

Trait gradient hypotheses

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2024-02-14

Biogeochemical Niche Hypothesis

The data-generating process is modeled following the Biogeochemical Niche Hypothesis as follows. A trait's value x of observation i , of species k , at site s is assumed to be exclusively determined by the identity of that species. All observed values of species k are equal to that species' mean plus an observational error ε_i .

$$x_{i,k,s} = \bar{x}_k + \varepsilon_i$$

An environmental filtering on species occurrence is modeled as a random draw (sample with replacement) of N_s individuals for each site from the population N_k species. The probability to draw a species k at site s depends on the site and is modeled using a functional form as shown in Figure 1. The “narrowness” of the the species distribution across different sites is controlled by a parameter k (`param_species_selection`).

The resulting trait gradient analysis (TGA) is shown in Figure 2. It demonstrates that the TGA identifies a data generating process following the Biogeochemical Niche Hypothesis by yielding within-species regressions with a slope of zero.

Perfect stoichiometric plasticity

The data-generating process is modeled following perfect stoichiometric plasticity as follows. Species occur randomly across sites and the site's environmental condition imprints a common effect on all species growing at the site - a site-specific mean value \bar{x}_s . Species are characterized by a random offset ($\delta_k \sim N(0, \sigma)$) of the leaf trait relative to the mean across all species growing at site s . ε_i is an observational error.

$$x_{i,k,s} = \bar{x}_s + \delta_k + \varepsilon_i$$

An environmental filtering on species occurrence is modeled as above, but with a slightly wider niche (smaller `param_species_selection`).

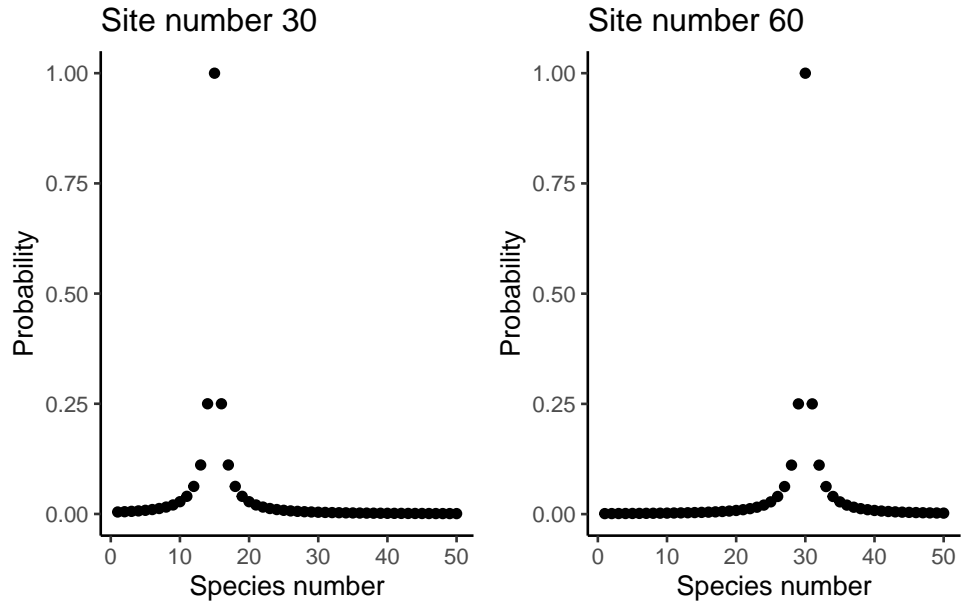


Figure 1: Probability for the occurrence of a given species at a given site.

