Functional Trait Analysis in Community Ecology

Traits/features: aspects of an organism including morphology, behavior, and physiology

- Taxon-free”
  - traits can be measured independent of species identity.
- Typically quantified/described for individuals
- But could also look at mean values across populations, species, communities or metacommunities (i.e., ecometrics, Eronen et al. 2017)

Traits are primarily used in three ways:

- Taxonomic ***identification***
- To infer something about the ***function*** of the organism
- To infer something about the ***environment*** of the organism

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- Overall, traits provide insight into how communities are assembled and structured across space and time.

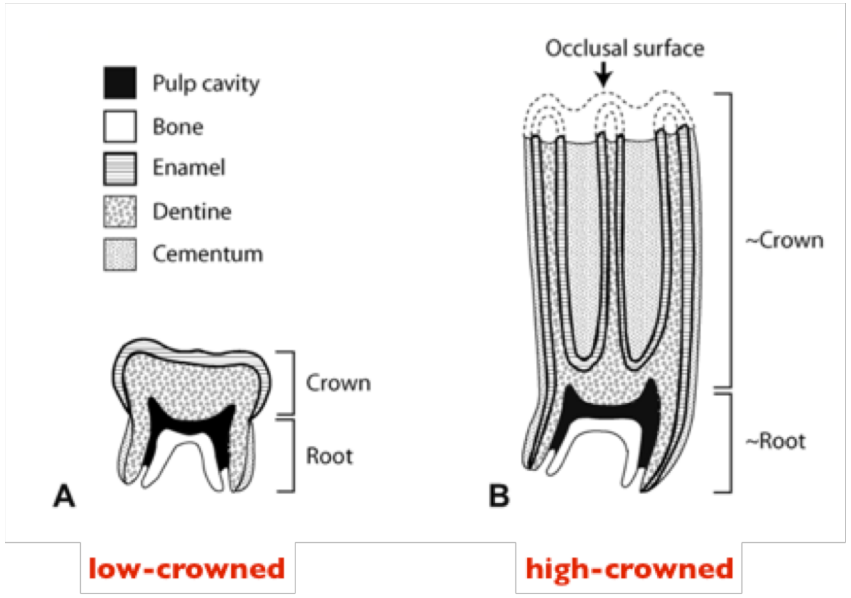
Environmental Inference

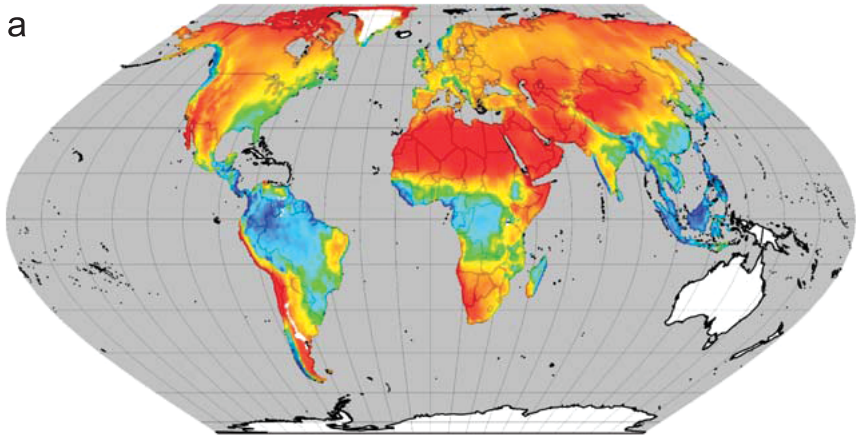
- Morphology often reflects the influence of the environment or habitat in which a species is located.
- Examples:
  - limb structure can reflect locomotion (function: walking, running, climbing, swimming, burrowing, etc.), which can indirectly indicate environment
  - tooth structure can reflect diet (function: carnivore, insectivore, herbivore, omnivore, frugivore) but can also reflect environment (e.g., enamel ridges on the grinding surface can indicate aridity)
  - leaf thickness or stomatal density & structure can reflect the amount of water stress in the environment
- At a community level, then, the mean value of a trait across all species in the assemblage may reflect important aspects of the environmental context

