

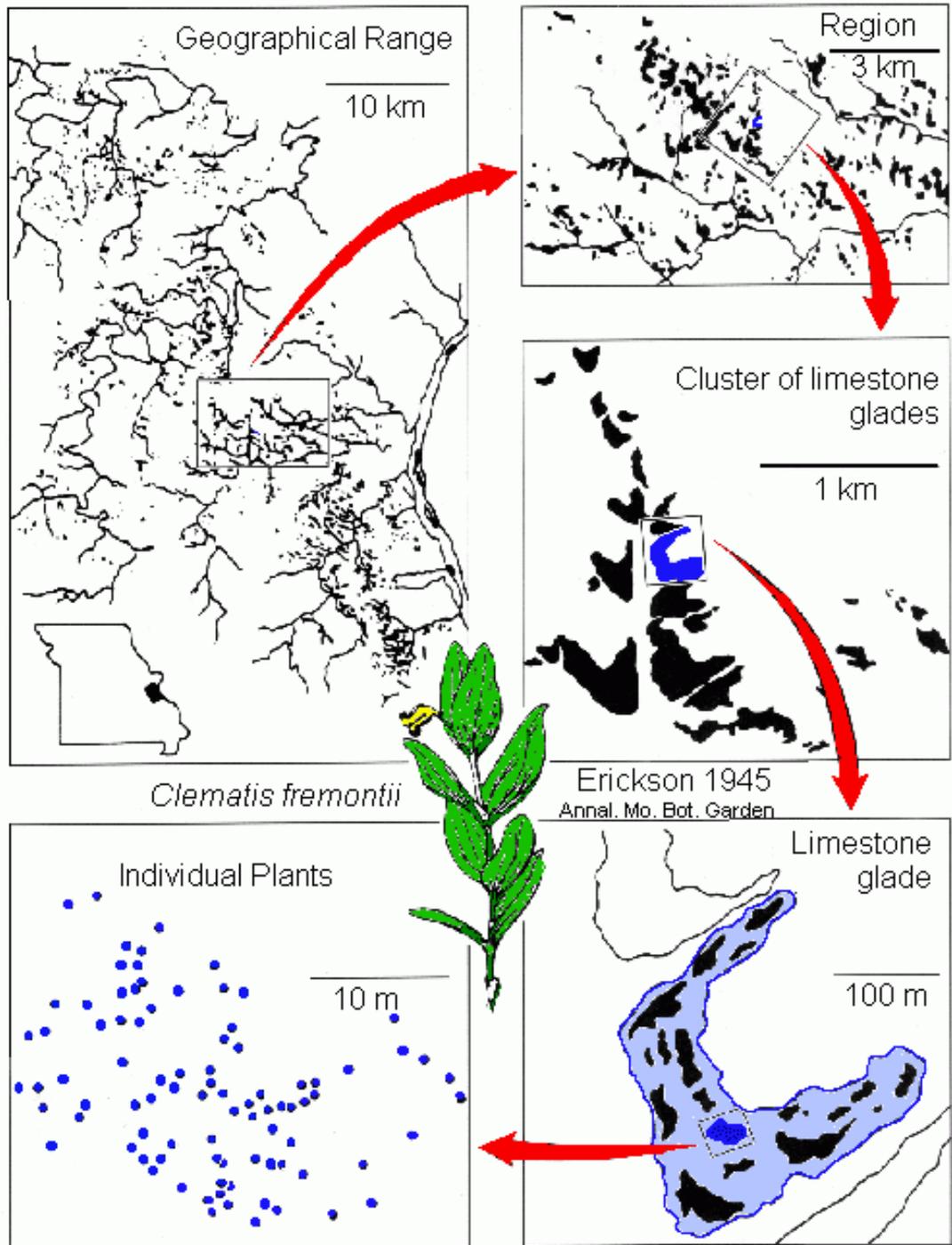
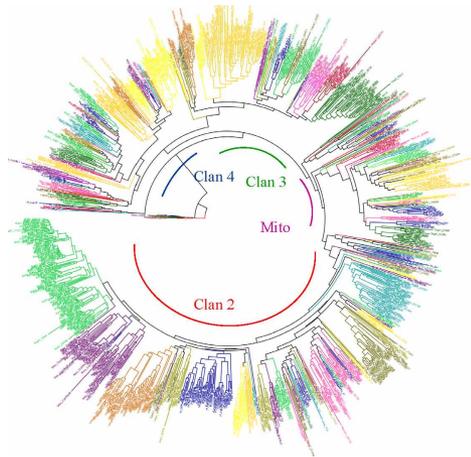
What is the range
of a taxon?

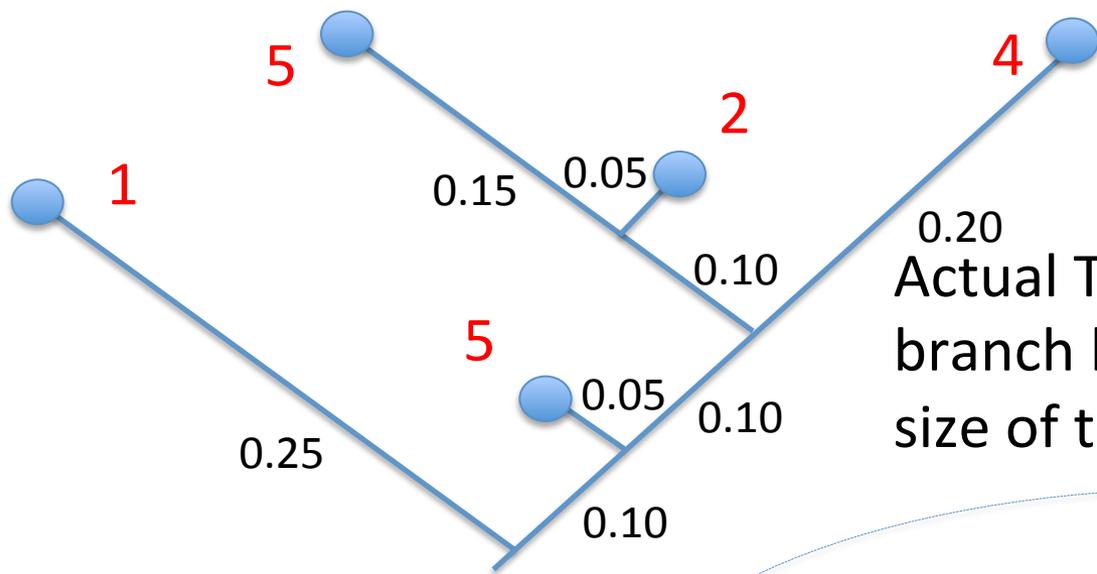
A scaling problem
at three levels:

Spatial scale

Phylogenetic depth

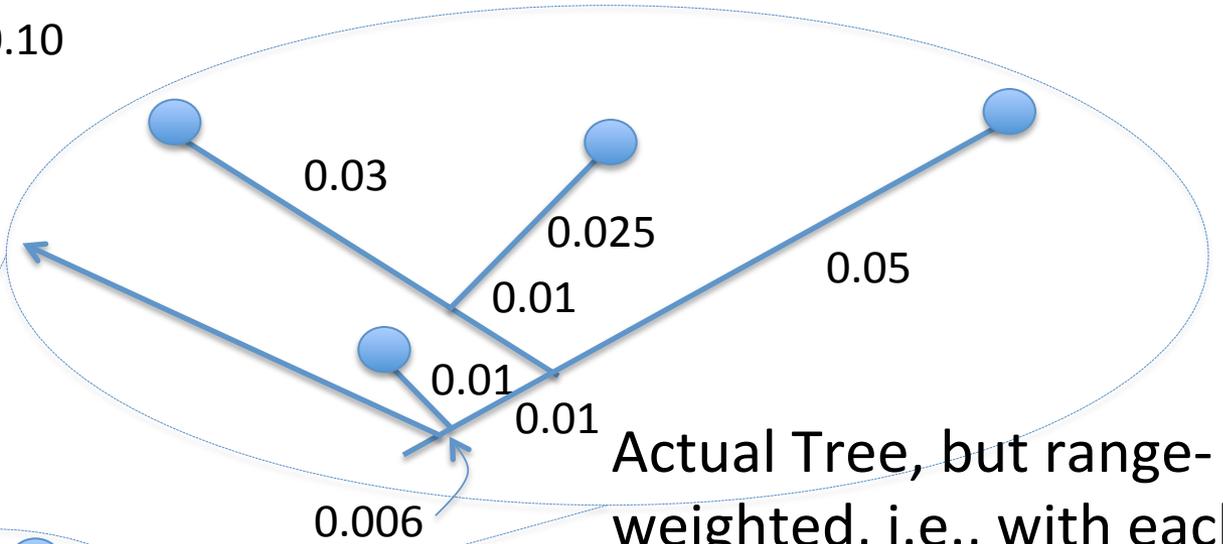
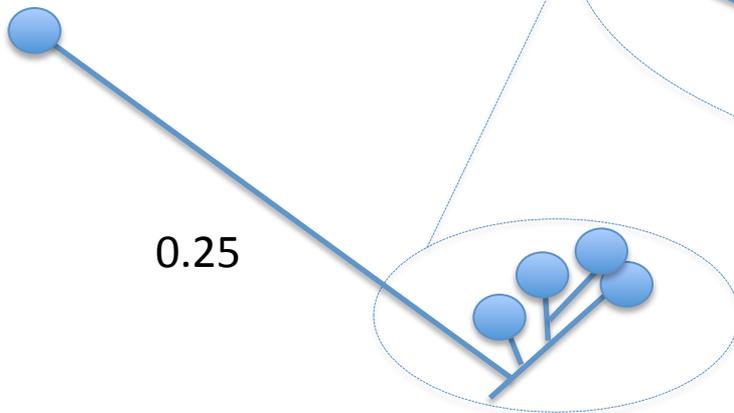
Time





Reminder of what a range-weighted tree is

Actual Tree again, with unmodified branch lengths, showing the range size of terminal taxa in red

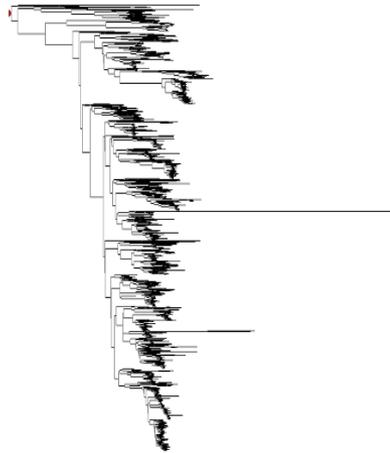


Actual Tree, but range-weighted, i.e., with each branch length divided by its range = PE

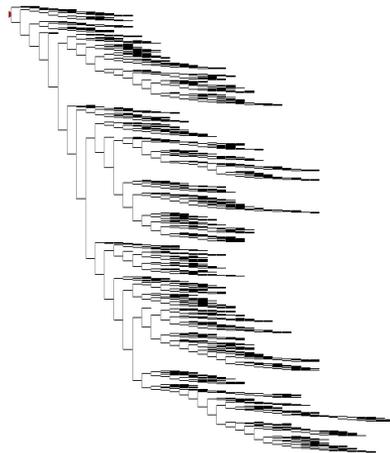
PE is PD of a range-weighted tree!

