

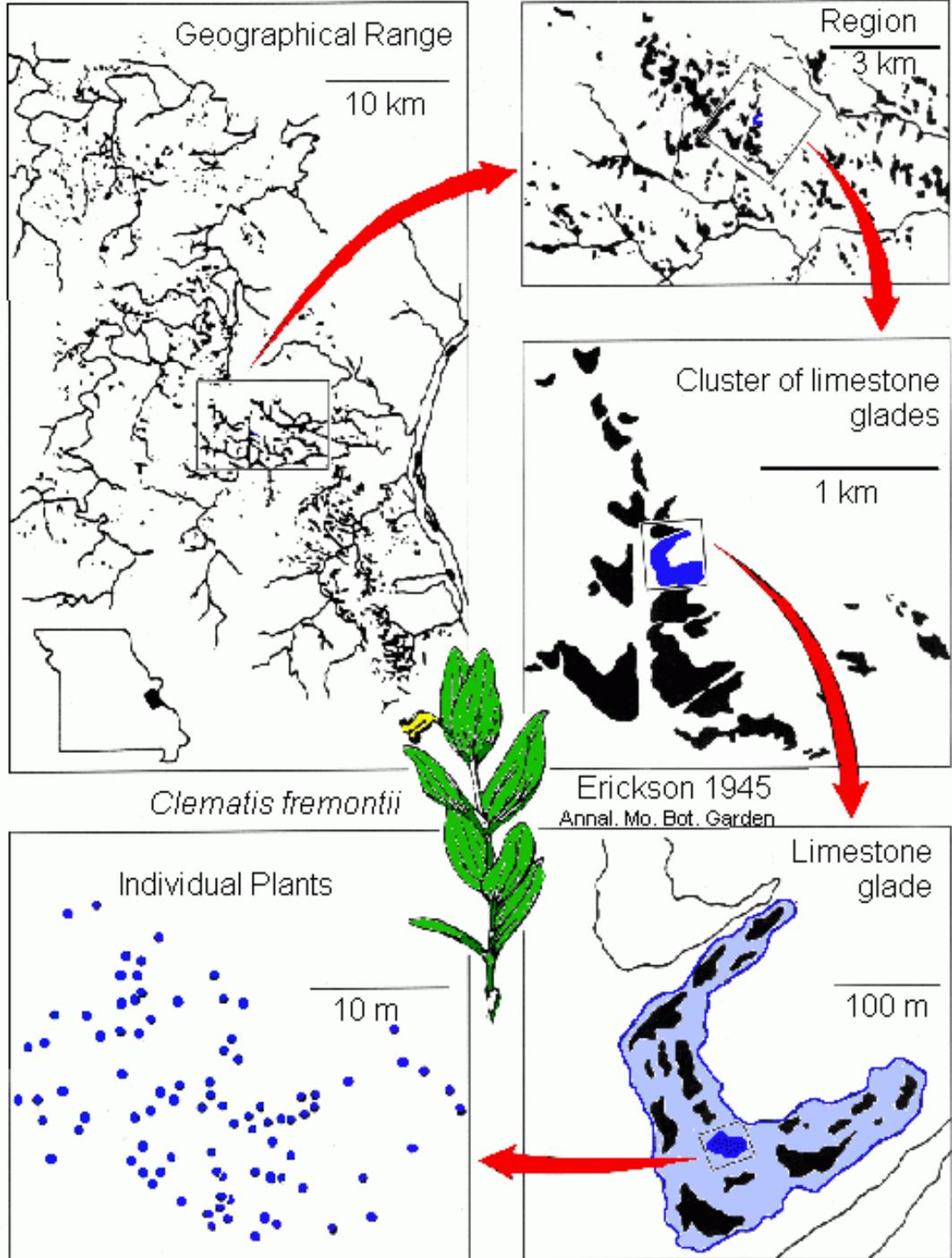
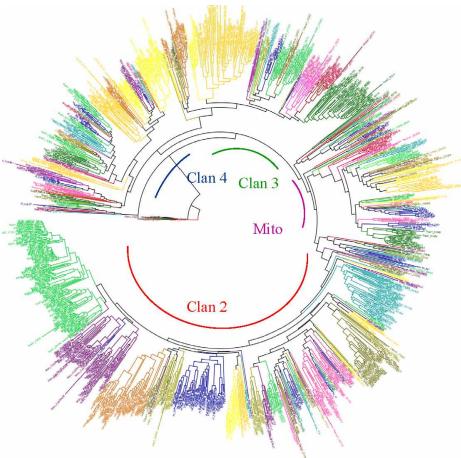
What is the range of a taxon?

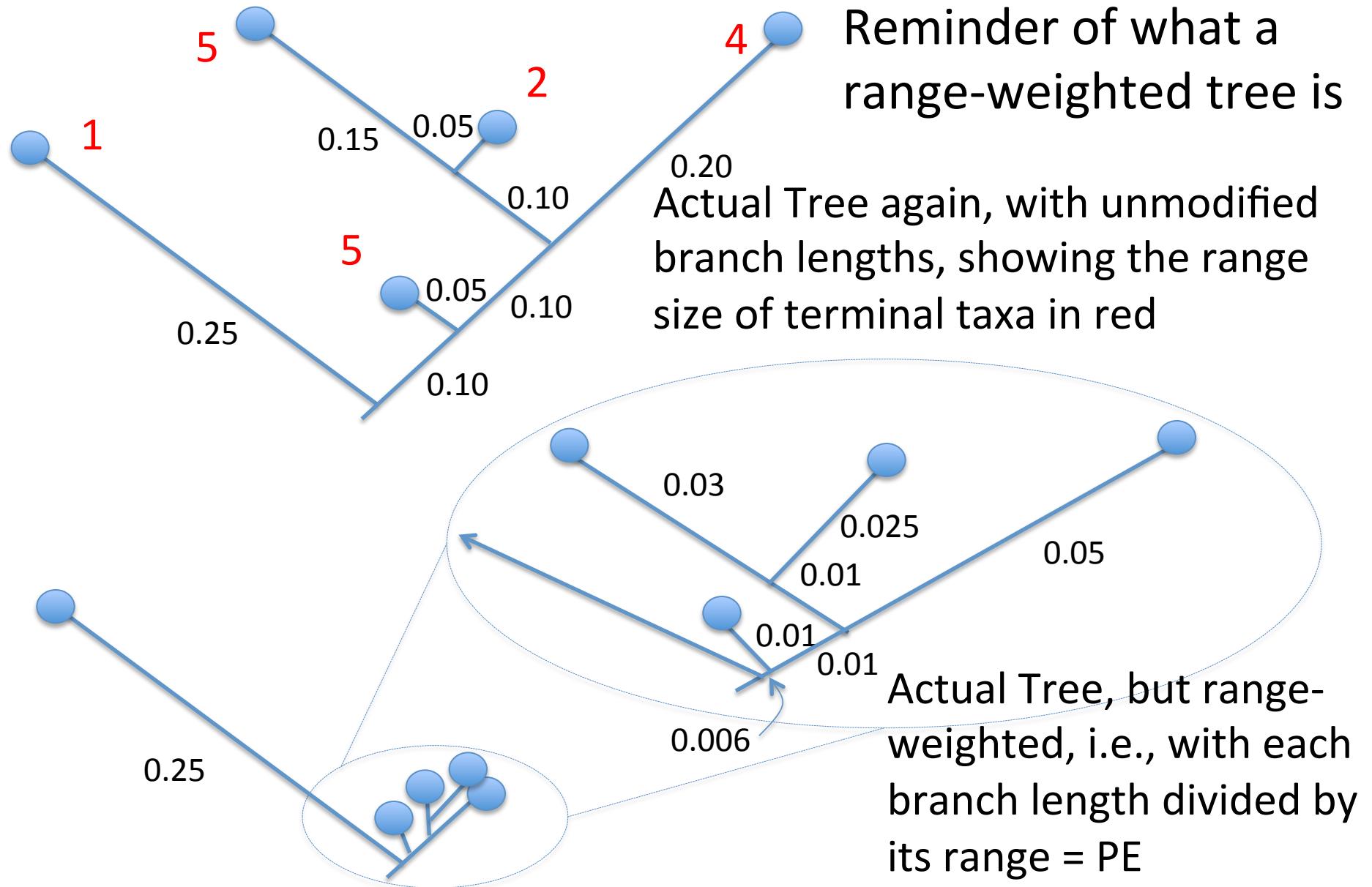
A scaling problem
at three levels:

Spatial scale

Phylogenetic depth

Time



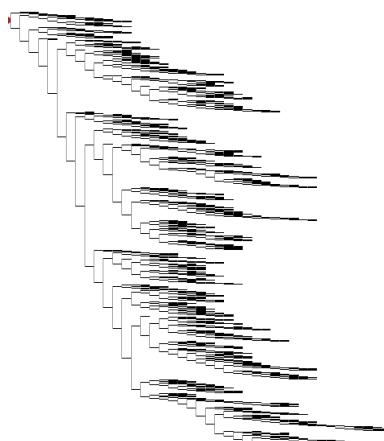
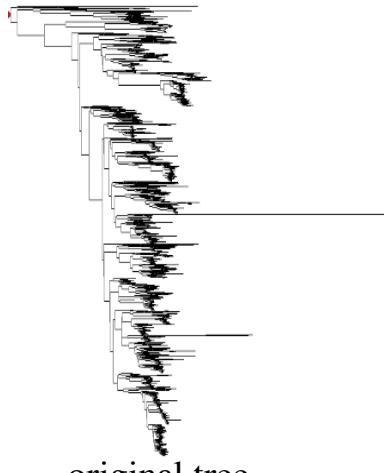


PE is PD of a range-weighted tree!