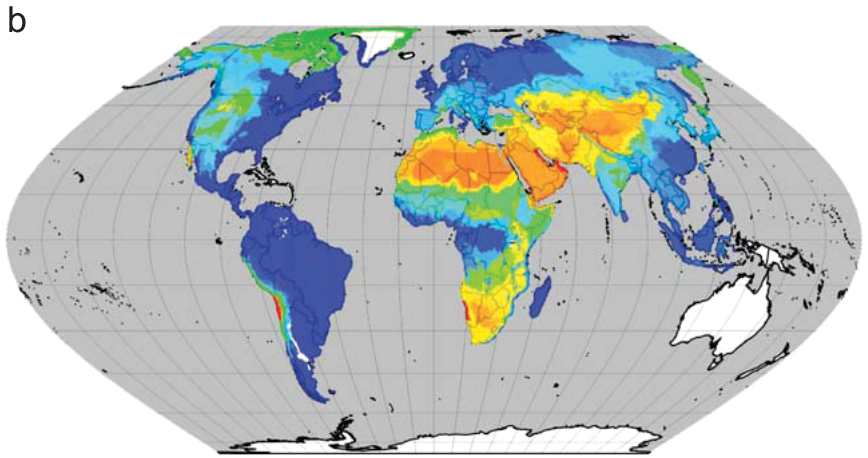
Eronen et al. 2010, Integrative Zoology

Environmental Inference

- Community mean tooth crown height in herbivorous large mammals is negatively related to precipitation.
- **Why?**

