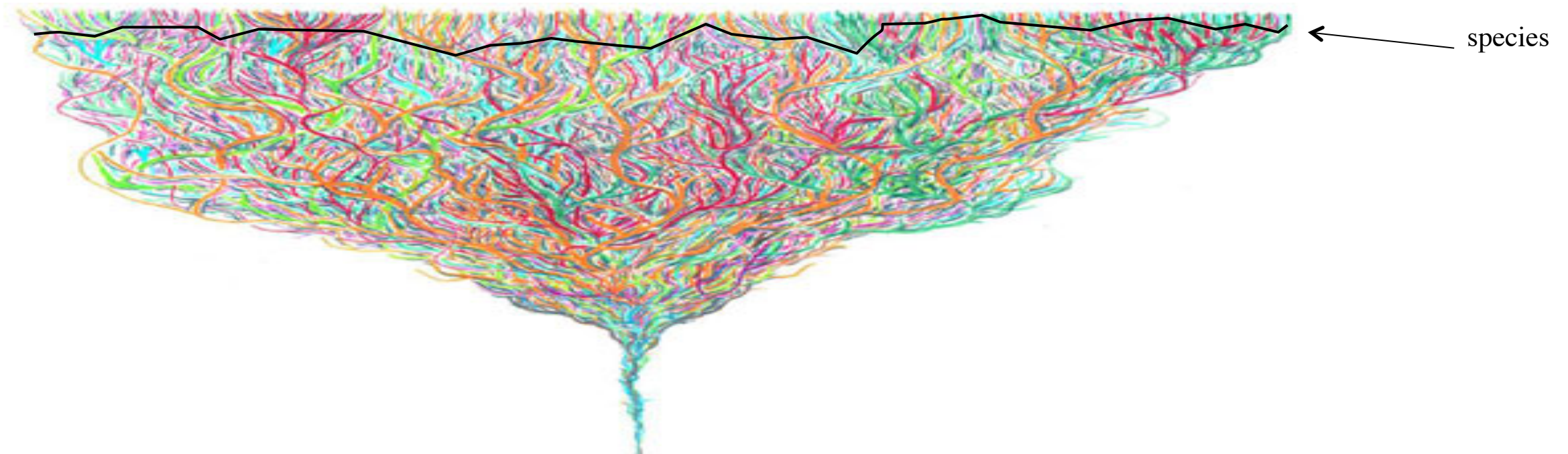# Biodiversity isn't just species

- Biodiversity should consider the *whole tree of life*, not just named species.

- There are clades smaller and larger than the traditional species level.

- Species are not comparable between lineages, just an arbitrary cut-off somewhere along a branch in the tree of life.
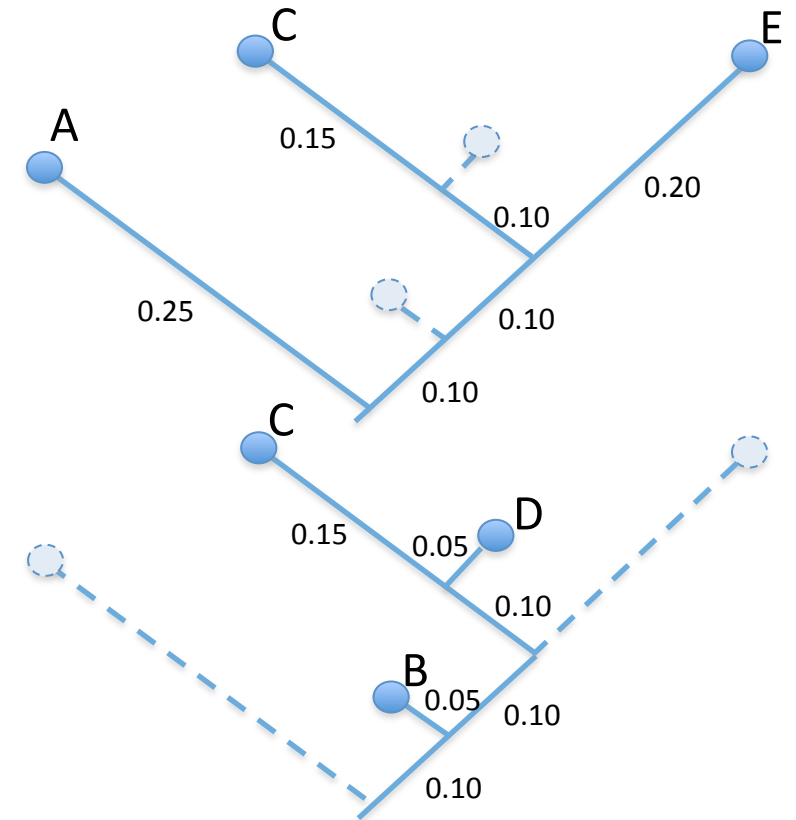

