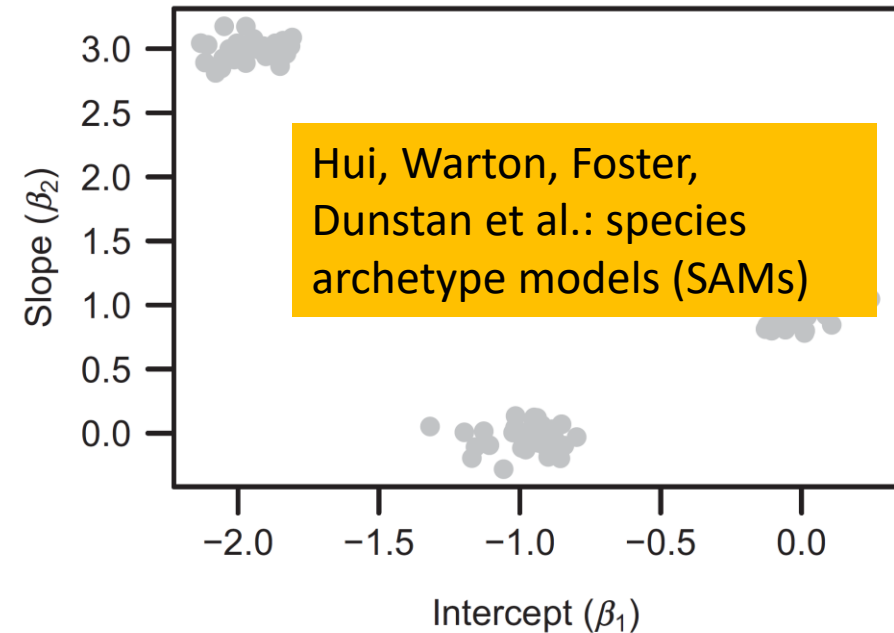
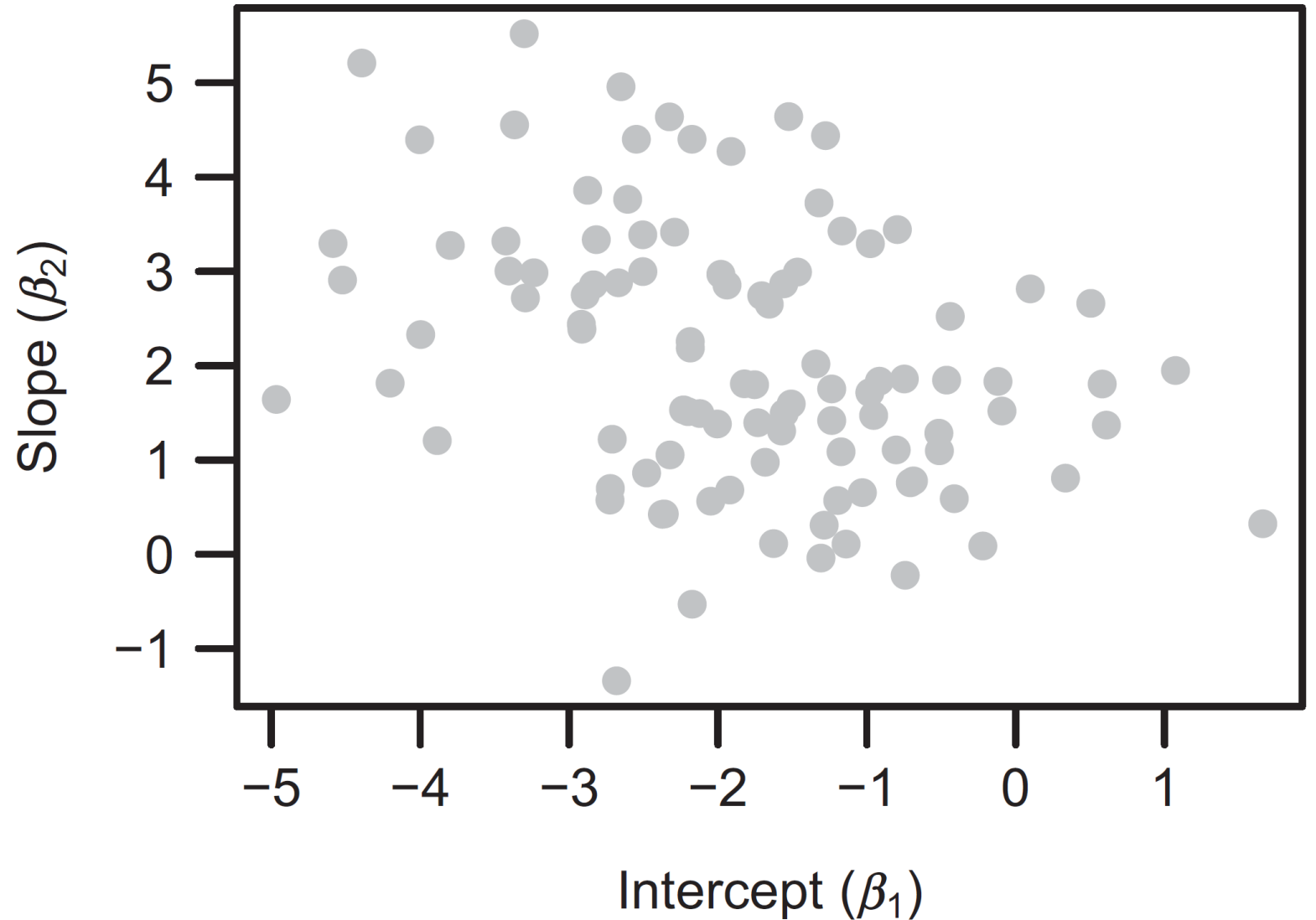


