

Tutorial: SDMs and Phylogenetic Diversity/Endemism

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Schedule

Tutorial 1 – SDMs in practice

1. Package install (ca. 3 min)
2. Download and prepare environmental data (ca. 2 min)
3. Download and prepare future environmental data (ca. 2 min)
4. Obtain species occurrence data from GBIF and spatially rarefy (ca. 5 min)
5. Build and evaluate SDMs (ca. 10 min)
6. Project SDMs from current to future climate (ca. 5 min)
7. Evaluate present vs future models

Example Region and data: Tutorial 1



- Australia
- Eastern Grey Kangaroo (*Macropus giganteus*)
- IUCN: Least Concern

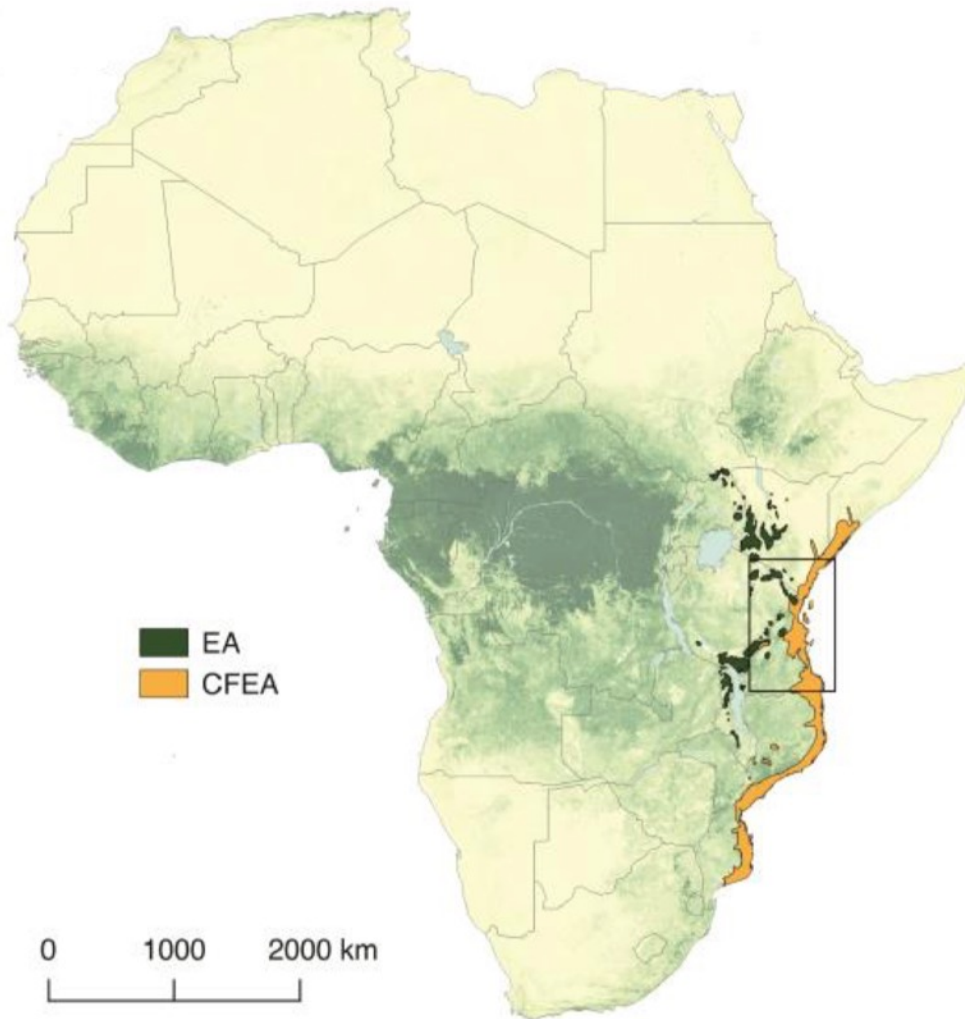


Schedule

Tutorial 2 – Phylogenetic Diversity and Endemism (a shorter tutorial)

1. Package install (ca. 3 min)
2. Download and prepare environmental data (ca. 2 min)
3. Process provided species occurrence data (ca. 5 min)
4. Build SDMs (ca. 10 min)
5. Calculate Phylogenetic Diversity and Endemism (from the SDMs and a provided phylogeny) (ca. 15 min)

Example Region: Tutorial 2



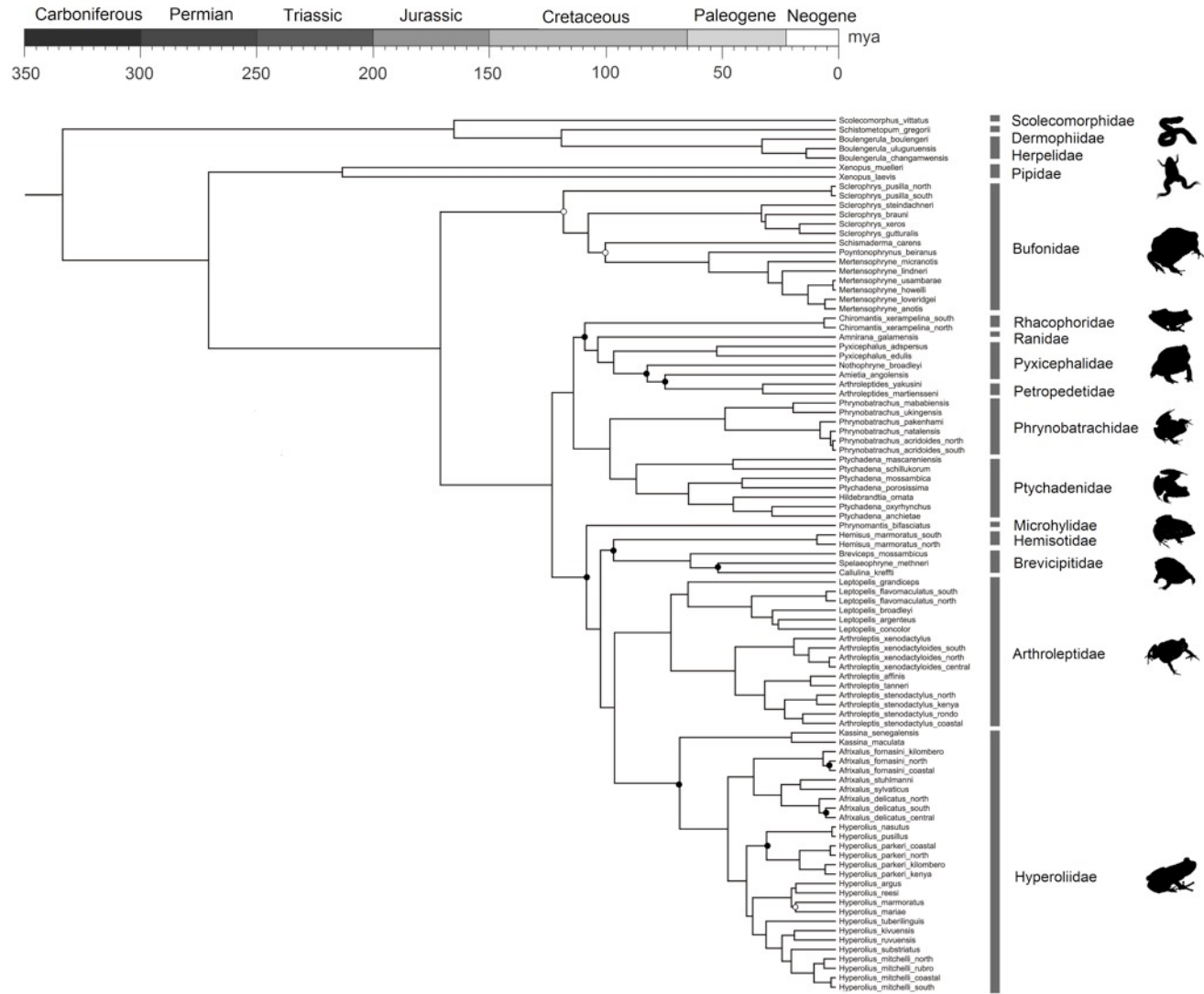
- Coastal Forests of Eastern Africa
- Global biodiversity hotspot
- Small proportion of original habitat remains due to habitat fragmentation

Example Data: Tutorial 2



- Subset of the coastal forest amphibian assemblage
- 20 of ~60 species
- Many generalists
- A few microendemics