species

Phylogenetic Diversity

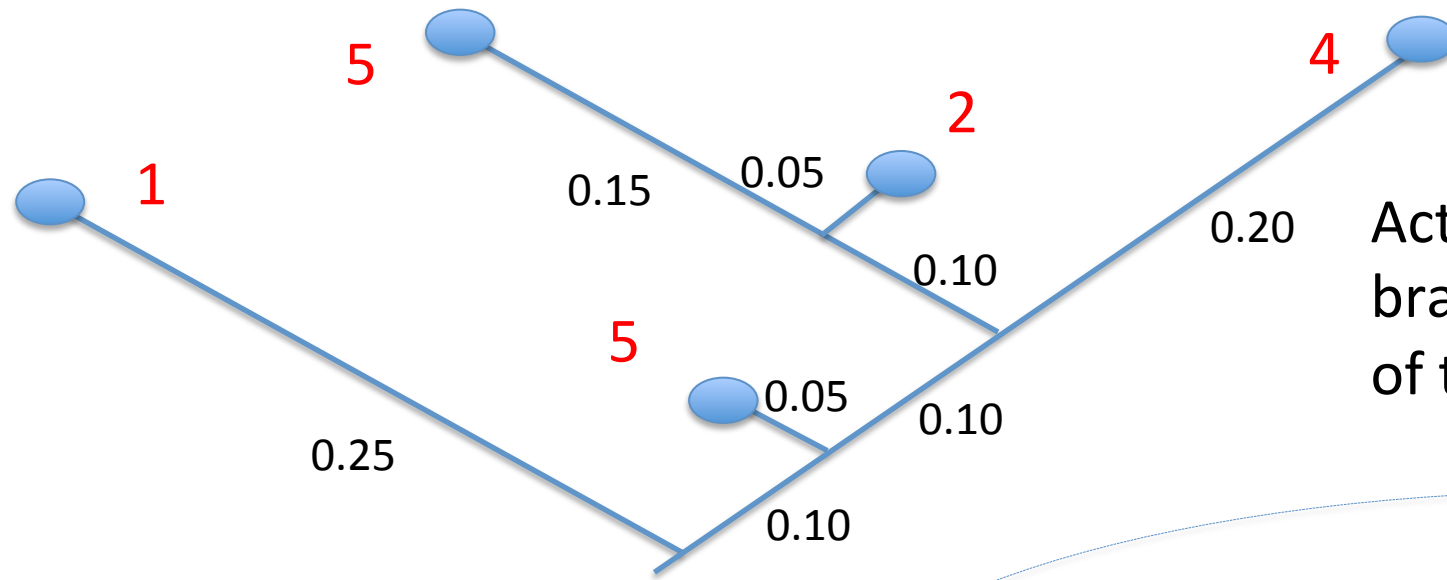PD (Faith, 1992) is the sum of the branches that lead to all terminals in an area
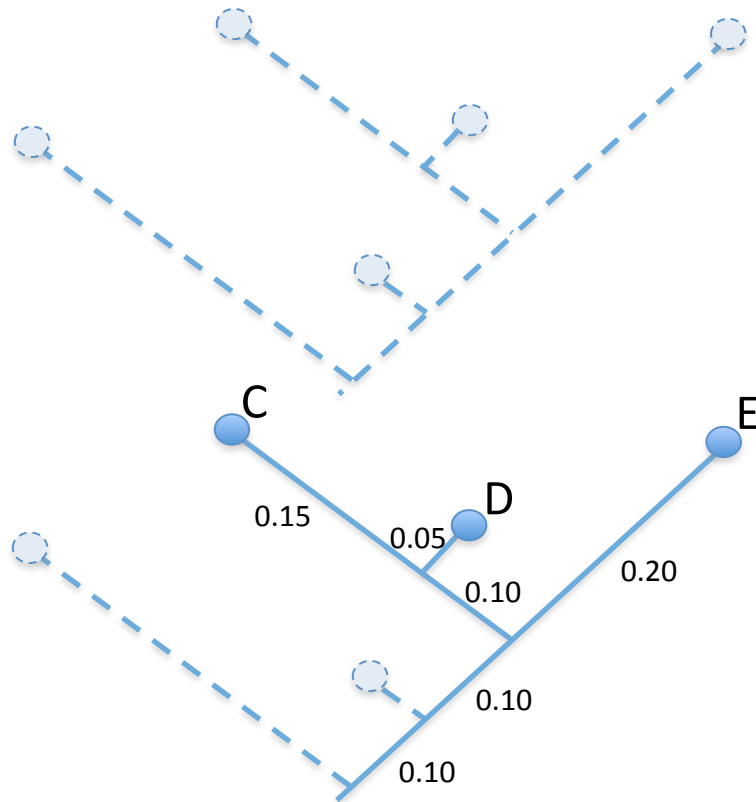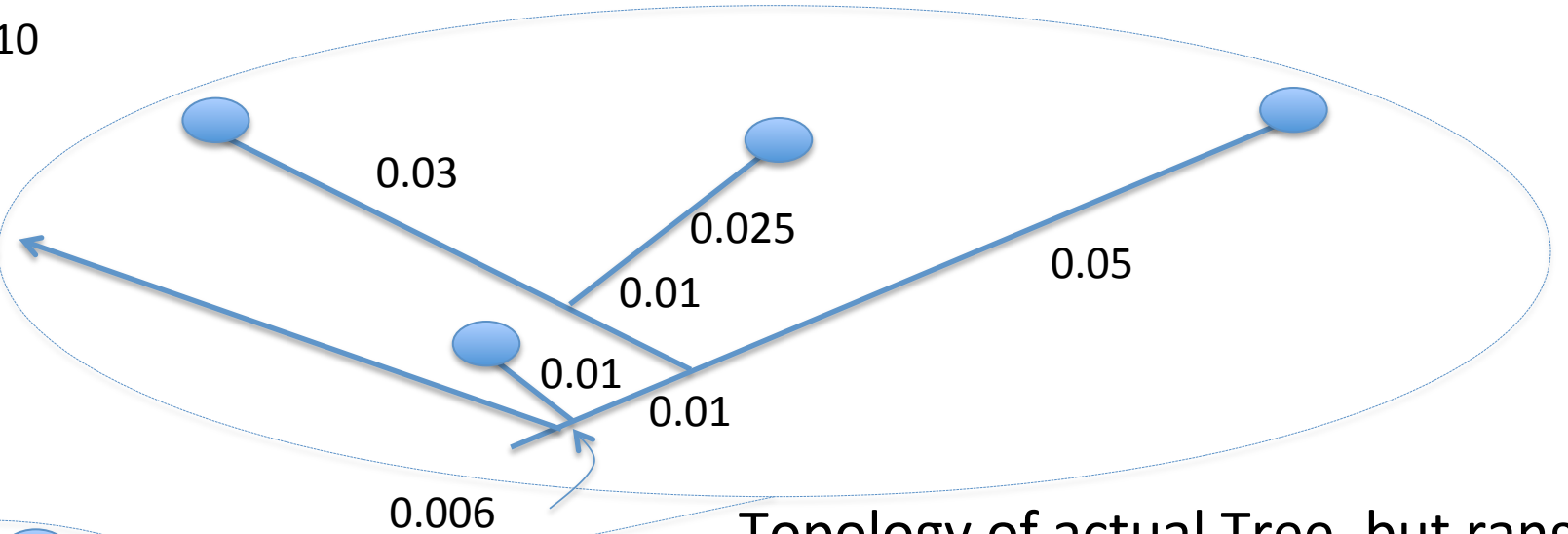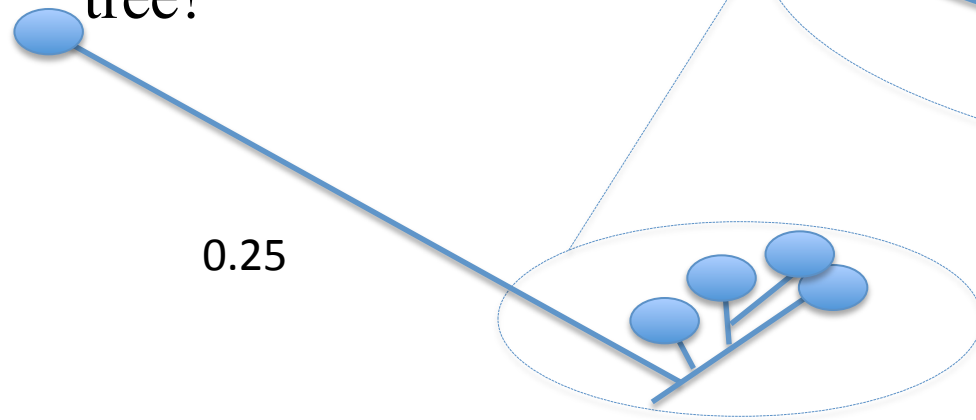
How is PE calculated?
Rosauer et al., (2009)

Actual Tree again, with unmodified branch lengths, showing the range size of terminal taxa in red
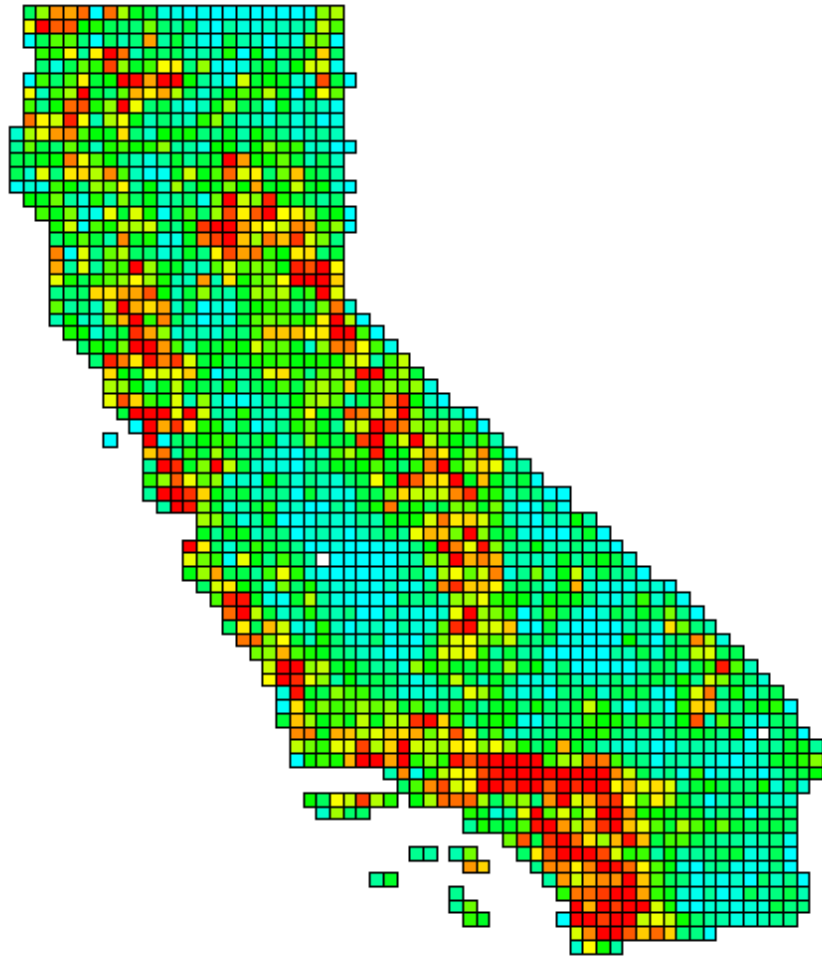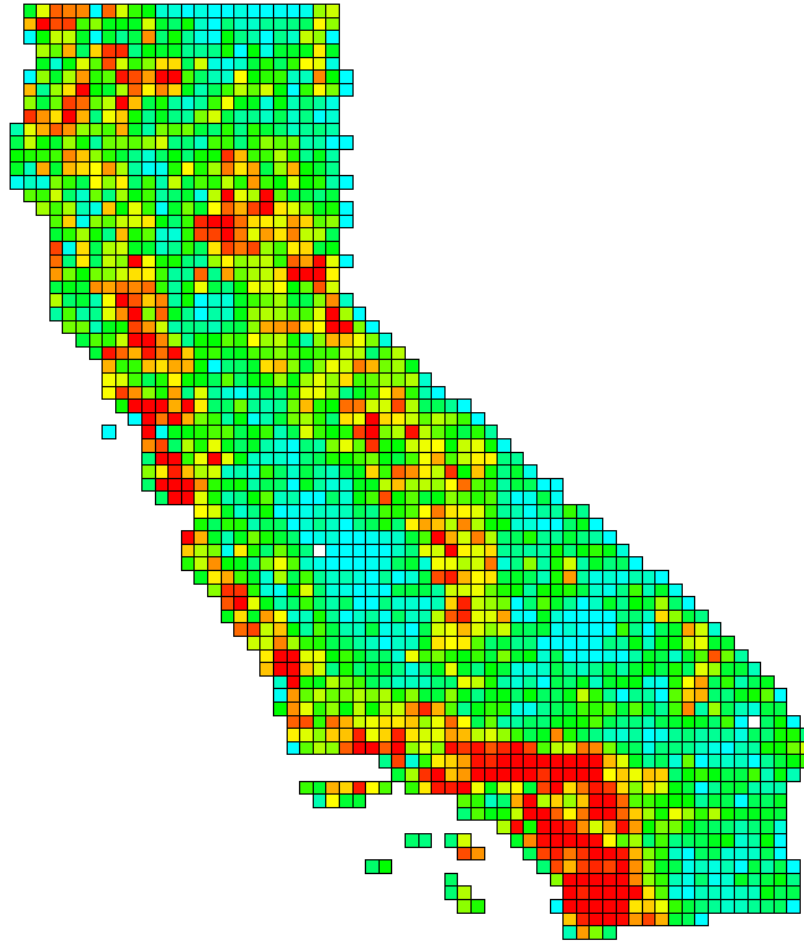
This is a range-weighted tree!