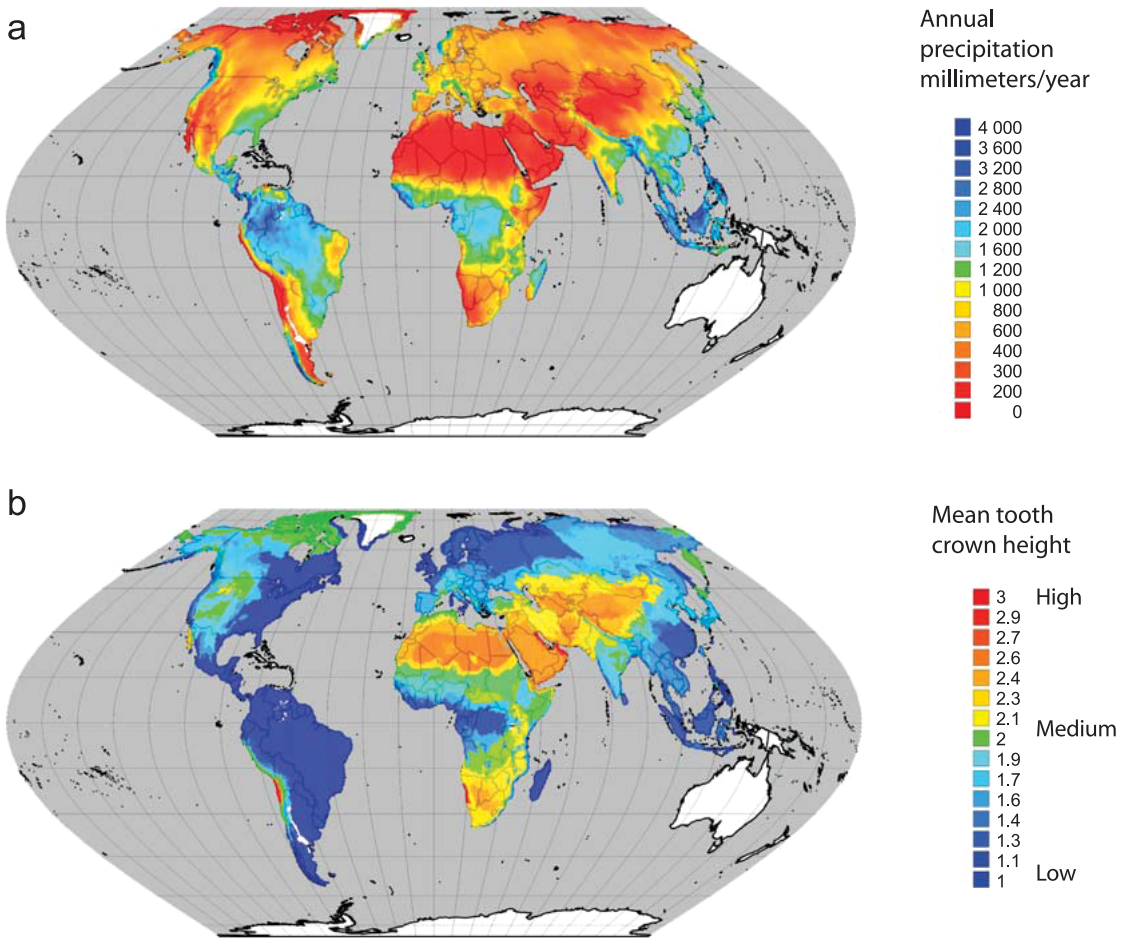




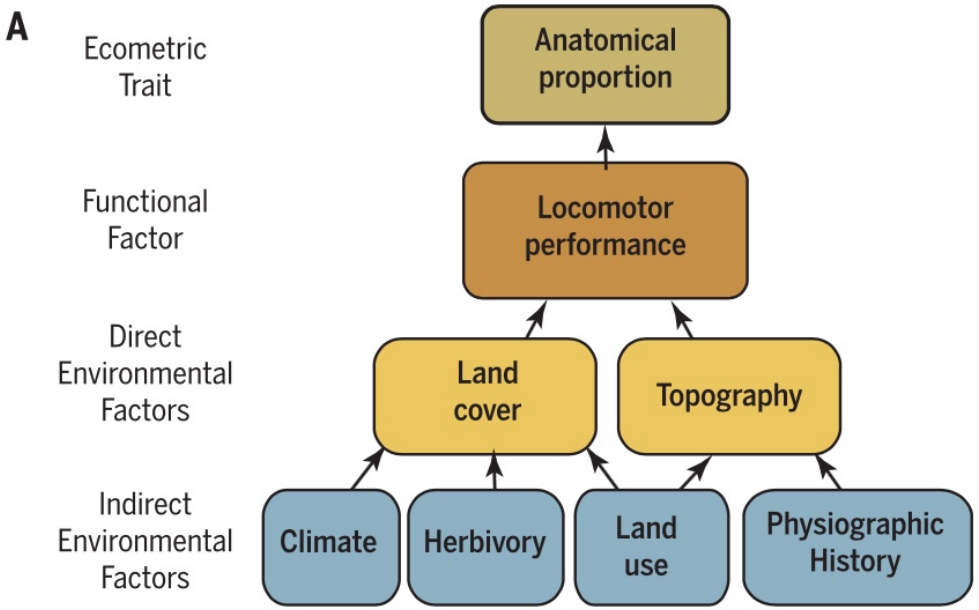


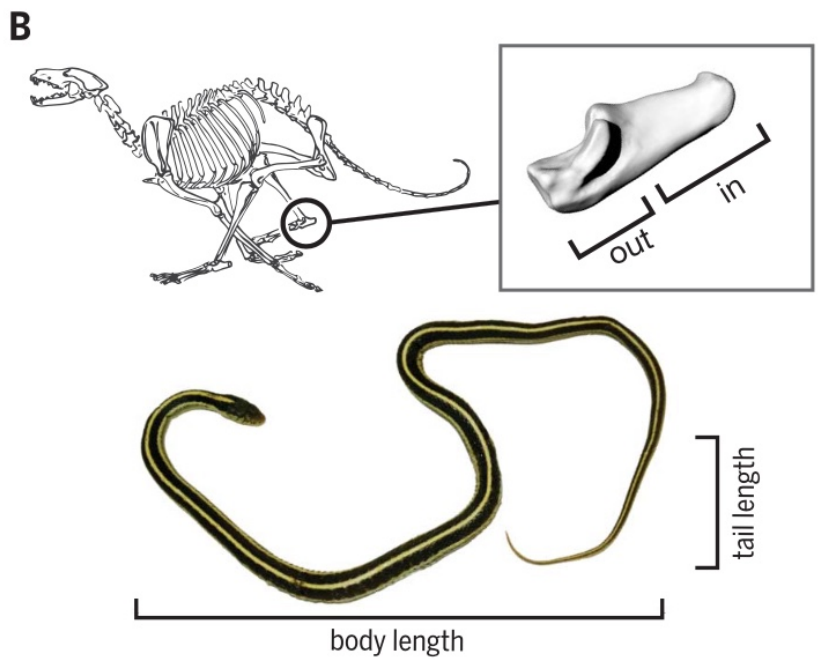
Environmental Inference

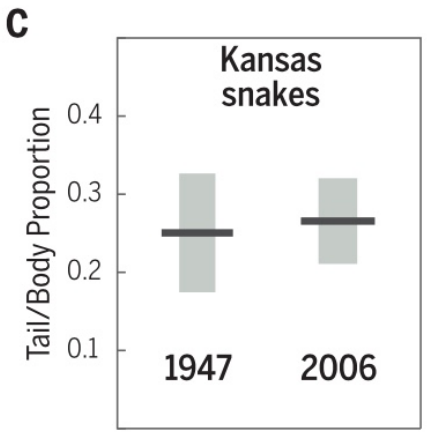
- Community mean tooth crown height in herbivorous large mammals is negatively related to precipitation.
- **Why?**
  - Tooth crown height related to tooth durability
  - Low-crowned teeth ~ eat relatively non-abrasive food such as soft browse in a relatively grit-free environment
  - High-crowned teeth ~ a diet that is more abrasive, usually containing greater amounts of grass, or plants from more arid areas
