Spatial distribution of phylogenetic and trait diversity of angiosperms

Intro

- Phylogenetic study of where on earth is the early history of angiosperms disproportionally preserved?
  - I.e. where communities with longer than expected branch lengths

Intro

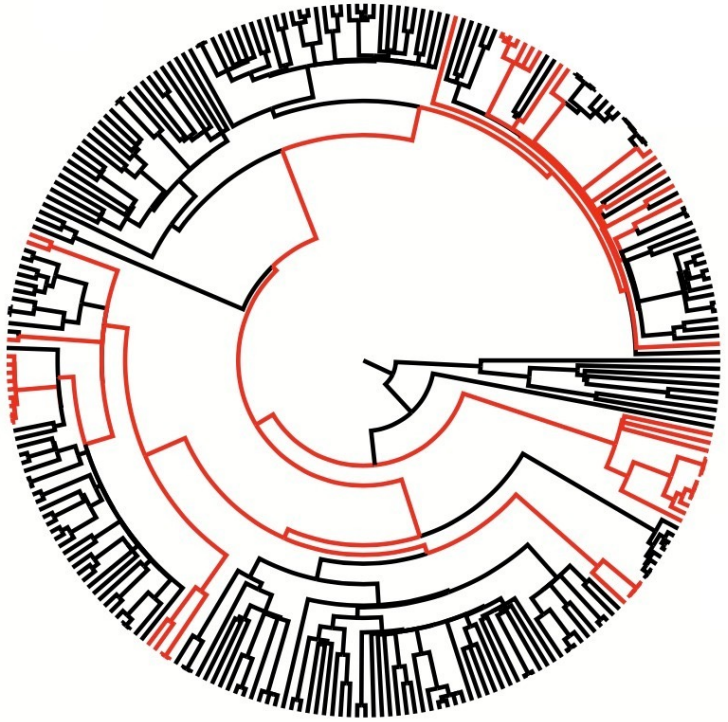
- How does this compare to traditional ideas about this
- Classic hypotheses
  - Traditionally focus on tropical rainforest, island environments and old geologies
  - Climatically stable ancient oceanic islands
  - New Caledonia, Madagascar, etc.
- OCBILs
  - Geologically old, climatically stable regions, with low fertility that allow for low extinction
  - South Africa, SW Australia, etc.

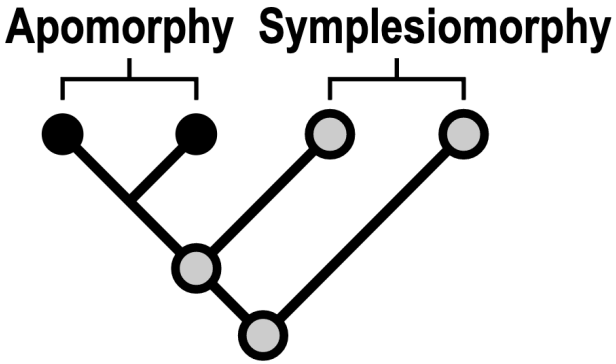
Intro

- Are PD &/or species richness higher in these areas
- Is the presence of plesiomorphic angiosperm traits associated with these areas?

How?

- First step – map where the early diversity of flowering plants is best preserved today
- Two ways to measure
  - Phylogenetic diversity
    - Popular modern method
    - Merge spatial and phylogenetic data, calculate one of several summary stats
  - Trait diversity
    - Often what early hypotheses referred to – plesiomorphic traits
- Wanted to assess in two ways – phylogenetic stats but traditionally morphologically conservative taxa were the focus