Figure 6.1 Illustration of variation in species niches. In both panels, each dot corresponds to one species in a community of 100 species. In panel A, there is continuous variation among species niches, whereas in panel B the species niches form three clusters.

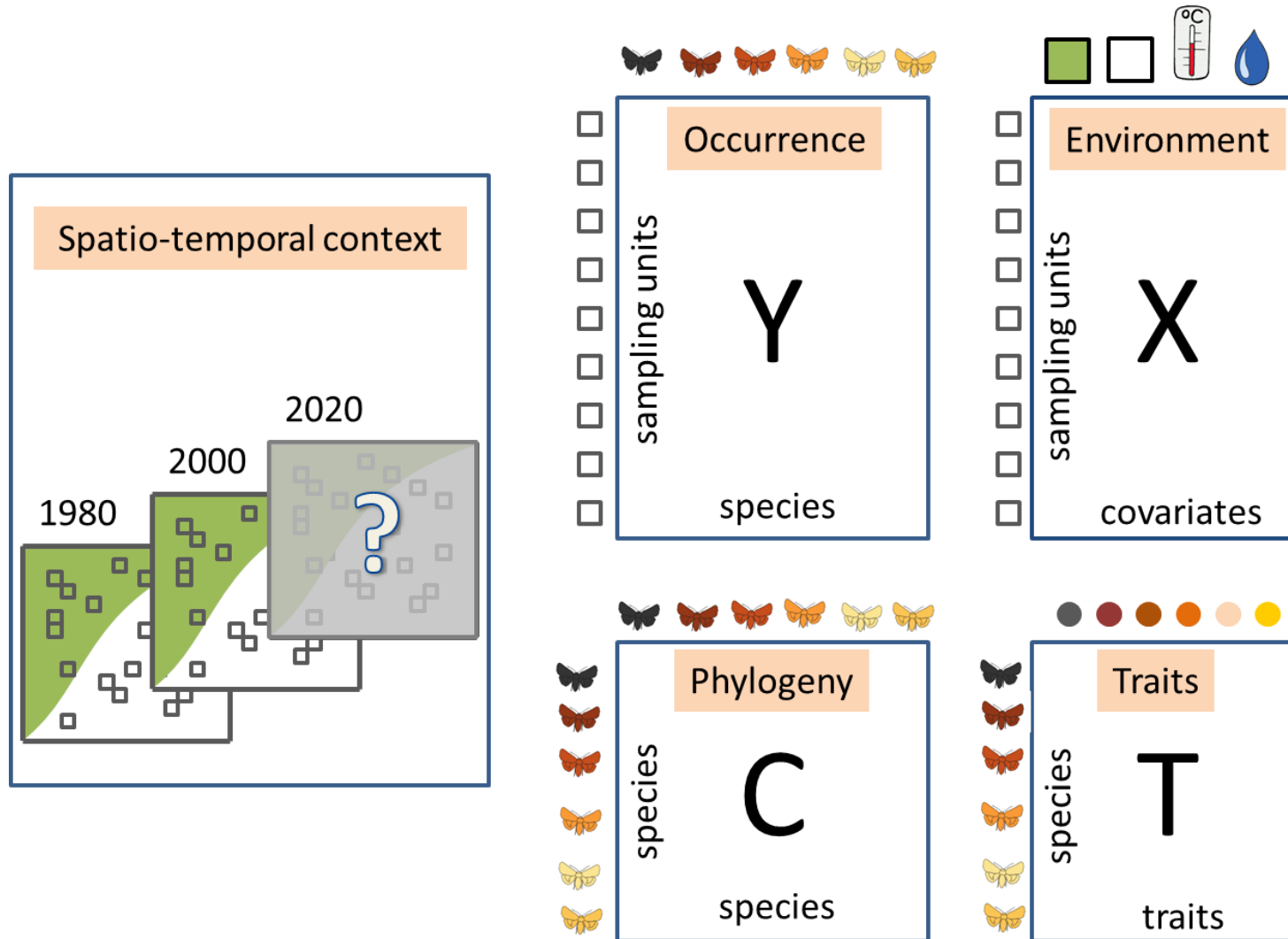
Variation in species niches among the species

