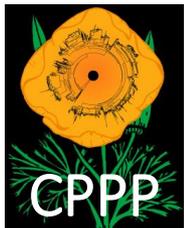


New phylogenetic methods for detecting, understanding, and conserving centers of endemism

Brent Mishler

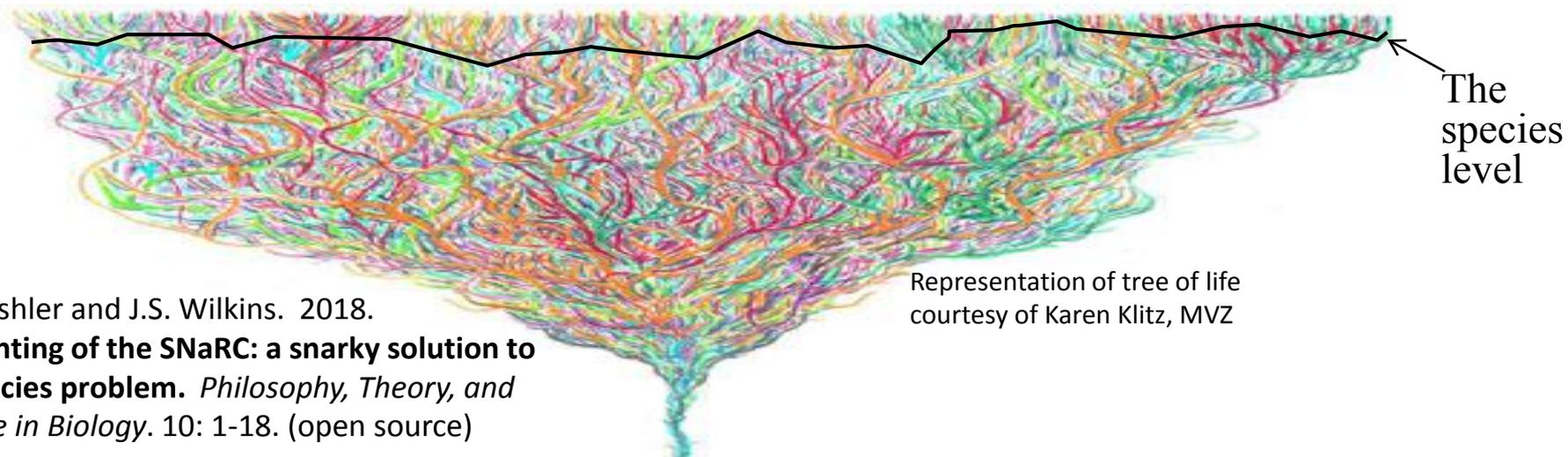
University and Jepson Herbaria
Dept. of Integrative Biology
UC Berkeley

With thanks to my collaborators in the California Plant Phylodiversity Project: Matt Kling, Andrew Thornhill, Bruce Baldwin, and David Ackerly.



Biodiversity is not just species

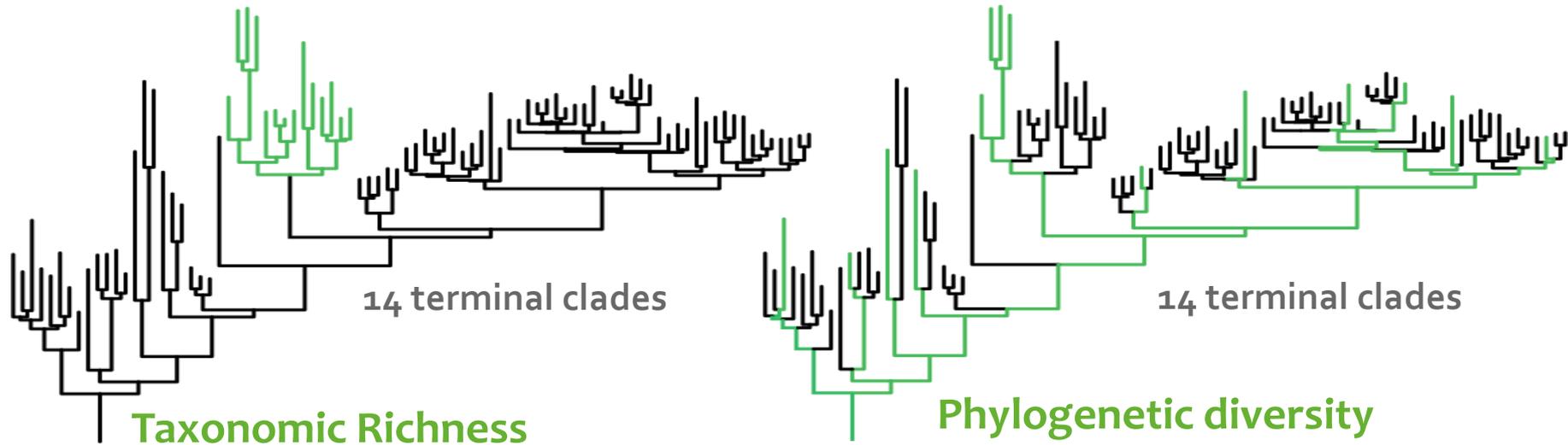
- Biodiversity is the *whole tree of life*, not just named species.
- There are lineages smaller and larger than the traditional species level.
- Species are not comparable among lineages, they are at best just an arbitrary cut-off somewhere along a branch in the tree of life.
- Likewise, endemism is not just about species, even though virtually all studies on endemism to the present focus solely on species. Clades at all levels can be endemic to a greater or lesser extent, and all levels are relevant to discovery and evaluation of centers of endemism.
- Thus for a true understanding of diversity and endemism, *we need to look at the whole tree*.