Topology of actual Tree, but range-weighted, i.e., with each branch length divided by its range = PE

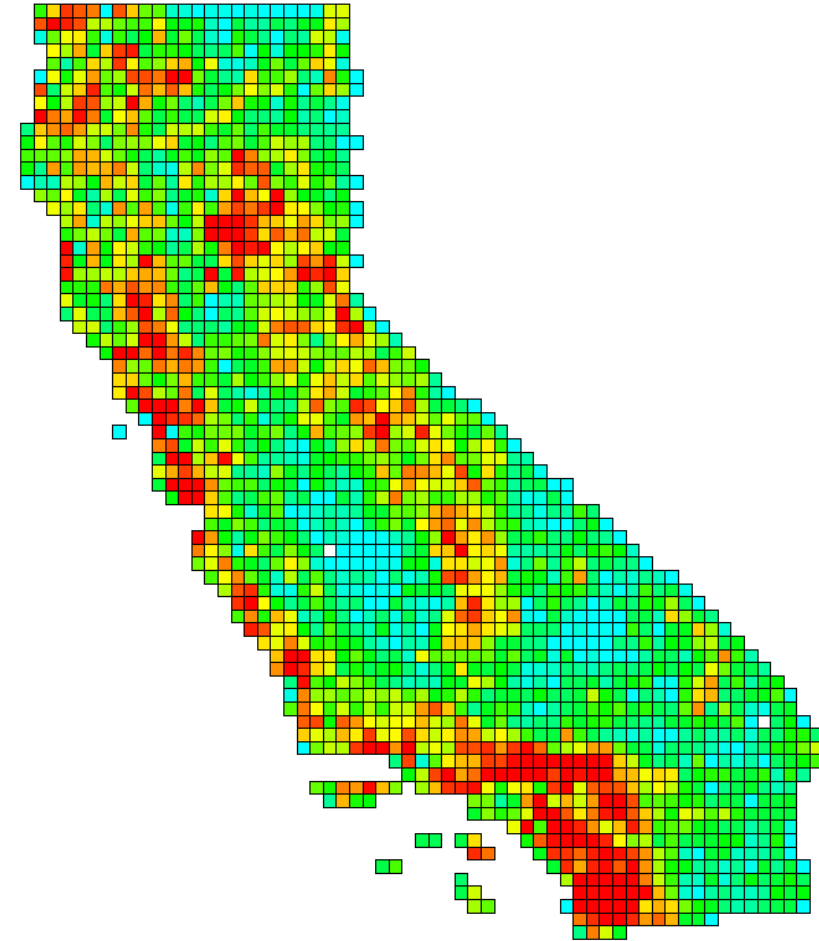So PE is PD of a range-weighted tree!

A comparison of richness measures

All species

Clades

PD

Randomizations are necessary

Observed values do not tell us much, unless we understand how much to expect.

No known null distribution for PD or PE → need to use a randomization test to generate a null expectation.

Biodiverse randomly reassigns the same number of terminal taxa to a grid cell without replacement (thus keeping constant the total number of grid cells each species occurs in, and the richness of each grid cell).

Repeated for 999 trials and compare against the observed (null) result.

Spatial phylogenetics

Investigations on species alone lacks the depth of a phylogenetic approach.

Spatial Phylogenetics combines two main elements, a phylogeny and a spatial dataset representing phylogeny terminals.

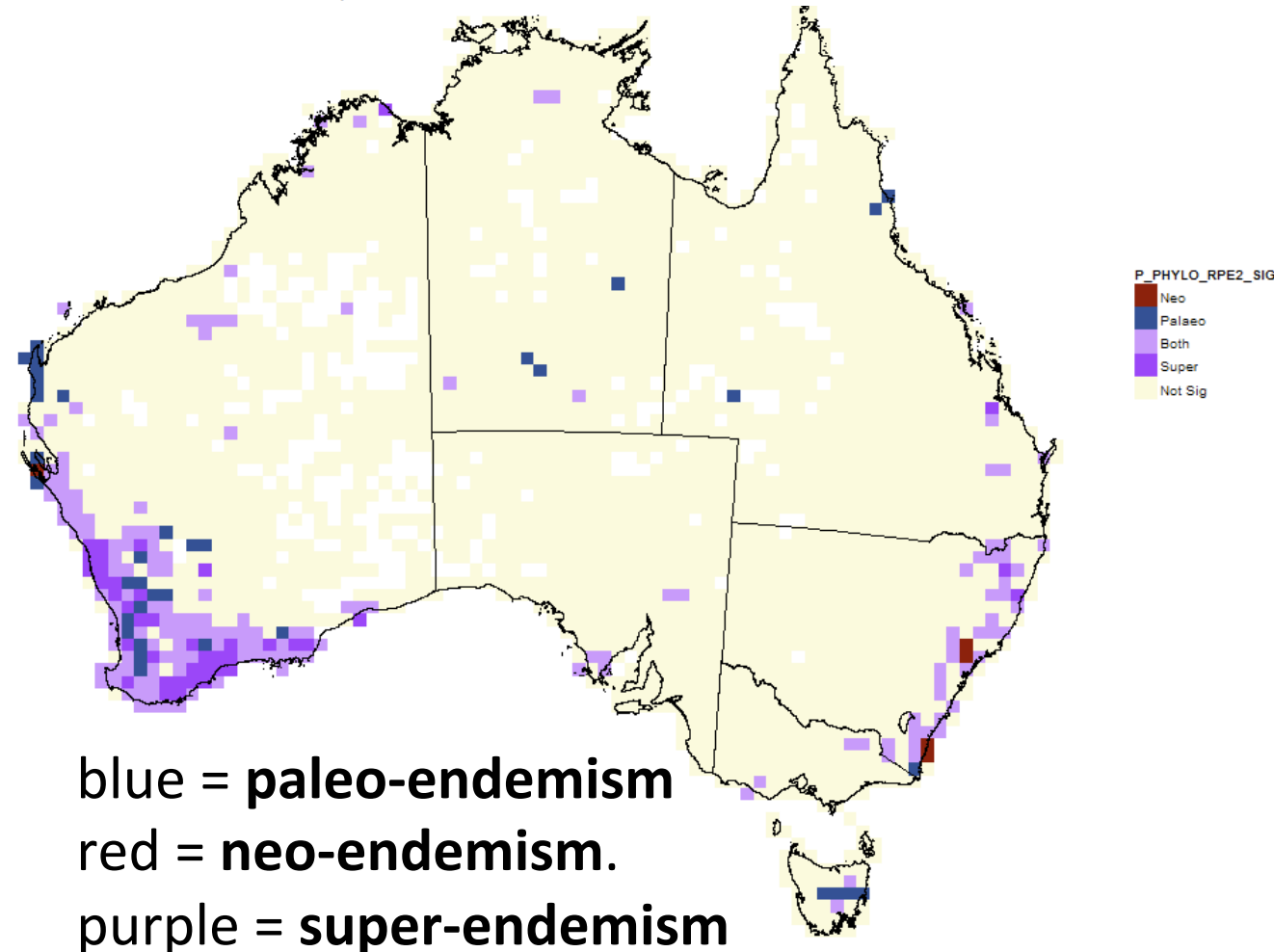Can be applied at any taxonomic and geographic level.

Measures diversity and endemism based on branch length and phylogenetic relatedness.

Because the approach is rank free it doesn't matter what taxonomic levels the terminals represent, as long as they are monophyletic.
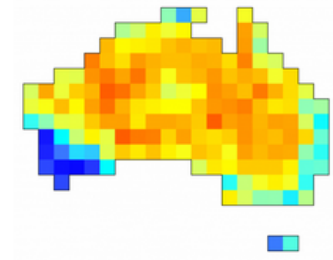
Relatively robust to lumping and splitting decisions.

