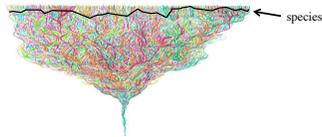
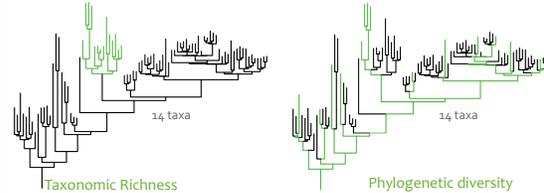


## Biodiversity isn't just species

- Biodiversity is the *whole tree of life*, not just the named species.
- There are clades smaller and larger than the traditional species level.
- Species are not comparable between lineages in any manner, just an arbitrary cut-off somewhere along a branch in the tree of life.



## Measuring biodiversity



- Traditional metric: species richness
- Alternative metric: phylogenetic diversity (PD)

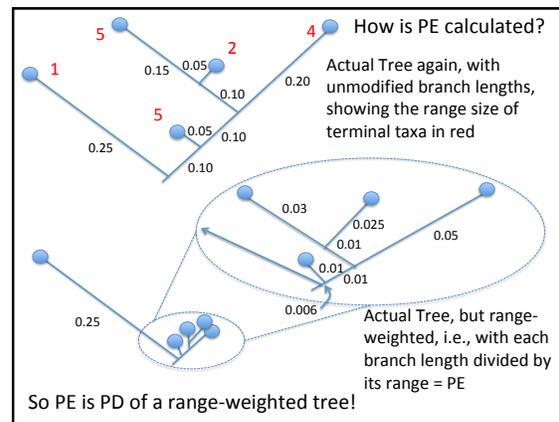
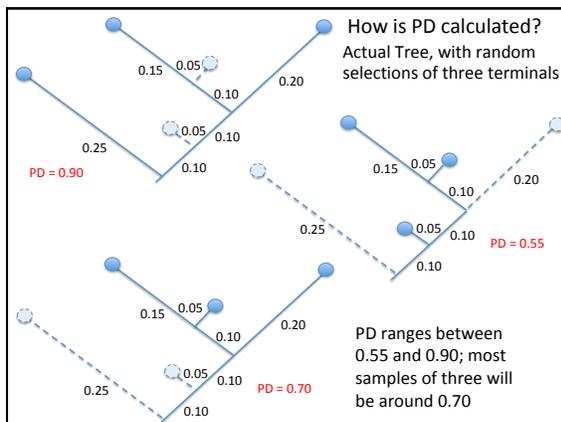
## Endemism isn't just species, either