B.D. Mishler and J.S. Wilkins. 2018.
The hunting of the SNaRC: a snarky solution to the species problem. *Philosophy, Theory, and Practice in Biology*. 10: 1-18. (open source)

Representation of tree of life
courtesy of Karen Klitz, MVZ

Measuring biodiversity & endemism



- Traditional metrics: species richness and weighted endemism (inverse of range size)
- Alternative metrics: **phylogenetic diversity** (PD) and **phylogenetic endemism** (a PD measure, but with each branch divided by its range size)

Spatial phylogenetics *→ Placing the tree of life on maps*

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.

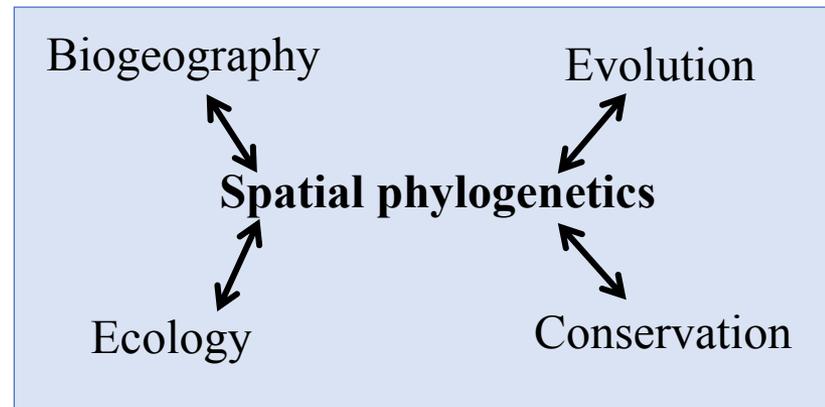
Relatively robust to lumping and splitting decisions.

A “big data” approach enabled by technological advances:

Advances in digitization and availability of natural history museums specimens

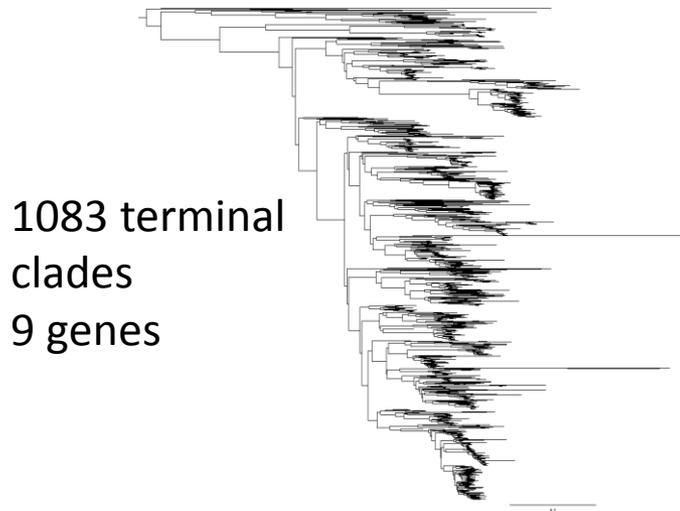
Plethora of DNA in GenBank; advances in mining software.

Major advances in computational methods for both tree-building and tree-using e.g. RAxML