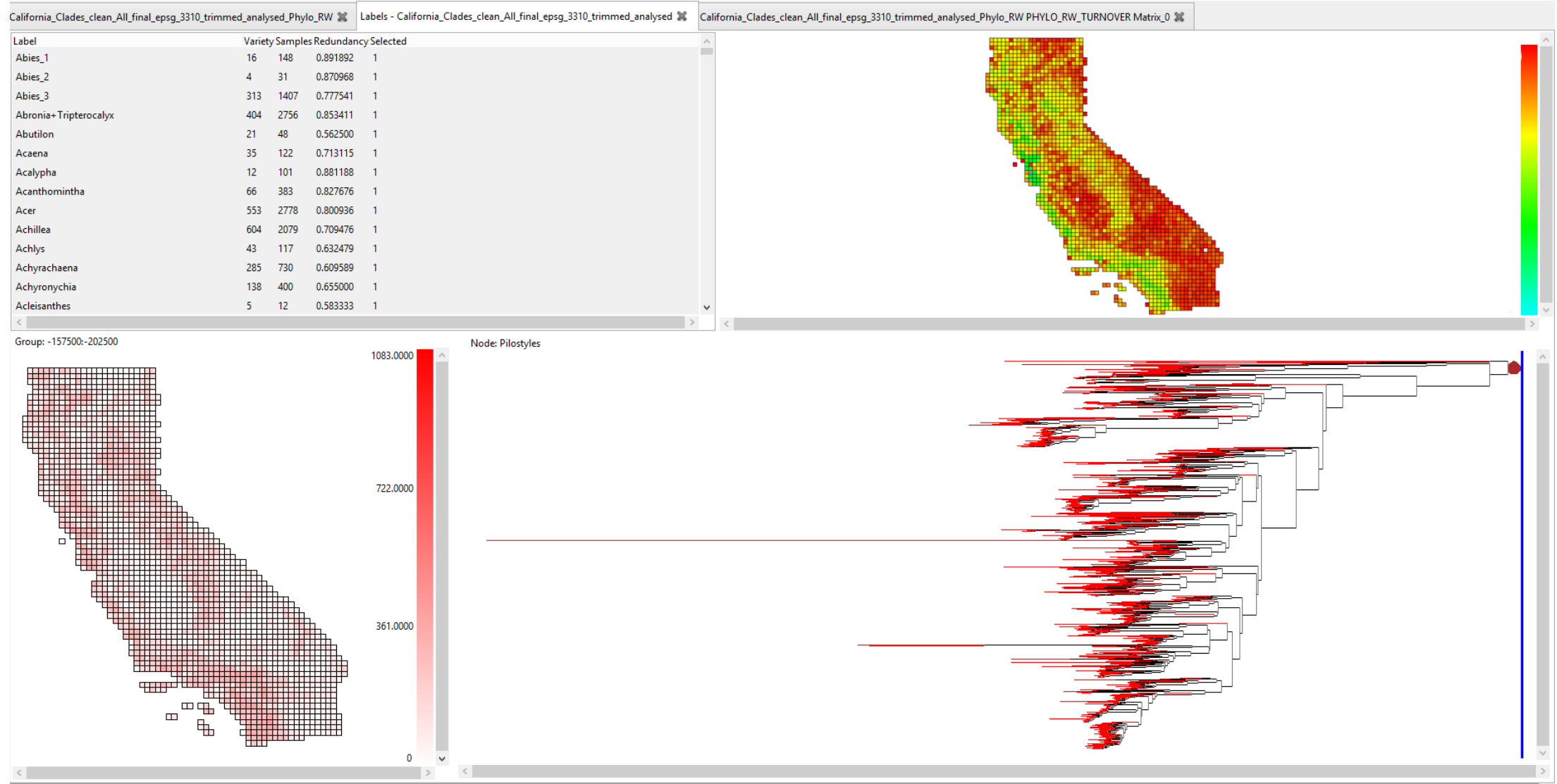Phylogenetic measures of biodiversity and neo- and paleo-endemism in Australian *Acacia*

Brent D. Mishler[1,2], Nunzio Knerr[1], Carlos E. González-Orozco[1,3], Andrew H. Thornhill[1,4], Shawn W. Laffan[5] & Joseph T. Miller[1]

P_PHYLO_RPE2_SIG
- Neo
- Palaeo
- Both
- Super
- Not Sig

blue = **paleo-endemism**
red = **neo-endemism**.
purple = **super-endemism**

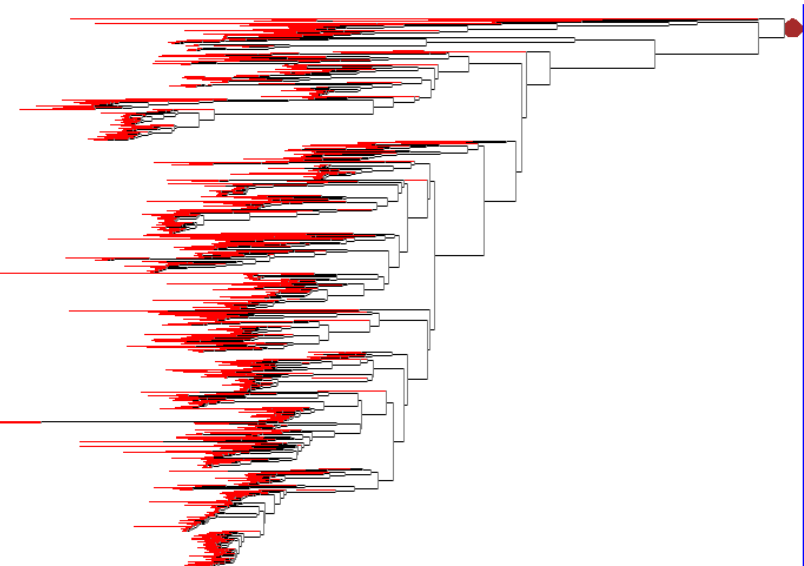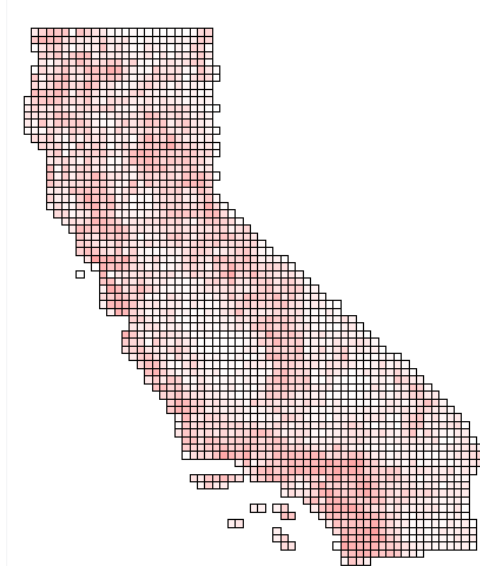# Diversity and endemism metrics calculated using Biodiverse

https://github.com/shawnlaffan/

Observed patterns

Tip Richness (**TR**)
A count of the number of taxa in each grid cell.

Weighted Endemism (**WE**)
A sum of the endemism values of each taxon in a cell
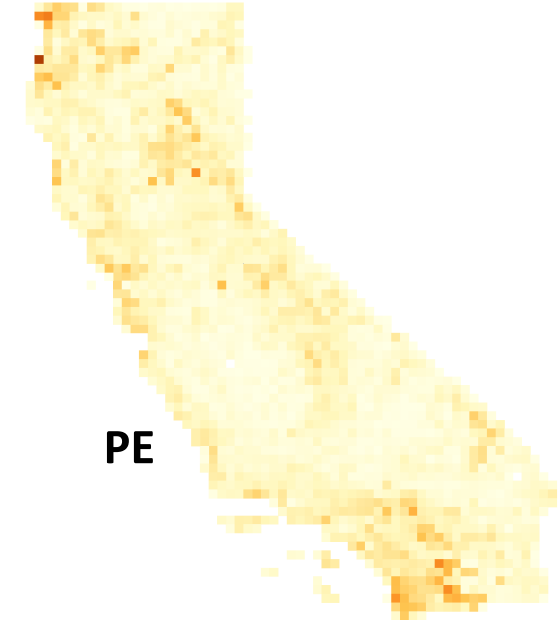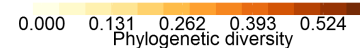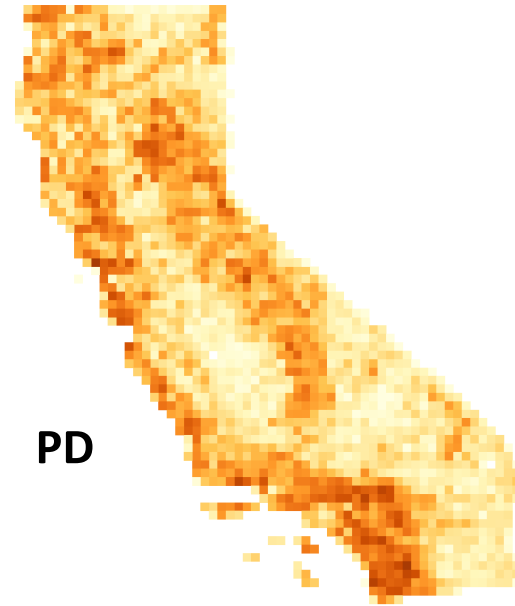
Phylogenetic Diversity (**PD**)
The sum of the phylogenetic branch lengths present in a site.