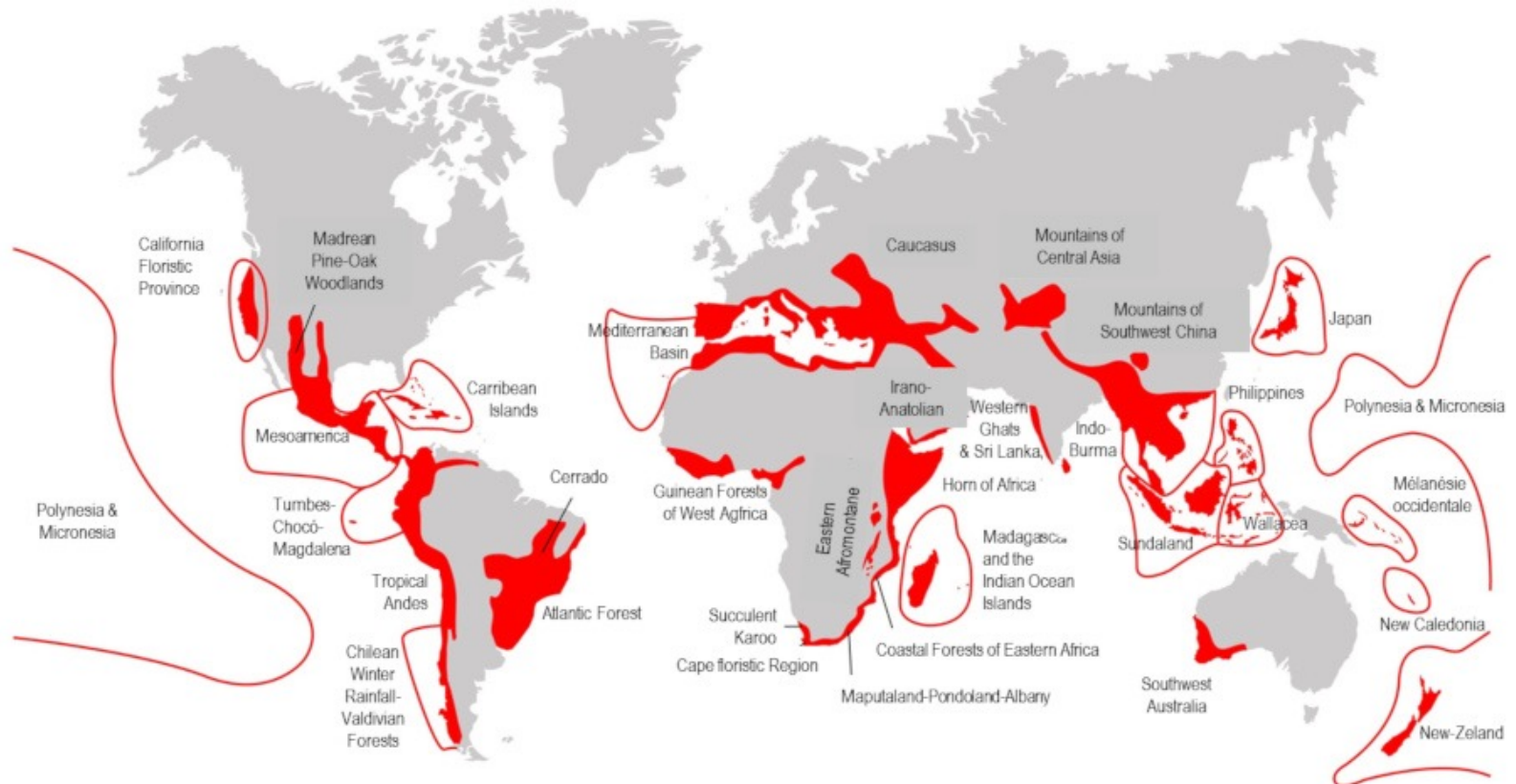
Example Data: Tutorial 2



Why?