Reminder of what RPD and RPE are

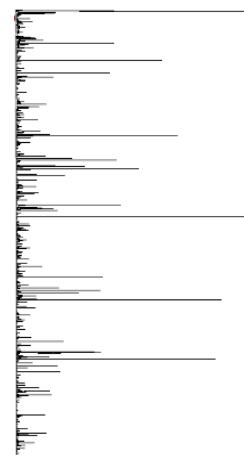
RPD (*relative phylogenetic diversity*) =
PD on the original tree

PD on a comparison tree with
all branch lengths equal

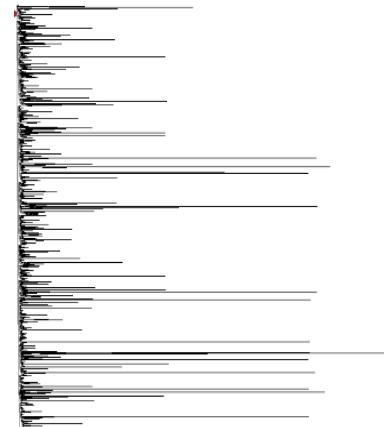


RPE (*relative phylogenetic endemism*) =
PD on the range-weighted original tree

PD on a range-weighted comparison tree
with all branch lengths equal

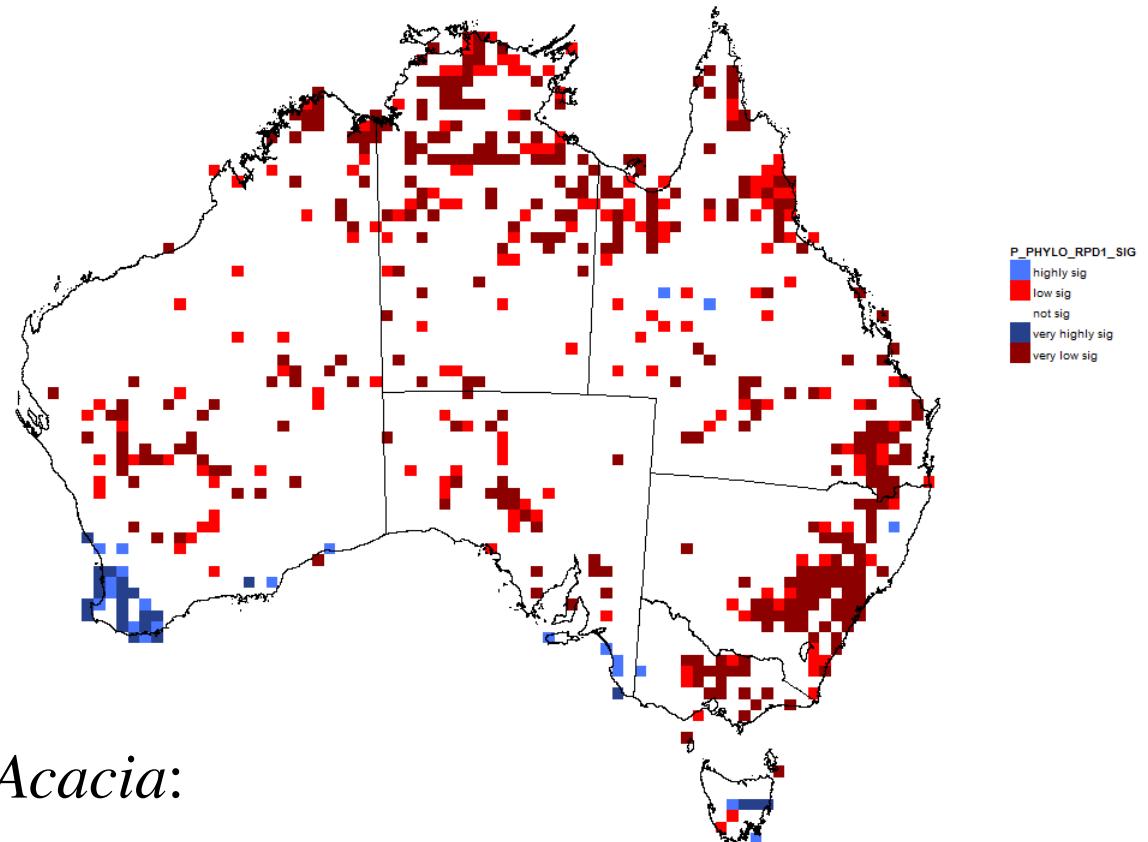


range-weighted original
tree

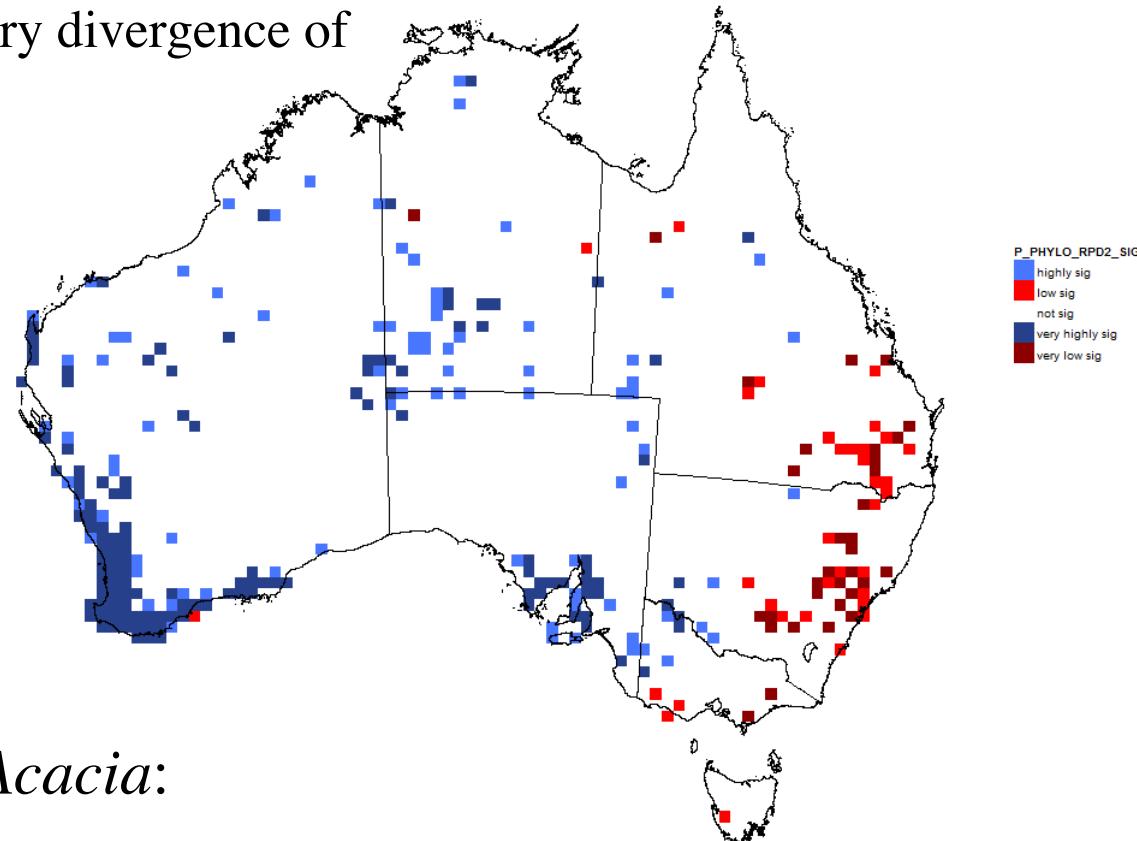


range-weighted comparison tree

- **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.