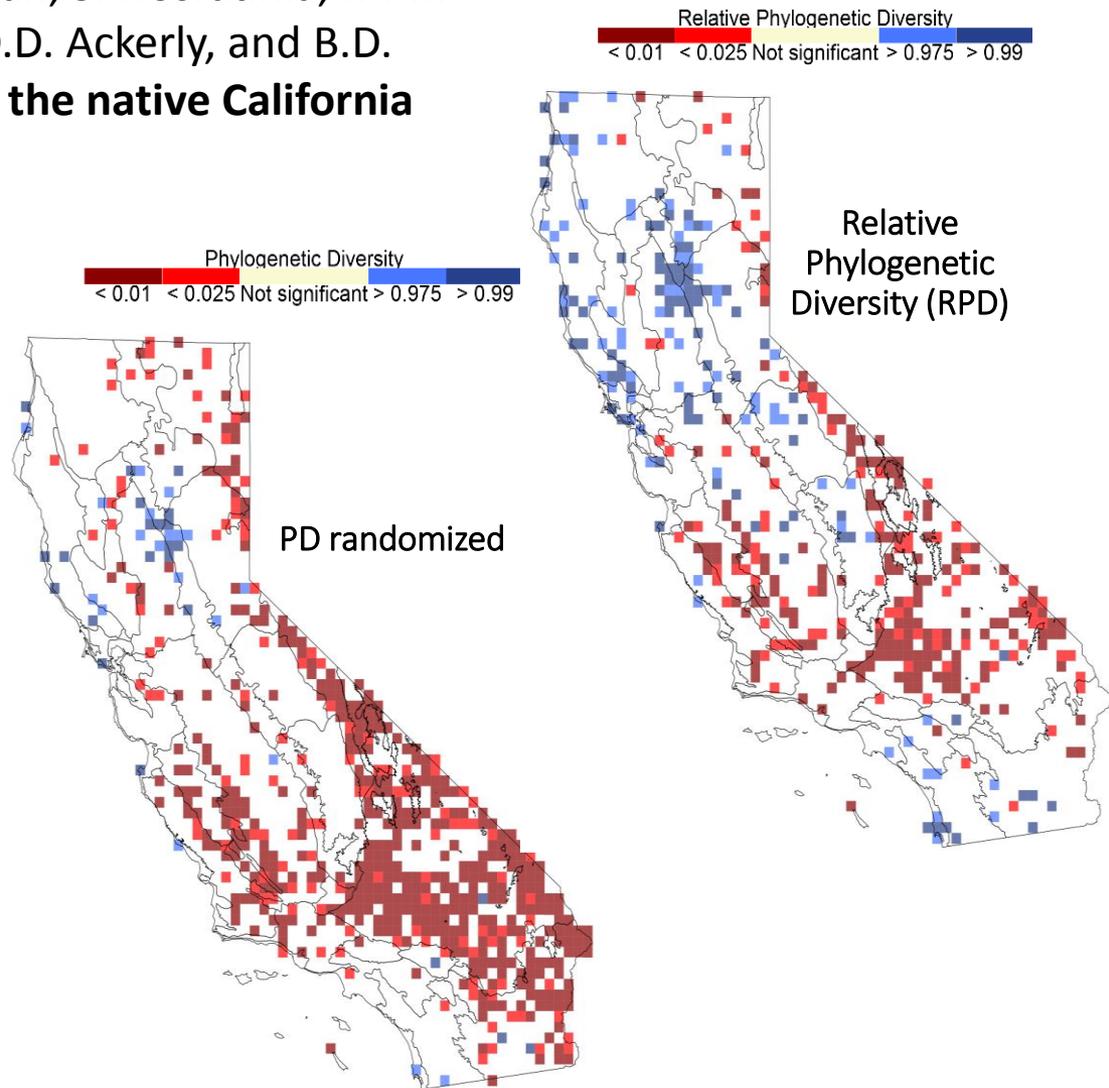


Quick review of:

A.H. Thornhill, B.G. Baldwin, W.A. Freyman, S. Nosratinia, M.M. Kling, N. Morueta-Holme, T.P Madsen, D.D. Ackerly, and B.D. Mishler. 2017. **Spatial phylogenetics of the native California flora.** *BMC Biology* 15:96.



1.4 million herbarium specimen records after cleaning – all datasets deposited online



We test statistical significance using spatial randomizations of the terminal taxa on the map, subject to two constraints: richness of each grid cell and range size of each taxon remains constant.

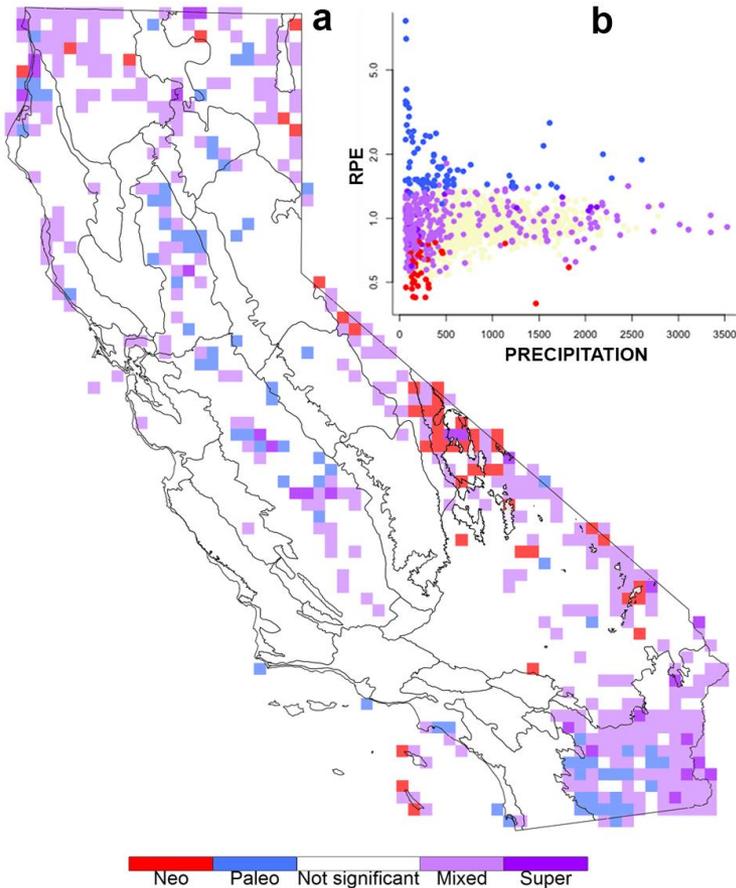
The
California Plant
Phylodiversity
Project