  - Communities containing primarily high-crowned herbivores imply more arid environments

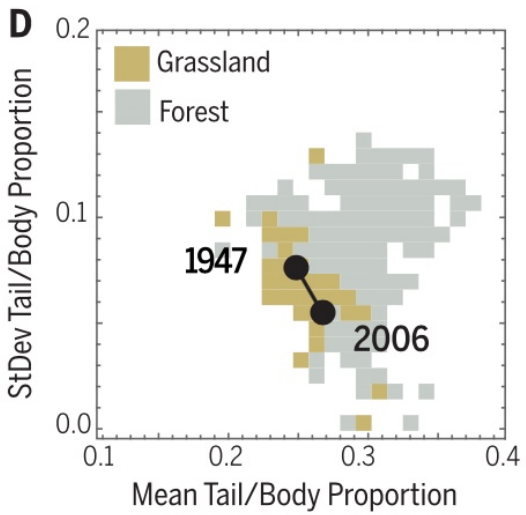


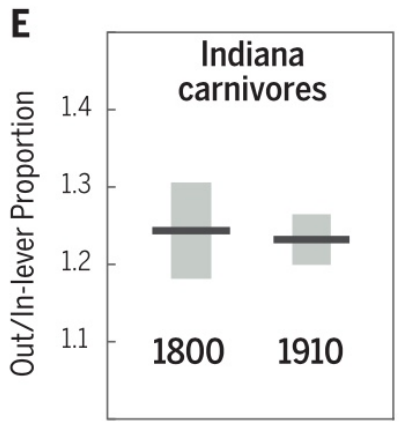
Link traits & environment through function











Barnosky et al. 2017

Environmental Inference

- But, which traits are most reflective of environment?
- What other processes besides environment might shape trait distributions within assemblages?

Community functional trait composition at the continental scale: the effects of non-ecological processes