Reminder of what RPD and RPE are

RPD (*relative phylogenetic diversity*) =
$$\frac{\text{PD on the original tree}}{\text{PD on a comparison tree with all branch lengths equal}}$$

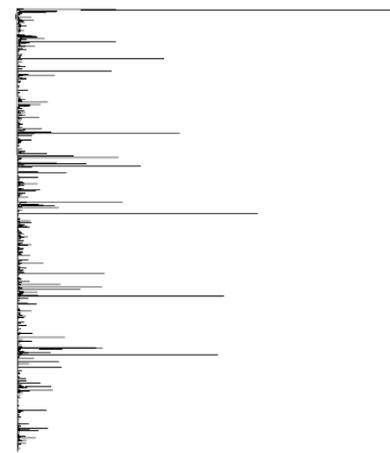


original tree

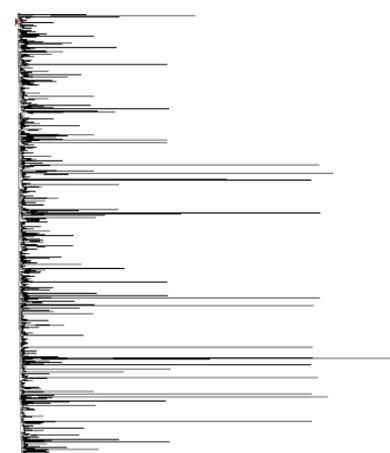


comparison tree

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

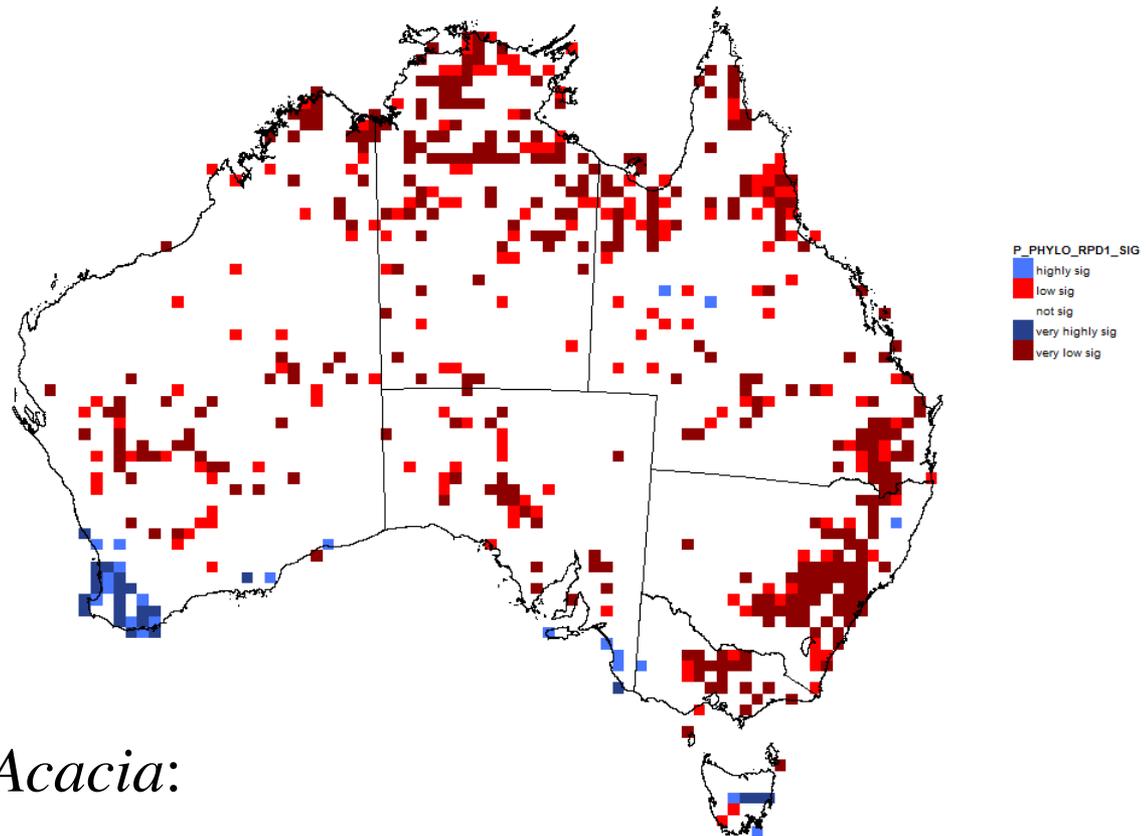


range-weighted original tree



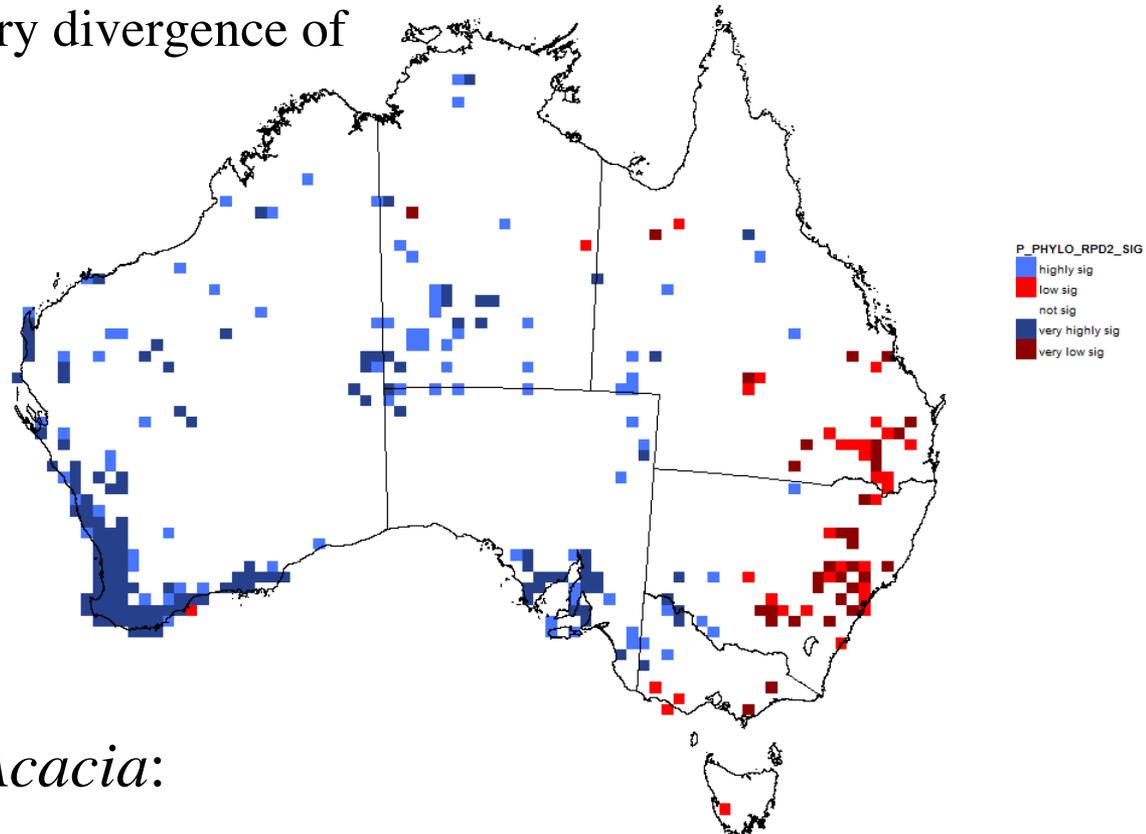
range-weighted comparison tree

- **Significantly high and low PD locations** may have an ecological explanation.
 - “Phylogenetic over-dispersion” (blue here) might be a result of competitive exclusion, if close relatives exclude each other.
 - “Phylogenetic clustering” (red here) might indicate that certain major clades have evolutionarily conservative habitat preferences and thus close relatives co-occur.