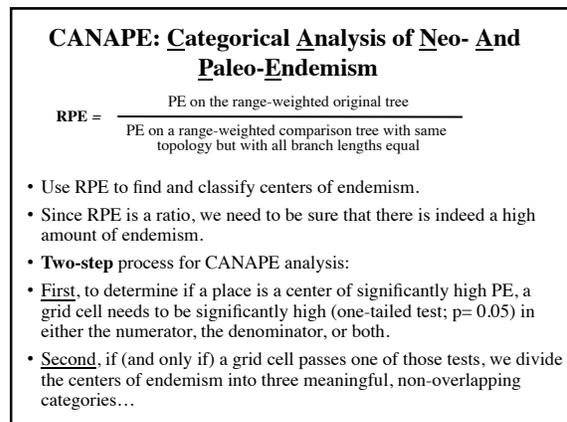
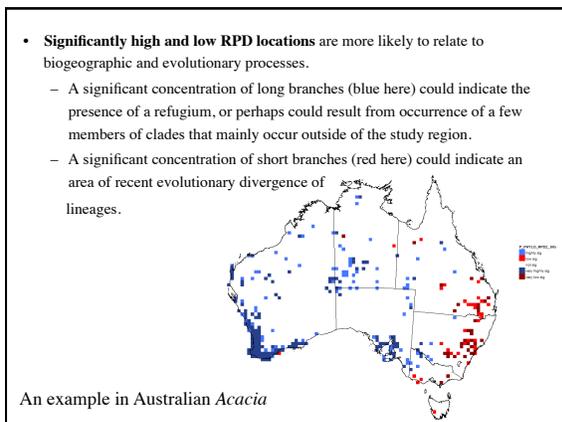
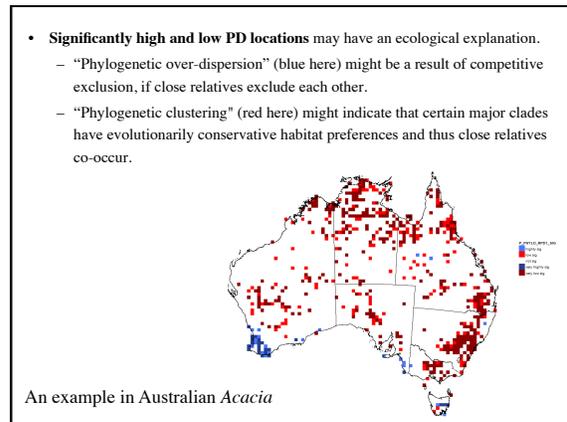
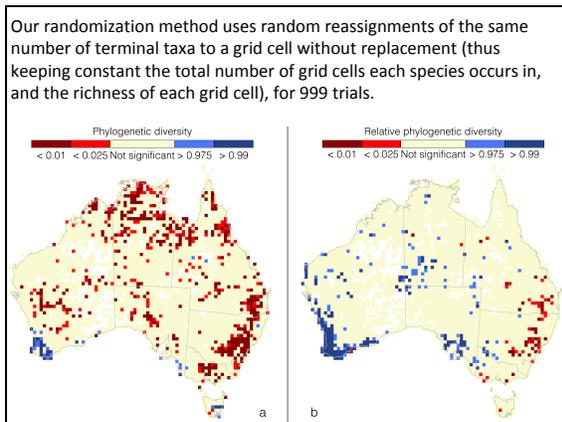
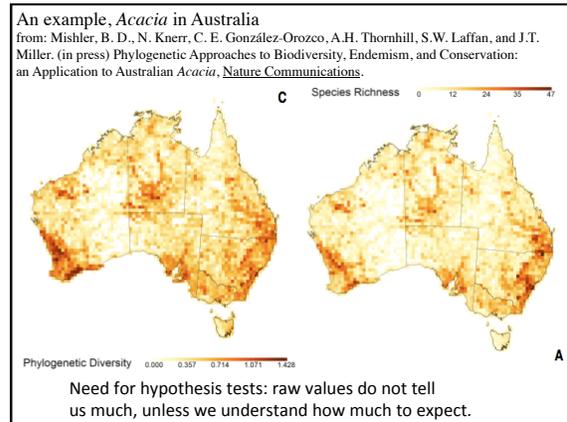
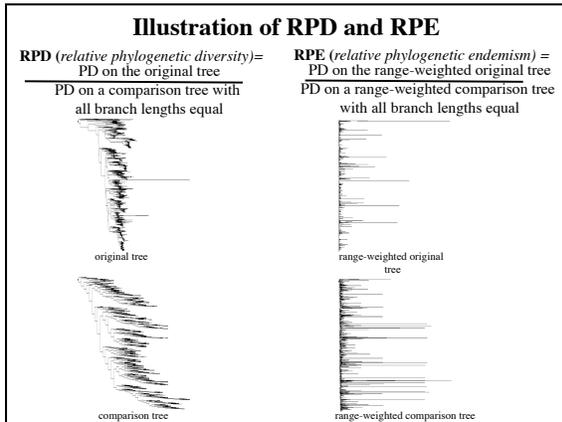
- Likewise, endemism is not just about species, even though virtually all studies on endemism to the present focus solely on species.
- Clades at all levels can be endemic to a greater or lesser extent, and all levels are relevant to discovery and evaluation of centers of endemism.
- Endemism, rather than being species-centric, should be more broadly defined to mean *the geographic rarity of that portion of a phylogenetic tree found in a given area*.
- Thus for a full understanding of diversity and endemism, *we need to look at the whole tree*.