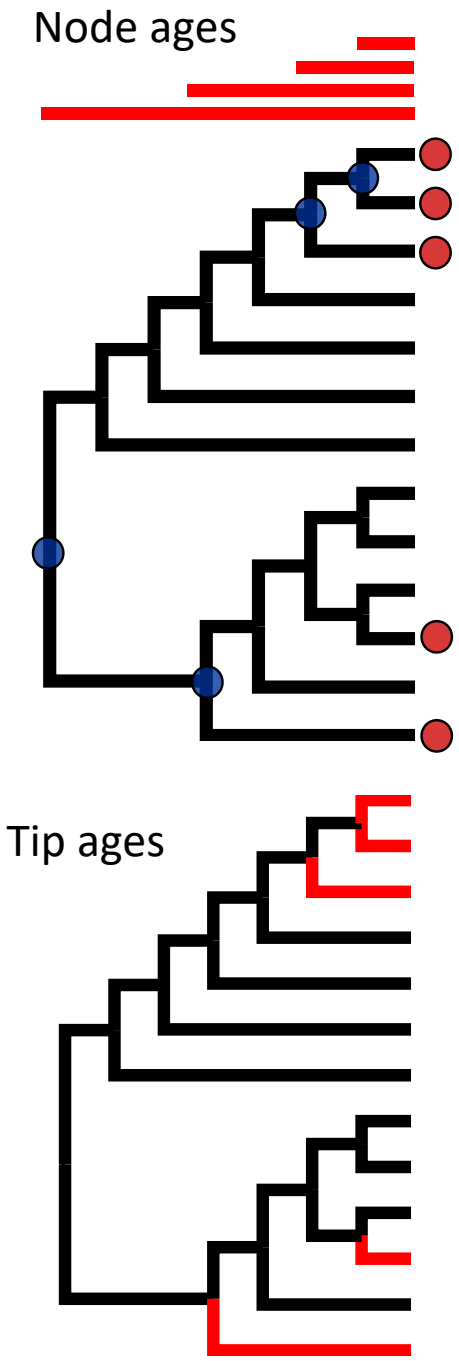


Biotaphy project

- Collaborative project between UF, KU, U Mich, MSU
- Preliminary analyses
- Data wrangling – linked ~40,000 SDMs with trait data, environmental predictors

Definitions

- Tip and node



Traits

- Made a list of 22 traits that
  - Are highly conserved
  - Able to be scored at the familial or ordinal levels
  - We will discuss 5: Laminar stamens, perianth phyllotaxis, stamen phyllotaxis, chloranthoid teeth, & ethereal oil cells

Traits

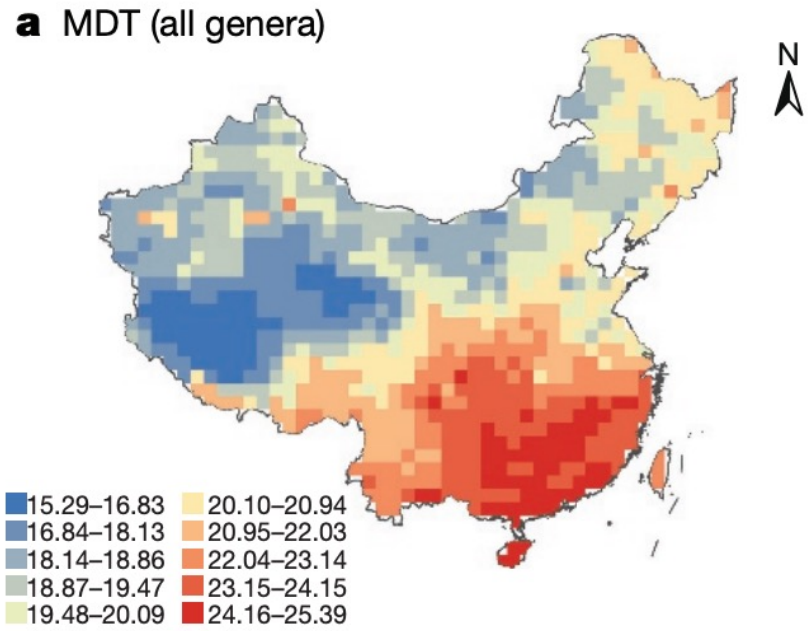
- Scored traits categorically as 0, 1, 2…, etc. at familial and ordinal levels
  - Traits recovered as ancestral by (Soltis et al. 2018) were assigned the “0 “ category
  - Any other number is assigned to derived states/ apomorphies
  - Traits were associated to individual taxa by GBIF backbone taxonomy

Traits

- Used these traits as a proxy for overall ancestral trait diversity
- Focused on proportion of the community with plesiomorphic traits
  - E.g. --A grid cell with 0.5 chloranthoid teeth = half of the community members in that grid cell have chloranthoid teeth
  - Considered both individual traits and means

Goals

- Determine global patterns of angiosperm community age
- Classic hypotheses about ”relicts” in climatically stable island environments – Madagascar, New Caledonia
- In many respects, expanding on a recent Nature paper on the flora of China – uncovered major age gradients related to climate stability and orogeny
  - Relied heavily on taxonomic ranks



LETTER

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Evolutionary history of the angiosperm flora of China

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Tip and node ages

- Largely measure the same thing… R^2 0.6467
- Typical problem – separating species richness effects from biodiversity measures
  - Not cumulative like Faith's PD but there could still be sampling effects
  - Node height ~ species richness R^2 0.1289
    - Could include species richness as predictor to separate
  - Tip length ~ species richness R^2 0.004349, continued with this
  - Explanatory power of environmental variables was also better for tip length (with ~0.4 more R^2)
- Focused on tip lengths