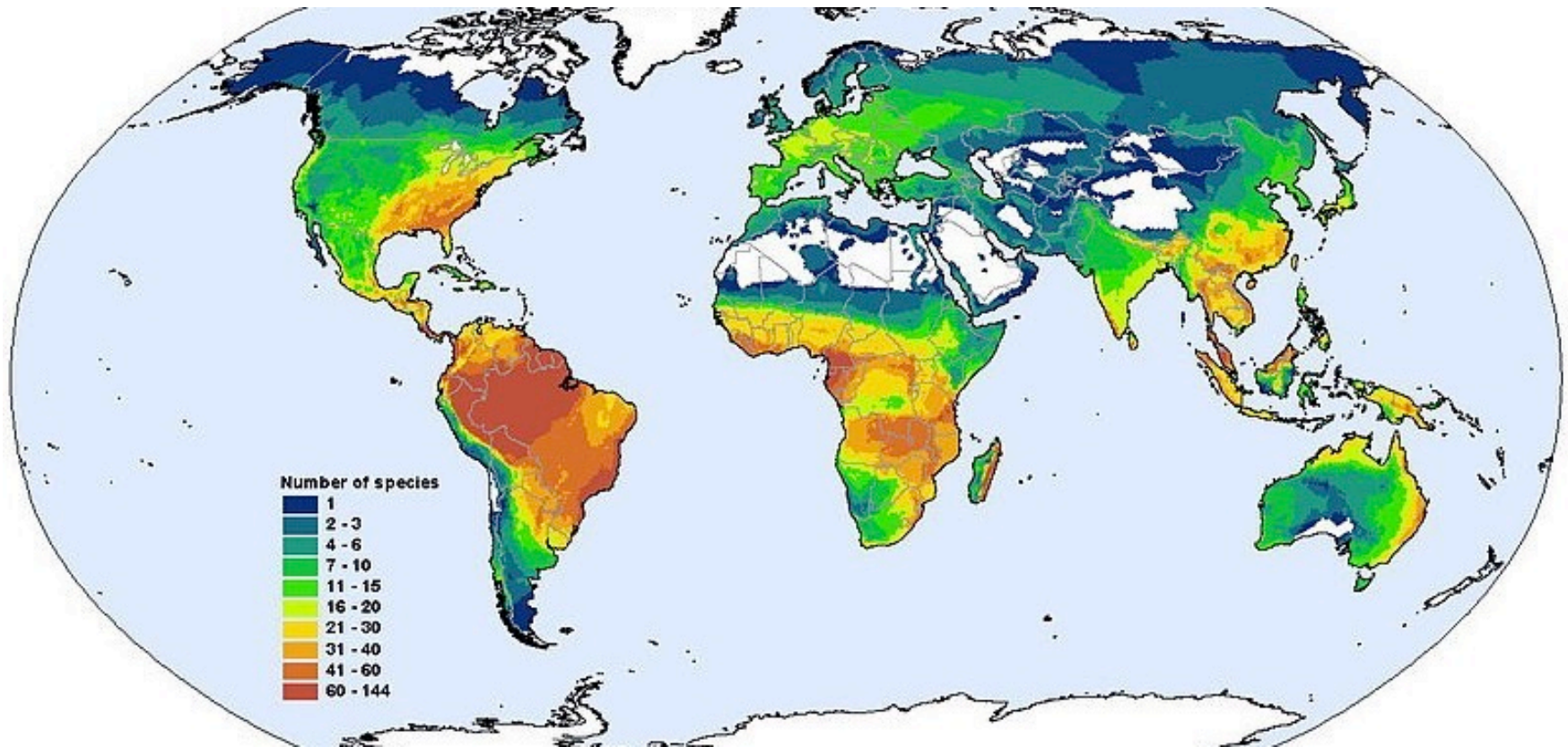
Biodiversity Hotspots

- We know biodiversity is unevenly distributed across the earth



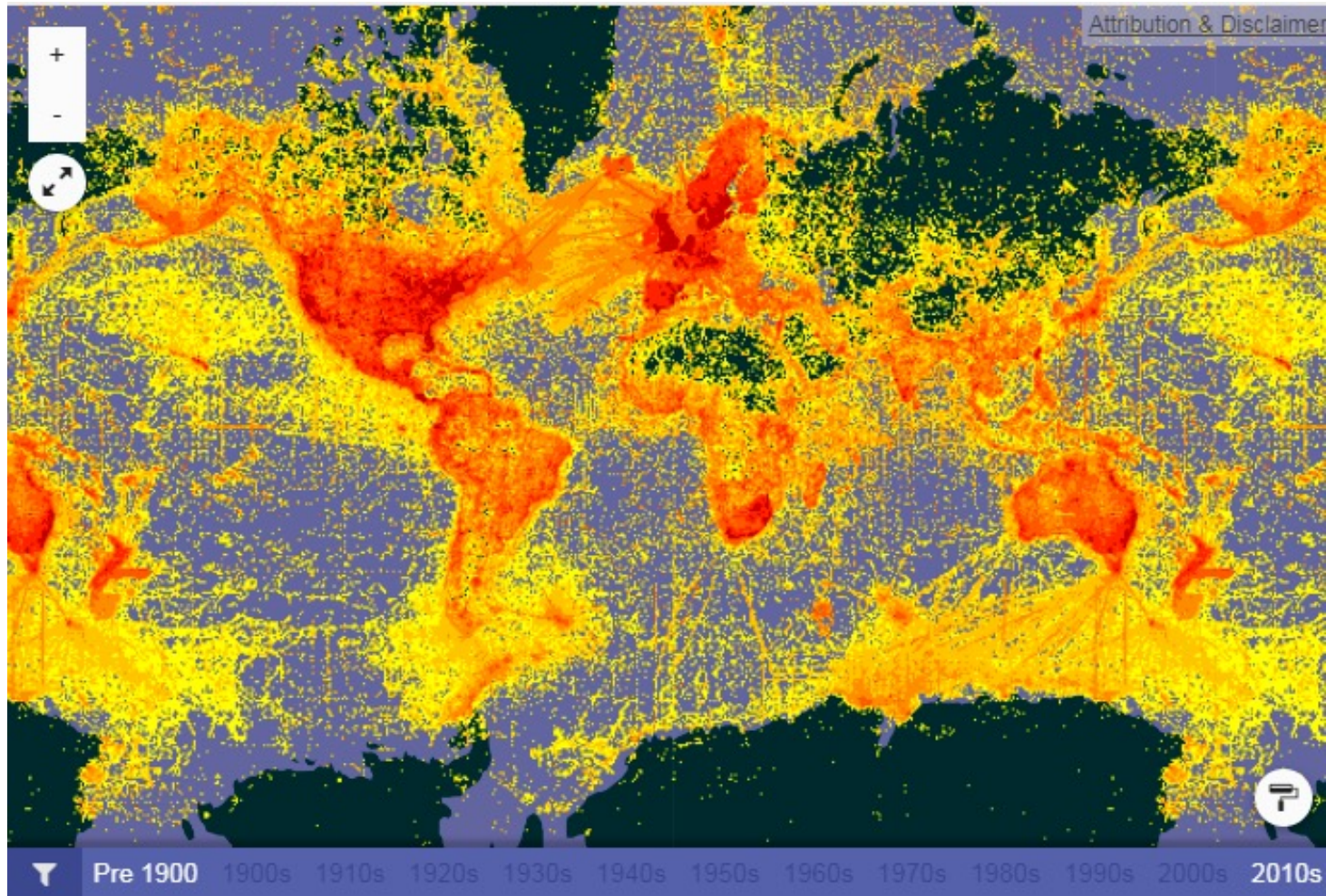
Wallacean shortfall: we need SDMs

- But we lack detailed knowledge on species ranges



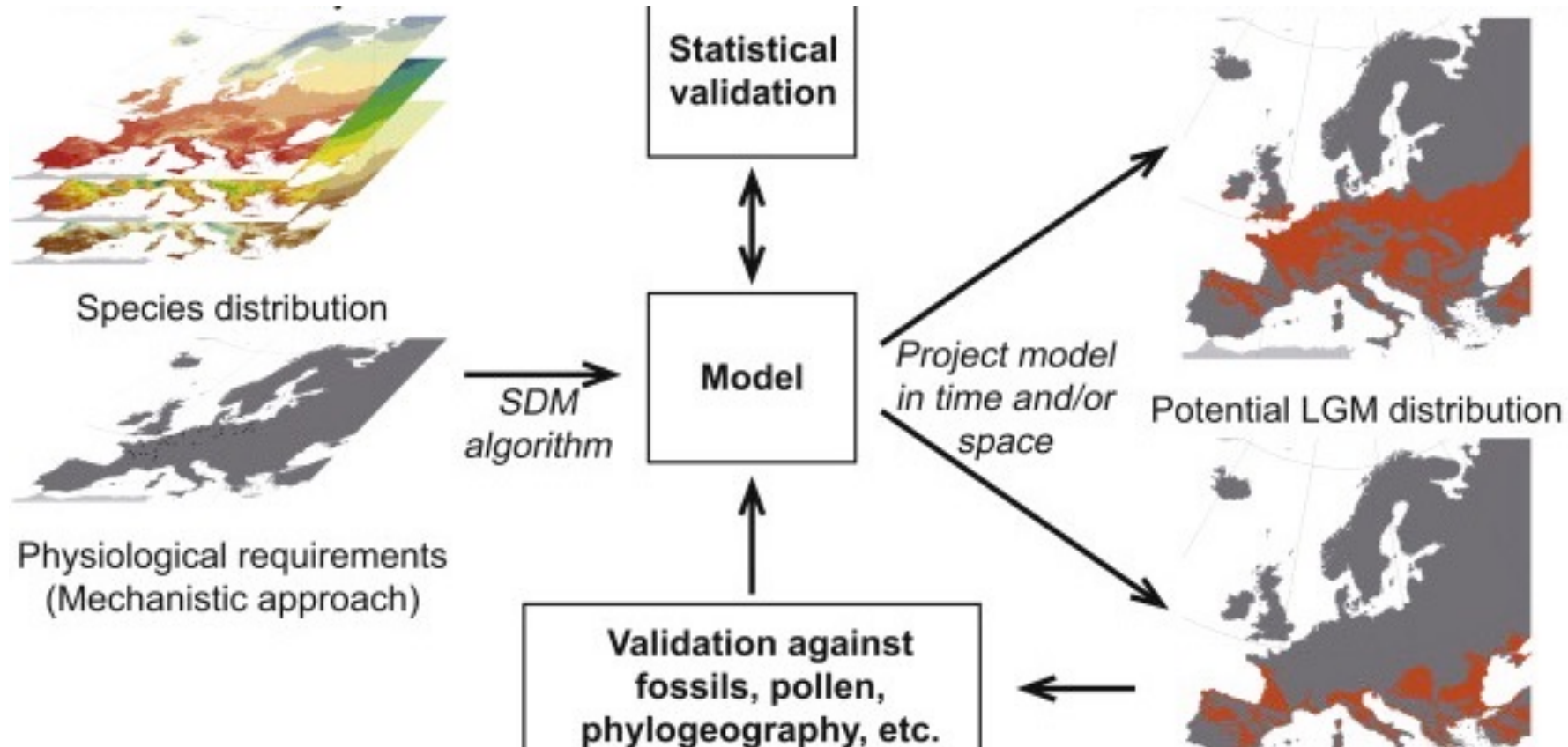
Wallacean shortfall: we need SDMs

- Thankfully new data is always becoming available...