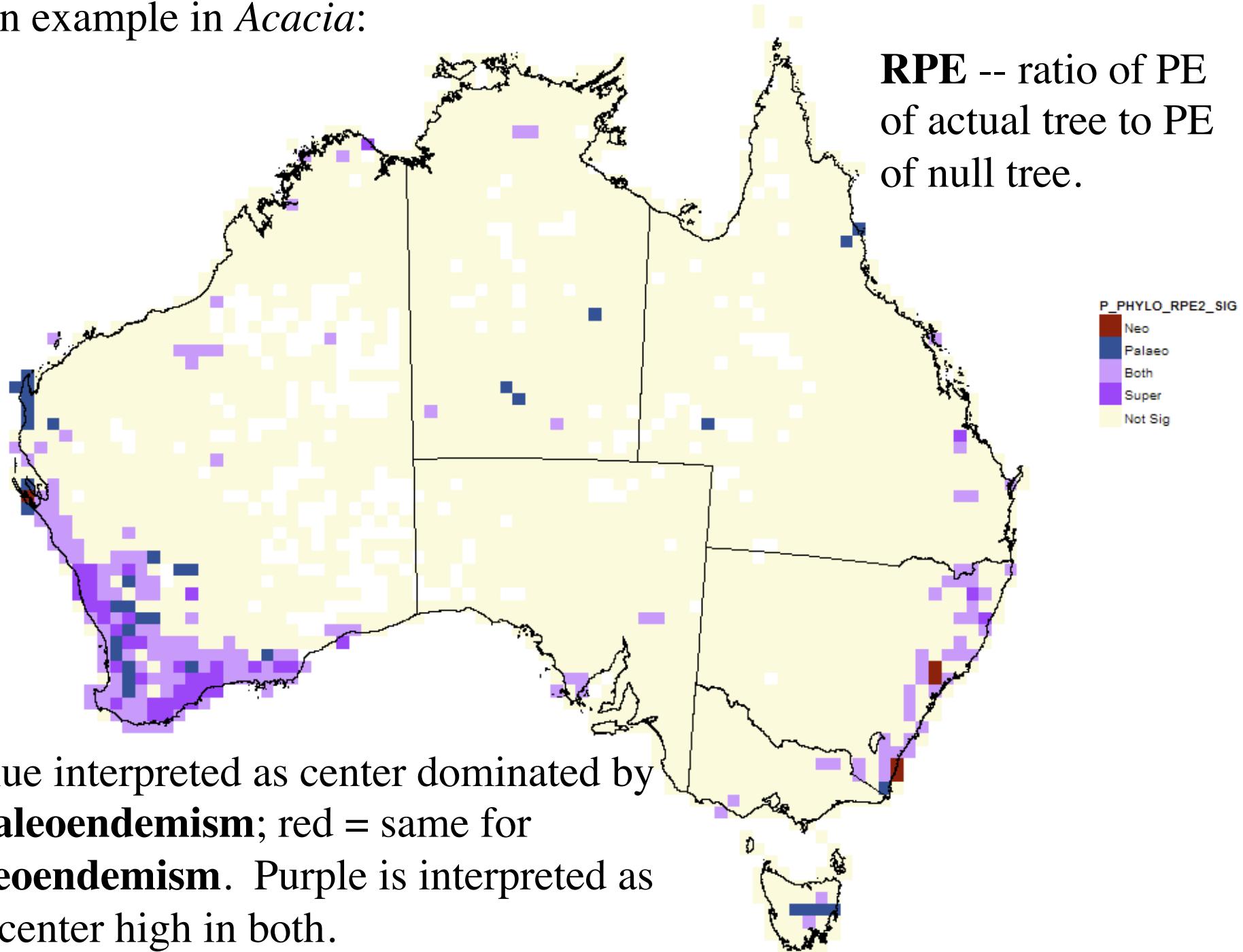


- **Significantly high and low RPD locations** are more likely to relate to biogeographic and evolutionary processes.
 - A significant concentration of long branches (blue here) could indicate the presence of a refugium, or perhaps could result from occurrence of a few members of clades that mainly occur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



Phylogenetic measures of geographic similarity

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

$$\textbf{Jaccard} = 1 - \frac{A}{A + B + C}$$

$$\textbf{Sorensen} = 1 - \frac{2A}{2A + B + C}$$

Phylo-Jaccard

Phylo-Sorensen

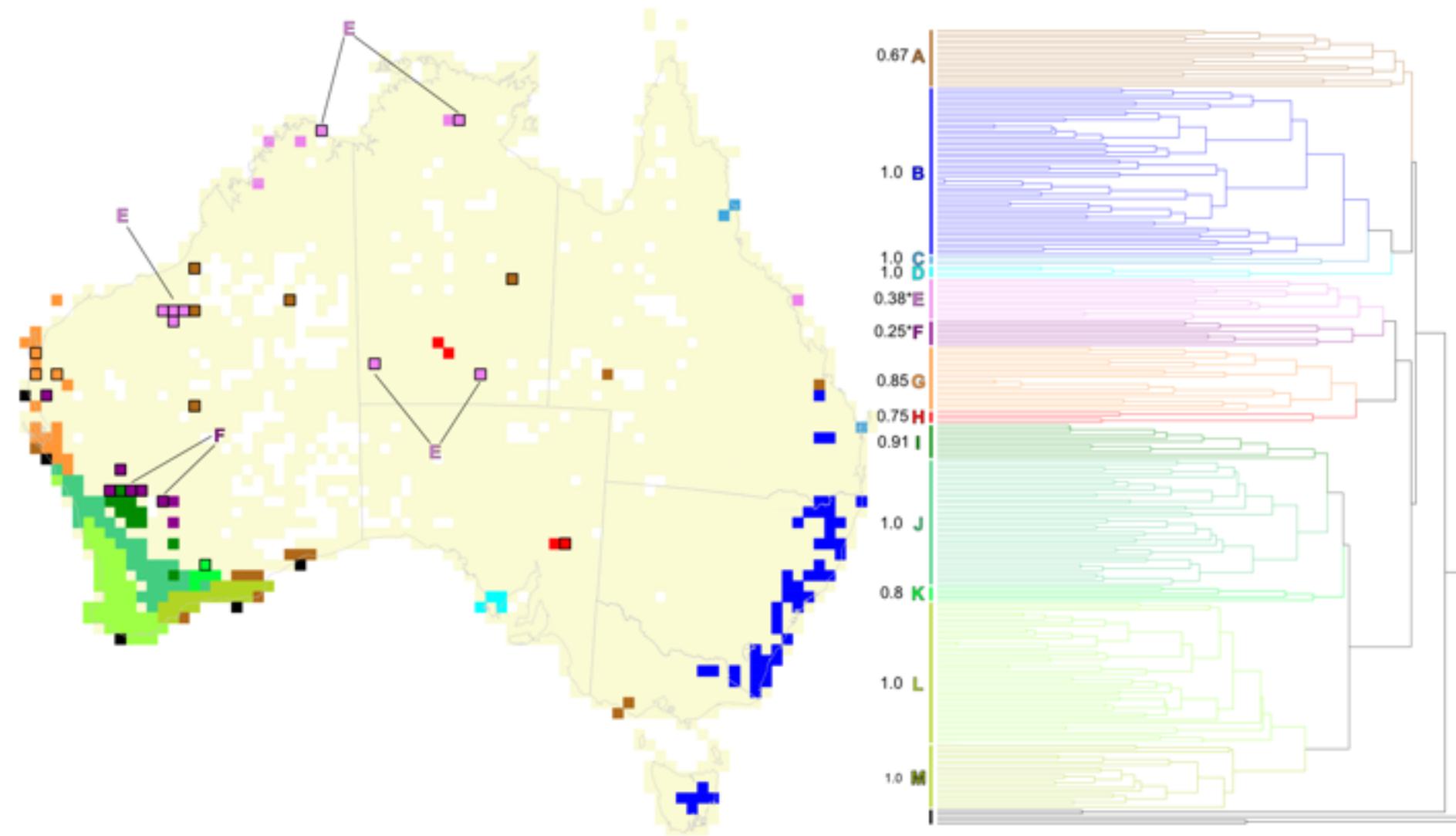
where A is the count of species found in both neighbor sets, B is the count unique to neighbor set 1, and C is the count unique to neighbor set 2.

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:

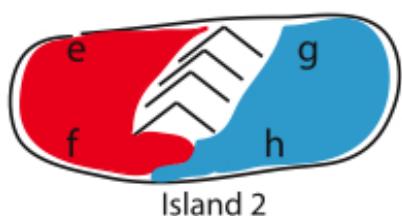
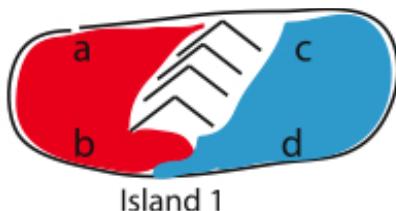
A UPGMA cluster analysis of phylo-Jaccard distances between all pairs of grid cells with significant endemism, done along with all these analyses using *Biodiverse* (Laffan et al.)