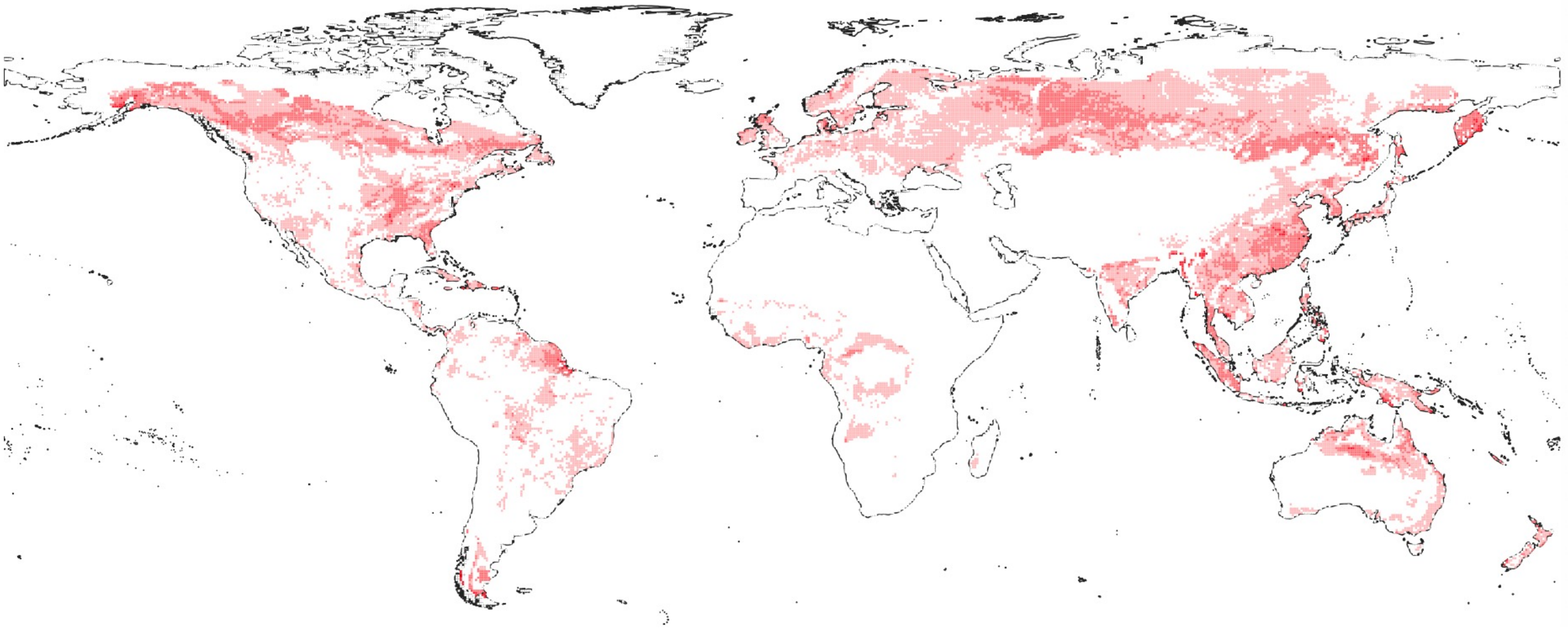
Dataset properties

- Are communities with phylogenetically old species enriched for plesiomorphic traits?
  - Plesiomorphic traits correlate weakly or not at all to phylogenetic measures of age
  - E.g., ethereal oil cells vs. mean node age, R^2 0.024