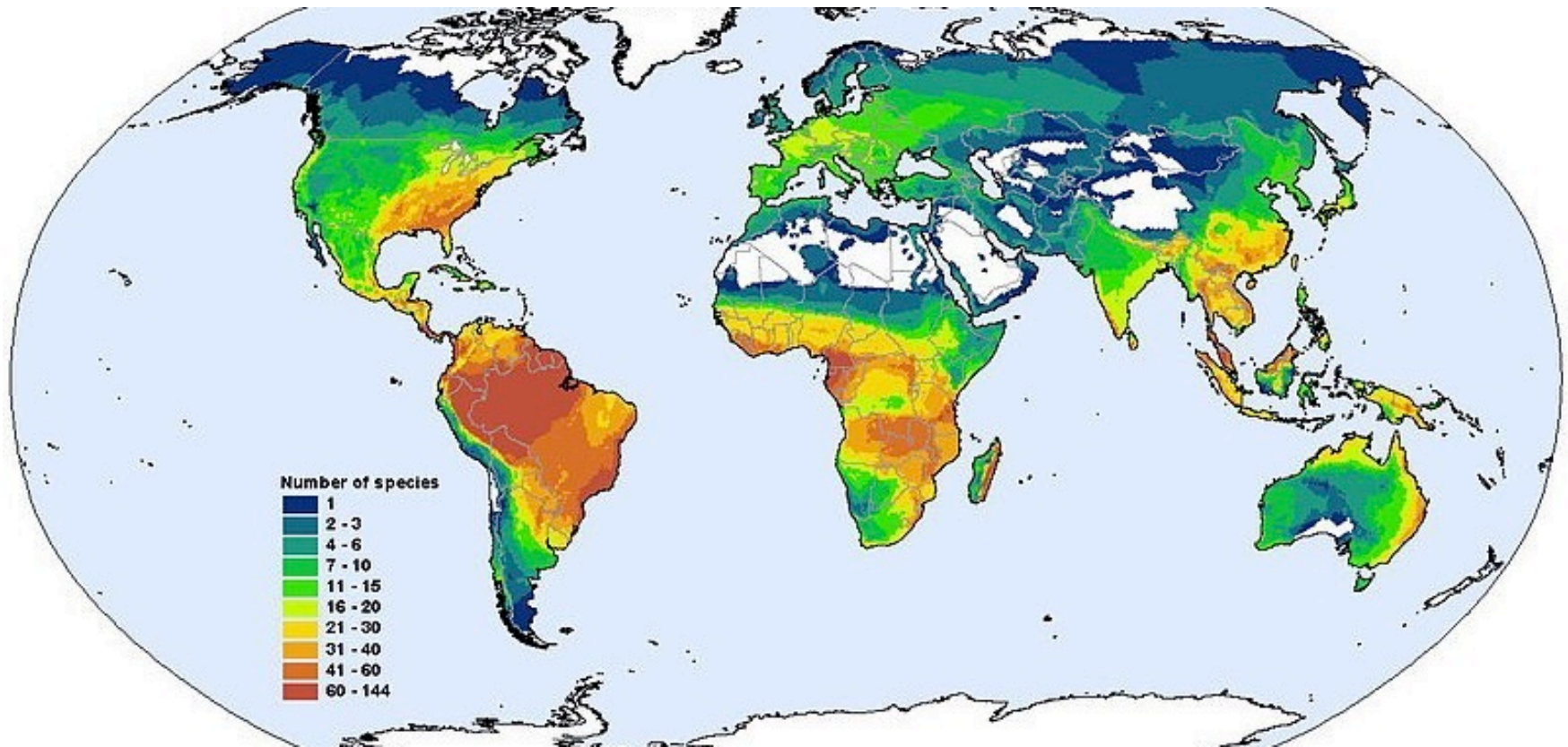
Wallacean shortfall: we need SDMs

- Along with techniques to model rather than sample every single place



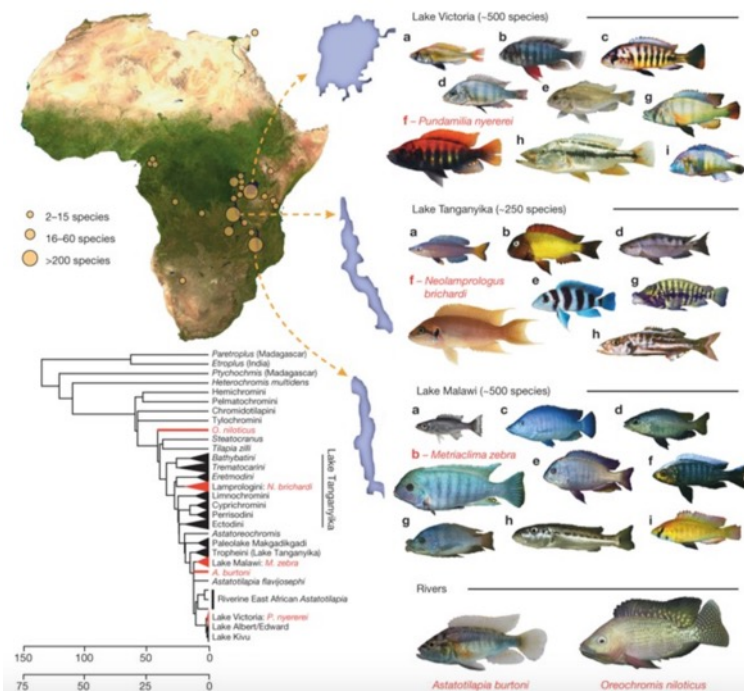
Darwinian shortfall: evolutionary data

- Species richness and endemism maps are great, but they don't tell us anything about evolutionary history, important for conservation



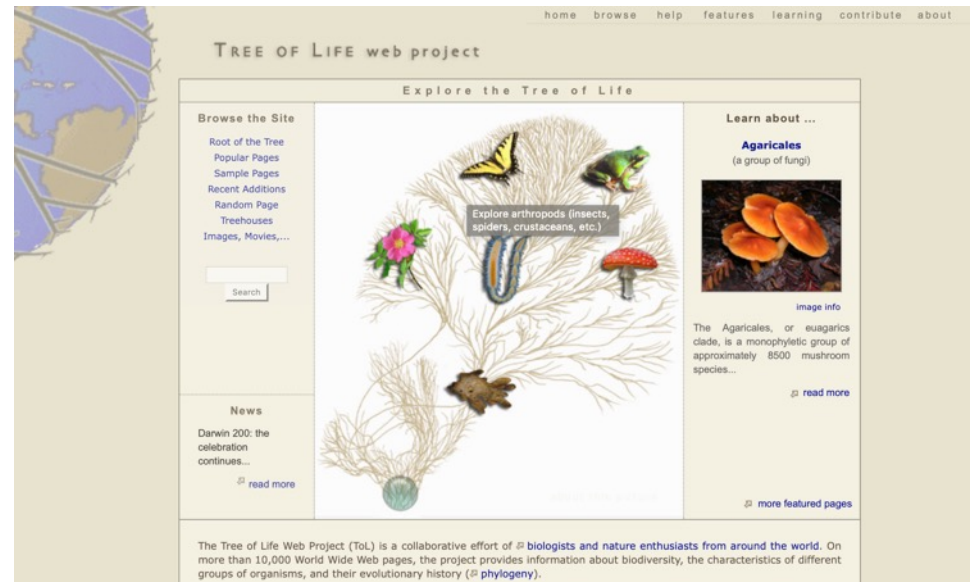
Darwinian shortfall: evolutionary data

- What about the very unique species? (e.g. sole survivors of previously widespread groups)
- Or recently diverged microendemics?

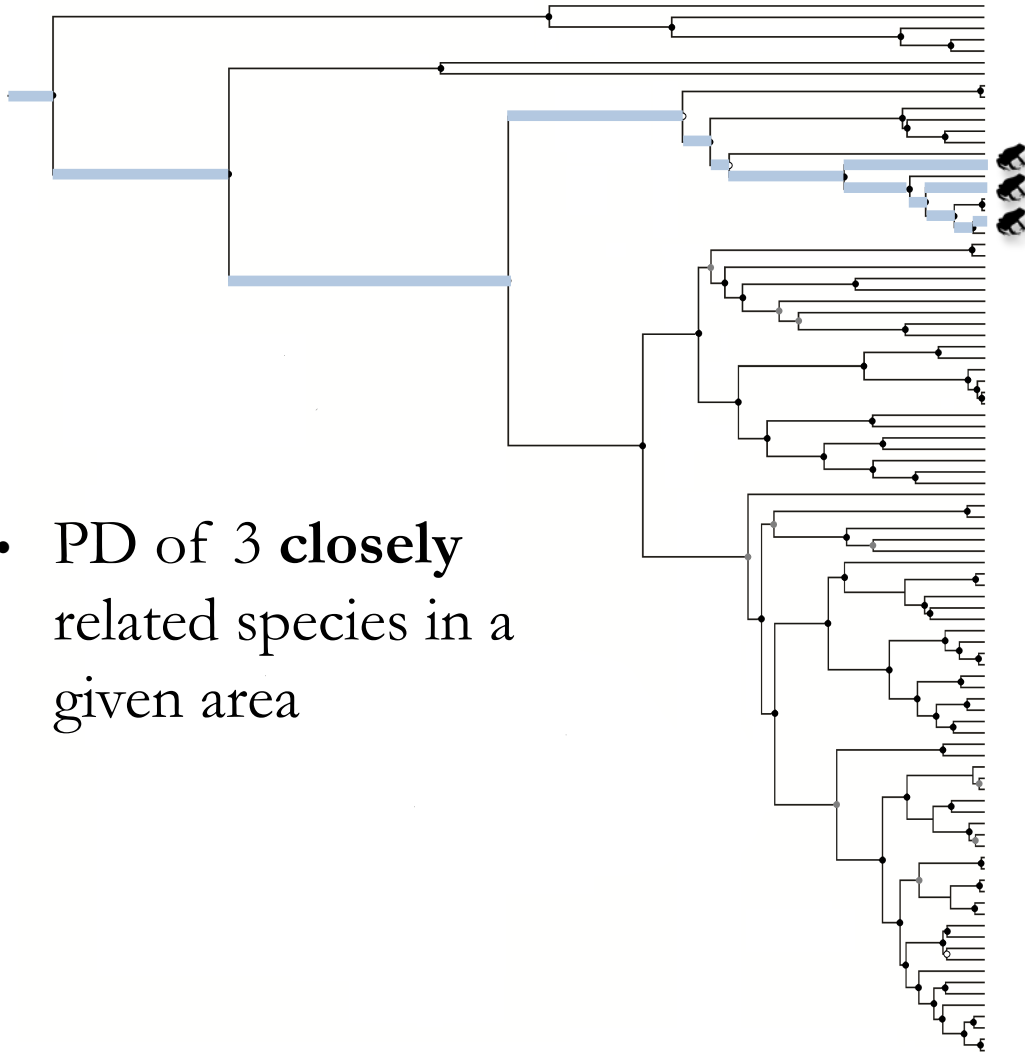


Darwinian shortfall: evolutionary data

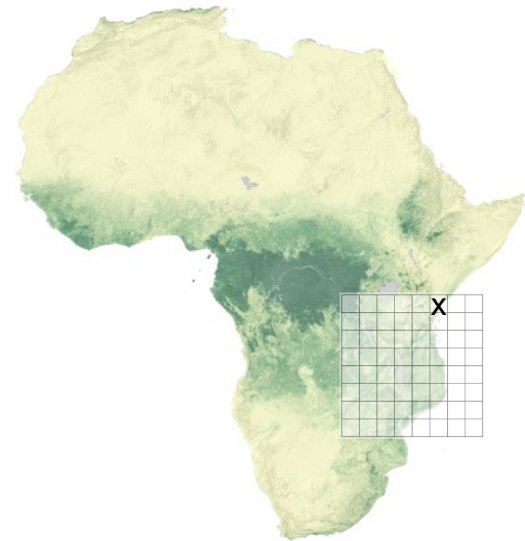
- Luckily lots of molecular data also available, and phylogenies