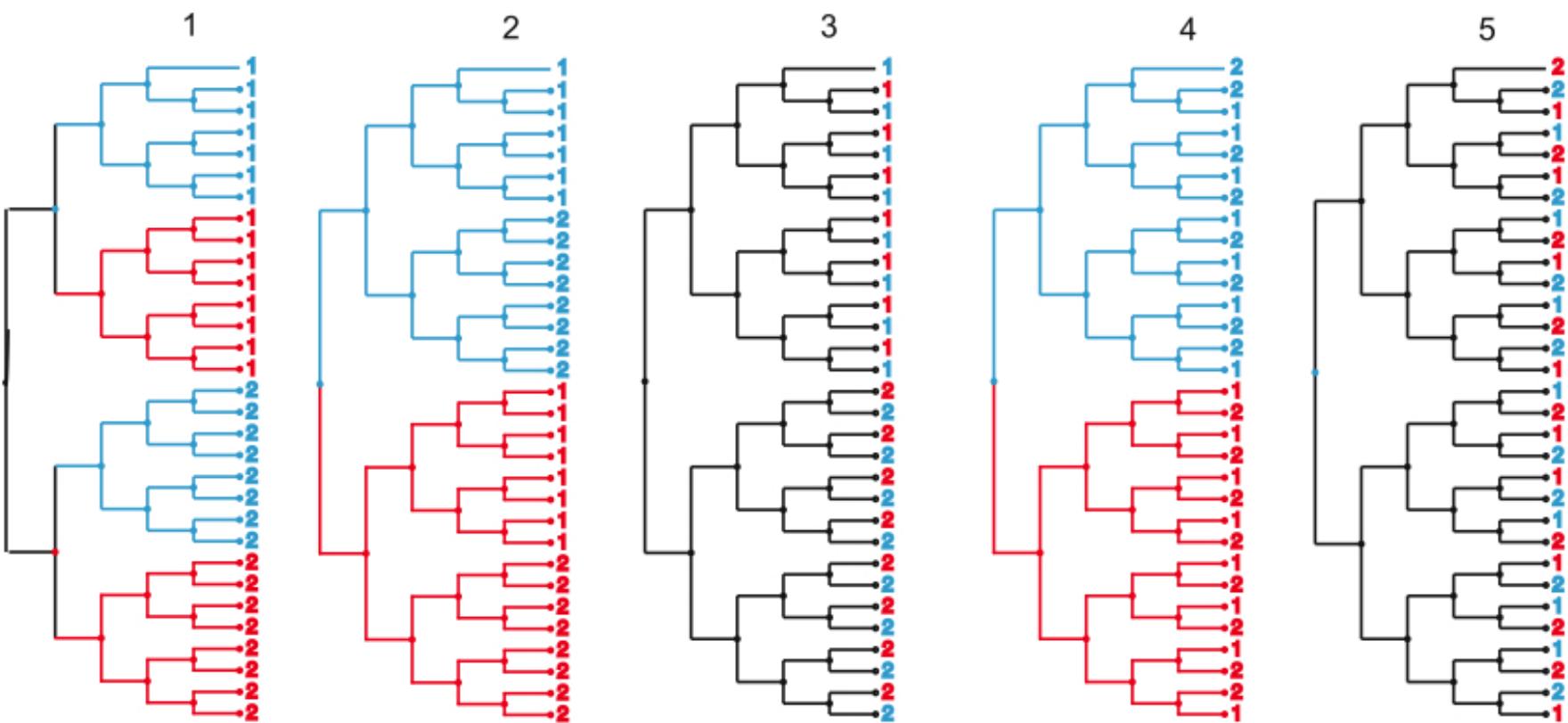
Phylo-betadiversity

- 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.

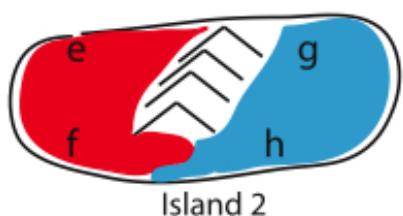
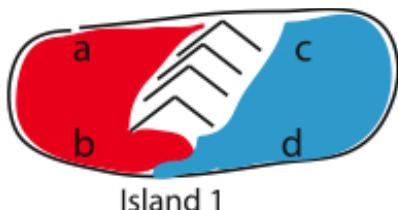
An example from Graham, C.H. & Fine, P.V.A. (2008) Phylogenetic beta diversity: linking ecological and evolutionary processes across space in time. *Ecology Letters*, 11, 1265-1277.



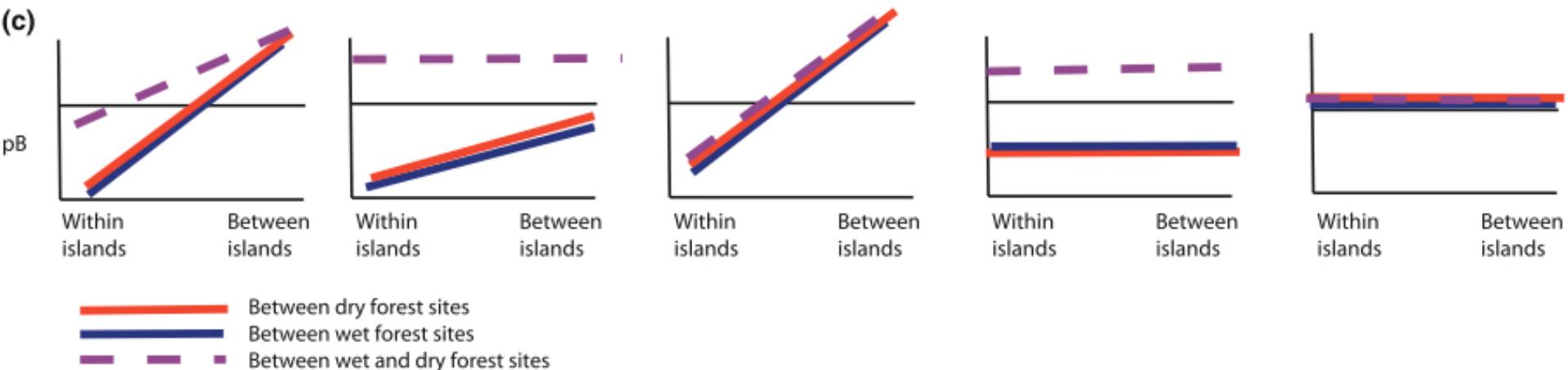
Site	Habitat	Species sampled	Community phylogenetic structure				
			Type1	Type2	Type3	Type4	Type5
Island 1	Dry	Random sample of all dry, island 1 taxa	C	C	c	c	r/o
		random sample of all wet, island 1 taxa	C	C	c	c	r/o
	Wet	Random sample of all dry, island 2 taxa	C	C	c	c	r/o
		Random sample of all wet,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



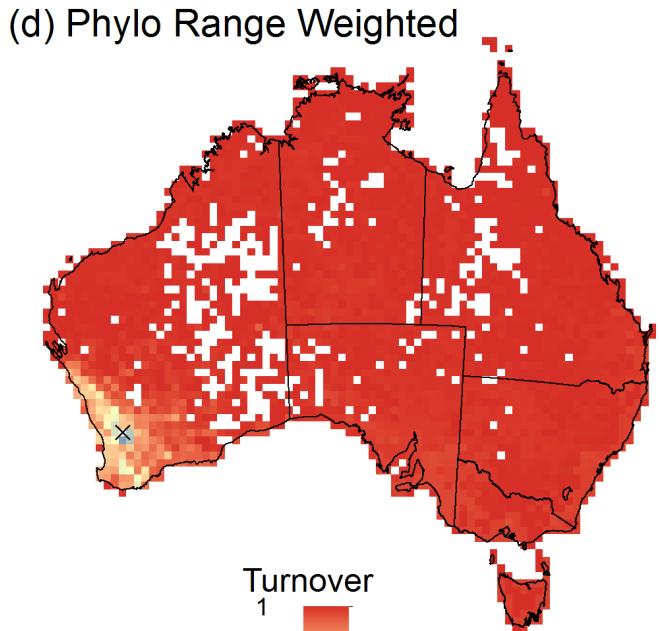
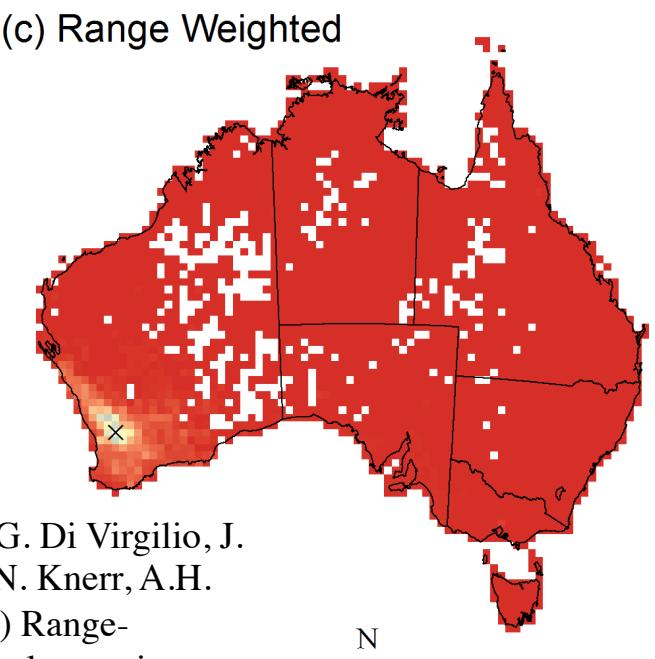
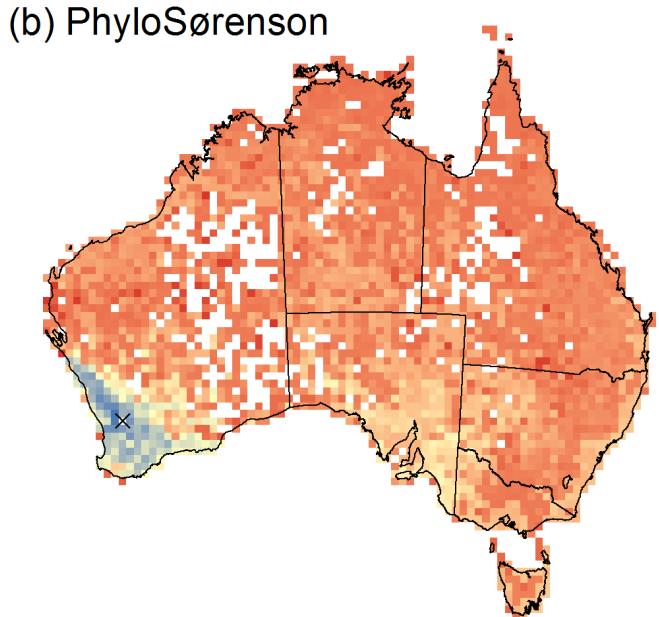
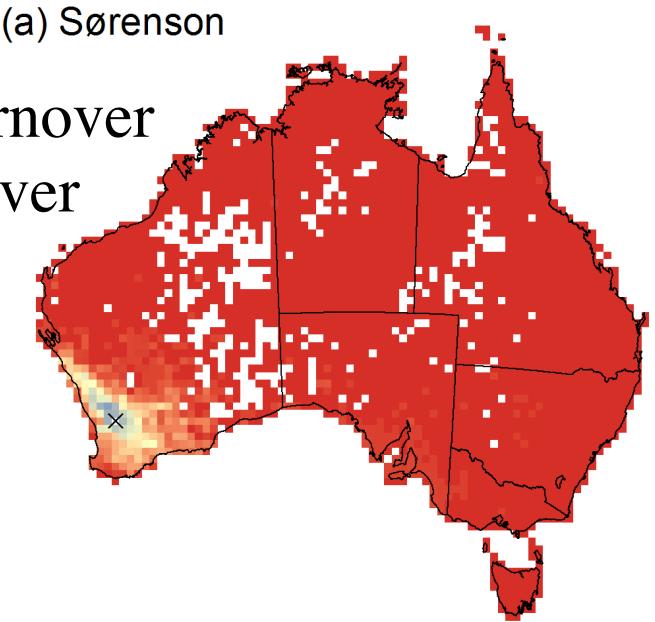
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Site	Habitat	Species sampled	Community phylogenetic structure				
			Type 1	Type 2	Type 3	Type 4	Type 5
Island 1	Dry	Random sample of all dry, island 1 taxa	C	C	c	c	r/o
		random sample of all wet, island 1 taxa	C	C	c	c	r/o
	Wet	Random sample of all dry, island 2 taxa	C	C	c	c	r/o
		Random sample of all wet, island 2 taxa	C	C	c	c	r/o