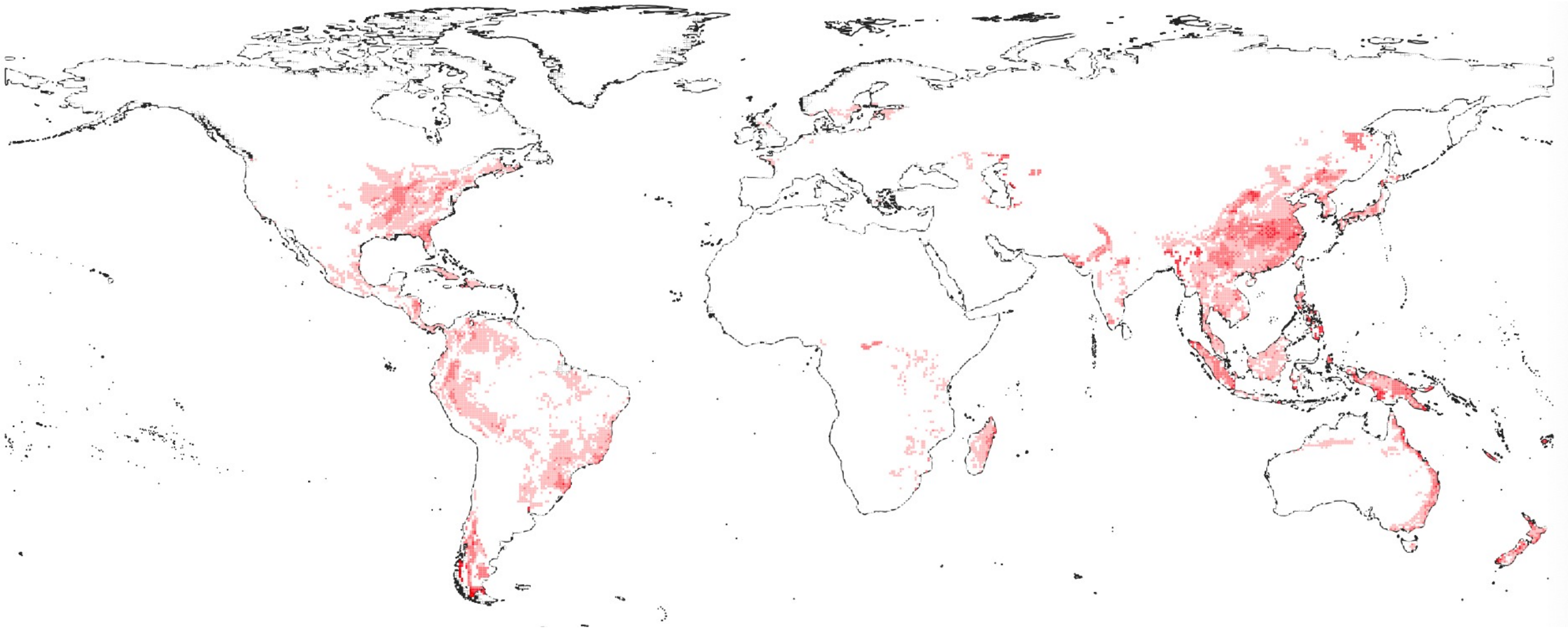
Maps of trait diversity

- Showing fractional richness of plesiomorphic trait
  - Each grid shows species richness for only taxa with the trait
- Color scale
  - Jenks natural breaks (scaling is long-tailed in many)
    - Deals with exponential and other distributions
    - Brings out contrast in the dataset
  - Scaling depends on variable (not 0% to 100%)