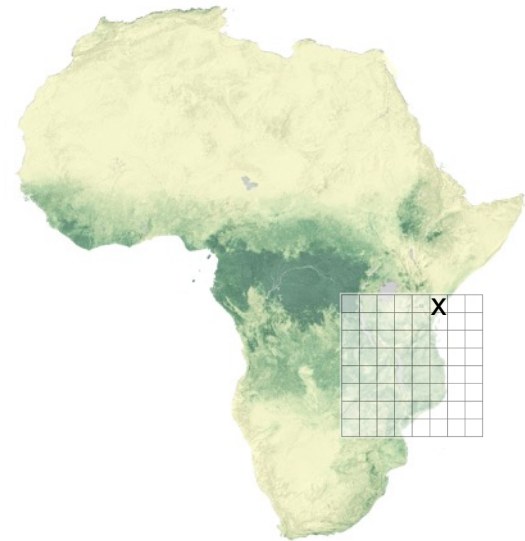
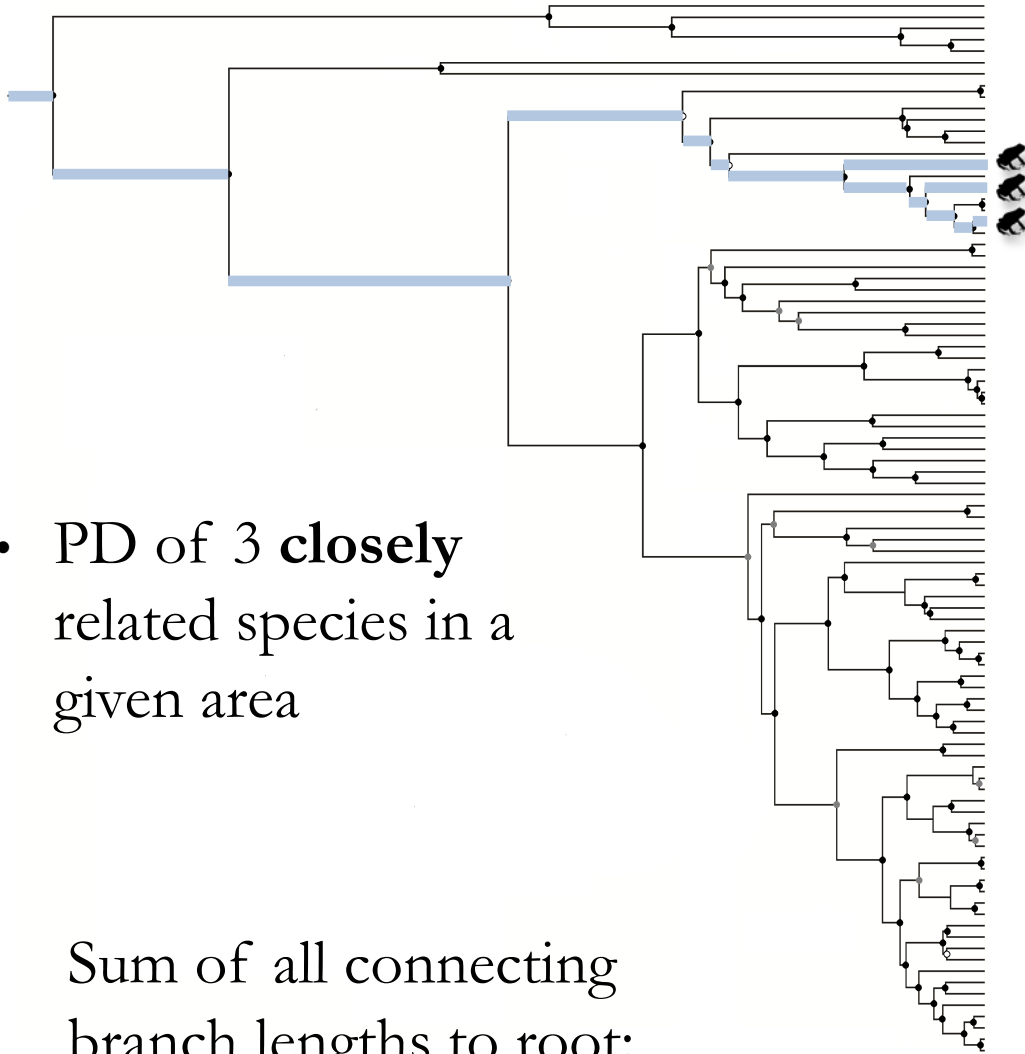
Phylogenetic Diversity