Range-weighted turnover vs. regular turnover measures

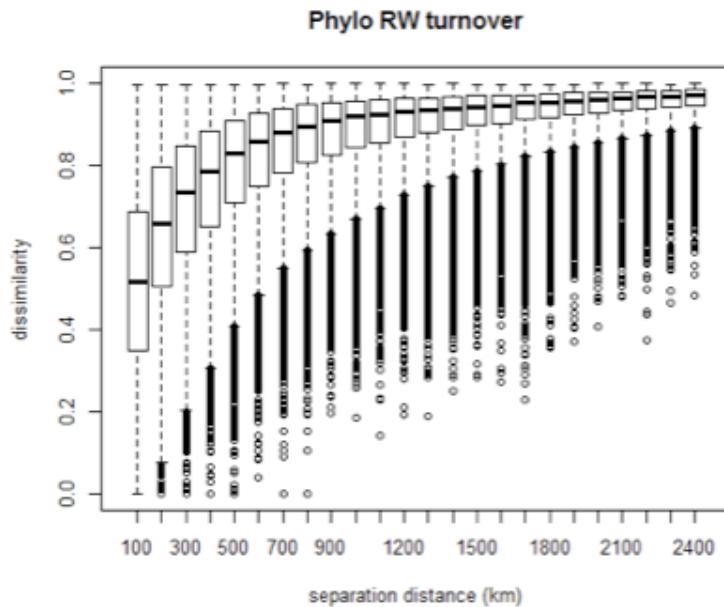
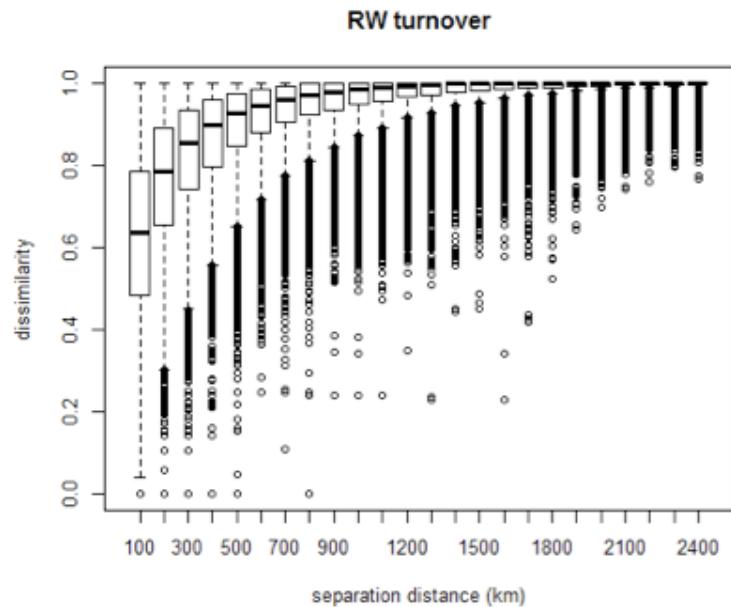
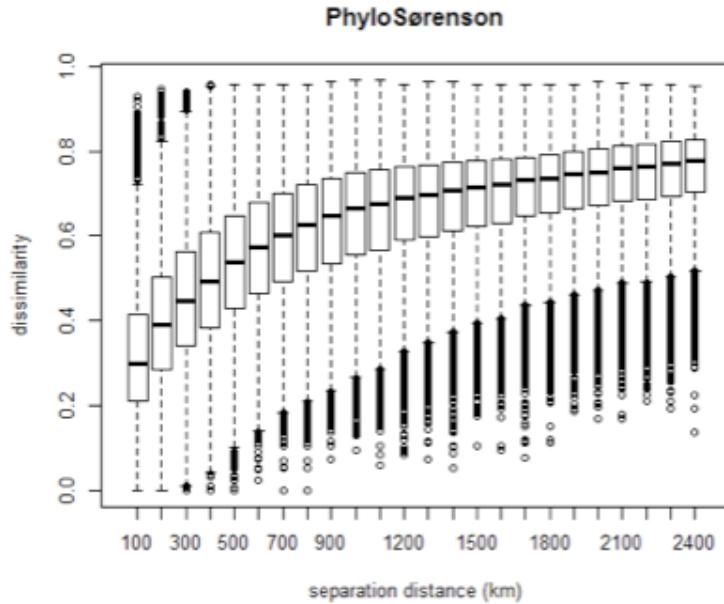
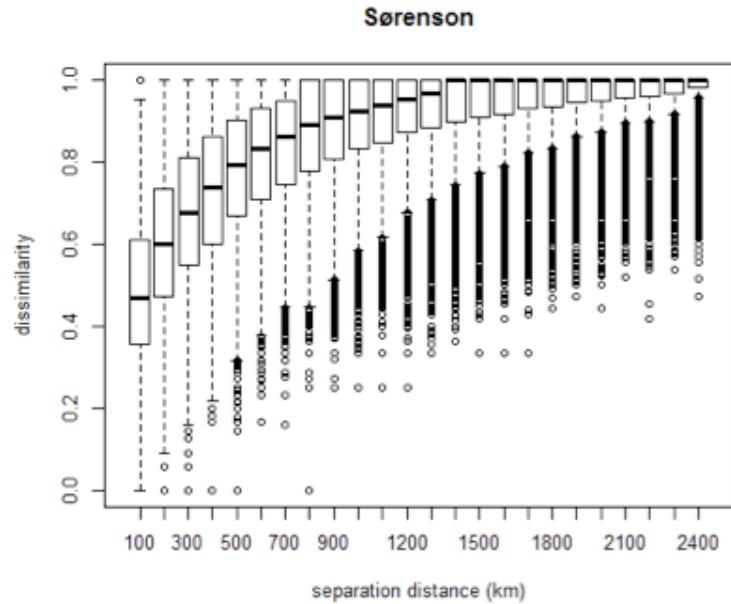