An example in Australian *Acacia*:

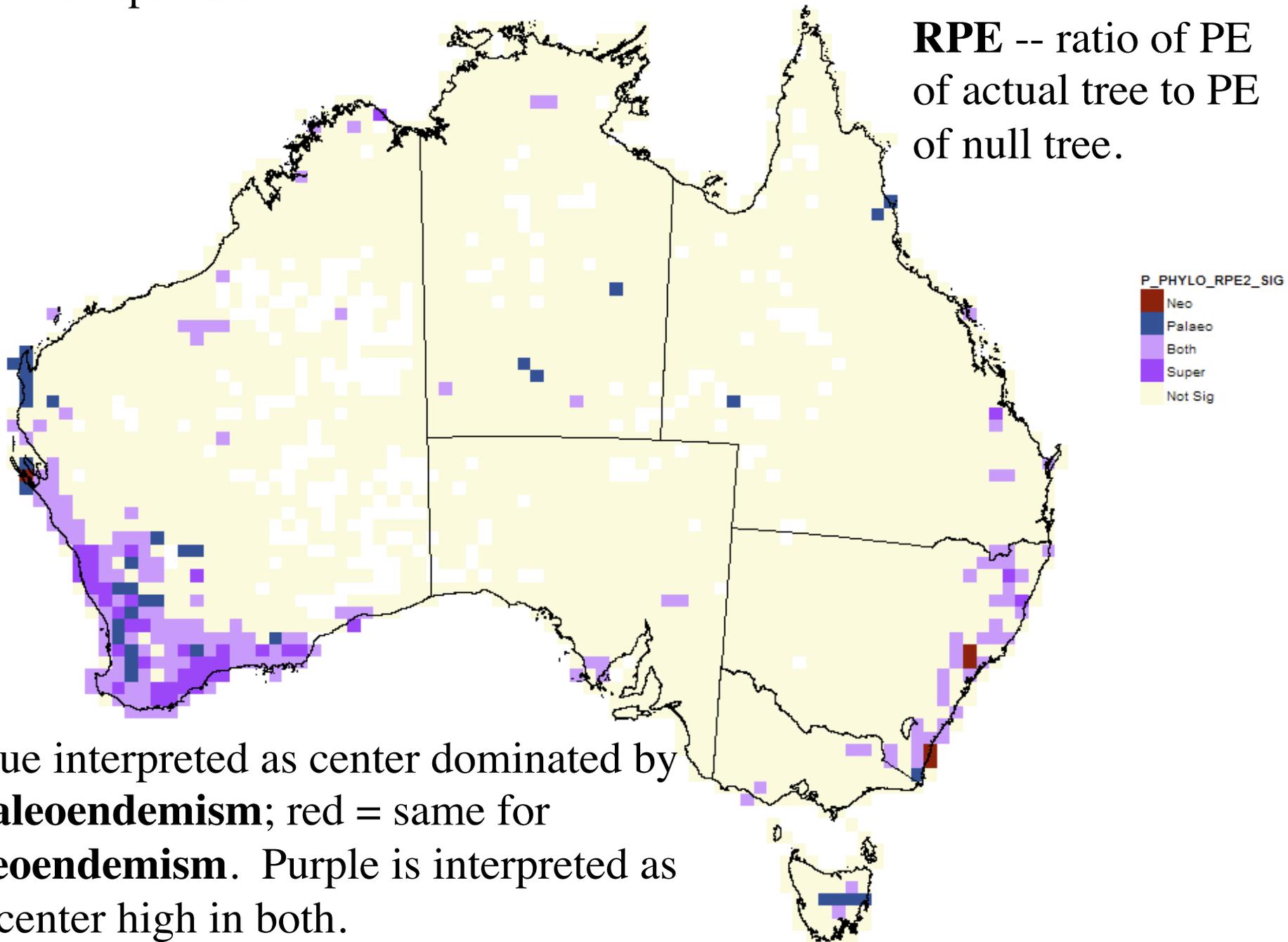
- **Significantly high and low RPD locations** are more likely to relate to biogeographic and evolutionary processes.
 - A significant concentration of long branches (blue here) could indicate the presence of a refugium, or perhaps could result from occurrence of a few members of clades that mainly occur outside of the study region.
 - A significant concentration of short branches (red here) could indicate an area of recent evolutionary divergence of lineages.



An example in Australian *Acacia*:

An example in *Acacia*:

RPE -- ratio of PE
of actual tree to PE
of null tree.



blue interpreted as center dominated by **paleoendemism**; red = same for **neoendemism**. Purple is interpreted as a center high in both.

Phylogenetic measures of geographic similarity

Typical measure looks at matching in species composition, measured via a dissimilarity index such as:

$$\mathbf{Jaccard} \quad = 1 - \frac{A}{A + B + C} \quad \mathbf{Phylo-Jaccard}$$

$$\mathbf{Sorensen} \quad = 1 - \frac{2A}{2A + B + C} \quad \mathbf{Phylo-Sorensen}$$

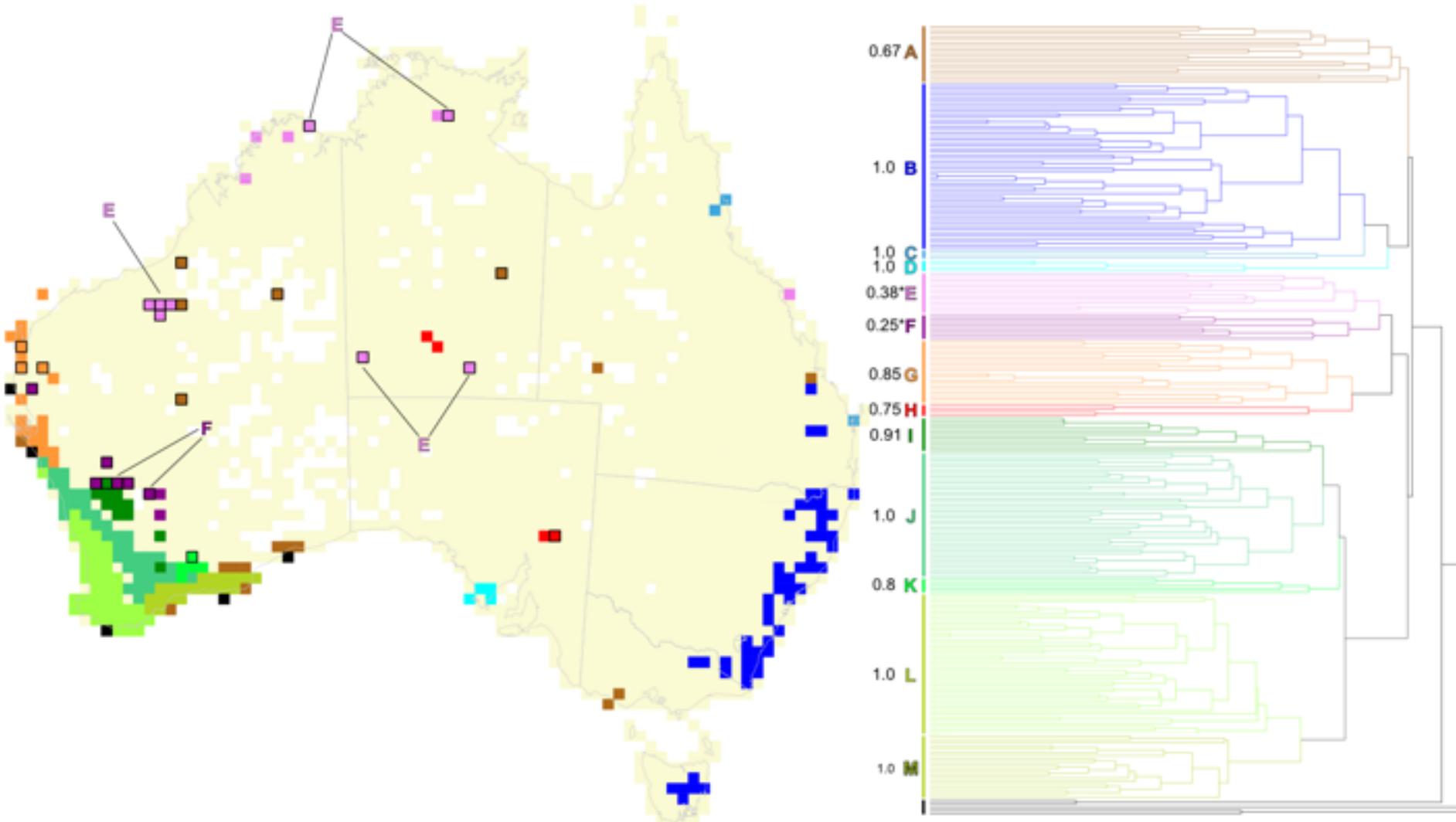
where A is the count of species found in both neighbor sets, B is the count unique to neighbor set 1, and C is the count unique to neighbor set 2.

There is an exact phylogenetic analog of these indices:

where A is the length of shared branches, and B and C are the length of branches found only in neighbor sets 1 and 2.

An example in Australian *Acacia*:

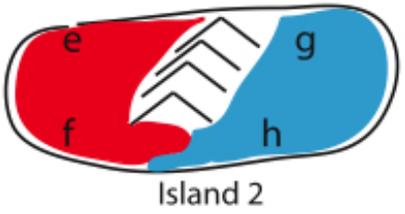
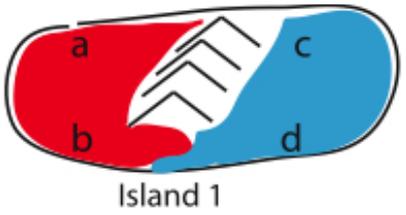
A UPGMA cluster analysis of phylo-Jaccard distances between all pairs of grid cells with significant endemism, done along with all these analyses using *Biodiverse* (Laffan et al.)