- PD of 3 **closely** related species in a given area

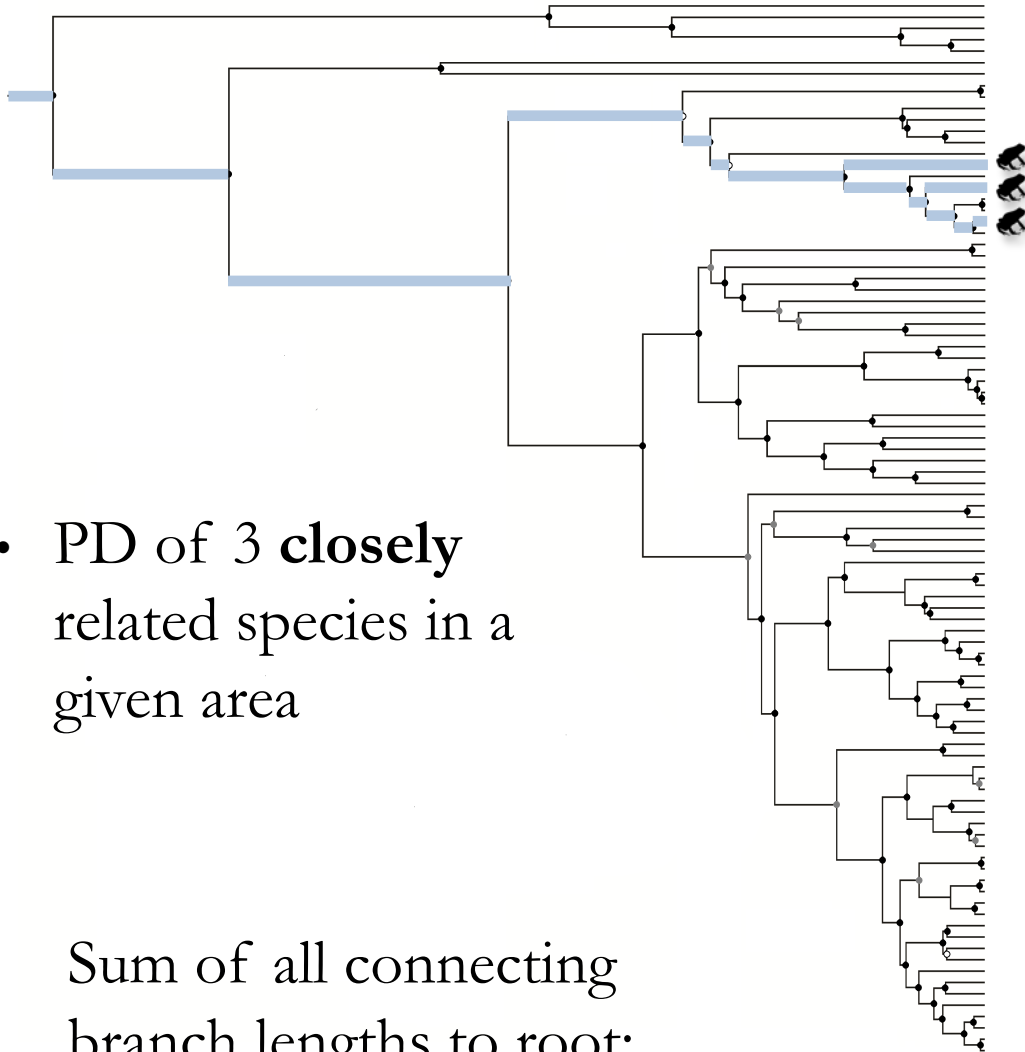


Phylogenetic Diversity

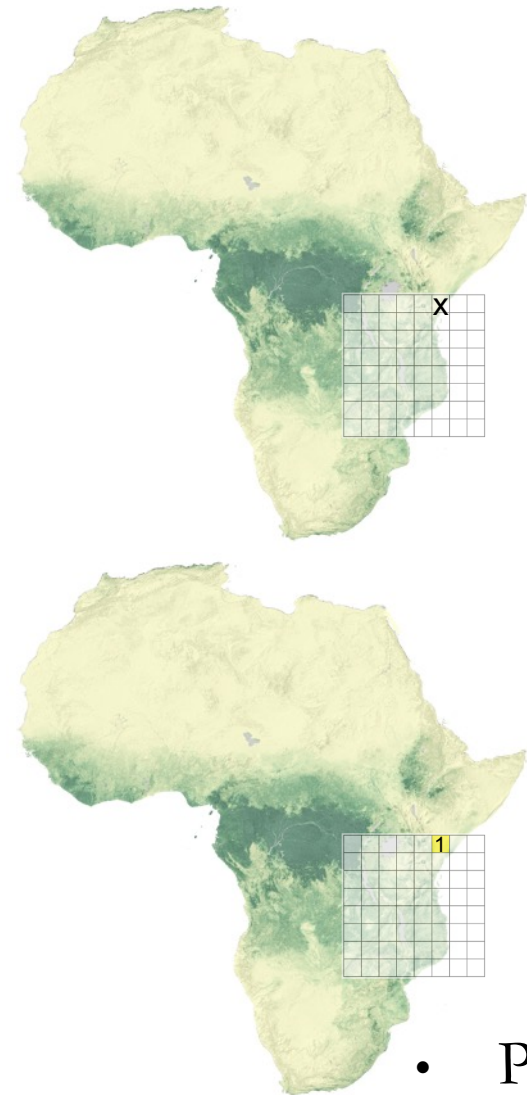


- PD of 3 **closely** related species in a given area
- Sum of all connecting branch lengths to root:

Phylogenetic Diversity

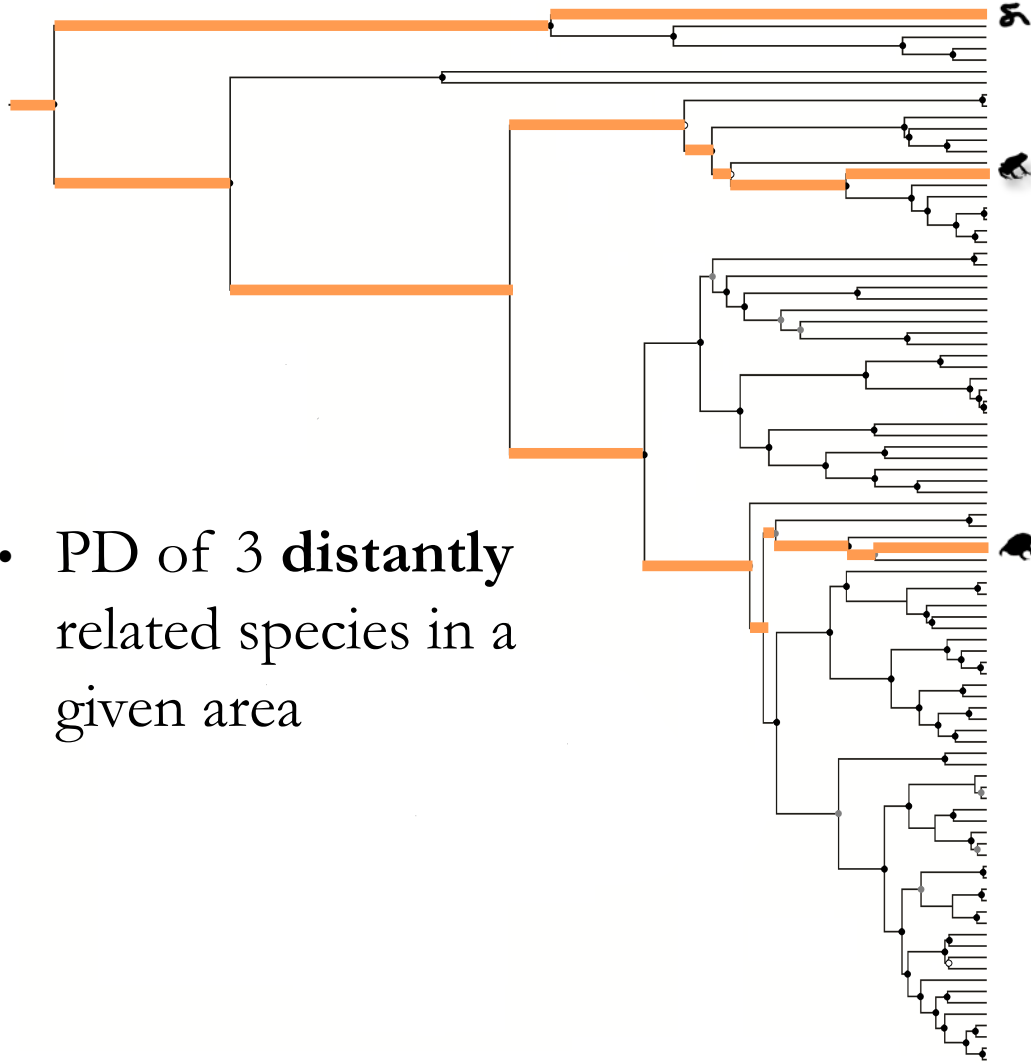


- PD of 3 **closely** related species in a given area
- Sum of all connecting branch lengths to root:

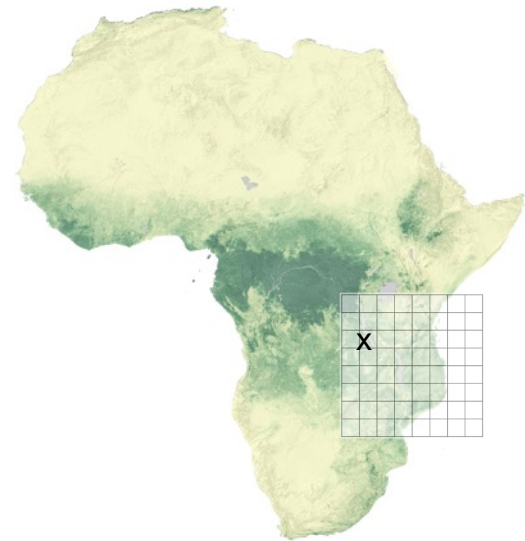


- PD per cell

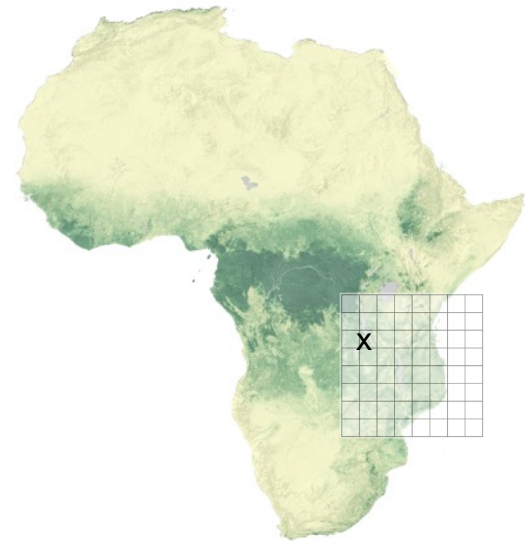
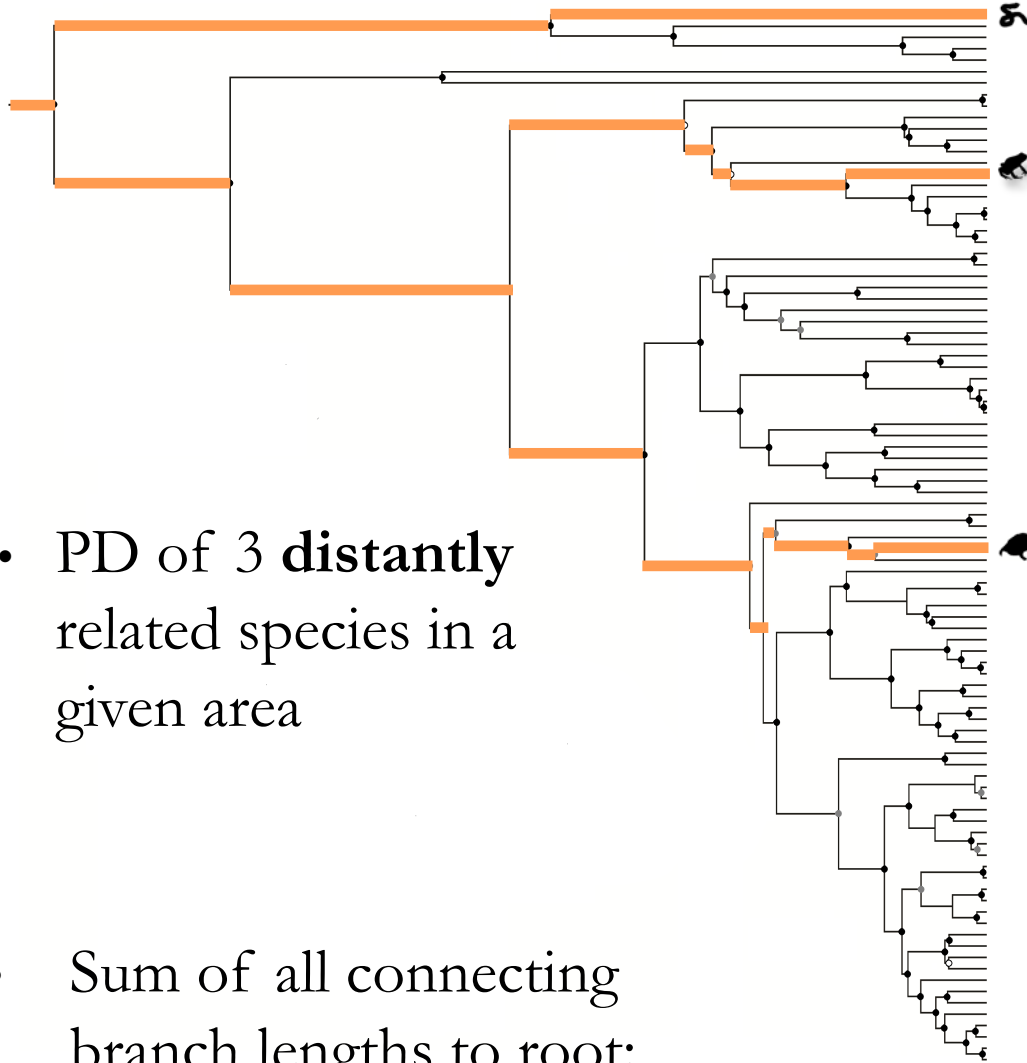
Phylogenetic Diversity