A simple statistical model for variation in species niches:

$$\boldsymbol{\beta}_{\cdot j} \sim N(\boldsymbol{\mu}, \mathbf{V})$$



How to utilize data on species traits & phylogenetic relationships?



Modelling the influence of species traits on their niches

Species-specific expected value:

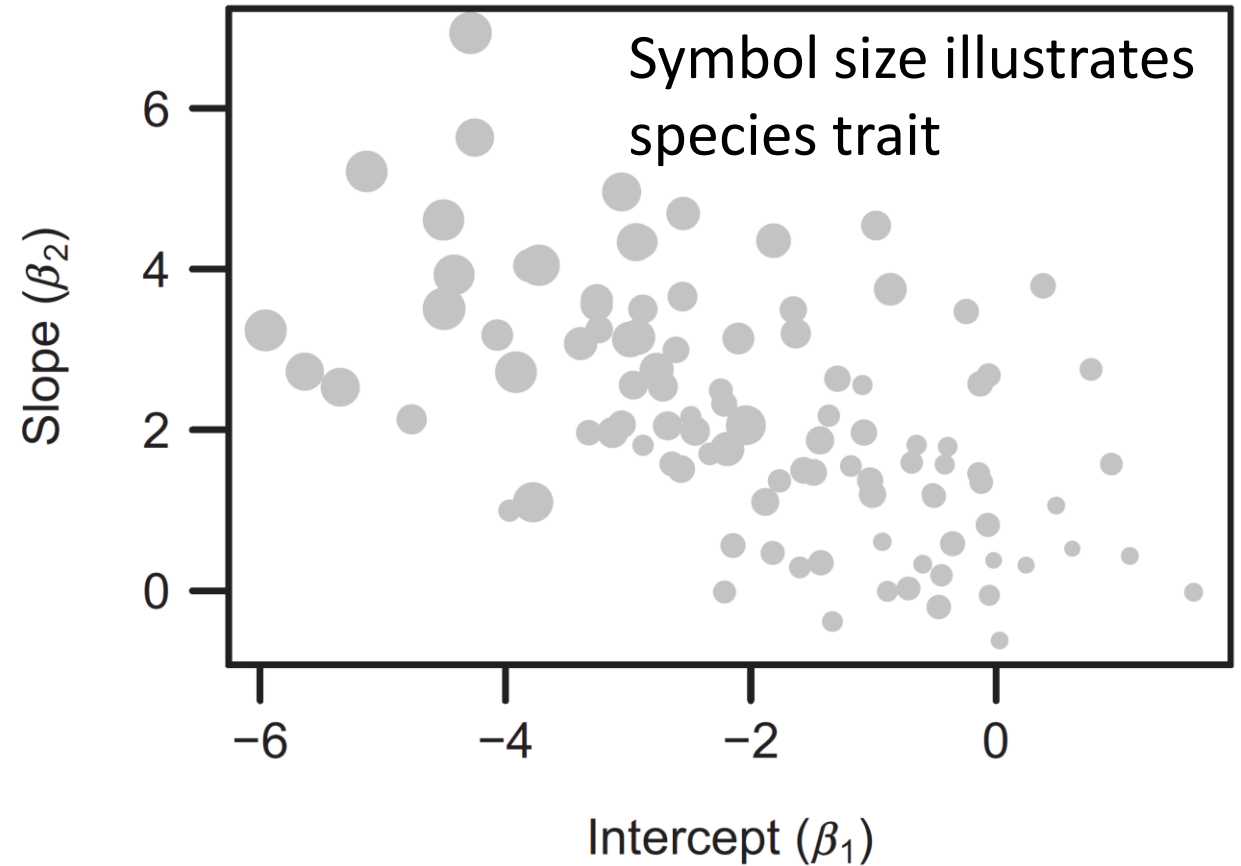
$$\boldsymbol{\beta}_{\cdot j} \sim N(\boldsymbol{\mu}_{\cdot j}, \mathbf{V})$$

Modelled as regression to species traits:

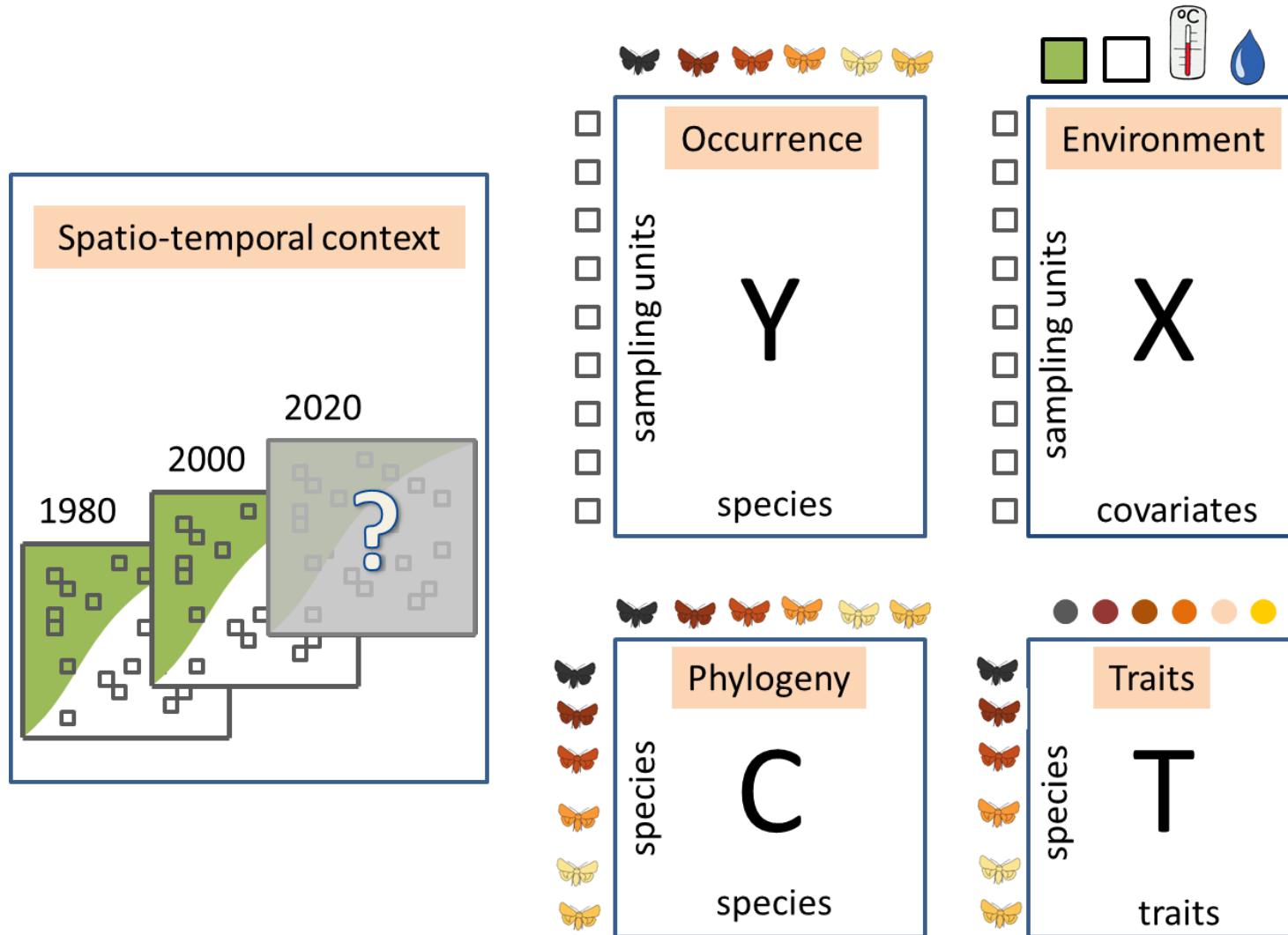
$$\mu_{kj} = \sum_{l=1}^{n_t} t_{jl} \gamma_{kl}$$