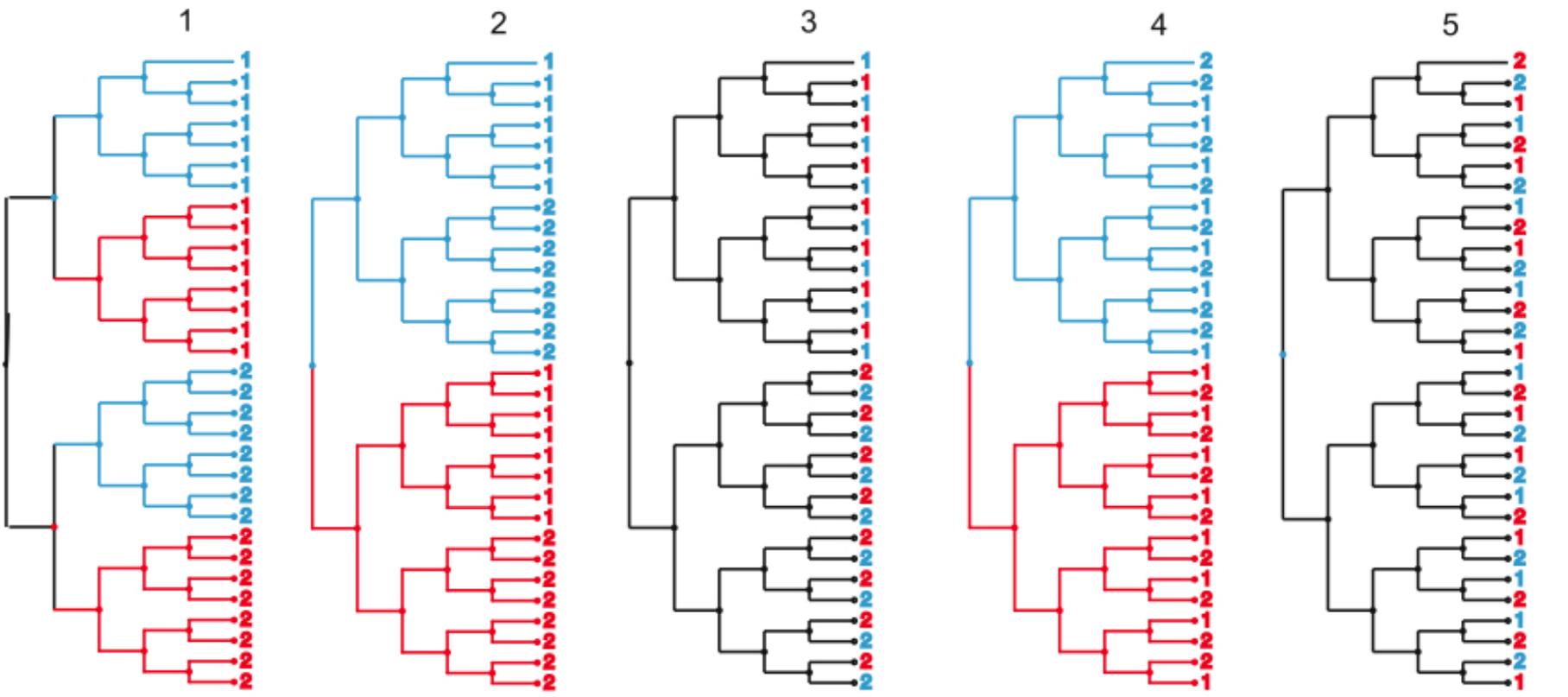
Phylo-betadiversity

- Biodiversity is conventionally partitioned into three levels: alpha, beta, and gamma.
- Gamma diversity is the total diversity across a study region, alpha diversity is the local diversity within subsets of that region, while beta diversity is the degree of compositional change, or turnover, of diversity between subsets.
- Turnover measures are all based on a partitioning of the alpha diversity of the combined sites. This means that, since measures of endemism are also alpha diversity metrics, range-weighted turnover metrics can be calculated as a direct modification of established range restriction metrics.

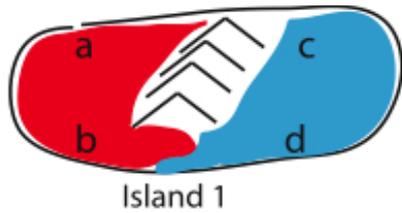
An example from Graham, C.H. & Fine, P.V.A. (2008) Phylogenetic beta diversity: linking ecological and evolutionary processes across space in time. *Ecology Letters*, 11, 1265-1277.



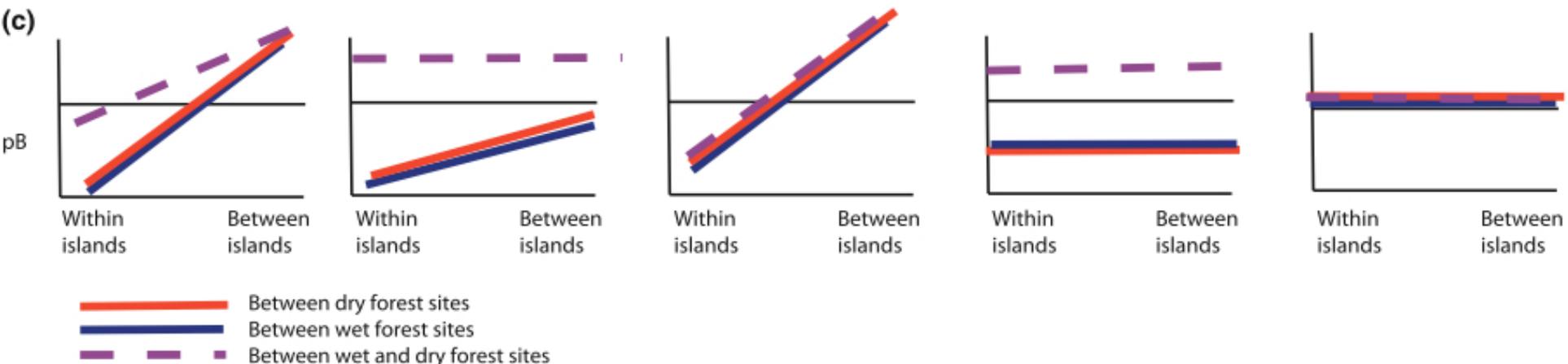
	Site	Habitat	Species sampled	Community phylogenetic structure				
				Type1	Type2	Type3	Type4	Type5
Island 1	a	Dry	Random sample of	C	C	c	c	r/o
	b		all dry, island 1 taxa	C	C	c	c	r/o
	c	Wet	random sample of	C	C	c	c	r/o
	d		all wet, island 1 taxa	C	C	c	c	r/o
Island 2	e	Dry	Random sample of	C	C	c	c	r/o
	f		all dry, island 2 taxa	C	C	c	c	r/o
	g	Wet	Random sample of	C	C	c	c	r/o
	h		all wet, island 2 taxa	C	C	c	c	r/o



An example from Graham, C.H. & Fine, P.V.A. (2008) Phylogenetic beta diversity: linking ecological and evolutionary processes across space in time. *Ecology Letters*, 11, 1265-1277.



	Site	Habitat	Species sampled	Community phylogenetic structure				
				Type1	Type2	Type3	Type4	Type5
Island 1	a	Dry	Random sample of	C	C	c	c	r/o
	b		all dry, island 1 taxa	C	C	c	c	r/o
	c	Wet	random sample of	C	C	c	c	r/o
	d		all wet, island 1 taxa	C	C	c	c	r/o
Island 2	e	Dry	Random sample of	C	C	c	c	r/o
	f		all dry, island 2 taxa	C	C	c	c	r/o
	g	Wet	Random sample of	C	C	c	c	r/o
	h		all wet, island 2 taxa	C	C	c	c	r/o

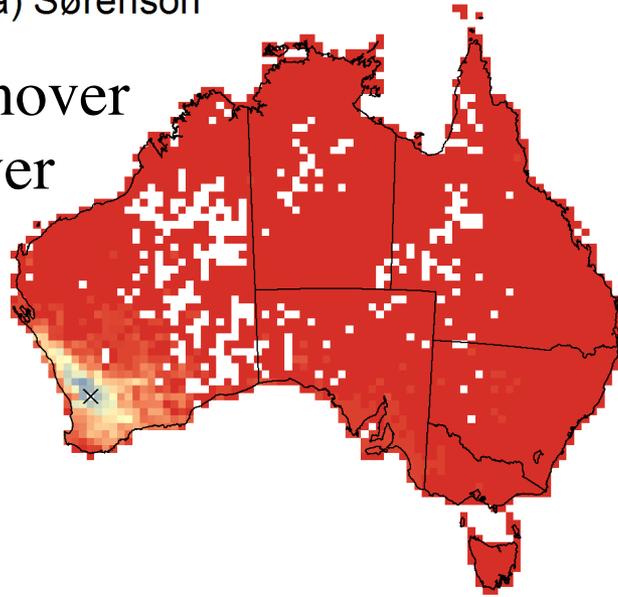


— Between dry forest sites
— Between wet forest sites
- - - Between wet and dry forest sites

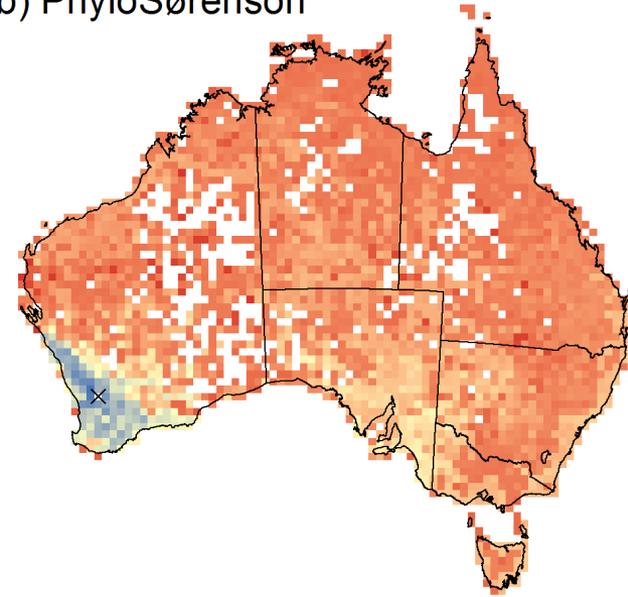
Range-weighted turnover vs. regular turnover measures

The range weighted turnover metrics represent the amount of weighted endemism, or phylogenetic endemism, shared between two location sets.