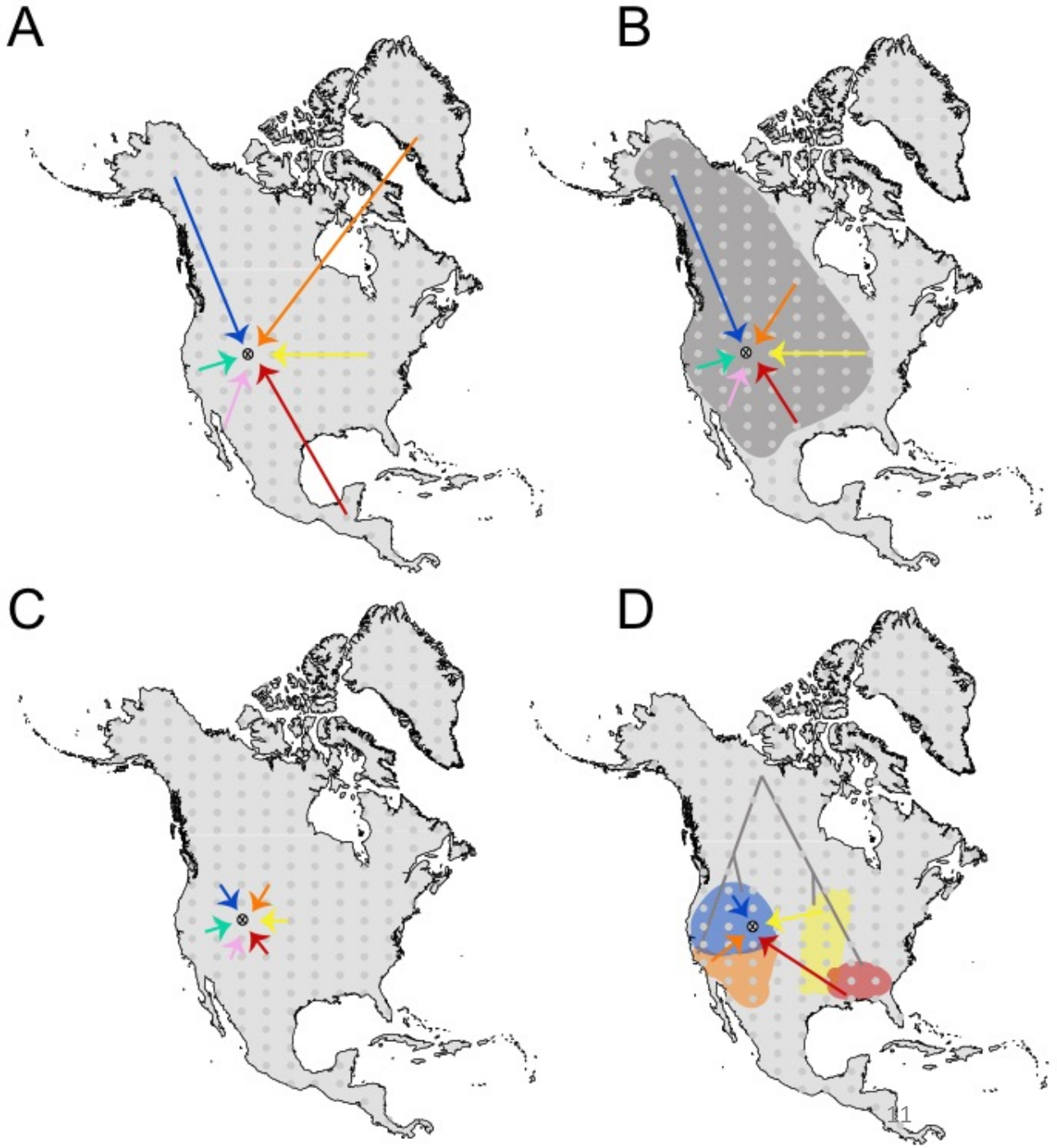
- We evaluated four null models using twelve mammalian traits and four climate variables to assess the extent to which trait–climate correlations can arise spuriously.
  - If spurious effects are small, then variation in the trait–climate correlation between the four data sets should be low.
  - The effect of correction should vary less between traits whose true correlations are strong because they are less likely to have arisen by chance than traits with weak correlations.