Phylogenetic Endemism (**PE**)
PD weighted by how common those branches of the tree are elsewhere in the region.

Taxon Richness

0   100   201   302   402

Weighted Endemism

0.00   0.90   1.81   2.71   3.62

TR

WE

PD

PE

0.000   0.131   0.262   0.393   0.524
Phylogenetic diversity

0.000   0.001   0.002   0.003   0.004
Phylogenetic endemism
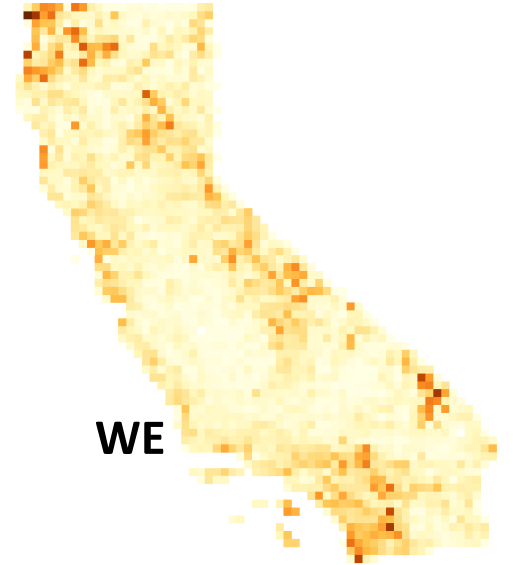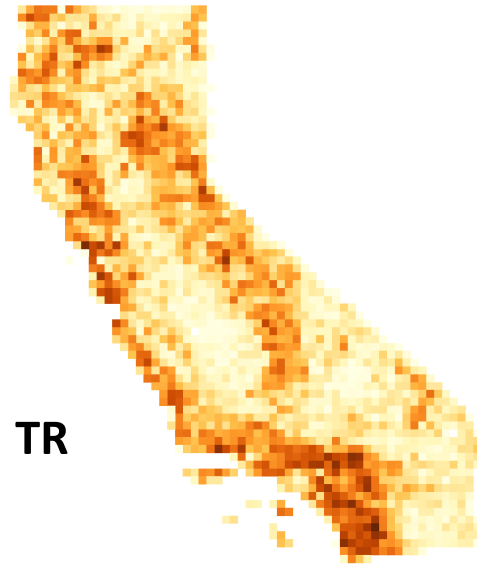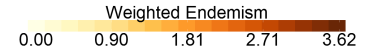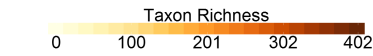
PD randomized

Compares the observed PD with the PD measured on the same tree for 999 randomly selected sets of the same number of taxa.

Are the co-occurring taxa in a grid cell more or less closely related to each other than would be expected by random?

Significant locations

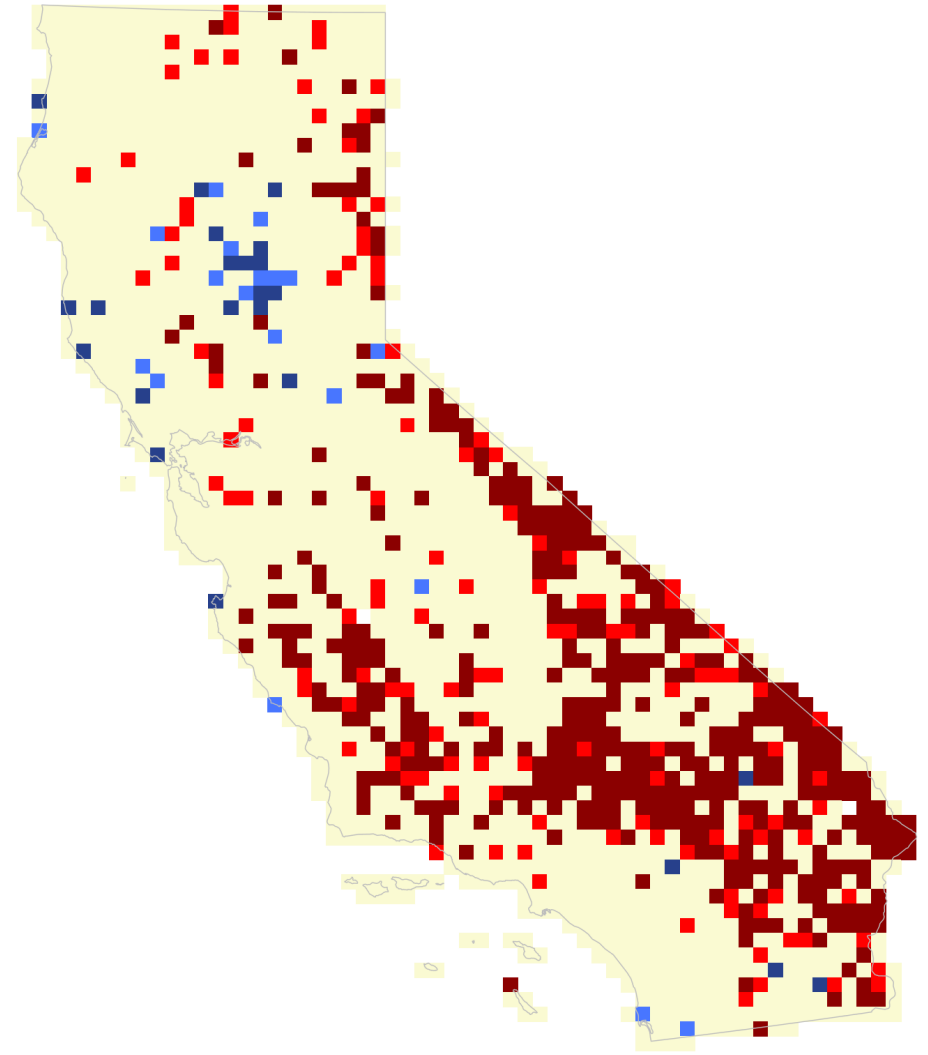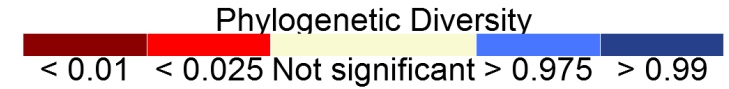may have an ecological explanation.

Phylogenetic over-dispersion (blue)

close relatives may exclude each other.

Phylogenetic clustering (red)

clades may have evolutionarily conservative habitat preferences and thus close relatives co-occur.

Phylogenetic Diversity

| < 0.01 | < 0.025 | Not significant | > 0.975 | > 0.99 |

Relative Phylogenetic Diversity (RPD)

$$\frac{\text{PD calculated using the original tree}}{\text{PD calculated using a comparison tree with all branch lengths equal}}$$
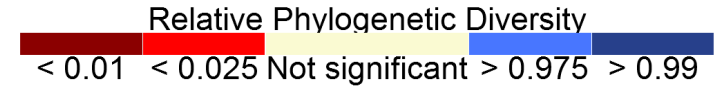
Is there an overrepresentation of long branches or short branches

in a grid cell as compared to what would be expected if the same

number of taxa had been selected at random?

Significant locations
more likely to relate to biogeographic and evolutionary processes.

Concentration of long branches (blue)
a refugium, or the dispersal of a few members of large clades that
mainly occur outside of the study region.

Concentration of short branches (red)
recent evolutionary divergence.