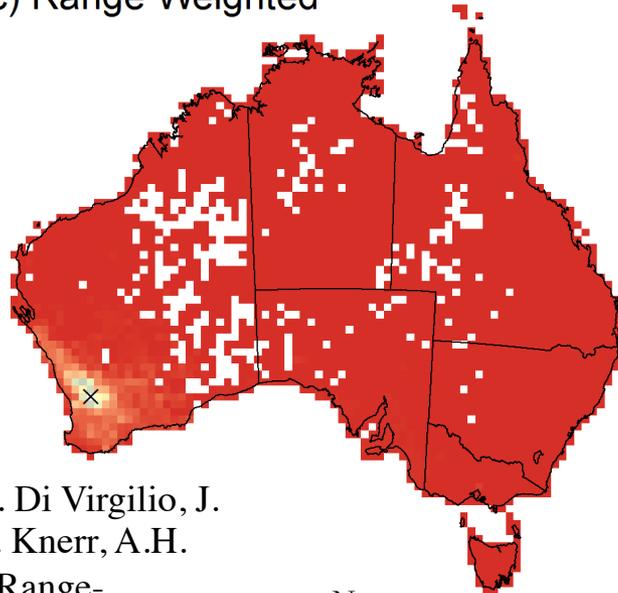
(a) Sørensen



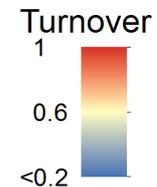
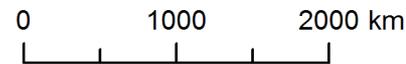
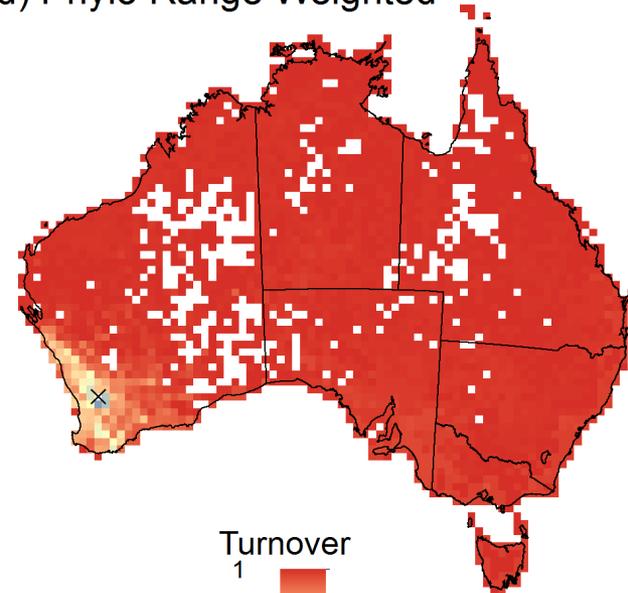
(b) PhyloSørensen



(c) Range Weighted

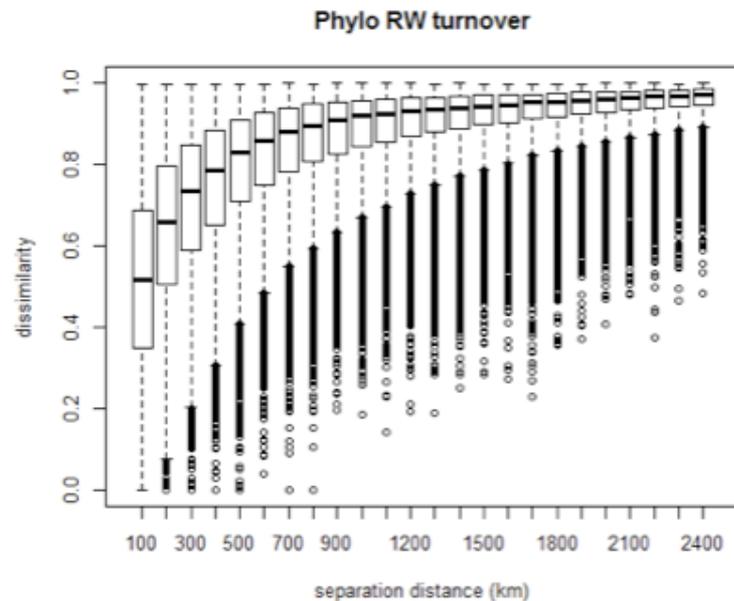
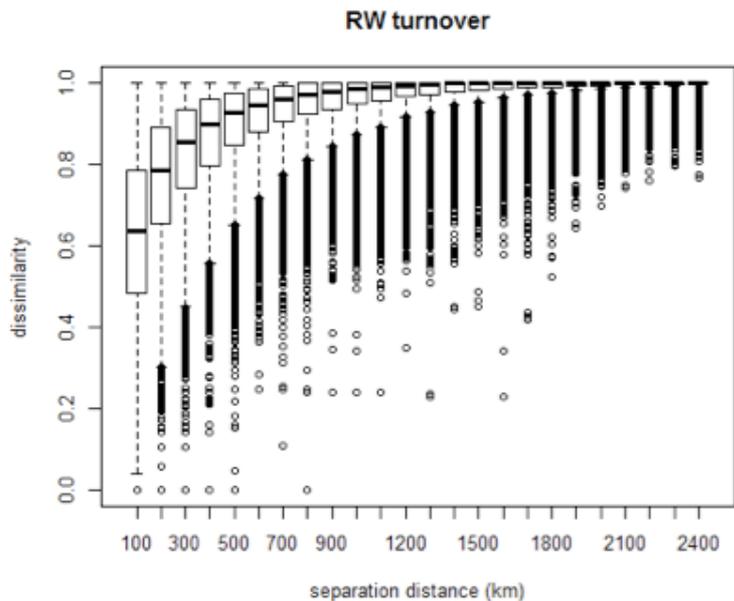
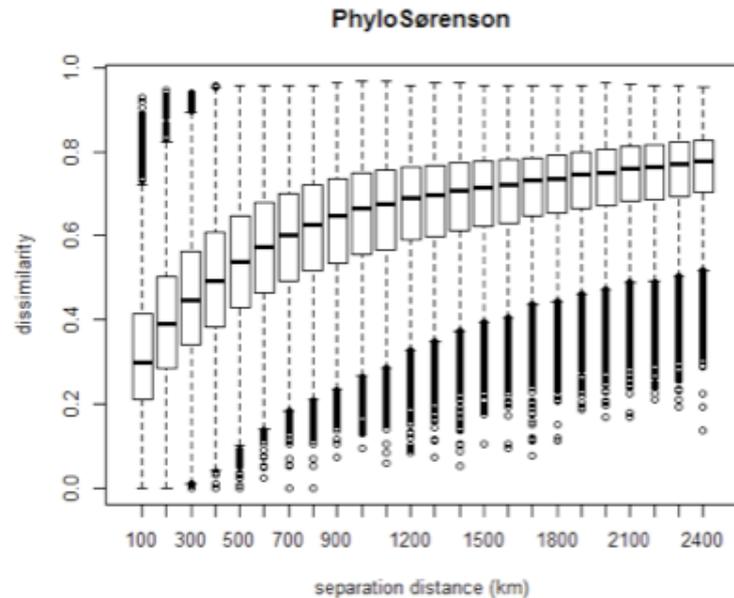
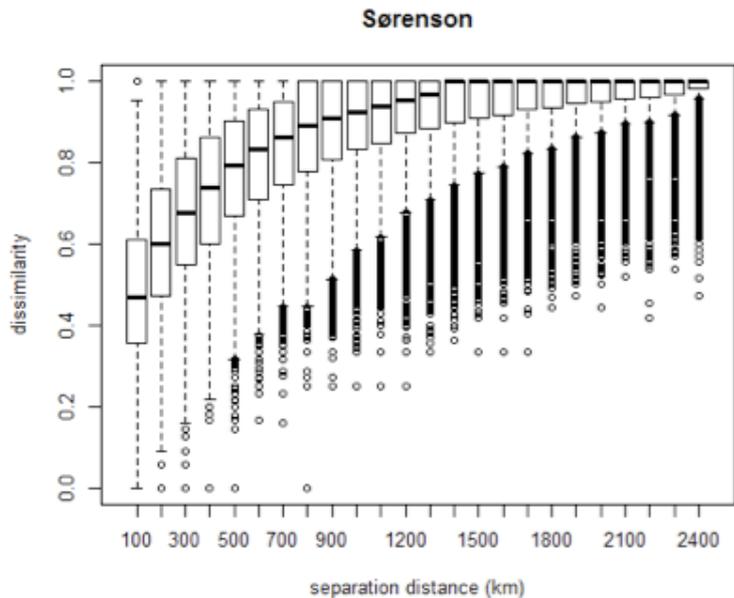