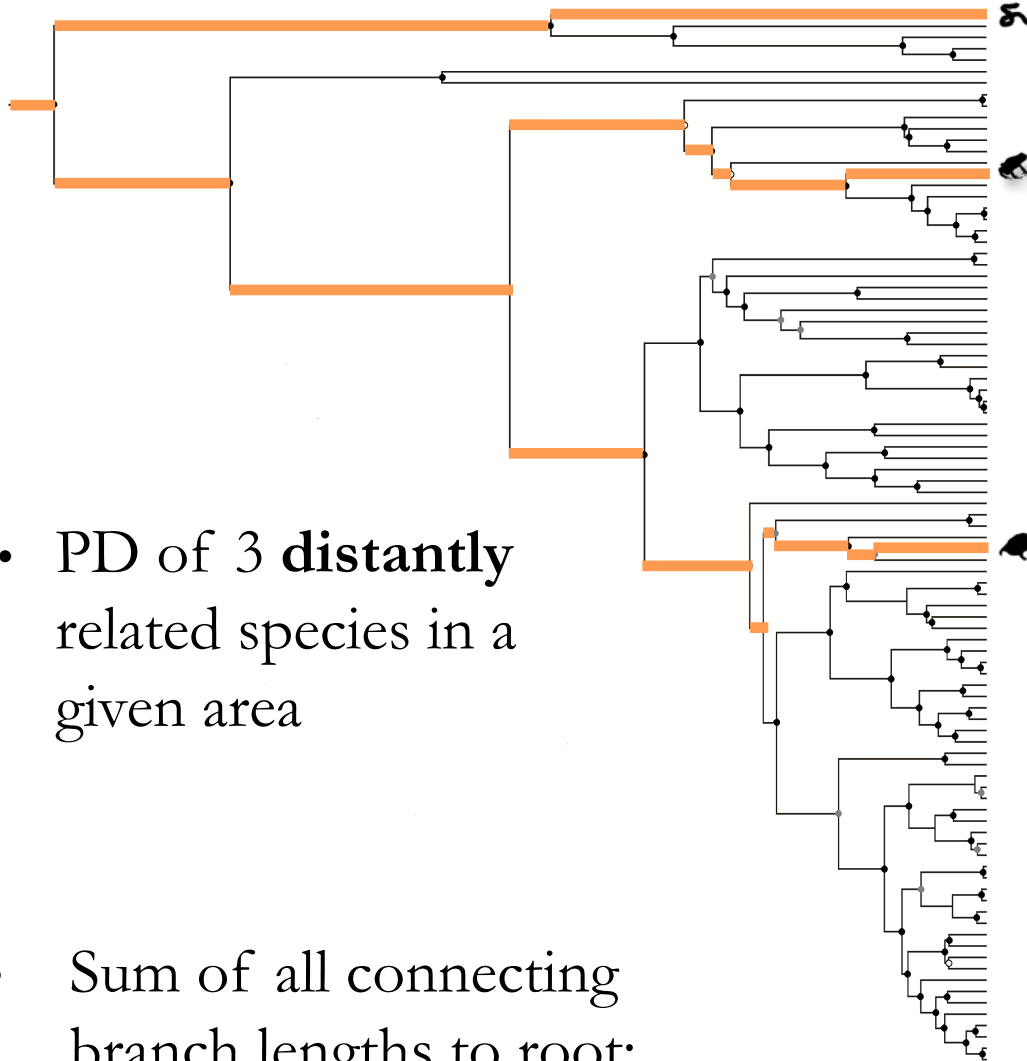
- PD of 3 **distantly** related species in a given area