0 1000 2000 km

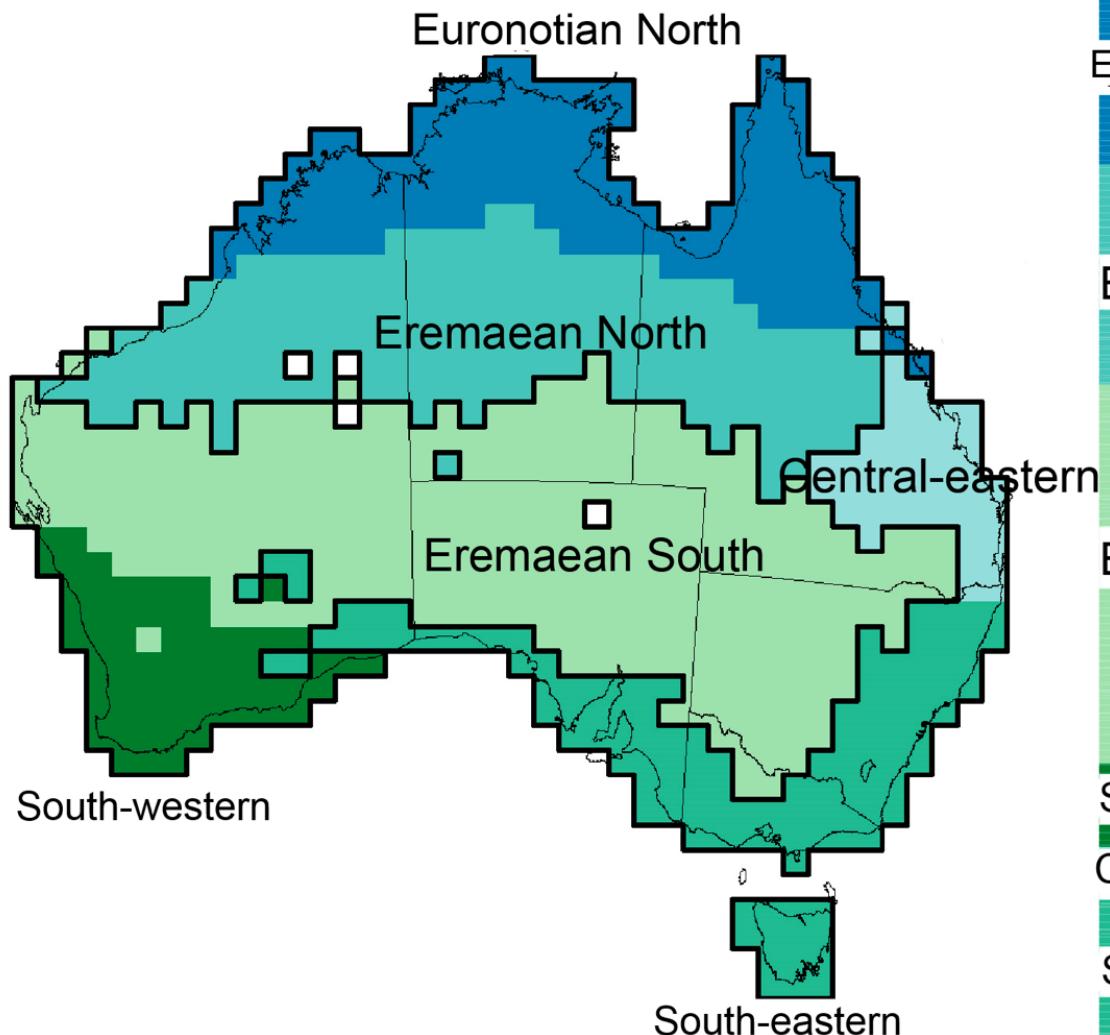
Turnover
1
0.6
<0.2

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*.

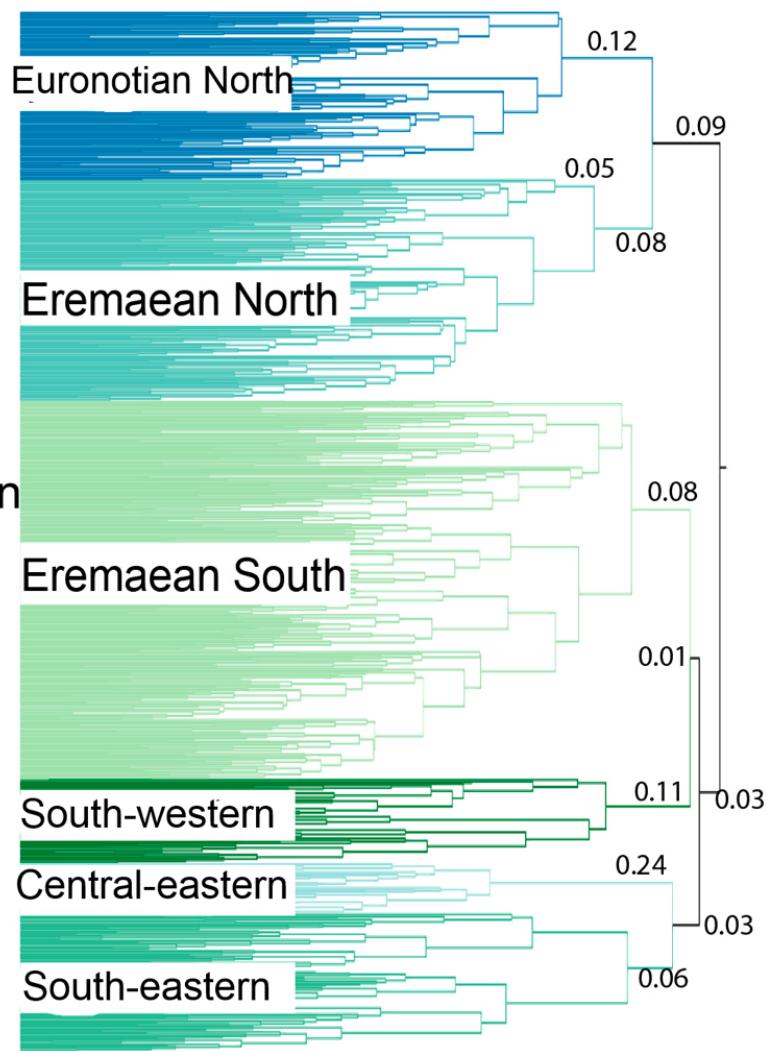
Range-weighted turnover vs. regular turnover measures

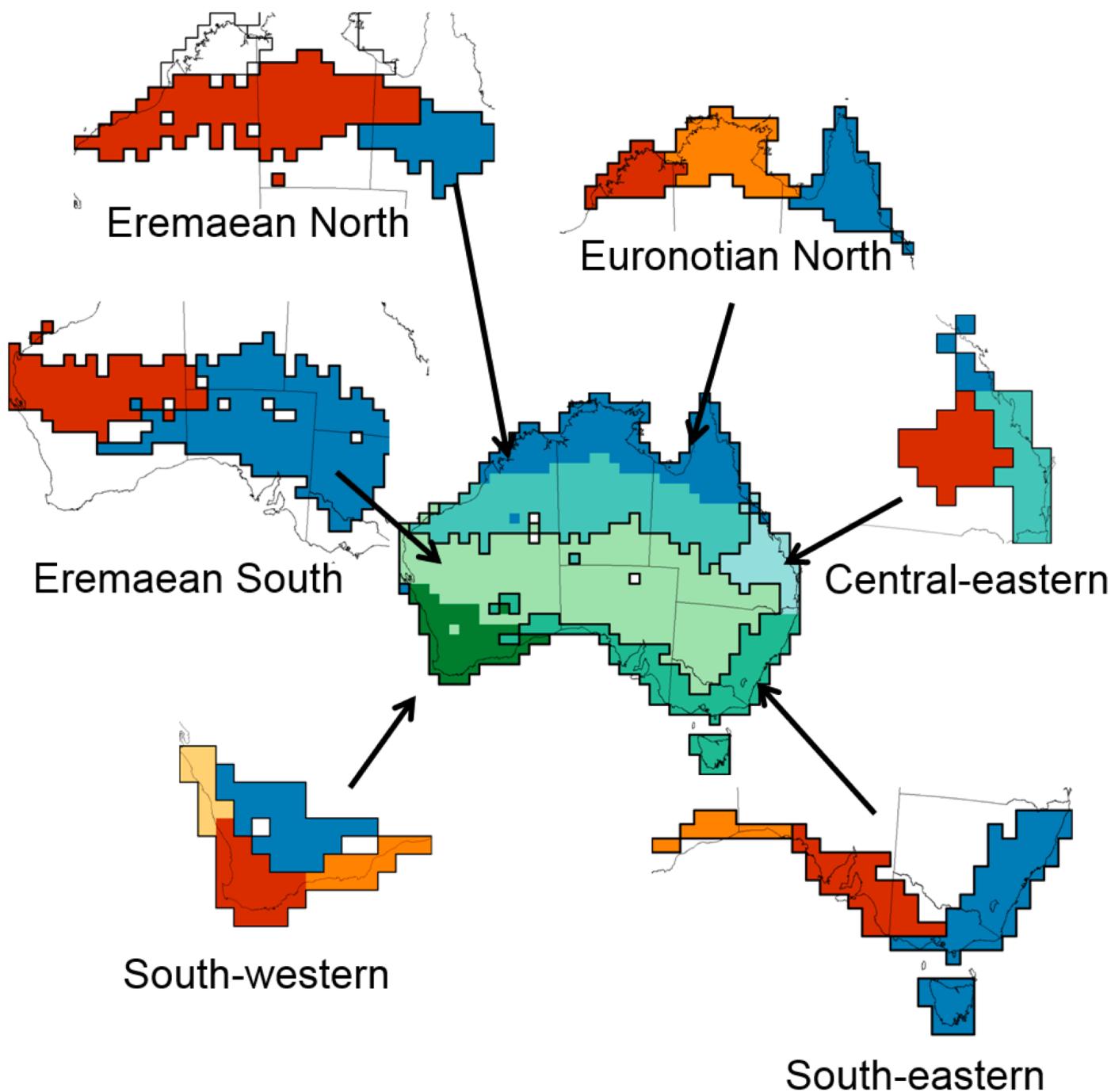


From: C. E. González-Orozco, M.C. Ebach, S. Laffan, A.H. Thornhill, N.J. Knerr, A.N. Schmidt-Lebuhn, C.C. Cargill, M. Clements, N.S. Nagalingum, B.D. Mishler, and J.T. Miller. 2014. Quantifying phytogeographical regions of Australia using geospatial turnover in species composition. *PLoS ONE* 9(3): e92558.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