(d) Phylo Range Weighted

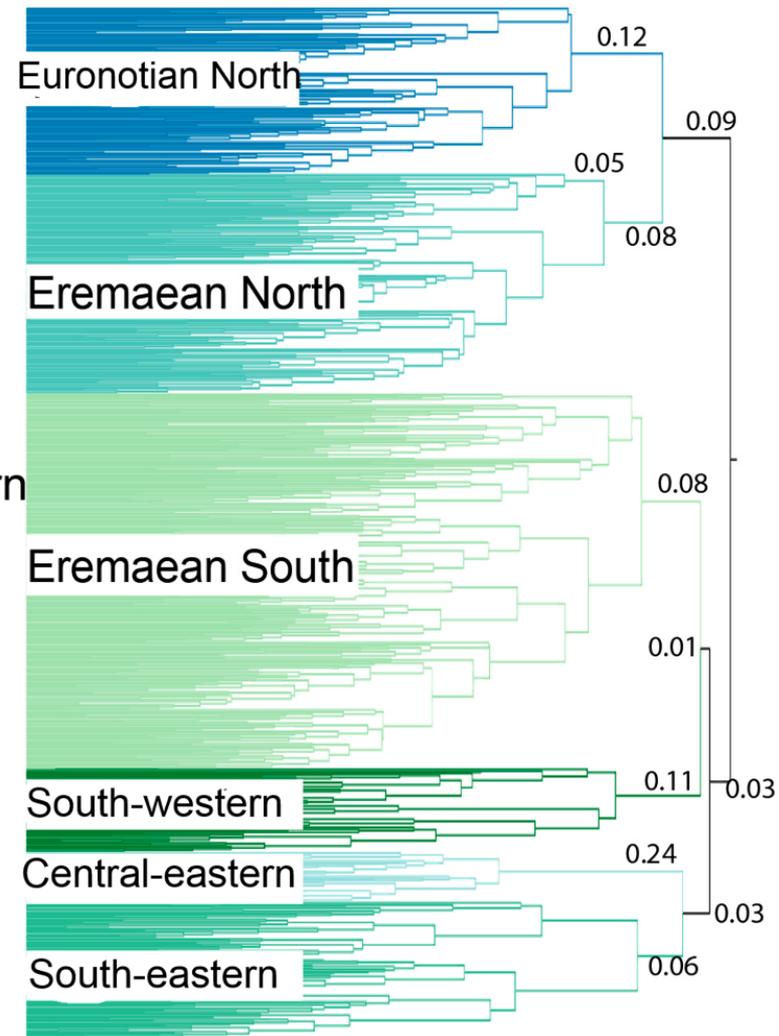
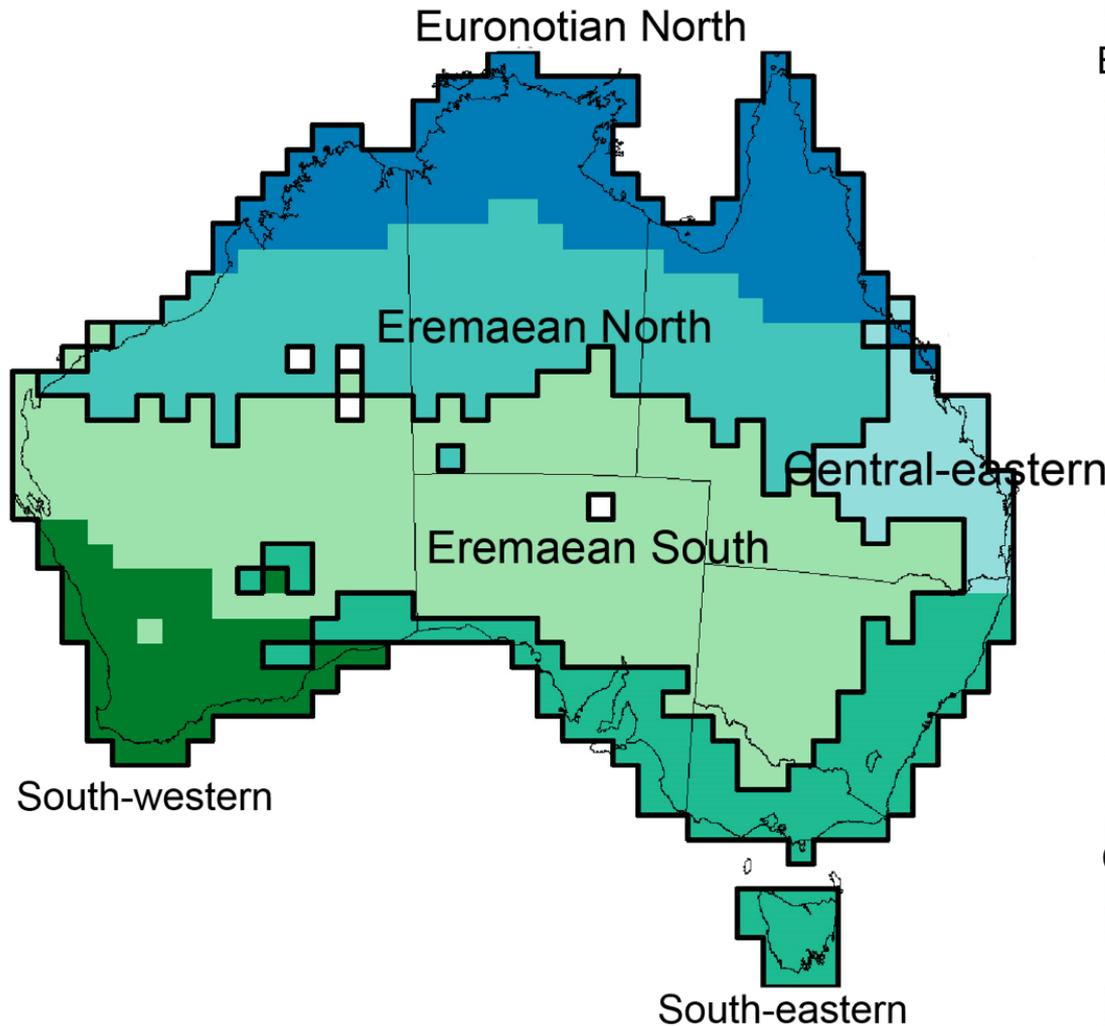


From Laffan, S.W., D.F. Rosauer, G. Di Virgilio, J. T. Miller, C.E. González-Orozco, N. Knerr, A.H. Thornhill, and B.D. Mishler (2016) Range-weighted metrics of species and phylogenetic turnover can better resolve biogeographic transition zones. Methods in Ecology and Evolution.

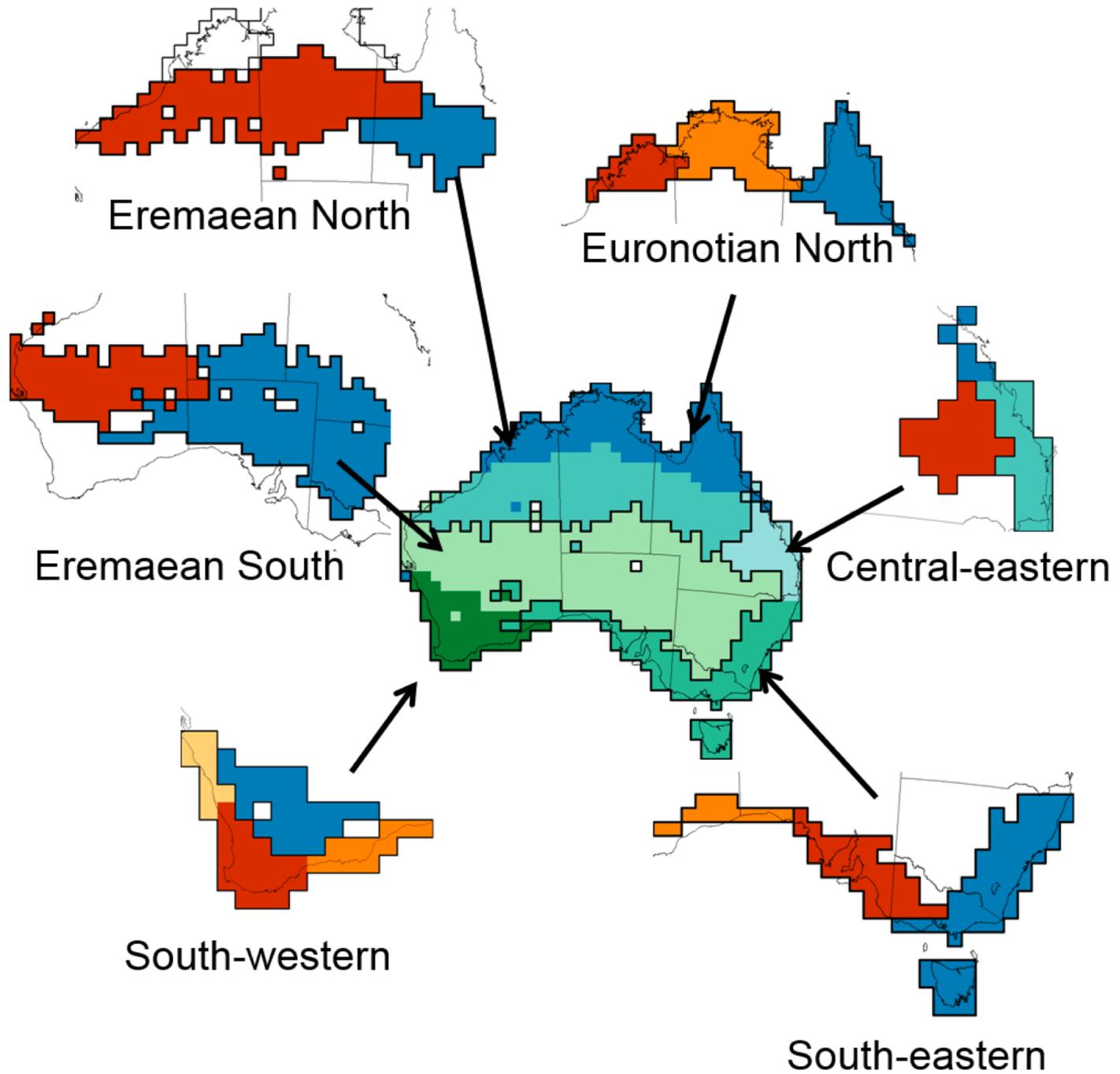
Range-weighted turnover vs. regular turnover measures