Relative Phylogenetic Diversity

< 0.01   < 0.025   Not significant   > 0.975   > 0.99
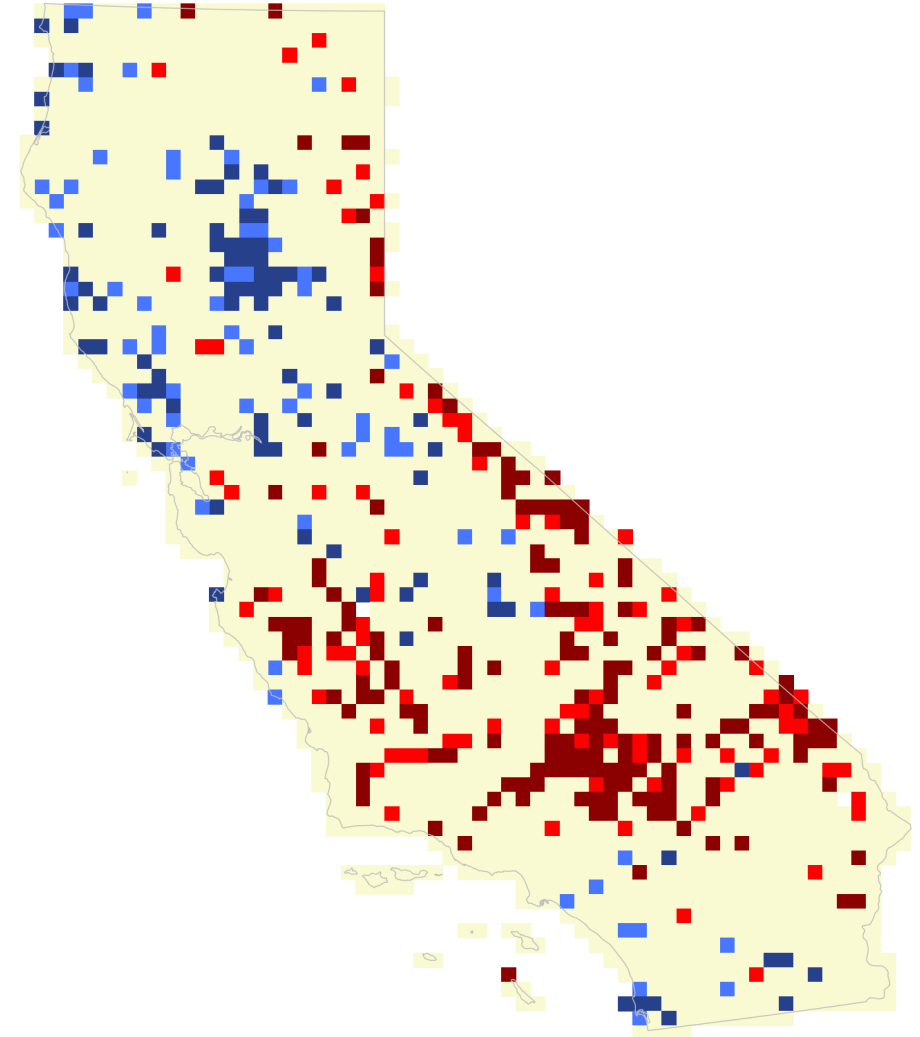
CANAPE: Categorical Analysis of Neo- And Paleo-Endemism

RPE - *relative phylogenetic endemism* = $\dfrac{\text{PE on the range-weighted original tree}}{\text{PE on a range-weighted comparison tree with all branch lengths equal}}$

- Use RPE to find and classify centers of endemism.

- Since RPE is a ratio, we need to be sure that there is indeed a high amount of endemism.

- **Two-step** process for CANAPE analysis:

- First, to determine if a place is a center of significantly high PE, a grid cell needs to be significantly high (one-tailed test) in either the numerator, the denominator, or both.

- Second, if (and only if) a grid cell passes one of those tests, we divide the centers of endemism into three meaningful, non-overlapping categories…

original tree

range-weighted original tree

comparison tree

range-weighted comparison tree
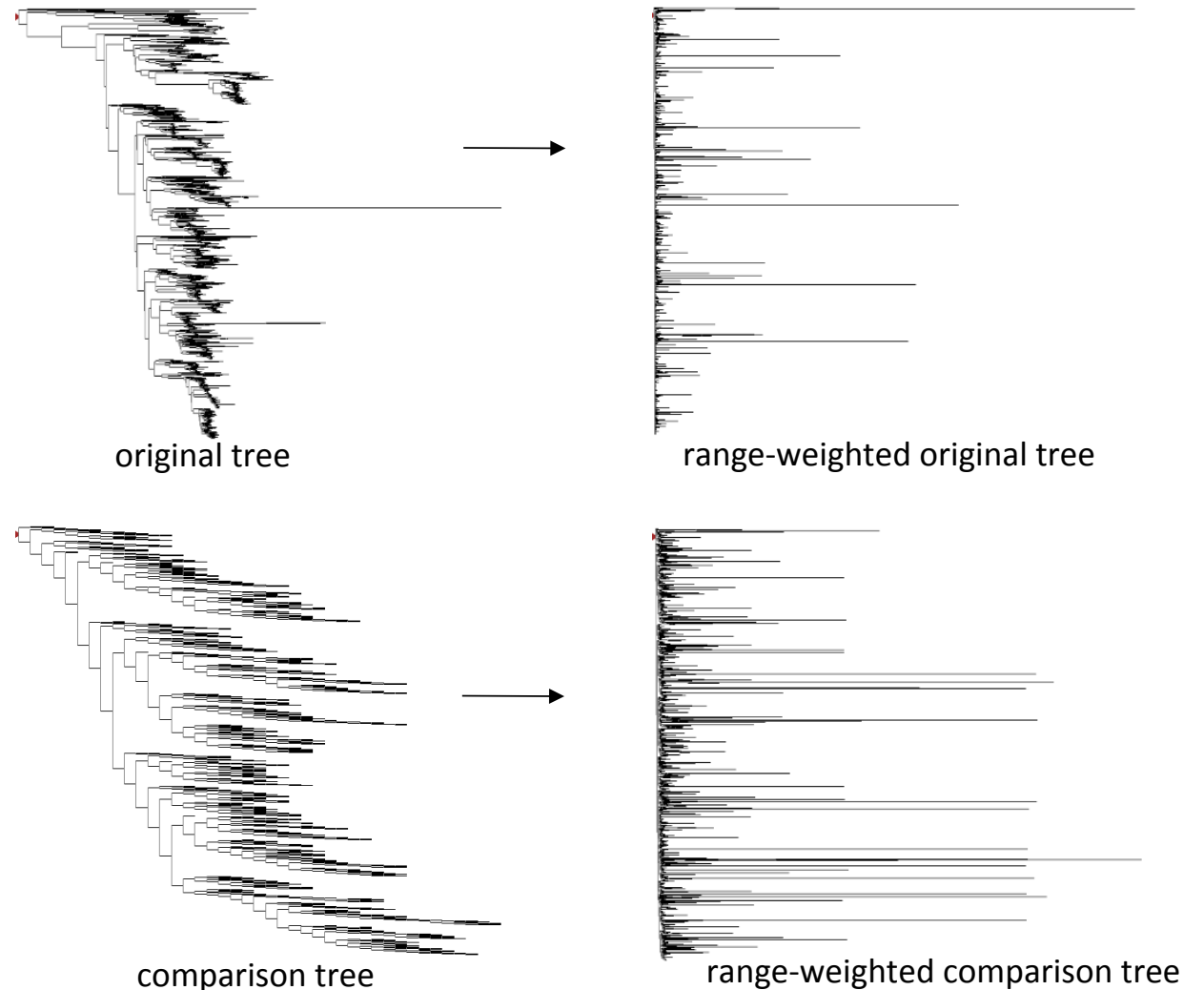
CANAPE: <u>C</u>ategorical <u>A</u>nalysis of <u>N</u>eo- <u>A</u>nd <u>P</u>aleo-Endemism

Is there an overrepresentation of range-restricted long or range-restricted short branches in a cell as compared to what would be expected if the same number of taxa had been selected at random?

- if a point is significantly high or low in RPE (two-tailed test), then it is a center of **paleo-endemism (blue)** or **neo-endemism (red)** respectively.