The trait l of species j

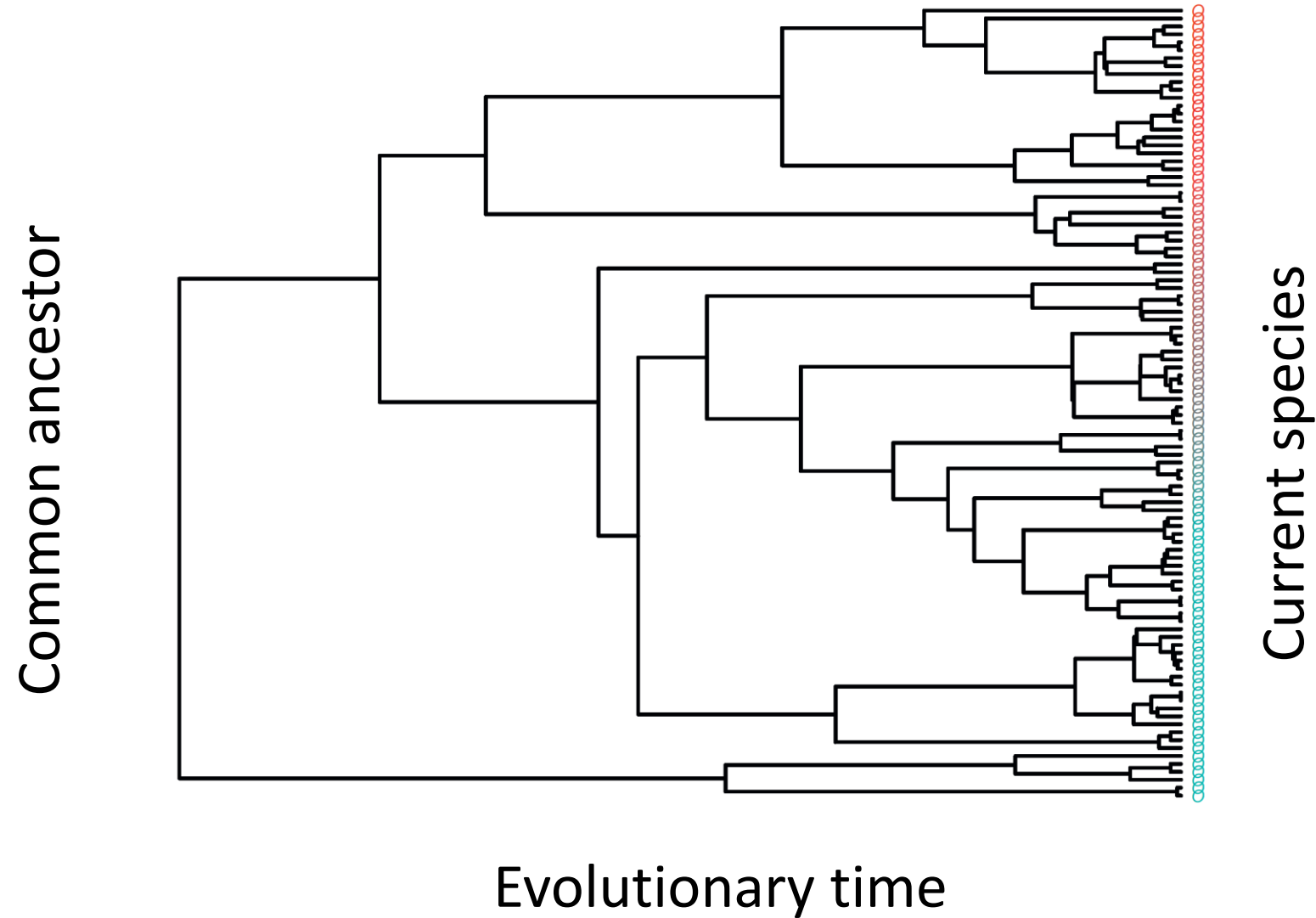
The influence of trait l on how the species is expected to respond to covariate k



How to utilize data on species traits & phylogenetic relationships?