CANAPE: Categorical Analysis of Neo- And Paleo-Endemism

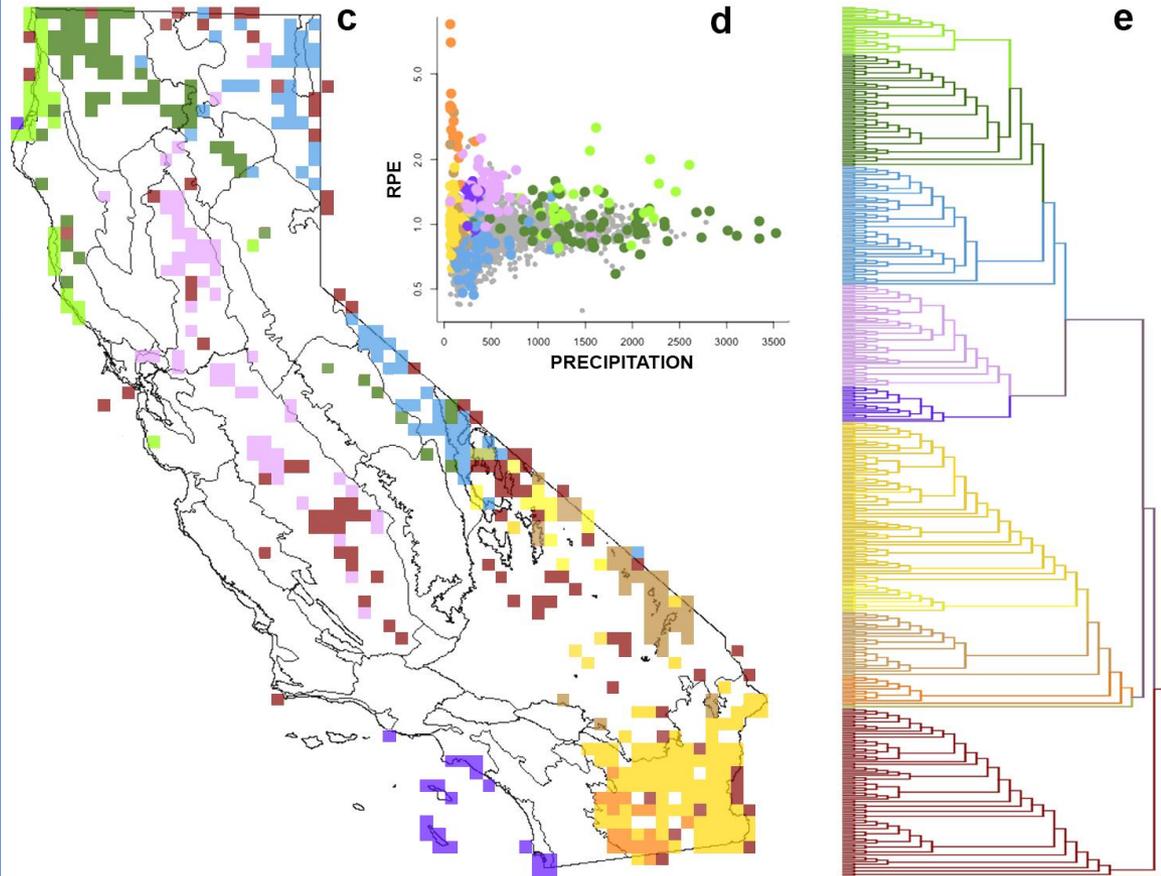
RPE - *relative phylogenetic endemism* =
$$\frac{\text{PE on the range-weighted original tree}}{\text{PE on a range-weighted comparison tree with all branch lengths equal}}$$

Blue = centers of paleoendemism
Red = centers of neoendemism
Purple = centers of mixed endemism



Beta-diversity:

Phyloturnover among centers of endemism.
Here colors indicate similarity among grid cells



The three facets of phylogenetic diversity

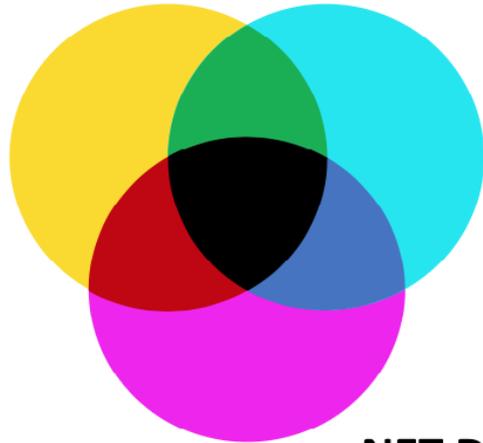
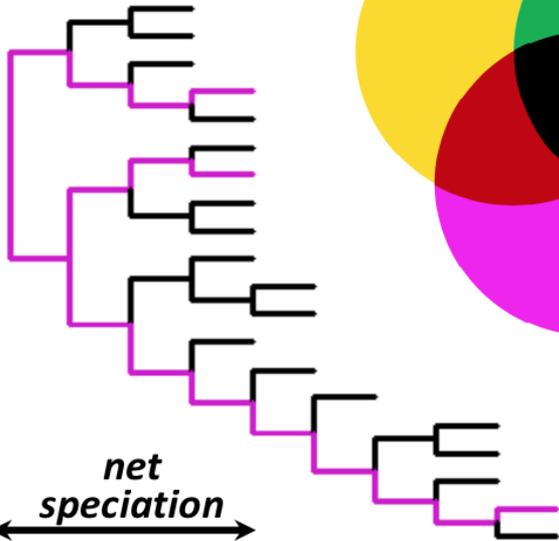
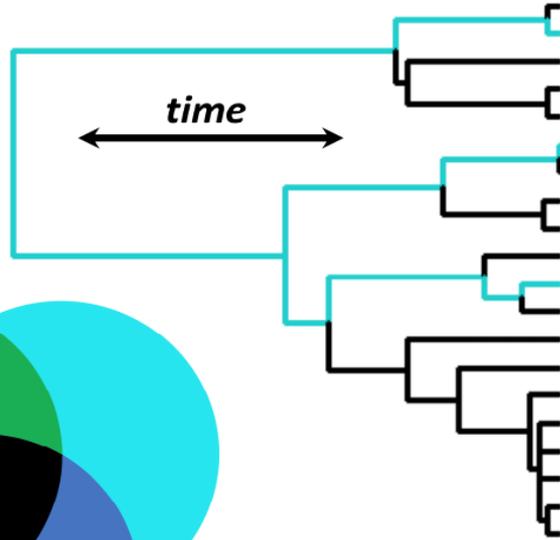
DIVERGENCE:

high PD on phylogram =
disparate assemblages



SURVIVAL TIME:

high PD on chronogram =
experienced assemblages



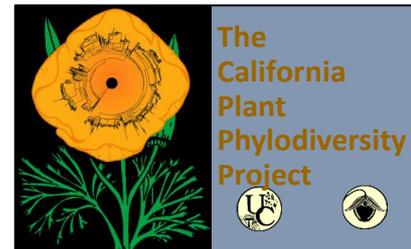
NET DIVERSIFICATION:

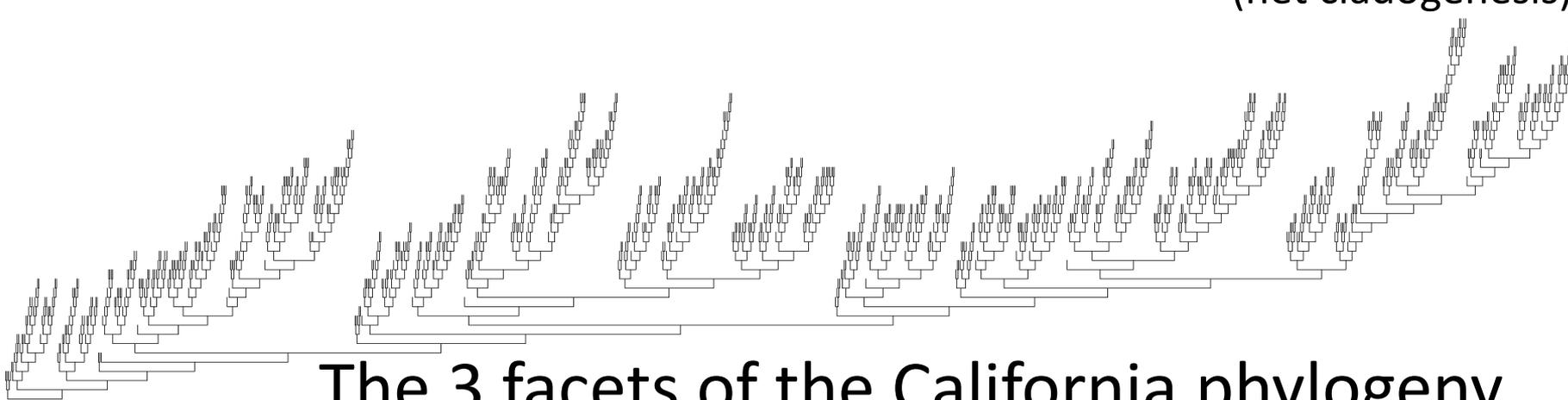
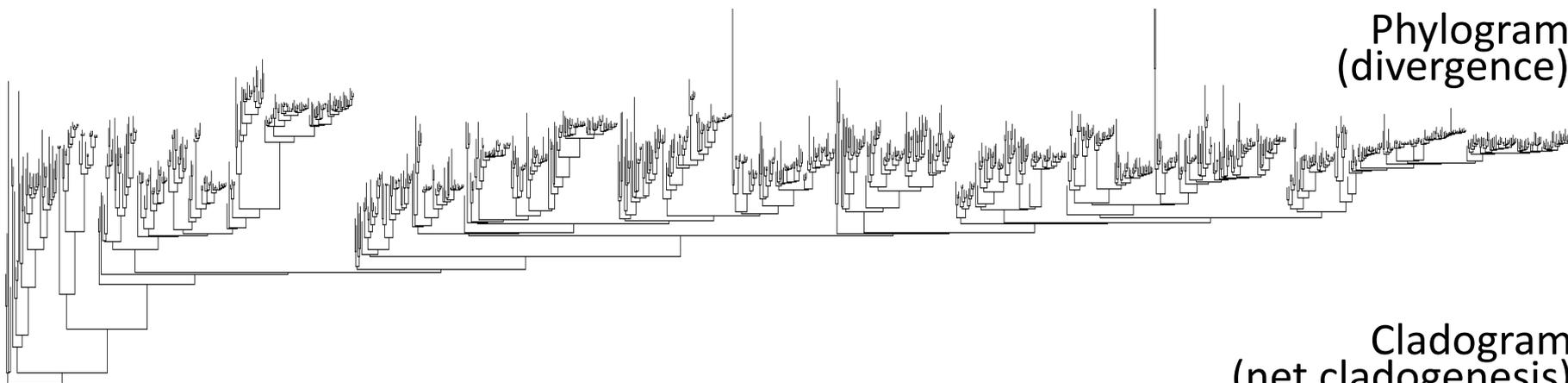
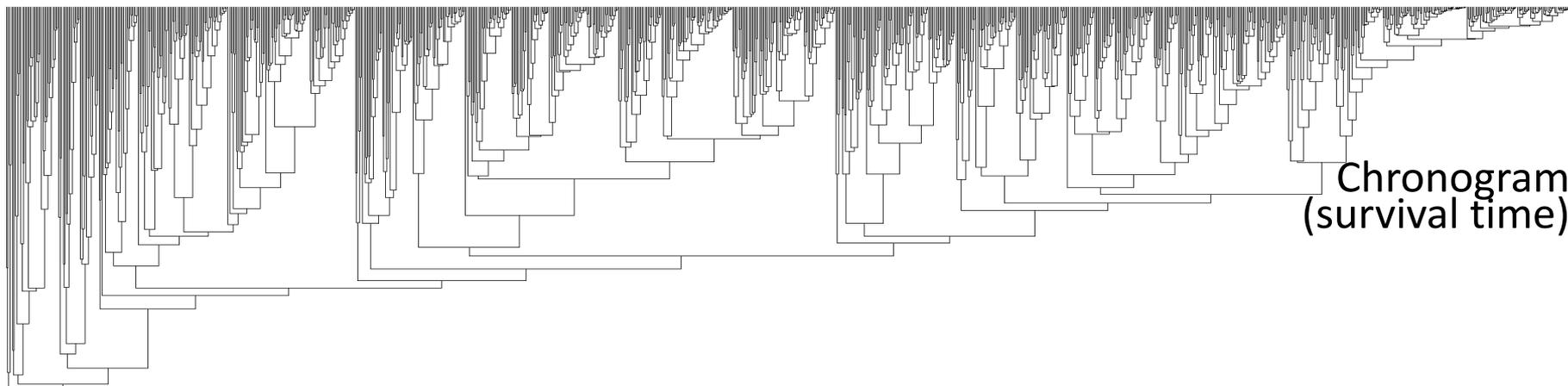
high PD on cladogram =
assemblages from
species-rich clades