A. Michelle Lawing*, Jussi T. Eronen*, Jessica L. Blois*, Catherine H. Graham and P. David Polly 2017 Ecography

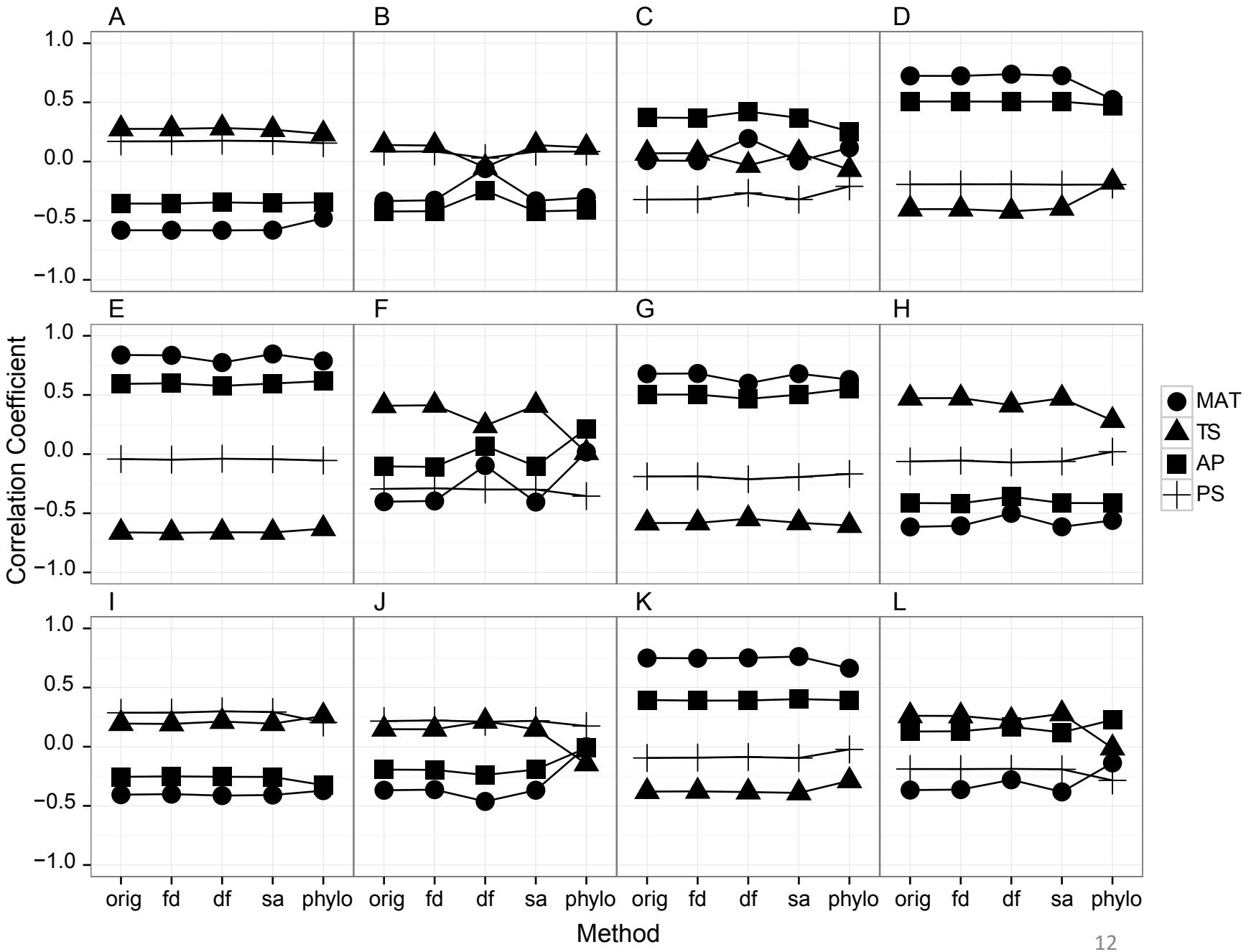
Null model analysis

Tested 4 different null models that reflect different biases:

1. free dispersal
2. dispersion field
3. spatial autocorrelation
4. phylogenetic autocorrelation



Results


A
B
C
D
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L
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Correlation Coefficient
orig
fd
df
sa
phylo
Method
MAT
TS
AP
PS

Methods

For each point in the sampling grid, we calculated the mean of each trait from the assemblage of species that co-occur there. ese are the observed local assemblage trait means (i.e. the ecometric mean). We calculated the Pearson's correlation coefficient (*r*) between each set of trait means and each of the four climate variables across all points in the grid (*orig*). We then recalculated the trait–climate correlations after adjusting the trait means for spurious patterns that arise from the each of the four null models as follows.

We randomly sampled *N* species (where *N* is the number of mammal species present at the sampling point), calculated the mean (simulated mean), and repeated 1000 times to generate an expected simulated mean (the average of the simulated means).

We subtracted the expected simulated mean from the original trait mean at each sampling point to produce anomalies (residuals) that indicate whether the observed trait mean is higher or lower than the mean expected from the model.

Trait–climate correlations were calculated from the anomalies of the original trait means from the means of the resampled data.