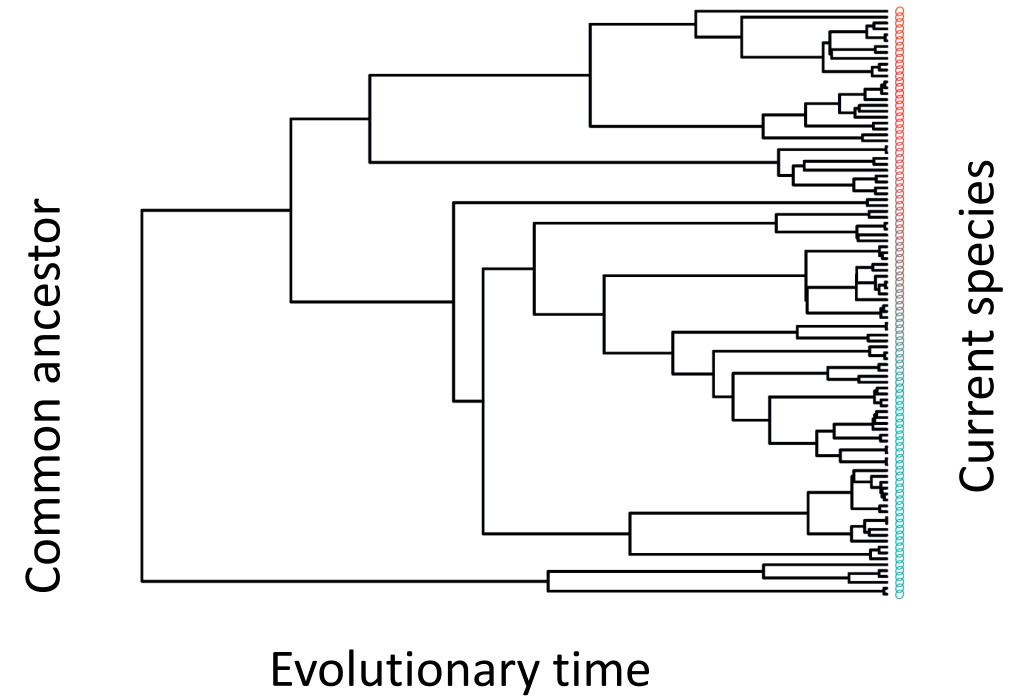
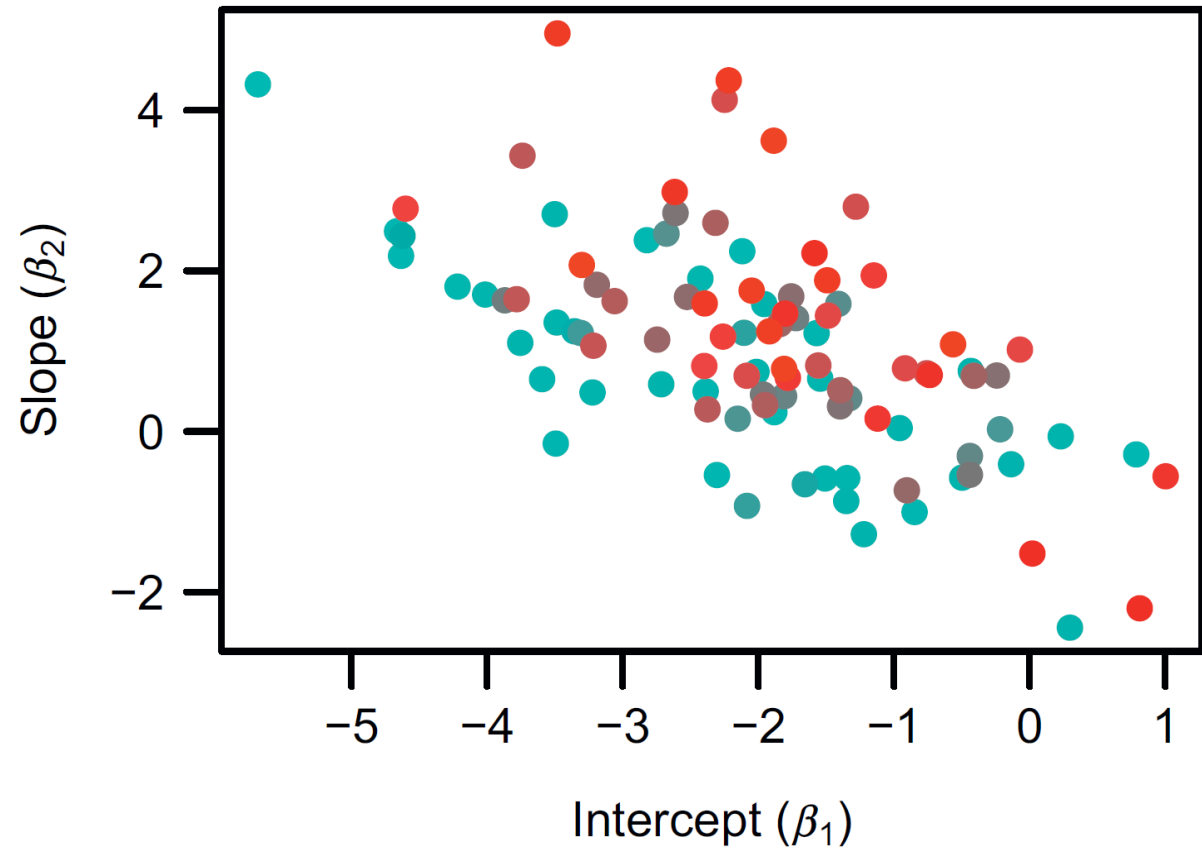


Modelling the influence of phylogeny on species niches



Modelling the influence of phylogeny on species niches

Illustration of systematic variation in species niches across the phylogeny



Modelling the influence of phylogeny on species niches

The basic model in matrix notation:

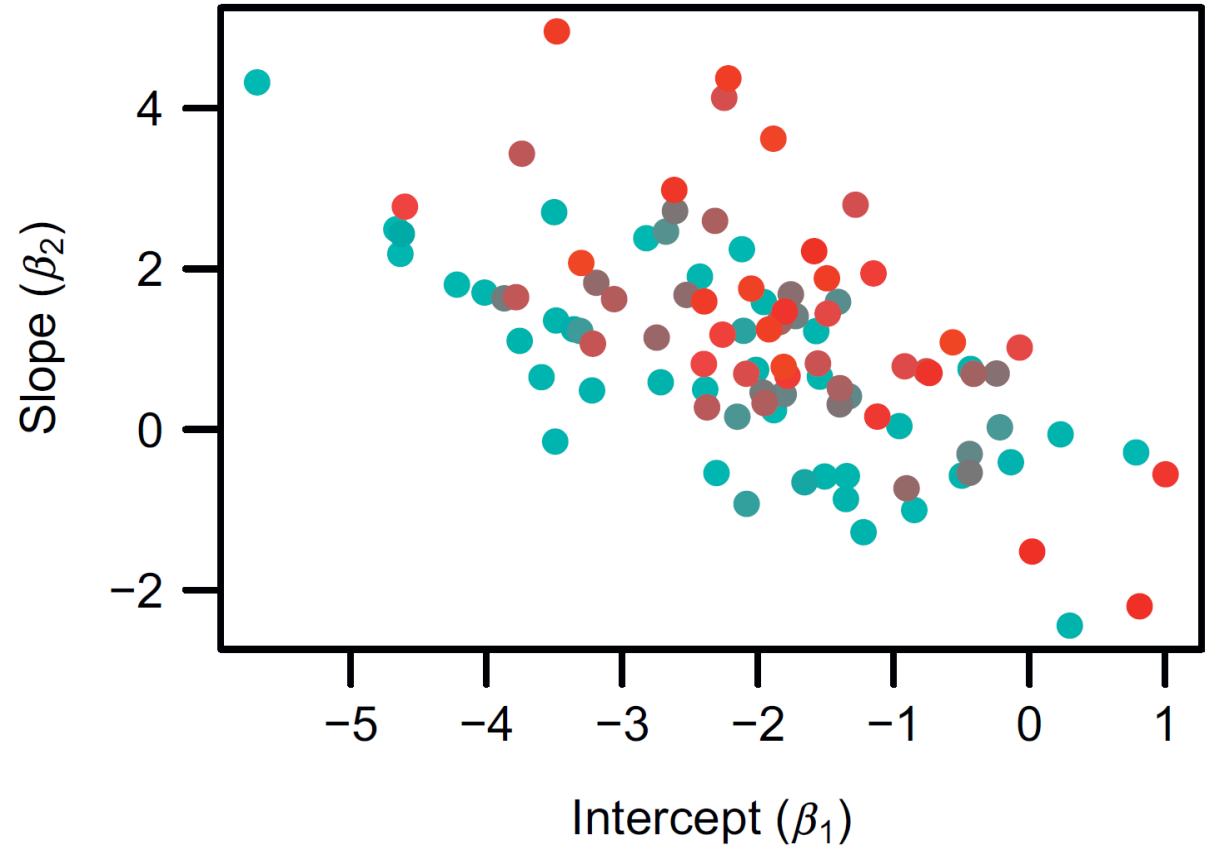
$$\boldsymbol{\beta}_{\cdot j} \sim N(\boldsymbol{\mu}, \mathbf{V})$$

$$\text{vec}(\mathbf{B}) \sim N(\text{vec}(\mathbf{M}), \mathbf{I} \otimes \mathbf{V})$$

Phylogenetically structured model
in matrix notation:

$$\text{vec}(\mathbf{B}) \sim N(\text{vec}(\mathbf{M}), \mathbf{W} \otimes \mathbf{V})$$