Now change focus from locations of hotspots of diversity and endemism in general.

Start from where we are at moment in land protection in California and decide what to do next.

From: M.M. Kling, B.D. Mishler, A.H. Thornhill, B.G. Baldwin, and D.D. Ackerly. 2018. **Facets of phylogenetic diversity: evolutionary diversification, divergence, and survival as conservation targets.** *Philosophical Transactions Royal Society B.* 374: 20170397

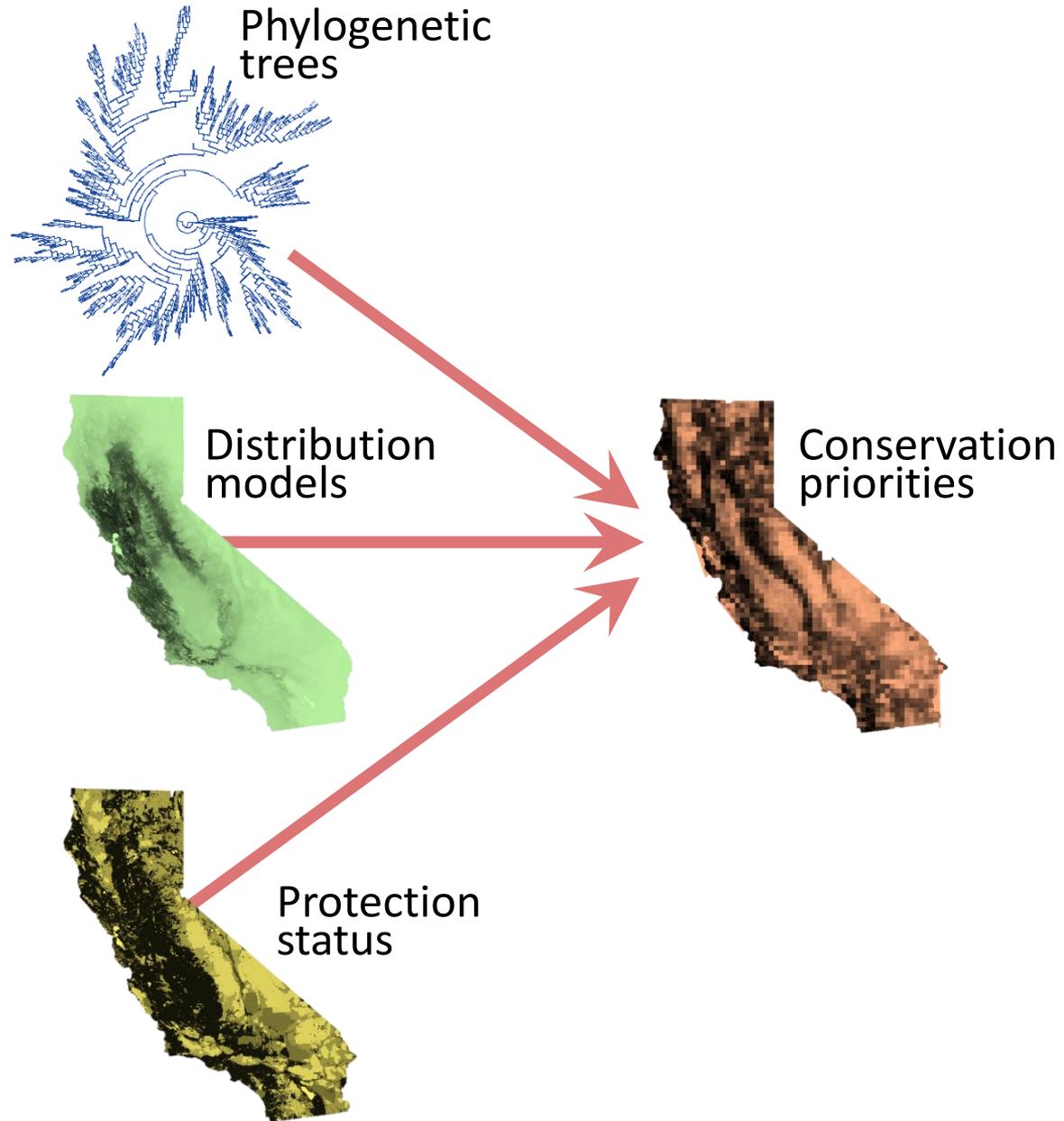


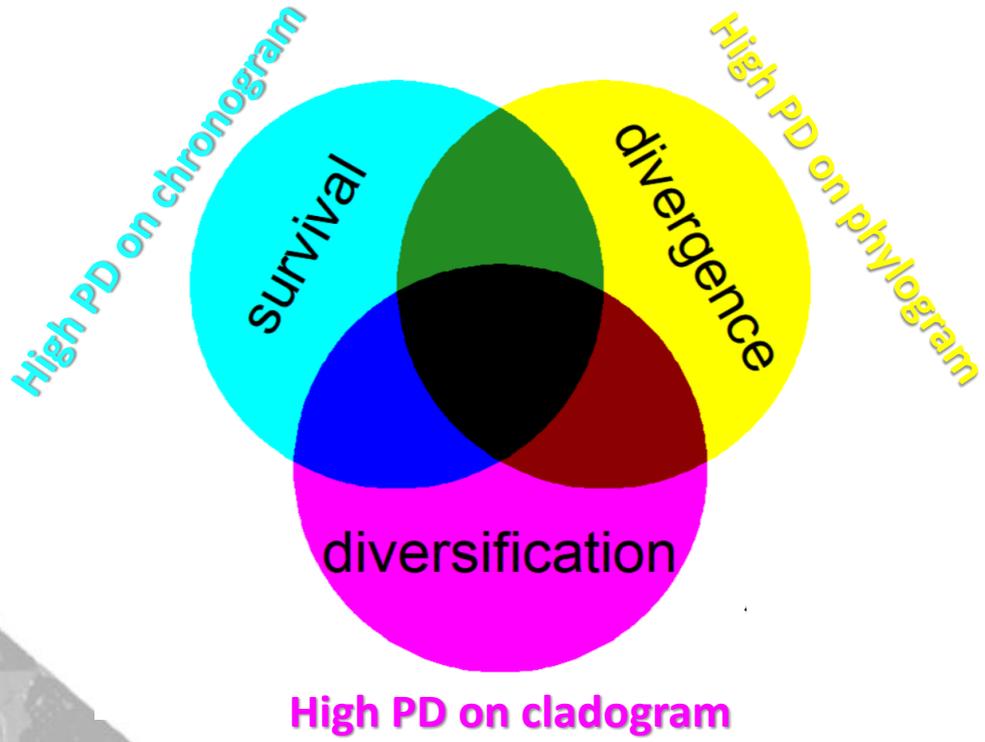
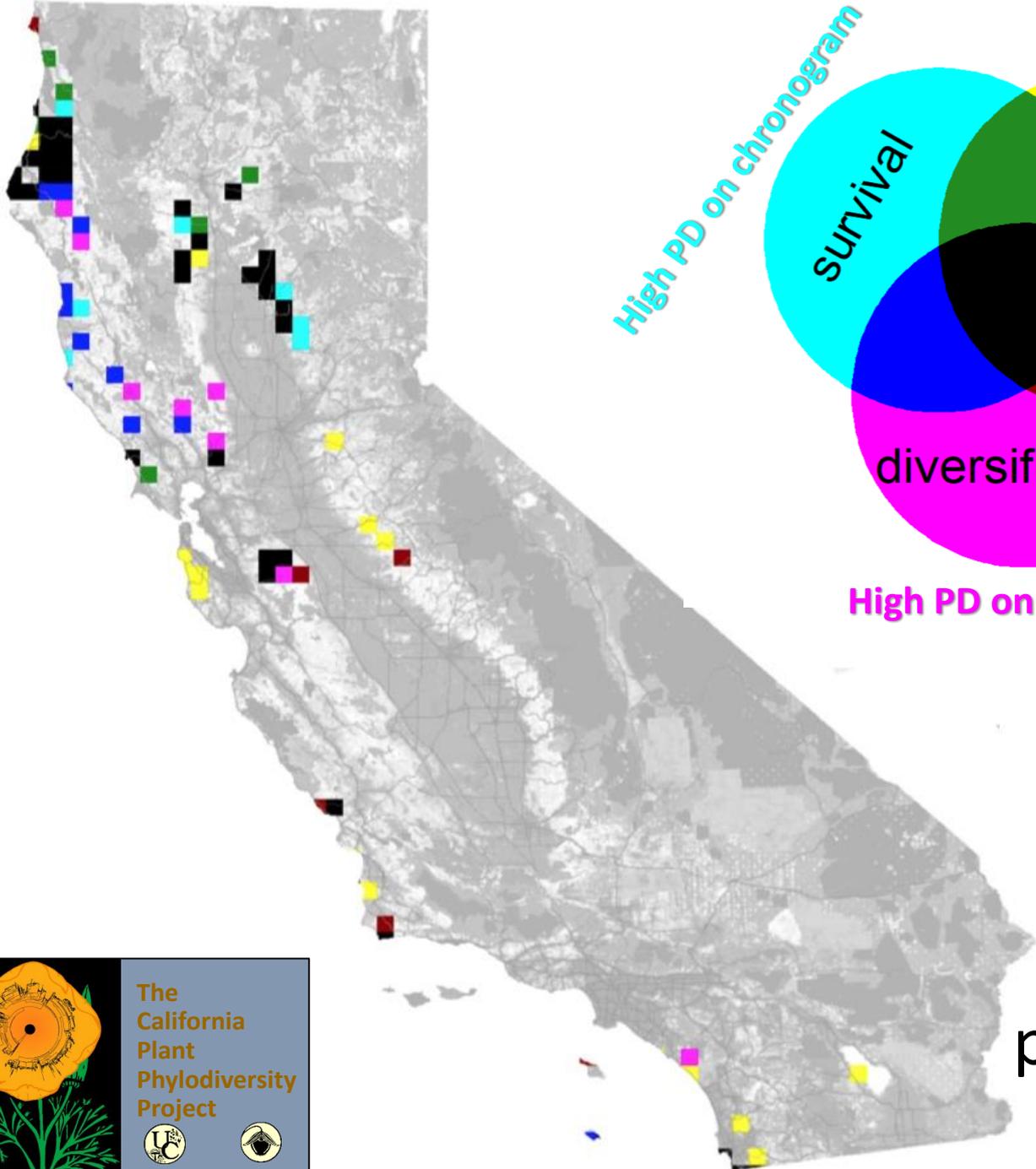