## Methods for studying phylogenetic diversity and endemism:

1. Two important measures to contrast with standard species diversity and endemism:
  - **PD** = *phylogenetic diversity*, the portion of a phylogenetic tree present in a site.
  - **PE** = *phylogenetic endemism*, PD weighted by how common those branches of the tree are elsewhere in the region.
2. Two derived measures that are proving to be powerful:
  - **RPD** = *relative phylogenetic diversity*, the ratio of PD to a null hypothesis based on the numbers of terminals present.
  - **RPE** = *relative phylogenetic endemism*, the ratio of PE to null hypothesis based on the endemism of terminals present. [significance of both is tested with a randomization approach]

*Biodiverse* software (<http://www.purl.org/biodiverse>)

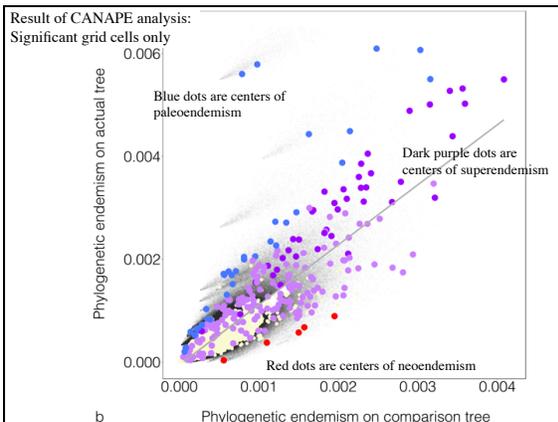
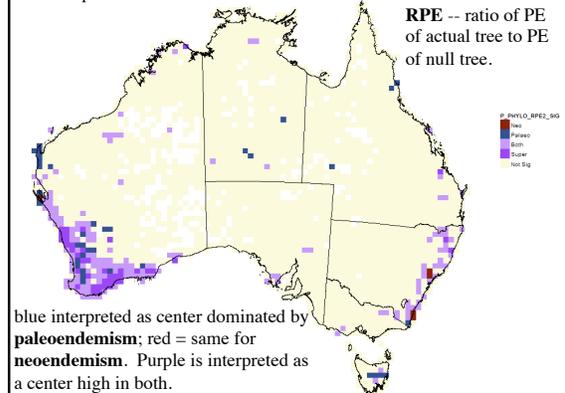




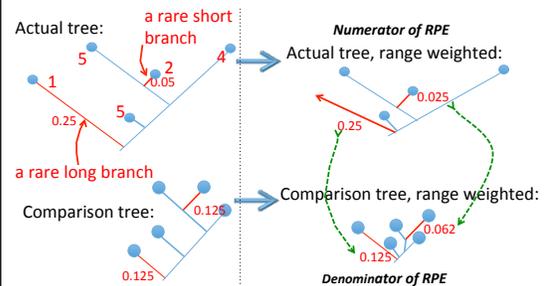
### CANAPE: Categorical Analysis of Neo- And Paleo-Endemism

- If a cell is significantly high or low in RPE (two-tailed test;  $p=0.05$ ), then it is a center of **paleo-endemism** or **neo-endemism** respectively.
- When the ratio is neither significantly high nor low, then it is a center of **mixed endemism**, the interpretation being that there is a mixture of lengths of range-restricted branches in that location that is not dominated by either neo-endemism or paleo-endemism.
- If a mixed endemism cell is significantly high in both the numerator and the denominator of RPE (one-tailed test) at the  $p=0.01$  level, then we have termed it a center of **super-endemism**.

An example in *Acacia*:



### How CANAPE works:



The rare long branch is longer in the RW actual tree than expected under the null.  
The rare short branch is shorter in the RW actual tree than expected under the null.

### Phylogenetic measures of geographic similarity

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

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

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

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.)