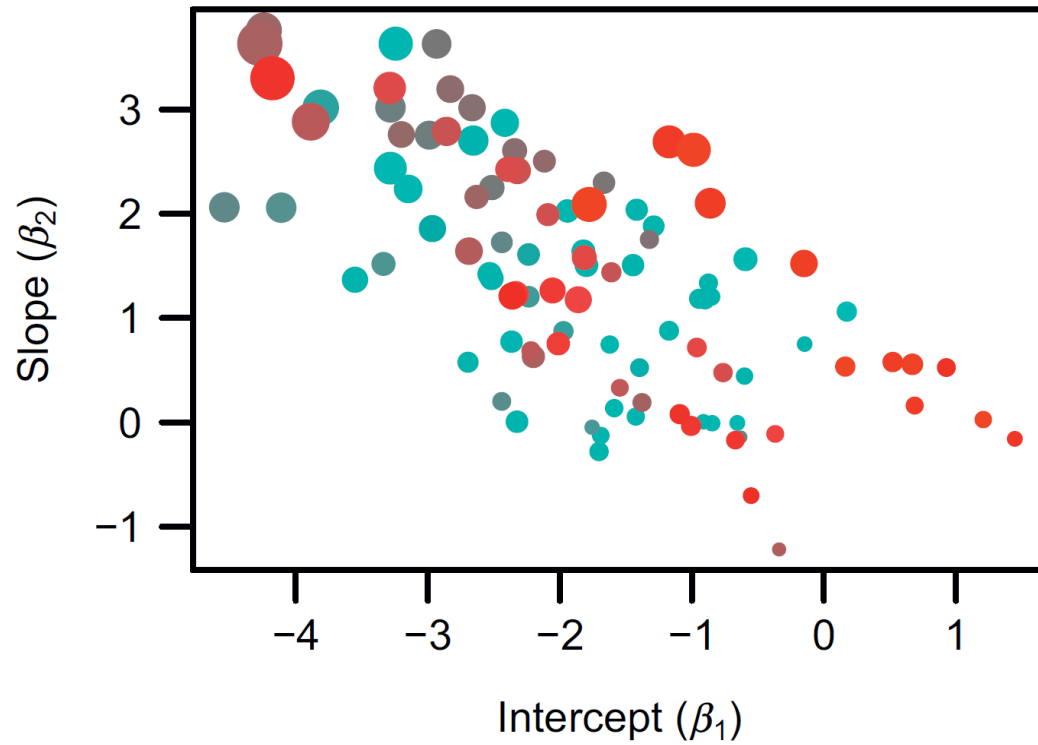
$$\mathbf{W} = \rho \mathbf{C} + (1 - \rho) \mathbf{I}$$



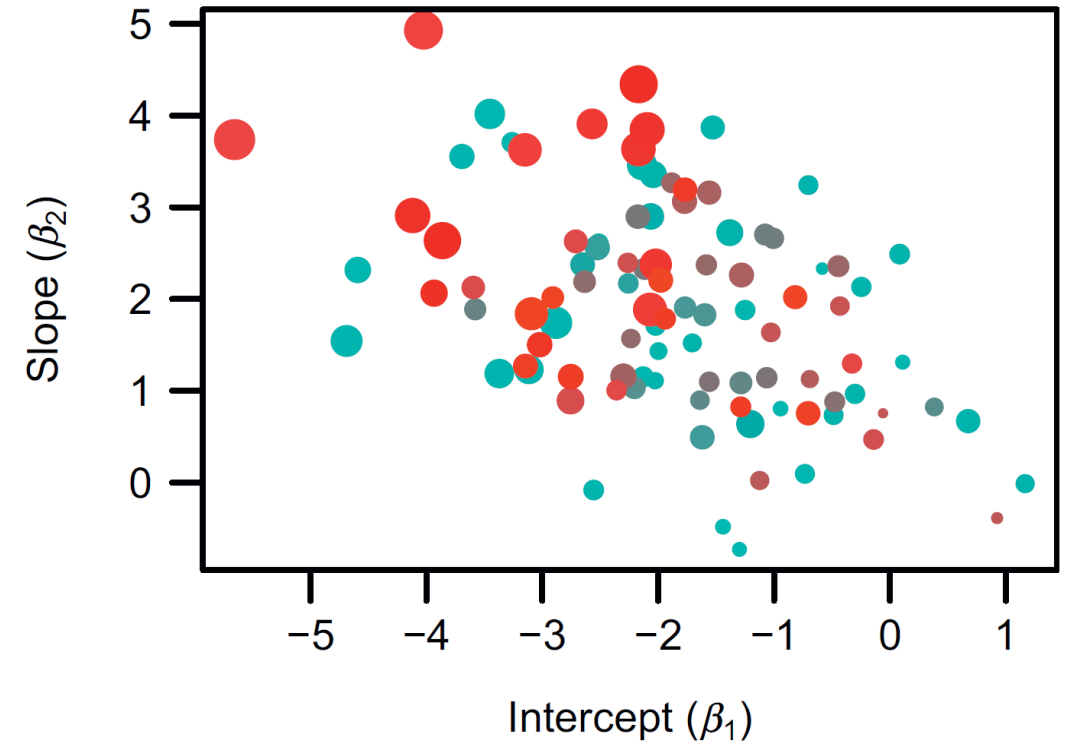
The parameter ρ measures the strength of phylogenetic signal in species niches

Modelling the joint influence of species traits and phylogeny on species niches

(A)



(B)



Distribution of species niches, as estimated with HMSC (BetaPlot)