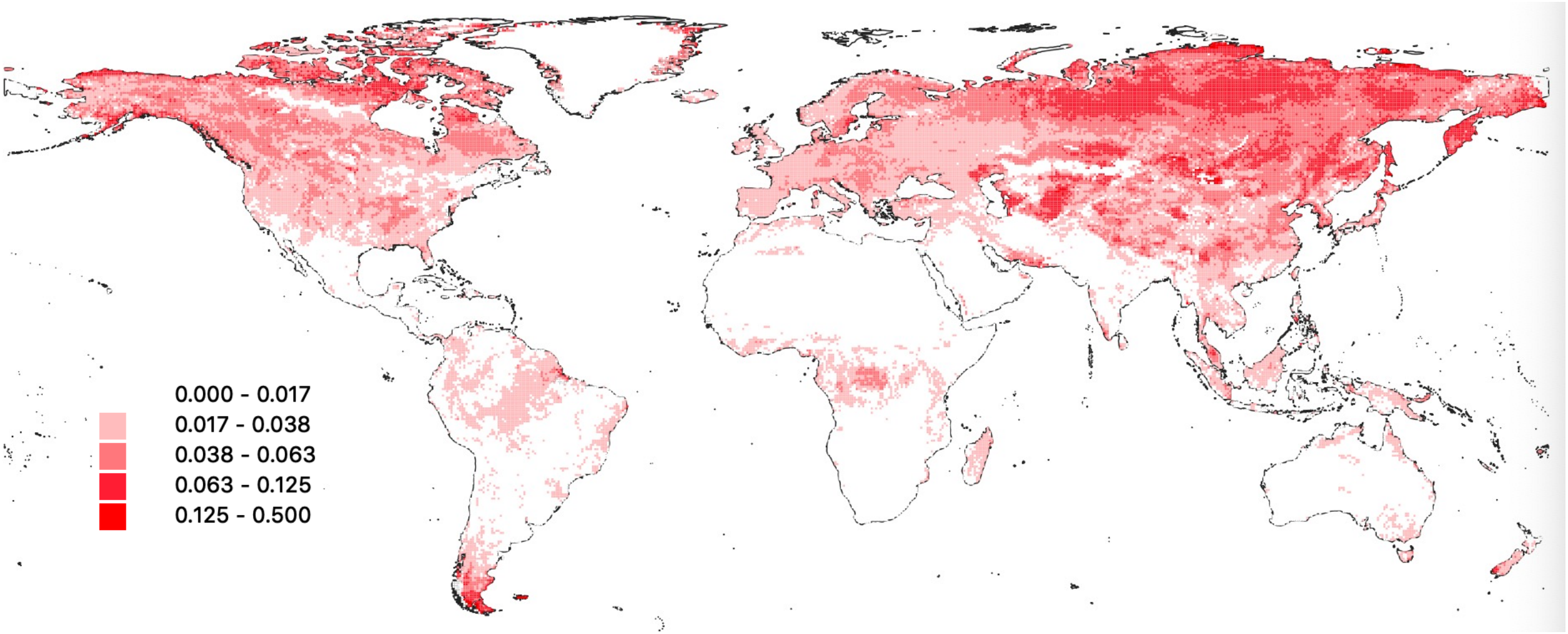
Laminar stamens



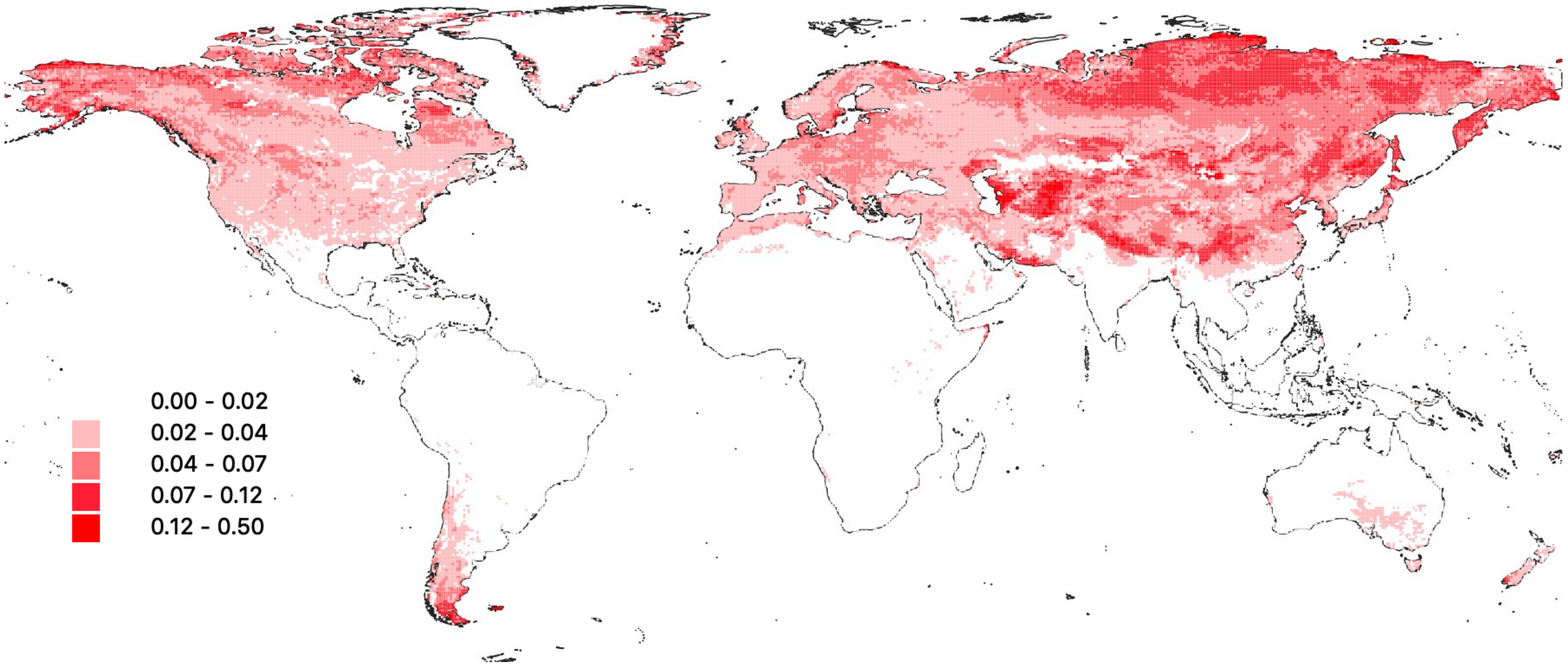
Perianth phyllotaxis



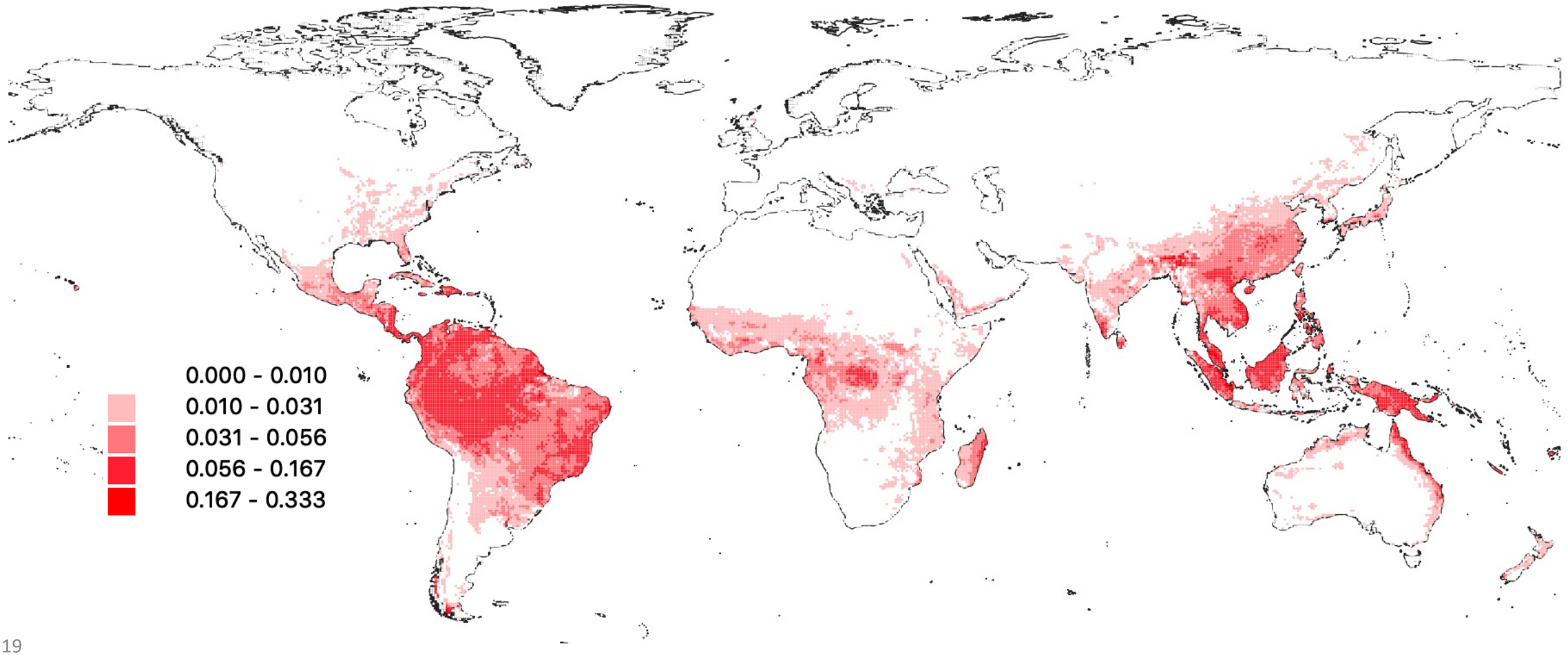
Stamen phyllotaxis



Chloranthoid teeth

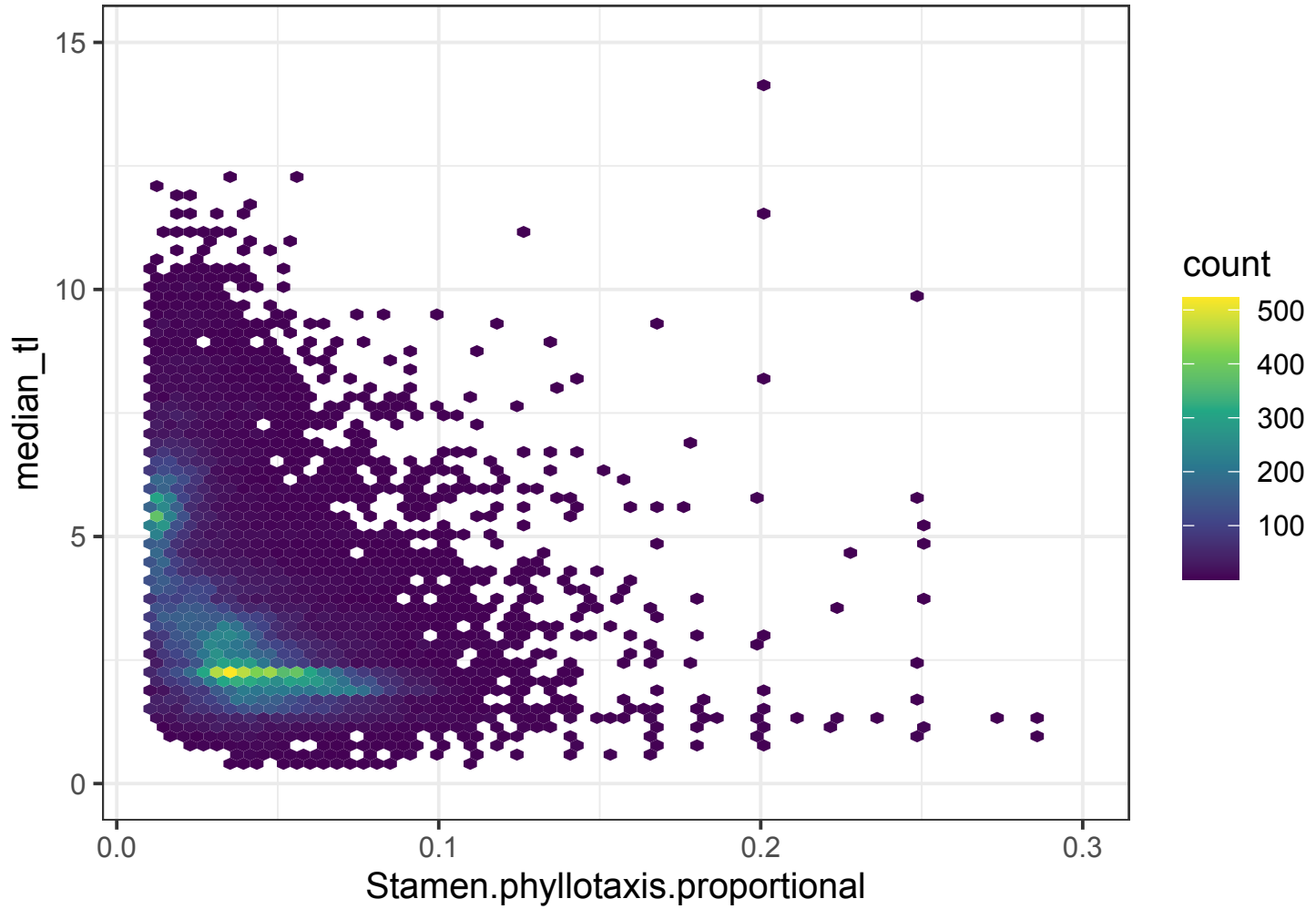


Ethereal oil cells

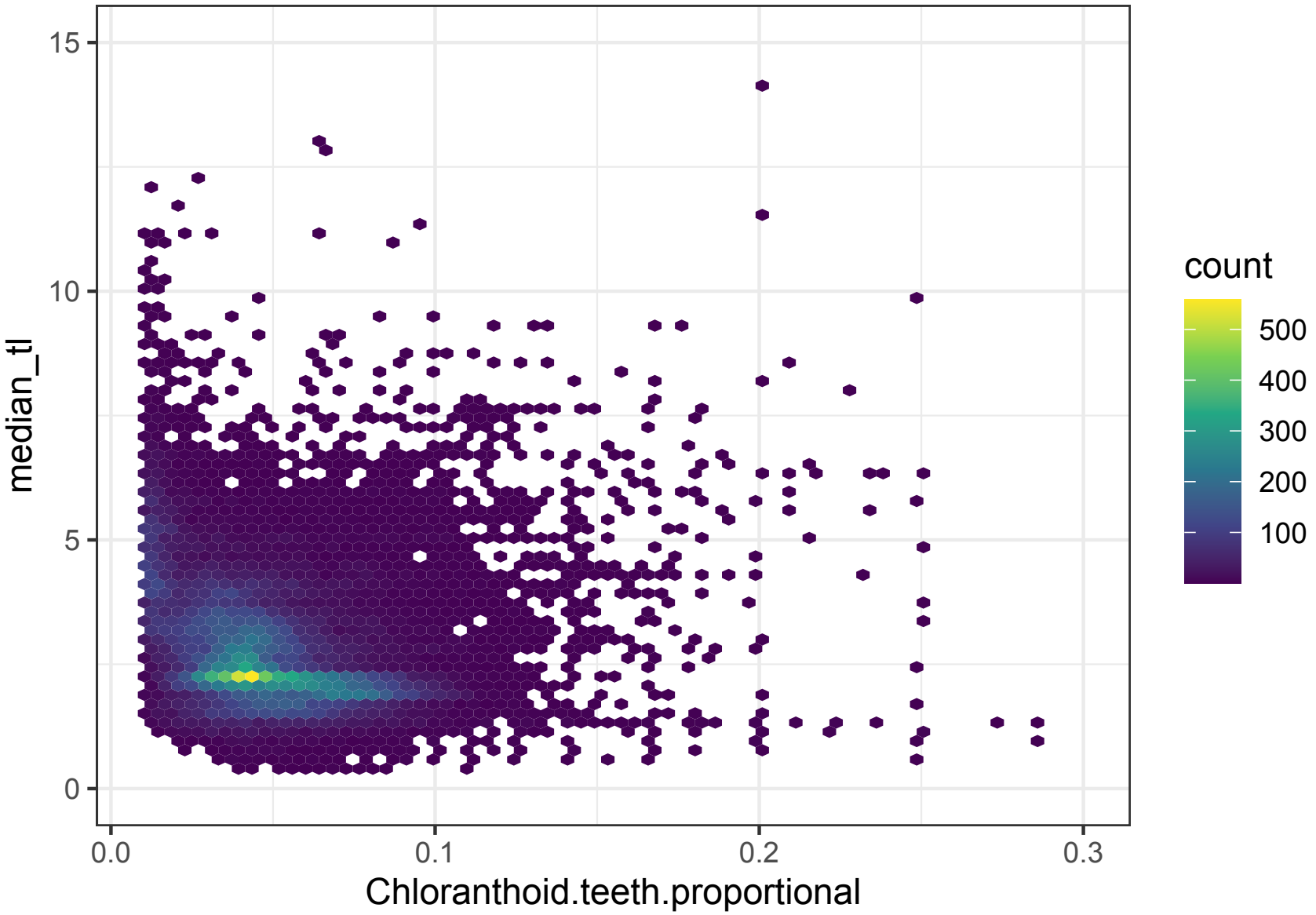


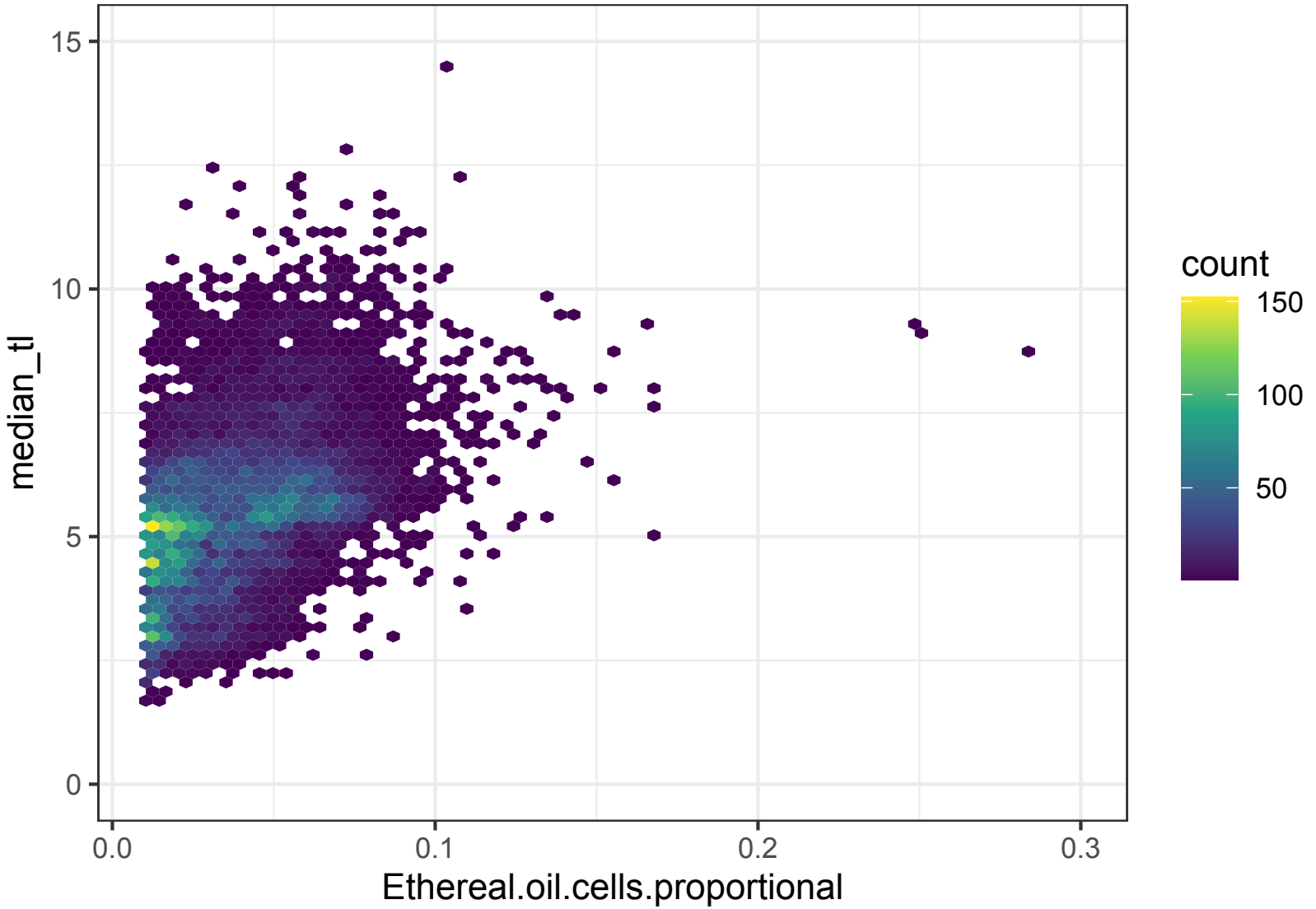
What have we learned?

- Not all traits share the same distribution
- We predicted we could find areas where ancestral traits were concentrated, but we found little concordance among them