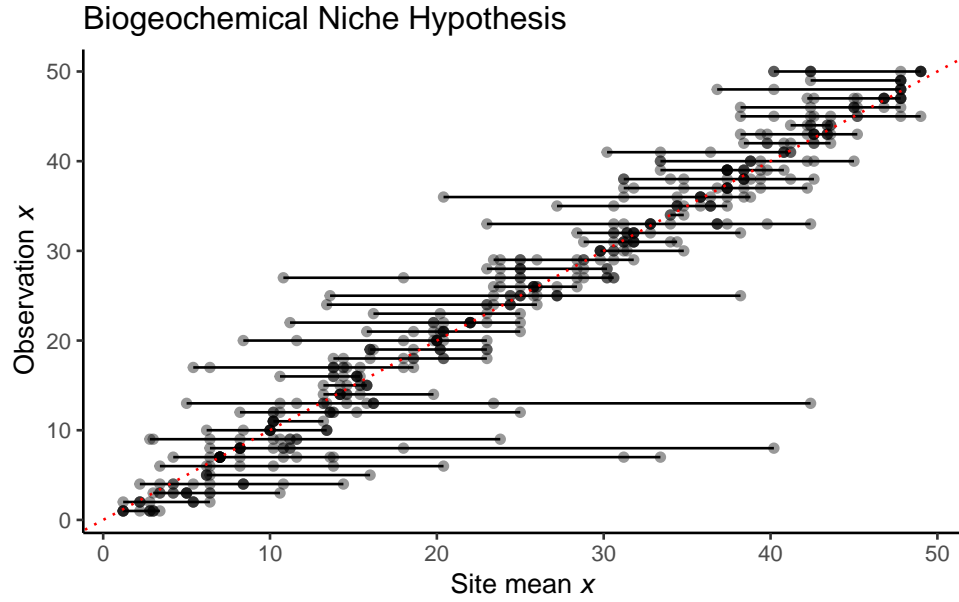


Figure 2: Trait gradient analysis for data generated assuming the Biogeochemical Niche Hypothesis. Solid lines represent the species-specific regressions of trait values observed at different sites vs. the respective site mean across all species growing at that site.

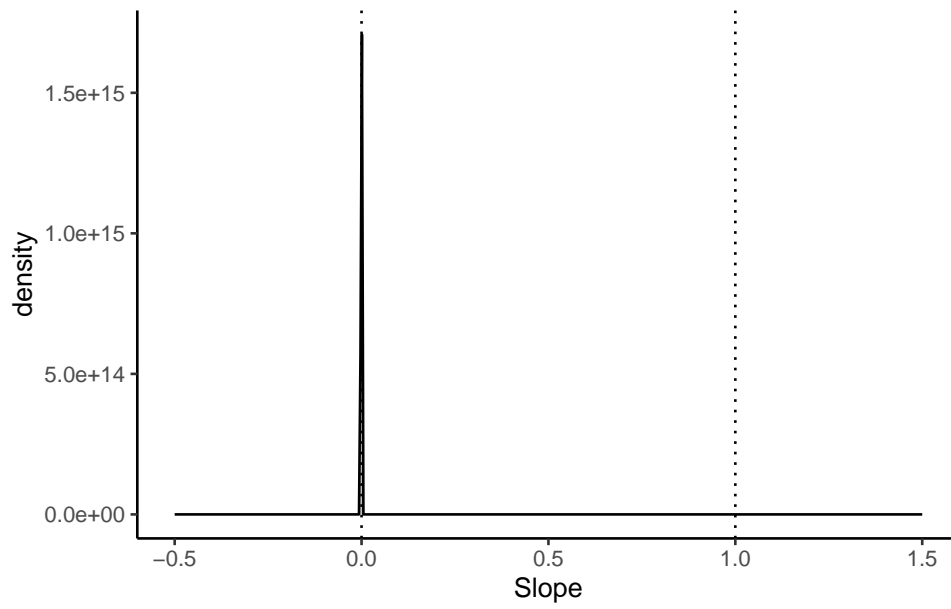


Figure 3: Distribution of slopes in the trait gradient analysis for data generated assuming the Biogeochemical Niche Hypothesis.

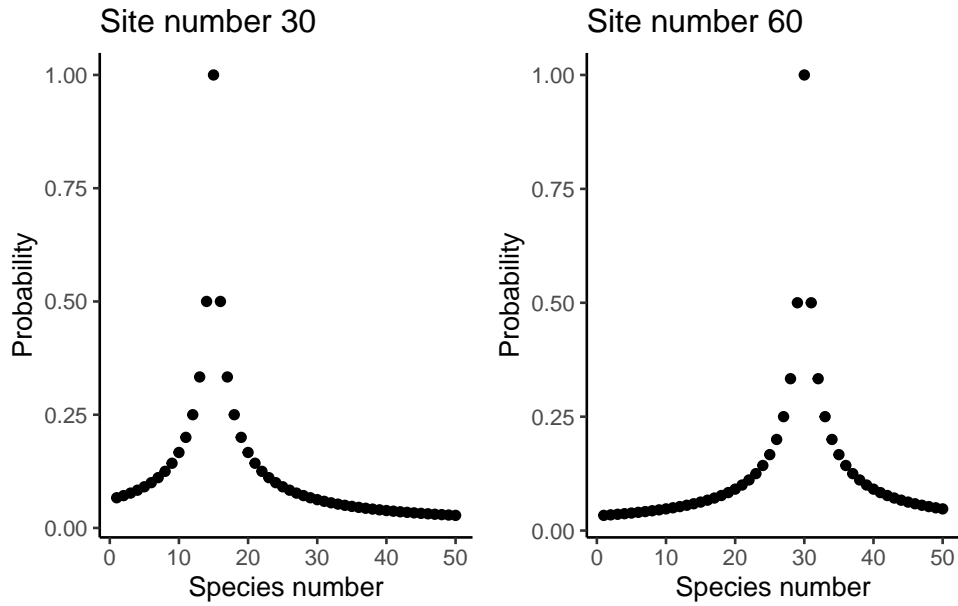


Figure 4: Probability for the occurrence of a given species at a given site. A wider niche is assumed here.