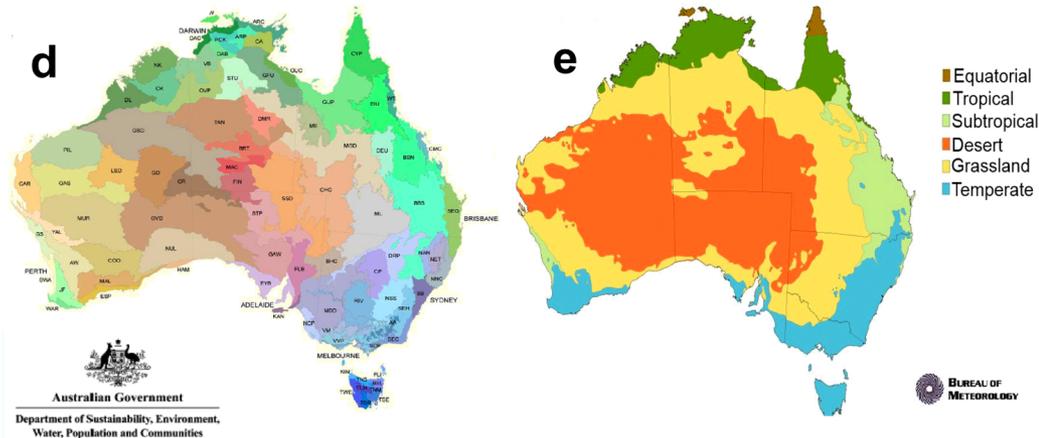
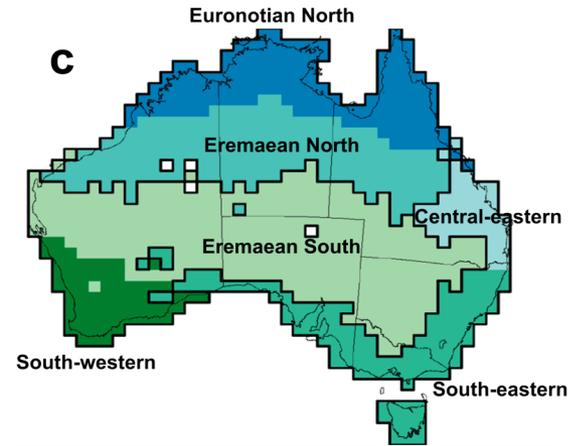
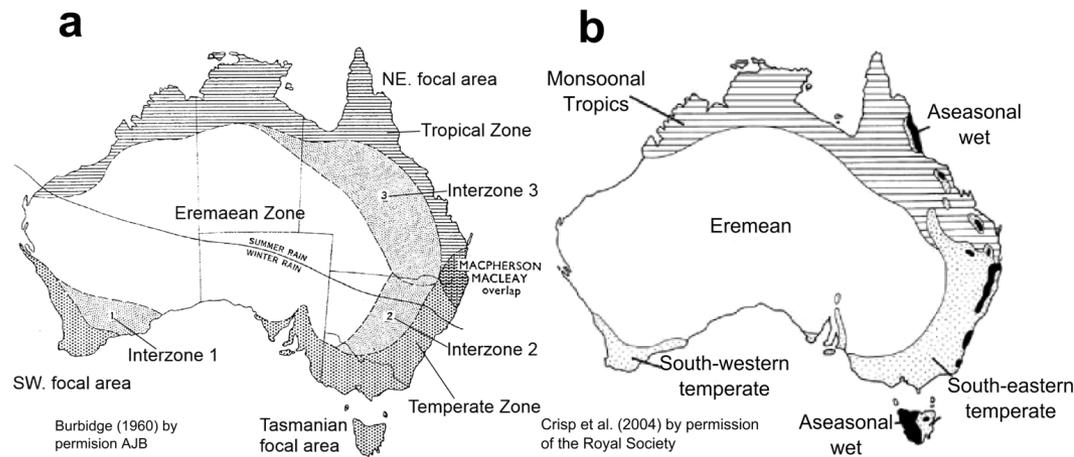
From: C. E. González-Orozco, M.C. Ebach, S. Laffan, A.H. Thornhill, N.J. Knerr, A.N. Schmidt-Lebuhn, C.C. Cargill, M. Clements, N.S. Nagalingum, B.D. Mishler, and J.T. Miller. 2014. Quantifying phytogeographical regions of Australia using geospatial turnover in species composition. *PLoS ONE* 9(3): e92558. doi:10.1371/journal.pone.0092558.



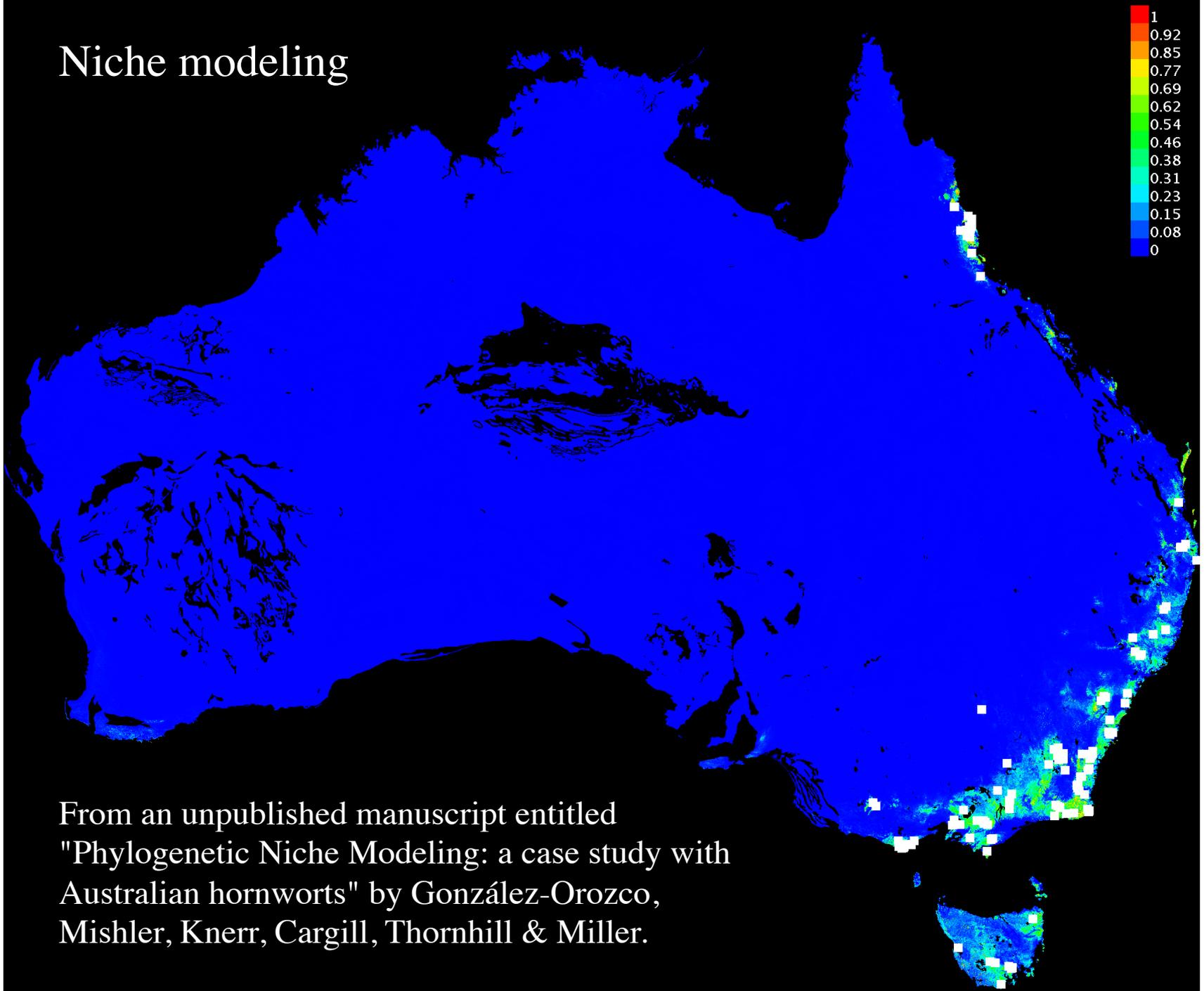
Land plant distributions in Australia (750,741 georeferenced herbarium records; 6,043 species).



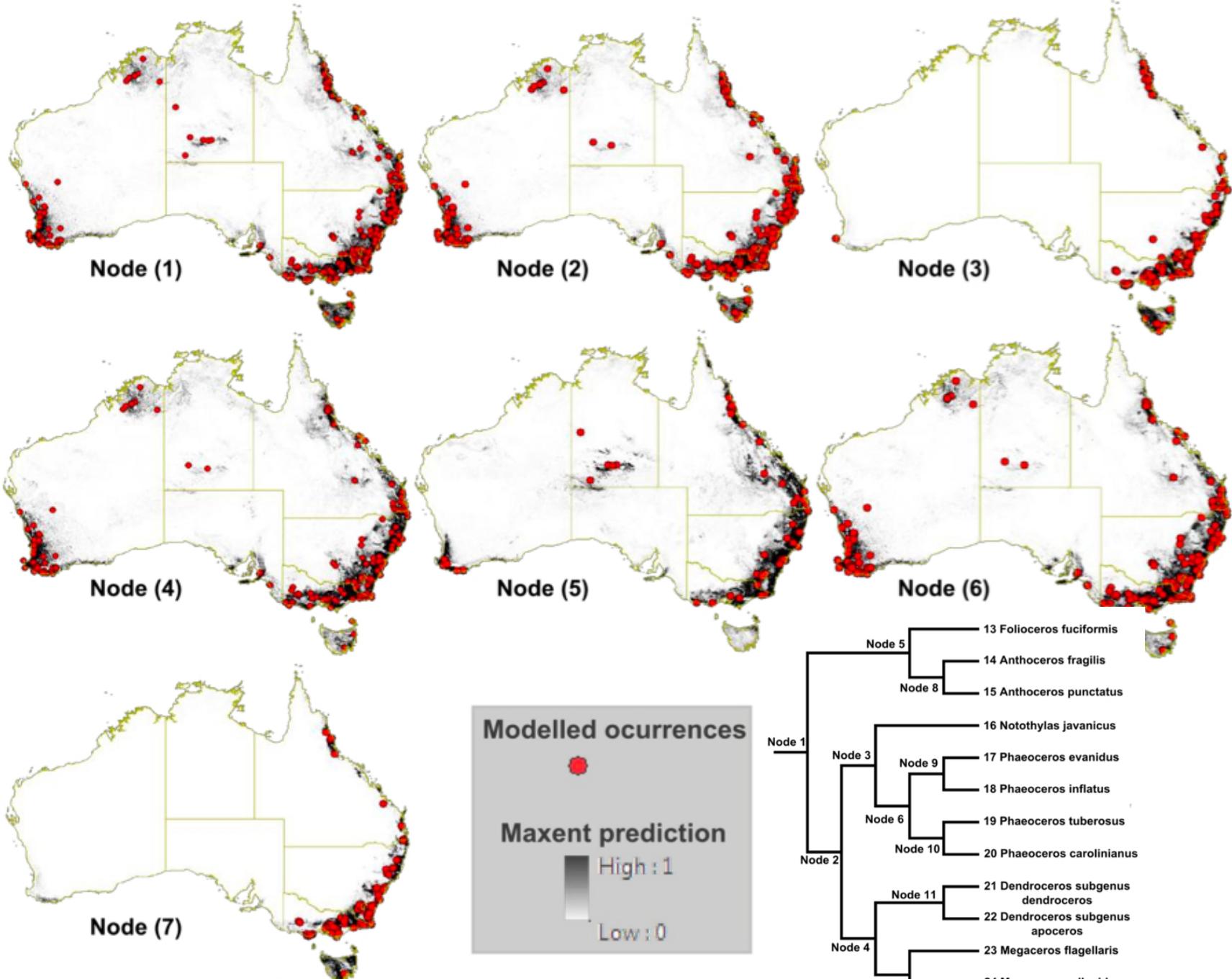
Comparison of our six phytogeographical regions of Australian flora (c) against major biogeographical classifications of Australia: Burbidges biomes [10] (a), Crisp et al biomes [49] (b), IBRA bioregions [4] (d) and Köppen's macro-climatic map of Australia (e).