The 3 facets of the California phylogeny

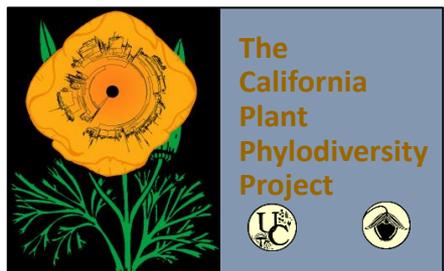
Optimal conservation targets:

- Poor protection
- High intactness
- High biodiversity value, i.e, many resident taxa with:
 - Long branches
 - Small ranges
 - Poor protection across ranges





Top 50
conservation
priorities for each
of the 3 facets



An app is available on the UC/JEPS website to explore the results in real time!

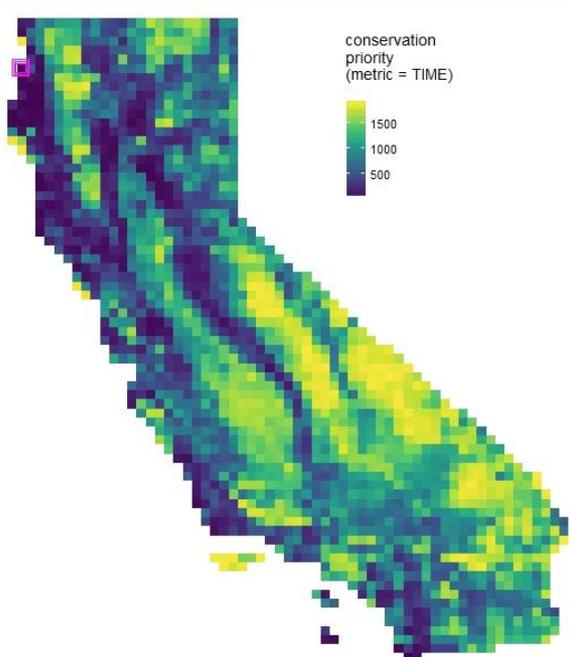
See: <http://ucjeps.berkeley.edu/phylodiversity/>

California plant phylodiversity atlas

Geography

Map variable: conservation priority

Overall conservation priority for this diversity facet. LOW values are HIGH priority sites, which contain concentrations of long-branch taxa with small ranges that are largely unprotected by current preserves or other top-priority sites.



Color scale: linear

Community

This table displays the floristic composition of the grid cell selected at left. The table is sortable and searchable.

Click to select a taxon. To map its range, change map variable to 'taxon range'. To view it in the evolutionary tree, change phylogeny variable to 'selected taxon'.

Show 10 entries

	name	combined benefit	presence	endemism	branch length
1	Lysichiton	1	0.3909	0.0466	0.469
2	Lycopodium	0.8587	0.3618	0.0206	0.759
3	Lycopodiella	0.549	0.4619	0.0189	0.759
4	Thuja	0.2799	0.3508	0.0121	0.544
5	Lycopodium & Lycopodiella (2-OTU clade)	0.2348	0.6565	0.0108	0.304
6	Armeria	0.1876	0.2829	0.0212	0.314
7	Empetrum	0.1646	0.2338	0.0962	0.090
8	Chrysosplenium	0.1324	0.3886	0.0338	0.100
9	Ribes_Heritiera	0.1051	0.3841	0.0218	0.121
10	Dryopteris_1	0.096	0.4875	0.0055	0.319

Showing 1 to 10 of 2,164 entries

Previous 1 2 3 4 5 ... 217 Next

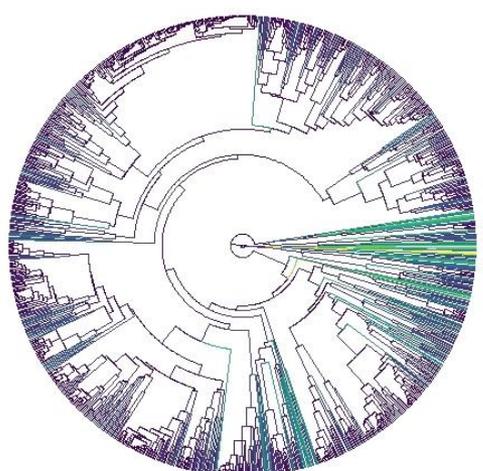
Note: 'range protection' values represent opportunity for protection increases, which is inversely related to actual current protection.

Phylogeny

Select biodiversity facet: time

Time as a measure of biodiversity based on a 'chronogram' represents the total number of years that independent ancestral lineages persisted to give rise to taxon assemblage.

Lineages colored by: branch length



Options

- Plot only the clade selected in table (not yet working)
- Show tip labels

Color scale