More common pattern – reverse of expectation


median_tl
15
10
5
0
0.0
0.1
0.2
0.3
Chloranthoid.teeth.proportional
count
500
400
300
200
100



Opposite pattern – follows expectations

Note – some traits are too rare to produce meaningful plots

Model fitting

- Put grid cells in a model fitting framework
- Generalized Linear Model
- Focused on tip lengths per reasons from previous slide
  - Treated tip length as response variable
- Seek to identify environmental drivers of community age metrics

Model fitting

- Model of environment – 12 temperature, precipitation, soil predictors, tip length as response
  - Adj. R2 0.663 – good explanatory power
  - Normalized coefficients with intuitive interpretation
  - Positive correlation (associated with older species): precipitation, temperature, elevation
  - Negative correlation (associated with younger species): seasonality, soil fertility
  - Variable importance (absolute value of standardized coefficients): Mean annual temperature → mean annual precipitation → soil predictors

Summary of initial observations

- Trait-based measures that try to capture classic hypotheses
- Traits based measures
  - don’t agree:
    - Among themselves
    - With phylogenetic measures of species age
  - Have different environmental correlates

Next steps

- Tease apart differing environmental relationships with measures of community “age” or PD
- Different ways of measuring climate disturbance – investigate central hypothesis of historical climate-trait relationships but for now looks like little relationship