Niche modeling



From an unpublished manuscript entitled
"Phylogenetic Niche Modeling: a case study with
Australian hornworts" by González-Orozco,
Mishler, Knerr, Cargill, Thornhill & Miller.

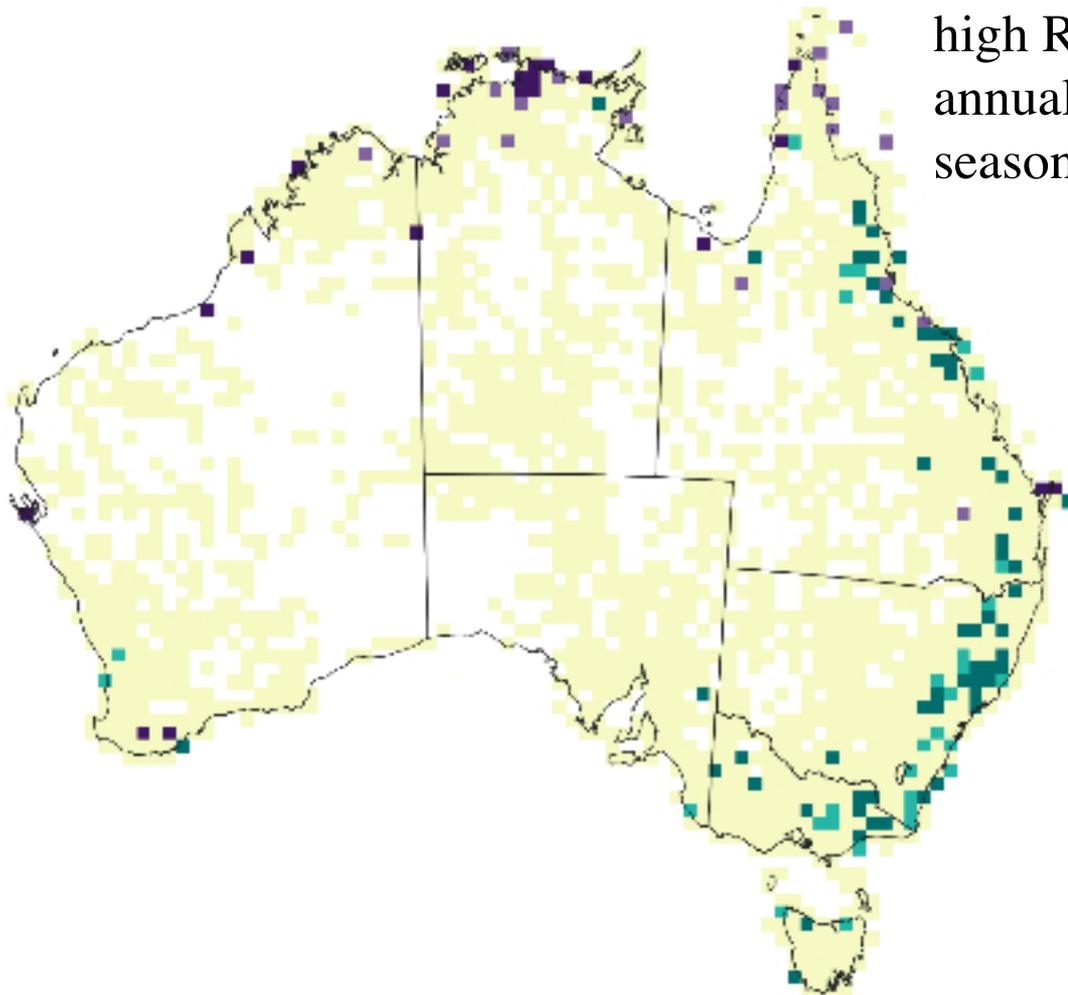


Phylogenetic Niche Modeling

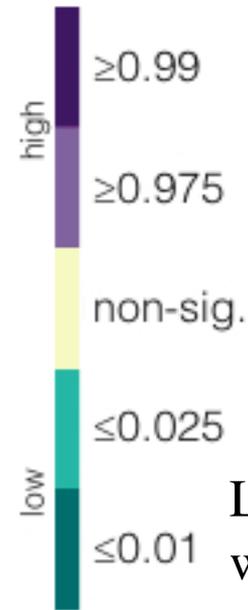
Ferns of Australia

Eleven environmental variables were assessed, encompassing temperature, precipitation, topography, and substrates.

C Relative phylogenetic diversity

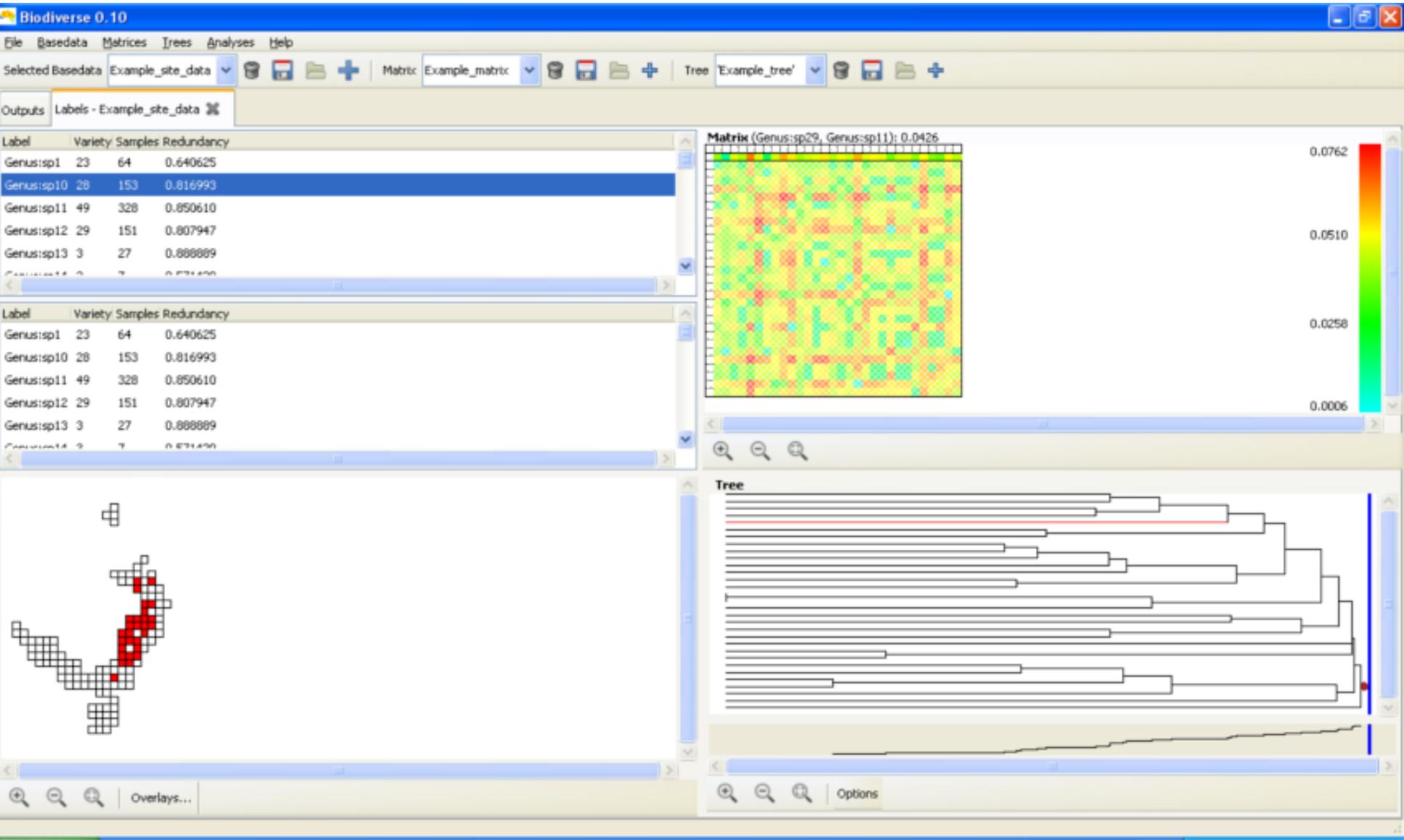


high RPD areas correlate with mean annual radiation and temperature seasonality



Low RPD areas correlate with temperature seasonality and annual precipitation.

Biodiverse software



Biodiverse software