- if it is significantly high (one-tailed test) in both the numerator and the denominator (taken alone), but not significant for RPE, then it is a center of **mixed or super-endemism (purple)**.
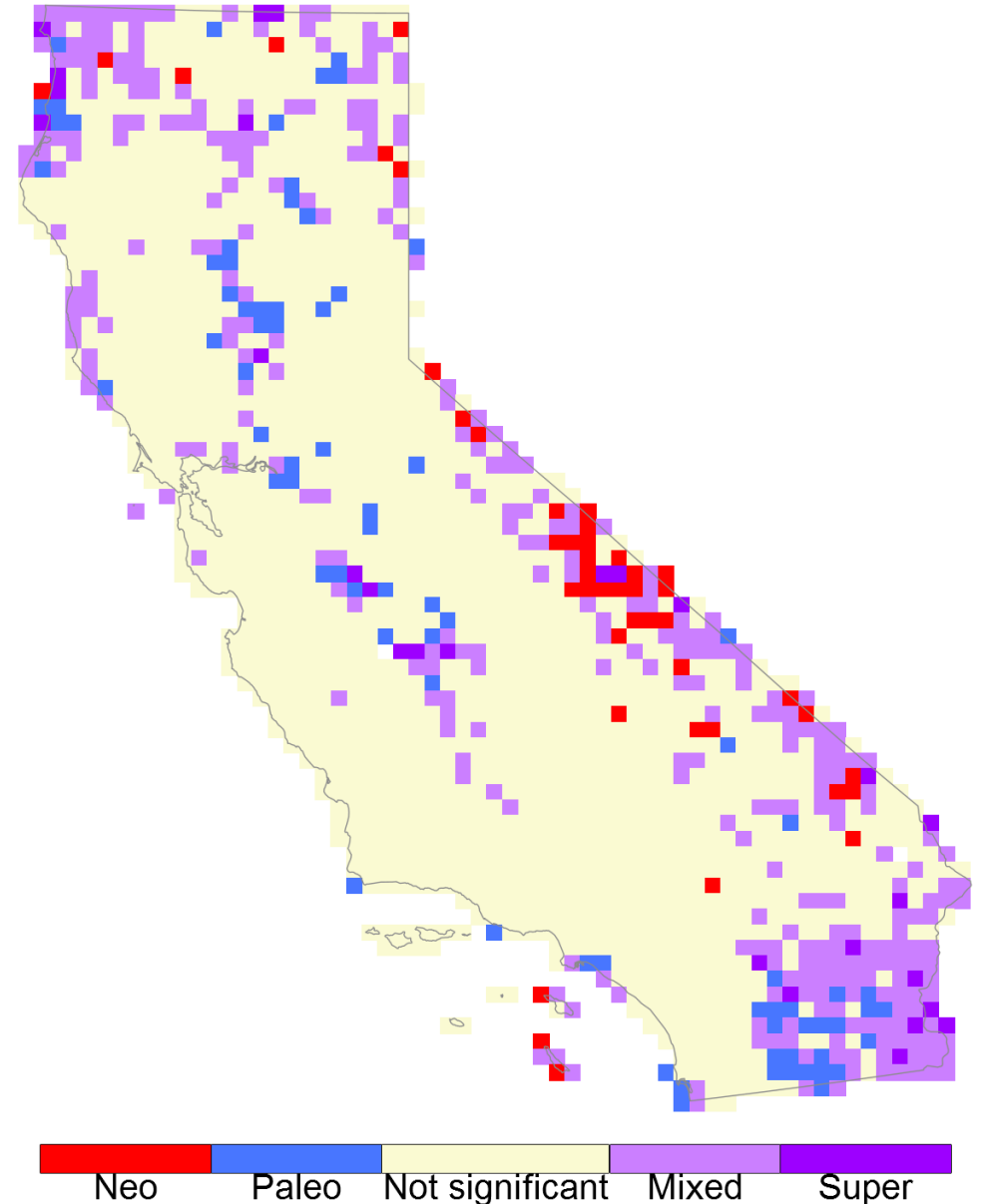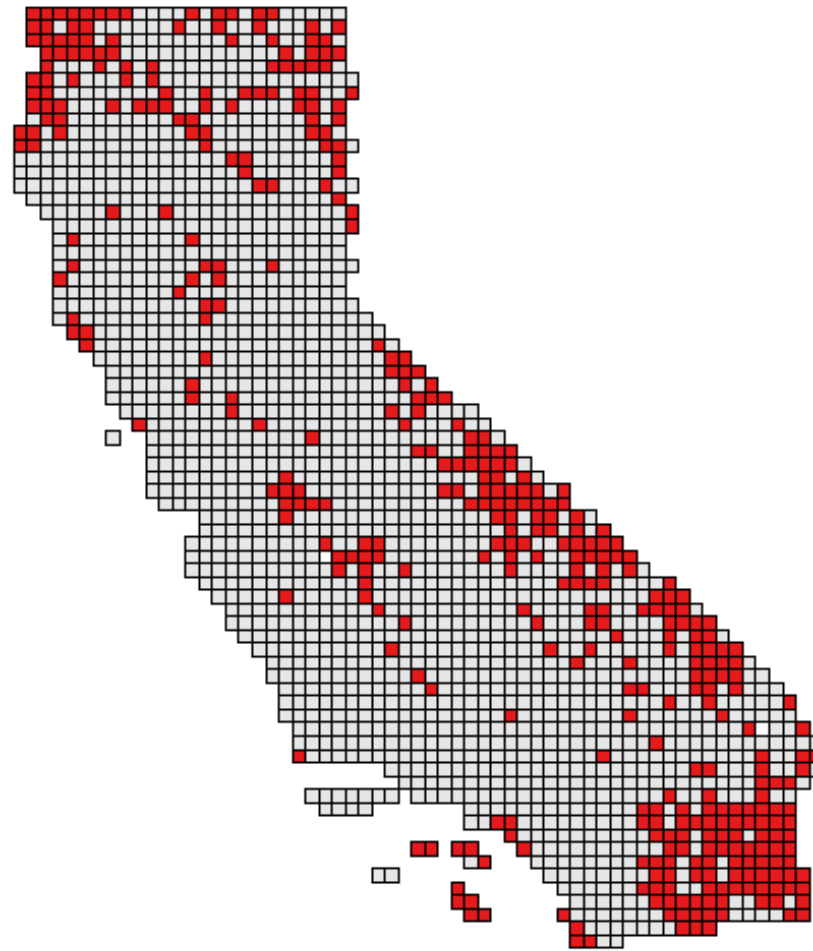