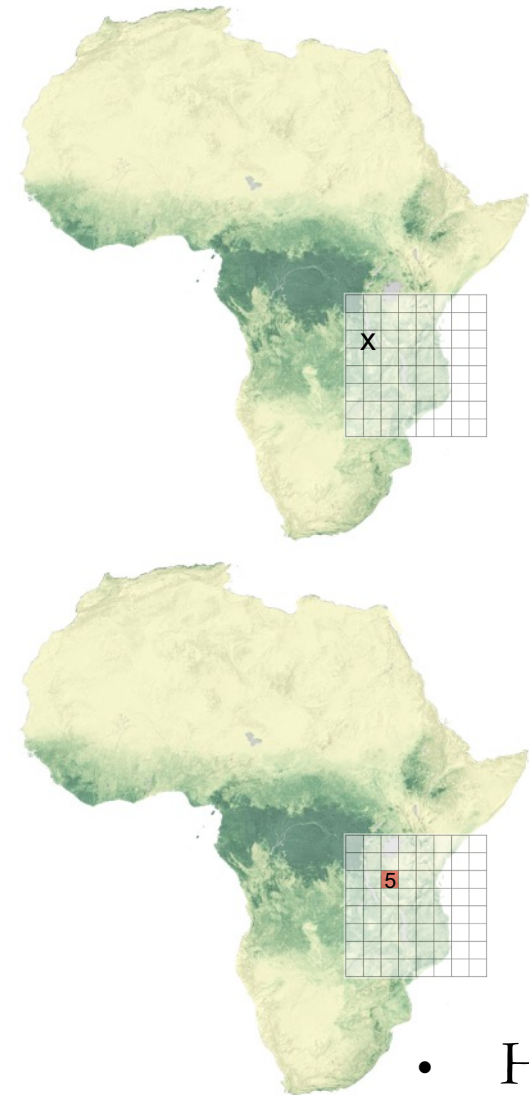
Phylogenetic Diversity



Phylogenetic Diversity

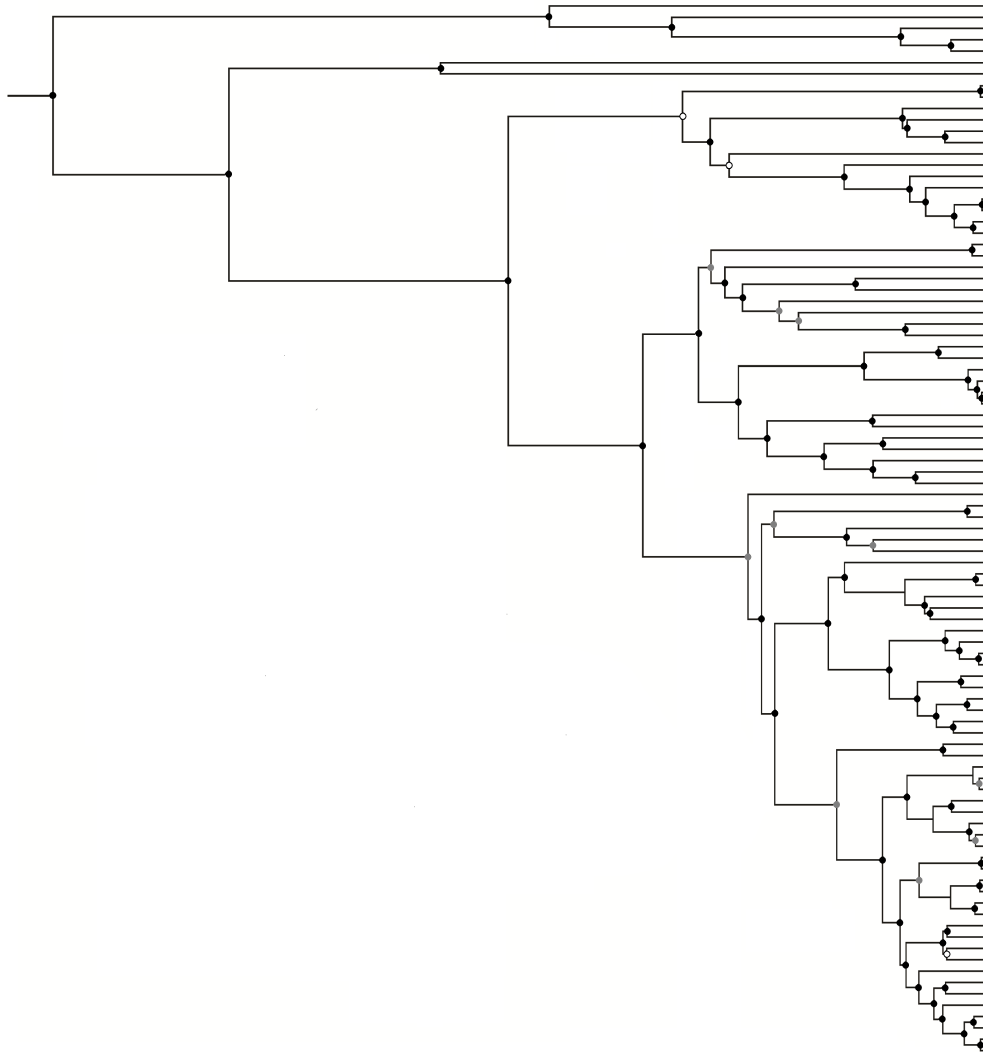


- PD of 3 **distantly** related species in a given area
- Sum of all connecting branch lengths to root:

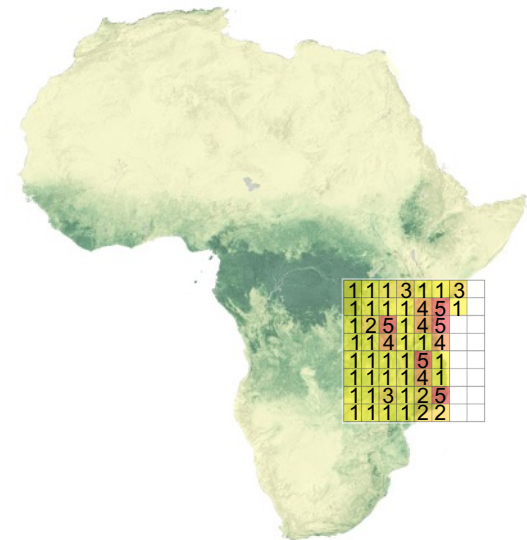


- Higher PD

Phylogenetic info for conservation

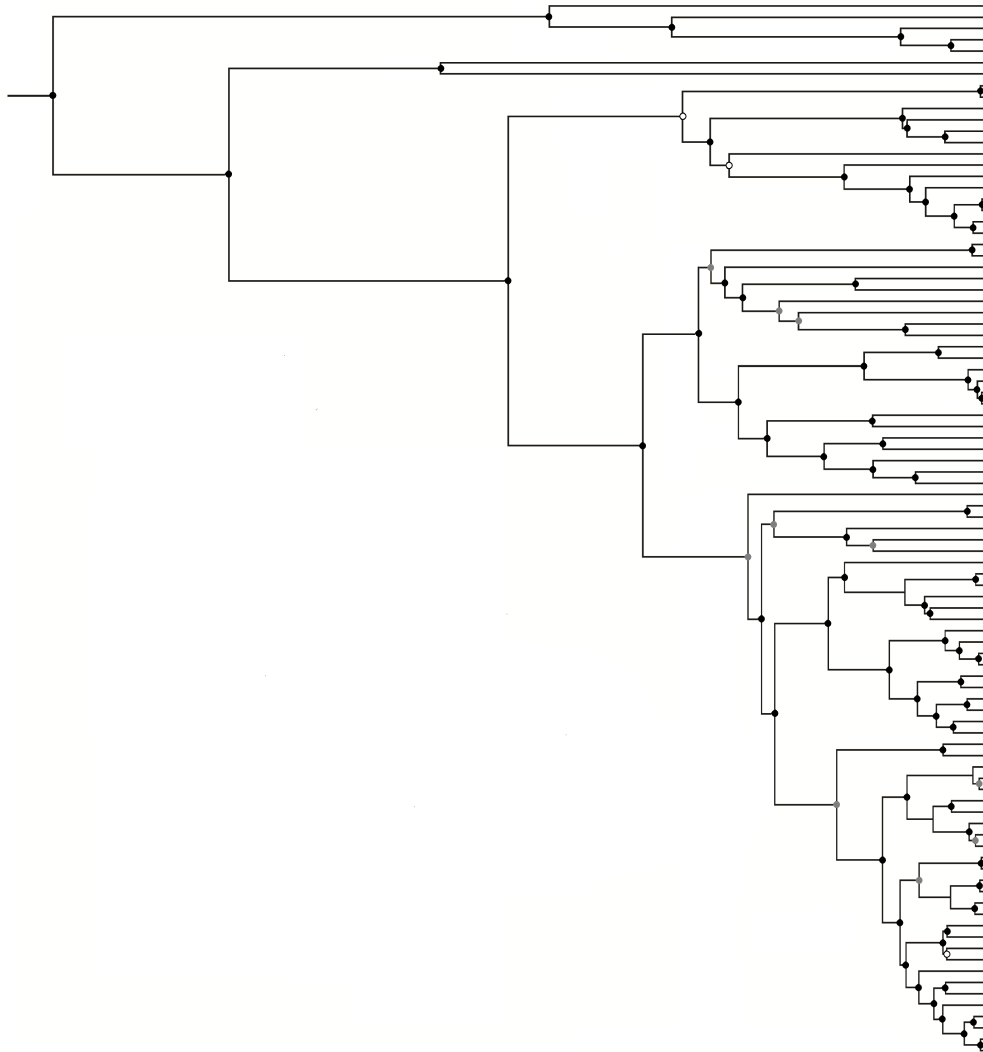


- Do this iteratively for every grid cell to map PD...

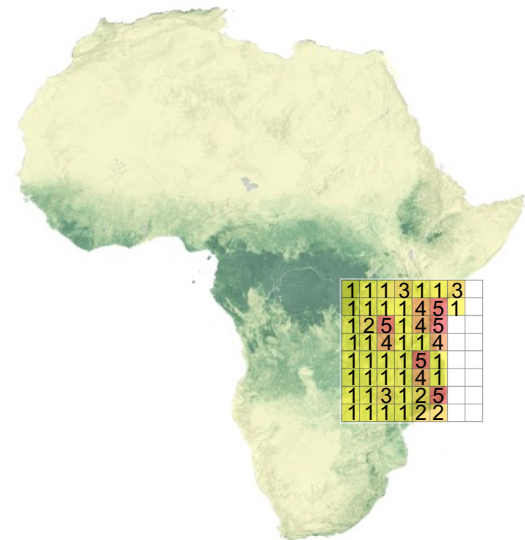


1	1	1	3	1	1	3
1	1	1	1	4	5	1
1	2	5	1	4	5	
1	1	4	1	1	4	
1	1	1	1	5	1	
1	1	1	1	4	1	
1	1	3	1	2	5	
1	1	1	1	2	2	

Phylogenetic Diversity



- Your input spatial data can also be a SDM!



Phylogenetic endemism

- PE is determined by how much PD is geographically restricted (based on Weighted Endemism, WE formula)

Rosauer et al. [7] extended the concept of SIR metrics to Faith's *phylogenetic* diversity (PD), which is a measure of the evolutionary history represented among a set of species, calculated as the sum of the branch lengths of a phylogenetic tree containing species in a particular community sample [8], [9], [10]. This *phylogenetic endemism* [7] (PE) was defined as (1):

$$PE = \sum_{\{c \in C\}} \frac{L_c}{R_c}$$

read as the sum of the lengths of each branch in a tree containing a community sample of species divided by the geographic range of each branch (i.e. based on the species terminating from that branch), where L is branch length, R is range size, C is the tree and c is a particular branch of the tree.