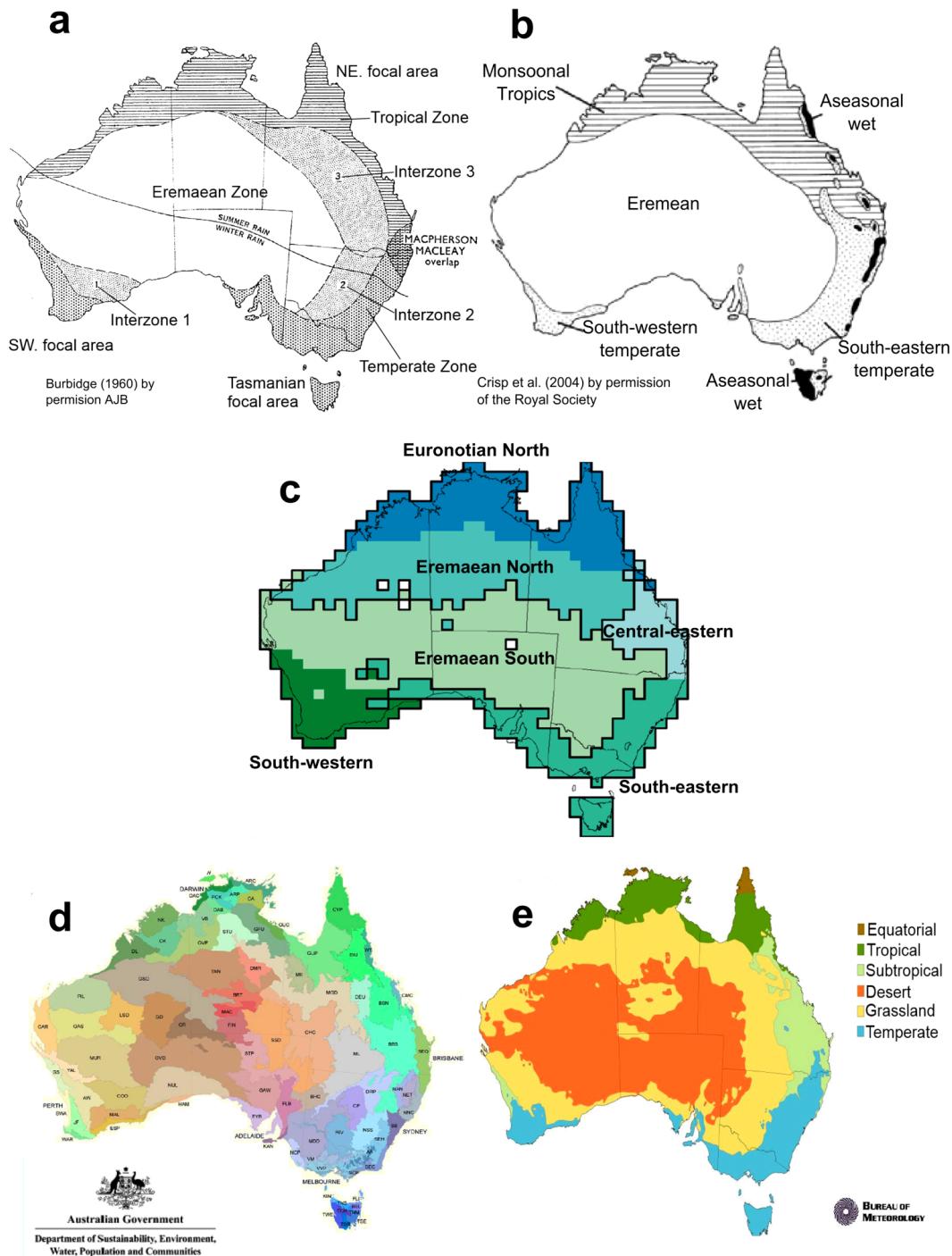


Land plant distributions in Australia (750,741 georeferenced herbarium records; 6,043 species).

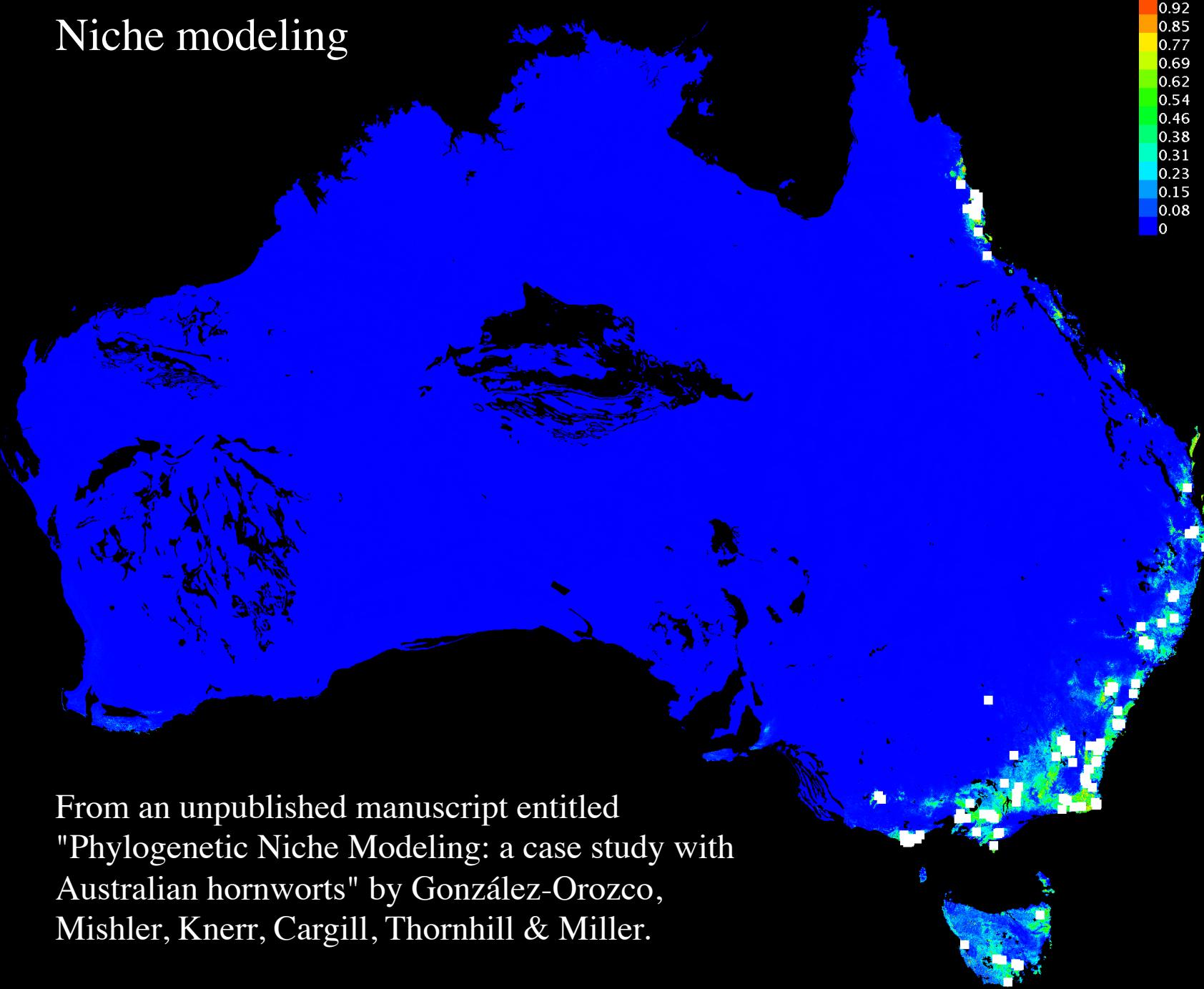




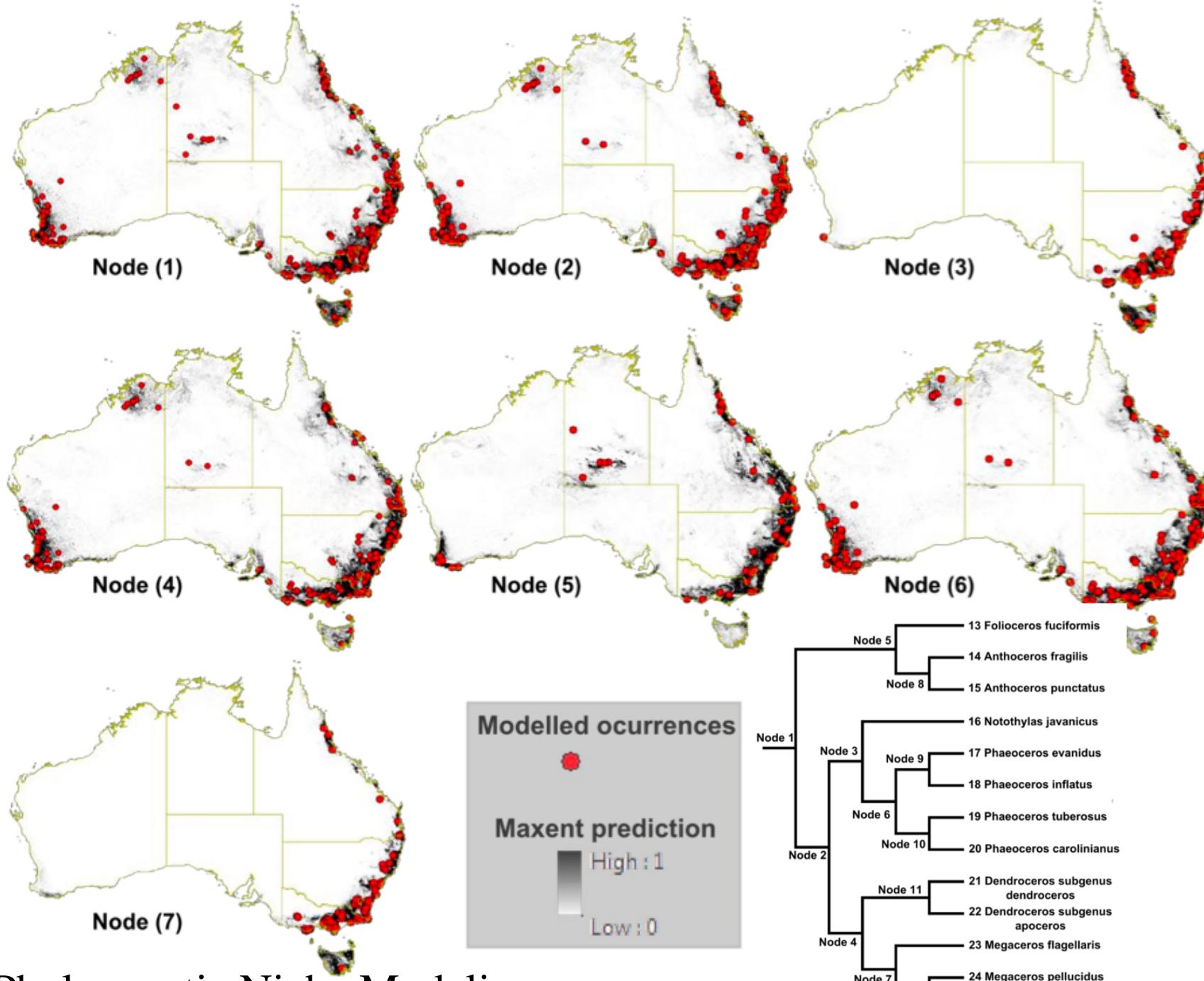
Comparison of our six phytogeographical regions of Australian flora (c) against major biogeographical classifications of Australia: Burbidges biomes [10] (a), Crisp et al biomes [49] (b), IBRA bioregions [4] (d) and Köppen's macro-climatic map of Australia (e).