The resulting trait gradient analysis (TGA) is shown in Figure 5. It demonstrates that the TGA identifies a data generating process following perfect stoichiometric plasticity by yielding within-species regressions with a distribution of slopes that has a peak at one.

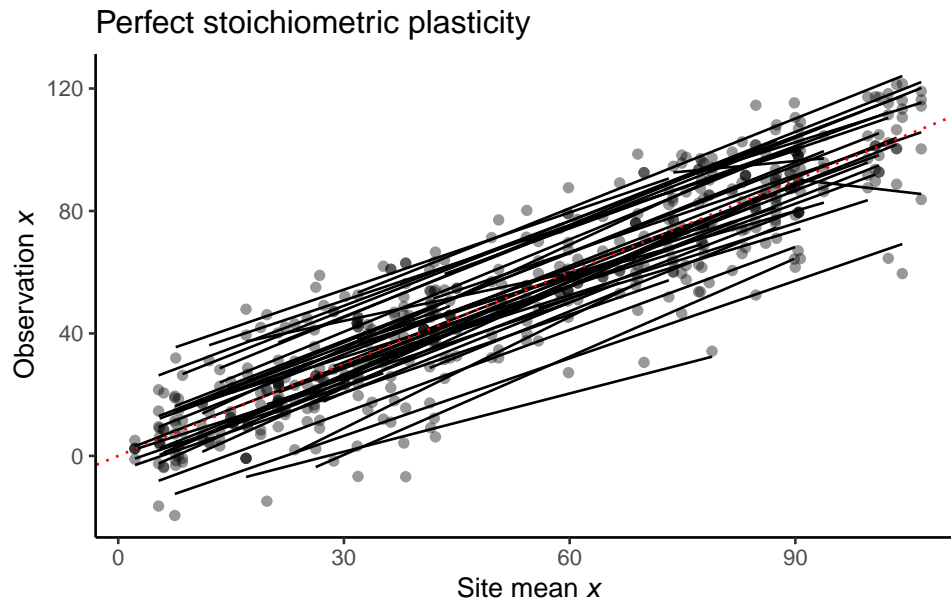


Figure 5: Trait gradient analysis for data generated assuming perfect stoichiometric plasticity. Solid lines represent the species-specific regressions of trait values observed at different sites vs. the respective site mean across all species growing at that site.

Publication figure

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`geom_smooth()` using formula = 'y ~ x'
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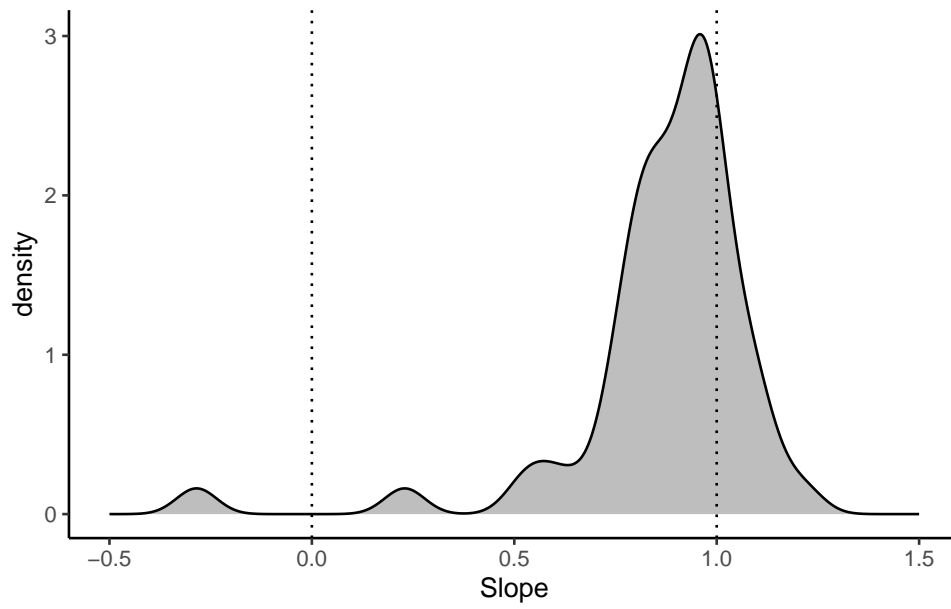


Figure 6: Distribution of slopes in the trait gradient analysis for data generated assuming the perfect stoichiometric plasticity.