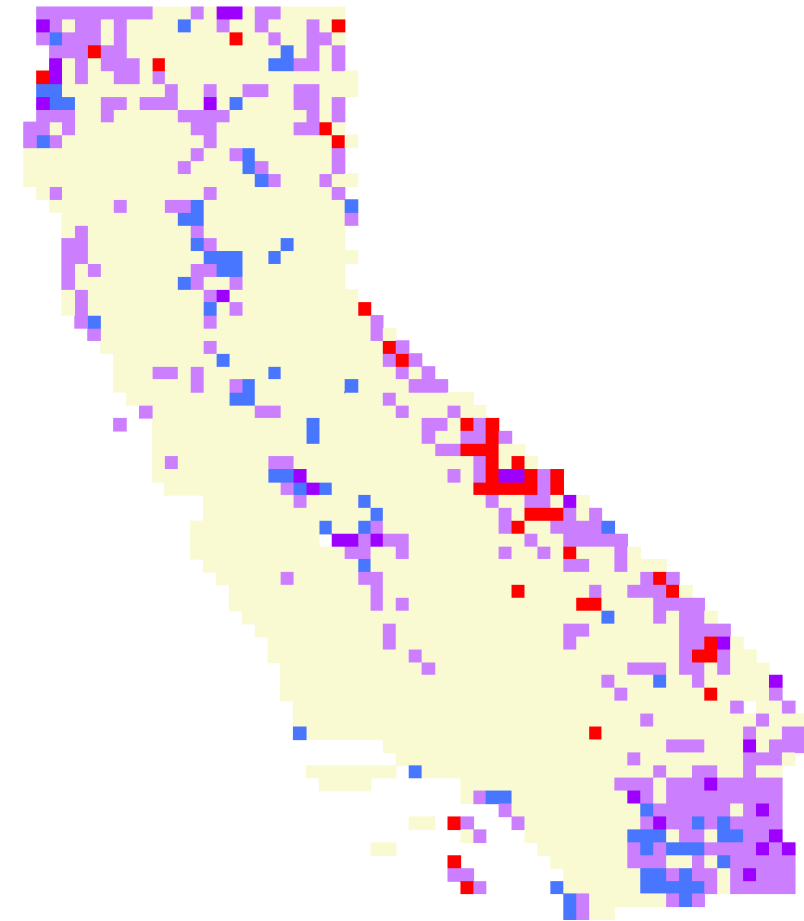# CANAPE: Categorical Analysis of Neo- And Paleo-Endemism
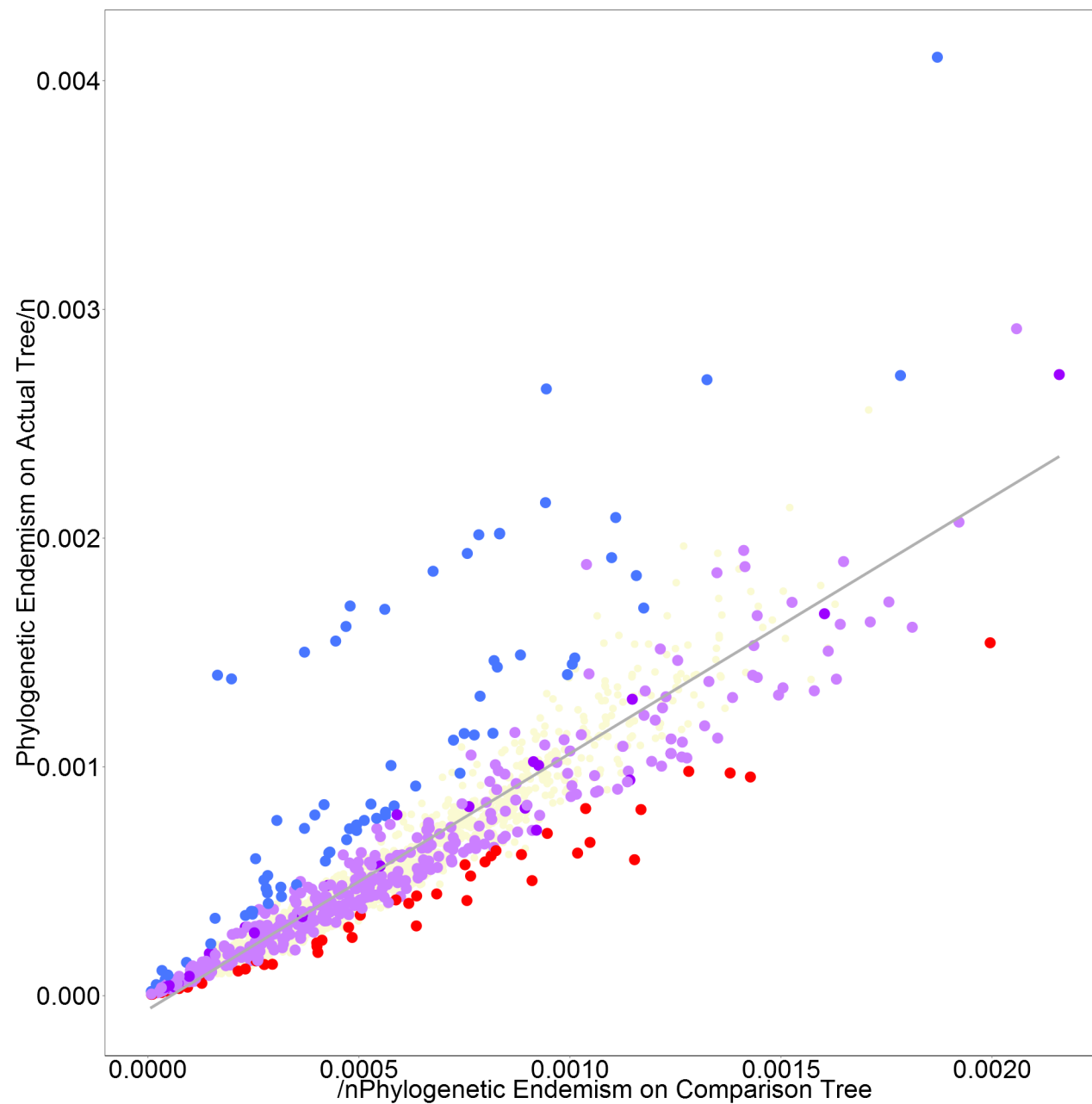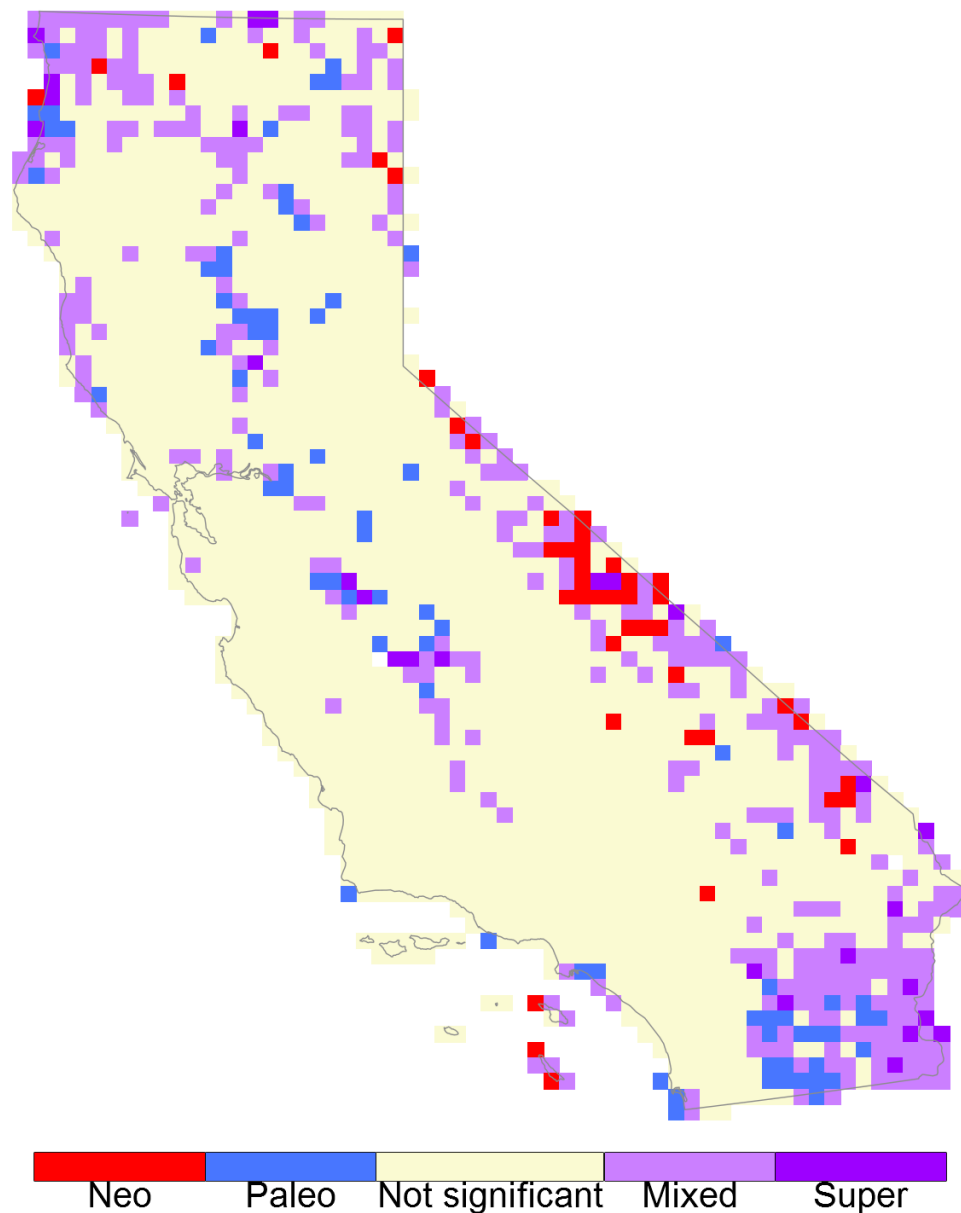
A comparison of areas of significant endemism
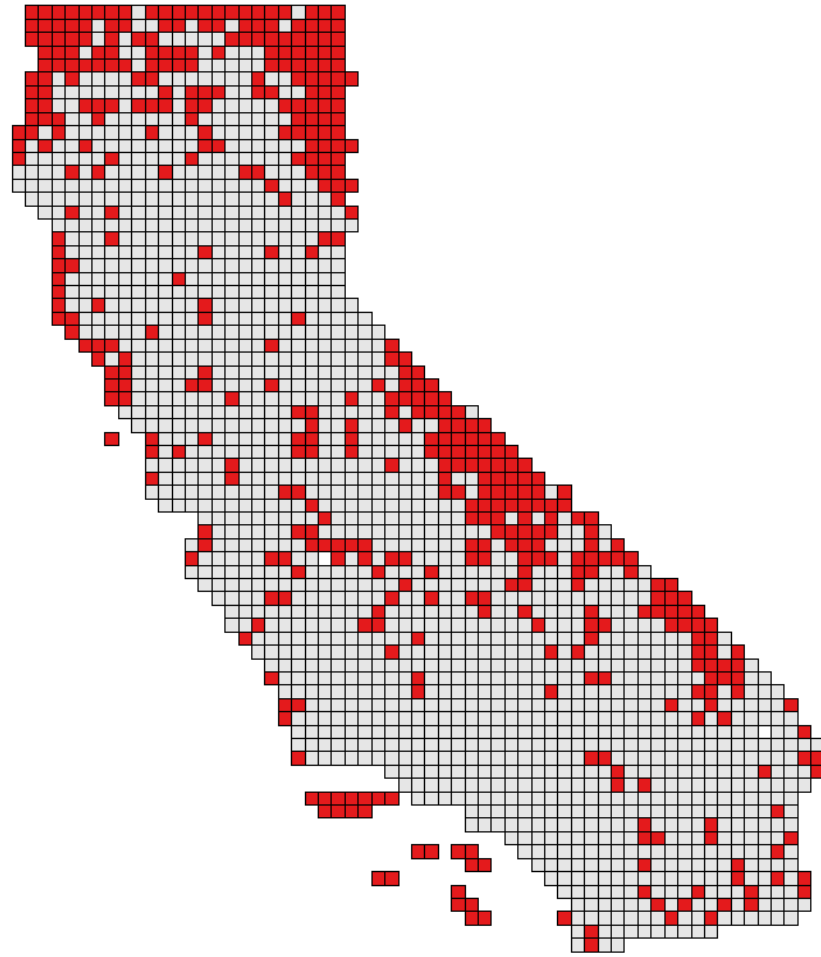
All species

Clades

Neo · Paleo · Not significant · Mixed · Super

Clades CANAPE