Niche modeling



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



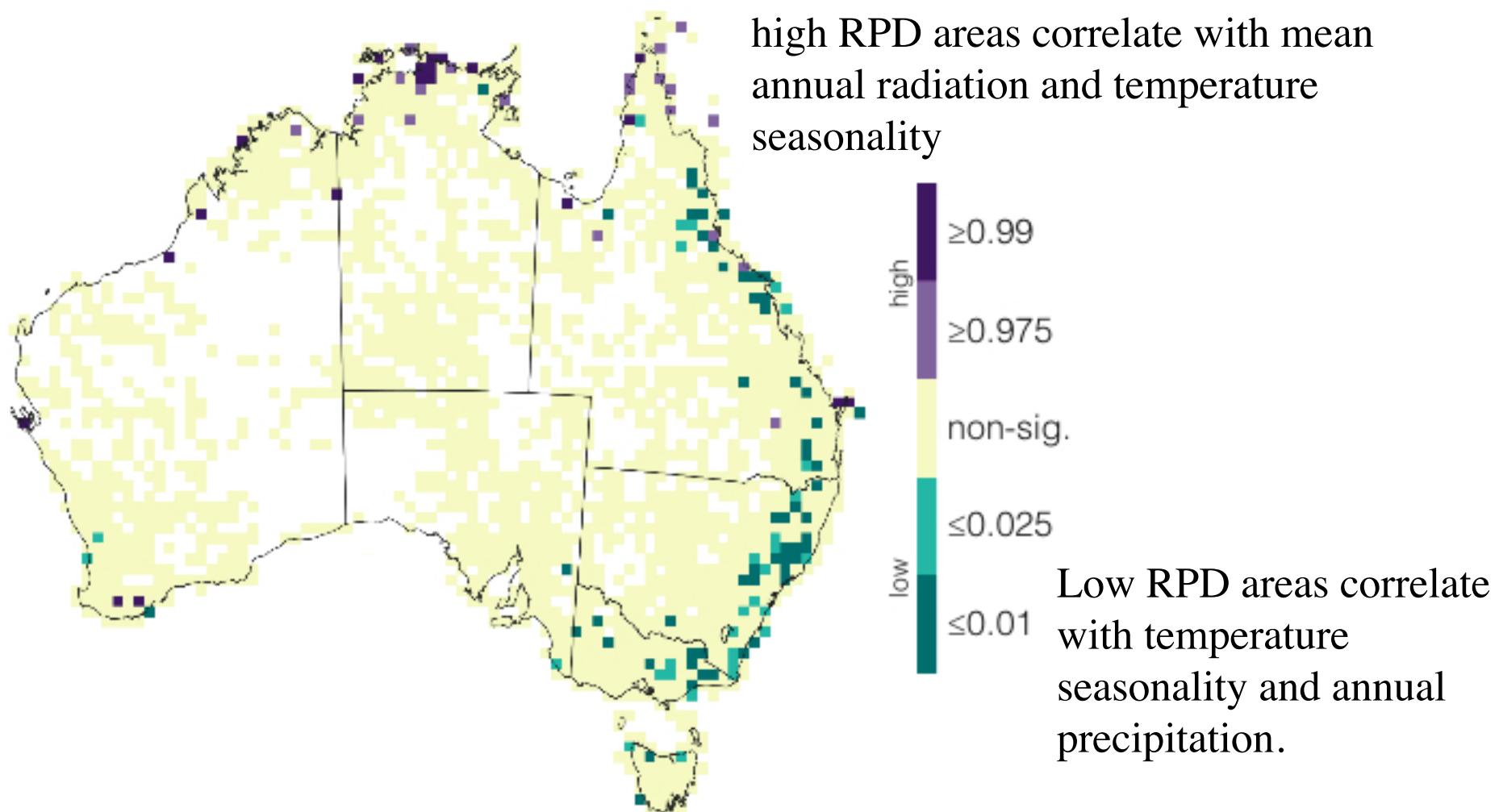
Phylogenetic Niche Modeling

Ferns of Australia

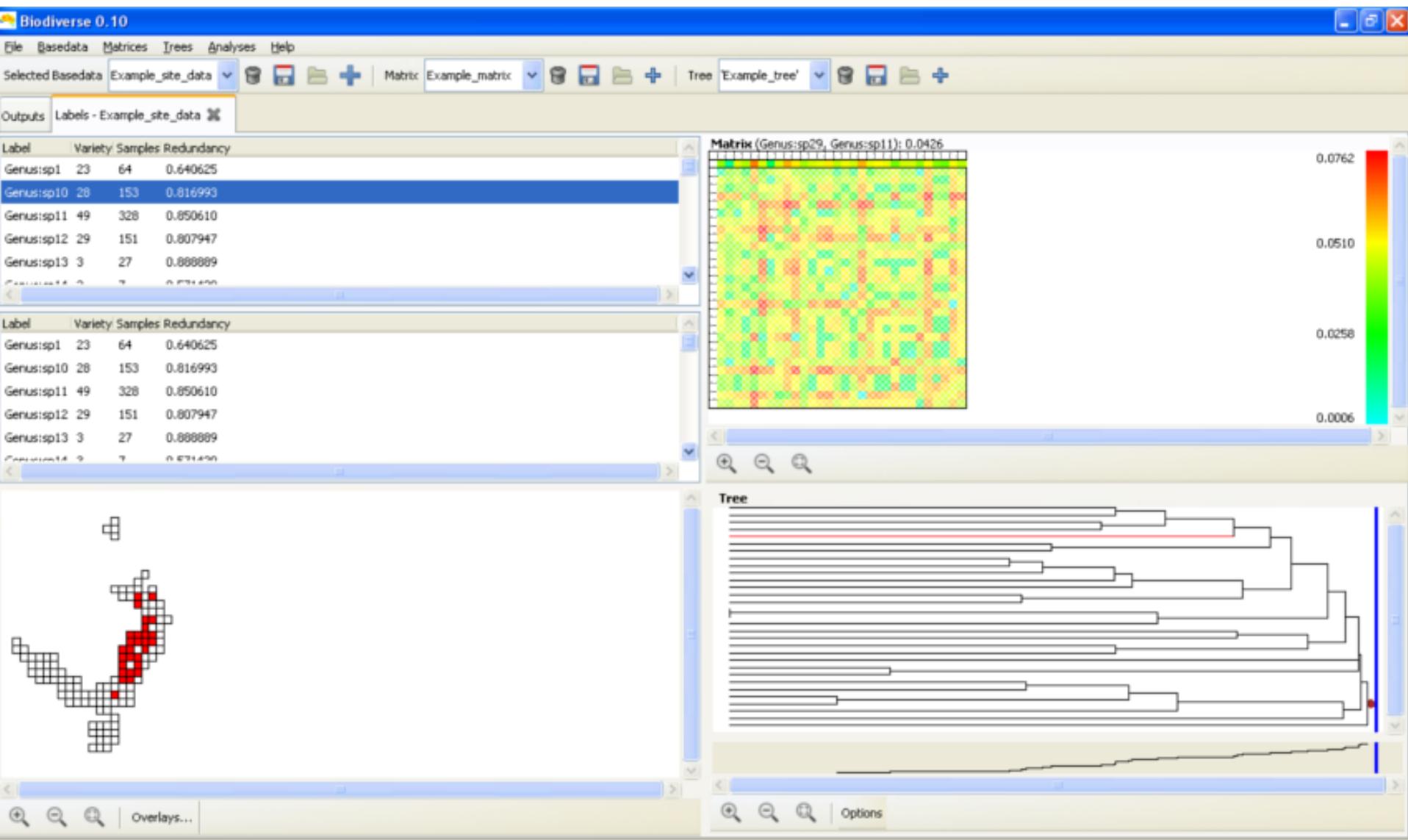
Eleven environmental variables were assessed, encompassing temperature, precipitation, topography, and substrates.

C

Relative phylogenetic diversity



Biodiverse software



Biodiverse software

