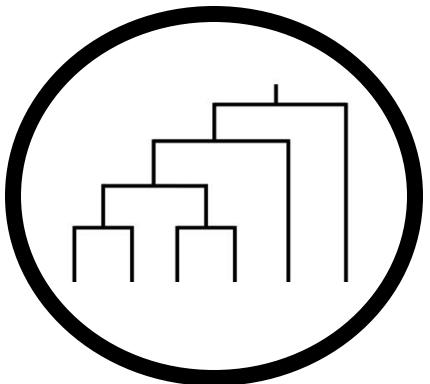


Community phylogenetics: Metrics and applications



Josep Padullés Cubino, PhD

josep.padulles@uab.cat

UAB
Universitat Autònoma
de Barcelona

Scheme of the presentation

- Aims of the talk
- Background: Why community phylogenetics?
 - Phylogenetic niche conservatism
- Calculation of phylogenetic diversity
 - Alpha diversity
 - Faith's PD
 - Mean Pairwise Distance (MPD)
 - Hot node
 - Mean Nearest Taxon Distance (MNTD)
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 - Beta diversity
 - PhyloSor
 - D_{pw}/D_{nn}
- R packages to calculate PD metrics
- Conclusions

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Aims of the talk

- Provide some context on **why to use community phylogenetics**, with its potential and limitations
- Introduction the some **metrics** to calculate phylogenetic diversity (PD)
- Provide some **examples** on the use of PD metrics

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- Conclusions

Personal background

filtering residential floras haikou climatic tropical understory filtering residential floras haikou climatic

phylogenetic years turnover patterns patterns

taxonomic continental spatial use

urban occur

size forest

across shoot

china structure

tree

composition

drive communities abundance

biodiversity alien

spain gardens habitat affect

city traits

yard

drivers

flamability management

cultivated

habitats richness

functional species

diversity

Background: Why community phylogenetics?



Annu. Rev. Ecol. Syst. 2002. 33:475–505

doi: 10.1146/annurev.ecolsys.33.010802.150448

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First published online as a Review in Advance on August 14, 2002

VOL. 156, NO. 2 THE AMERICAN NATURALIST AUGUST 2000

Exploring the Phylogenetic Structure of Ecological Communities: An Example for Rain Forest Trees

Campbell O. Webb*

Ecology Letters, (2009) 12: 693–715

doi: 10.1111/j.1461-0248.2009.01314.x

REVIEW AND
SYNTHESIS

The merging of community ecology and phylogenetic biology

Abstract

The increasing availability of phylogenetic data, computing power and informatics tools has facilitated a rapid expansion of studies that apply phylogenetic data and methods to community ecology. Several key areas are reviewed in which phylogenetic information

Jeannine Cavender-Bares,^{1*}
Kenneth H. Kozak,² Paul V. A.
Fine³ and Steven W. Kembel³⁺

PHYLOGENIES AND COMMUNITY ECOLOGY

Campbell O. Webb¹, David D. Ackerly², Mark A. McPeek³,
and Michael J. Donoghue¹

¹Department of Ecology and Evolutionary Biology, Yale University, New Haven, Connecticut 06511; email: campbell.webb@yale.edu, michael.donoghue@yale.edu

²Department of Biological Sciences, Stanford University, Stanford, California 94305;

Review

Cell
PRESS

Phylogenetic analysis of community assembly and structure over space and time

Brent C. Emerson¹ and Rosemary G. Gillespie²

¹Centre for Ecology, Evolution and Conservation, School of Biological Sciences, University of East Anglia, Norwich NR4 7TJ, UK

²Department of Environmental Science, University of California, Berkeley, CA 94720, USA

Background: Why community phylogenetics?

Advantages of using community phylogenetics in biology and ecology:

- 1) Insight into evolutionary processes
- 2) Understanding functional diversity
- 3) Detecting non-random assembly patterns
- 4) Conservation applications
- 5) Global comparisons
- 6) Multiscale analyses

Background: Why community phylogenetics?

Functional Ecology



Functional Ecology 2015, **29**, 600–614

doi: 10.1111/1365-2435.12425

COMMUNITY PHYLOGENETICS AND ECOSYSTEM FUNCTIONING

Phylogenetic patterns are not proxies of community assembly mechanisms (they are far better)

Pille Gerhold^{*1}, James F. Cahill Jr², Marten Winter³, Igor V. Bartish⁴ and Andreas Prinzing^{5,6}



Ecology Letters, (2010) **13**: 1085–1093

doi: 10.1111/j.1461-0248.2010.01509.x

IDEA AND
PERSPECTIVE

Opposing effects of competitive exclusion on the phylogenetic structure of communities

Abstract

Though many processes are involved in determining which species coexist and assemble into communities, competition is among the best studied. One hypothesis about competition's contribution to community assembly is that more closely related species are less likely to coexist. Though empirical evidence for this hypothesis is mixed, it

Margaret M. Mayfield^{1*} and
Jonathan M. Levine²

¹The University of Queensland,
School of Biological Sciences,

Background: Why community phylogenetics?

Disadvantages of using community phylogenetics in biology and ecology:

- 1) Assumptions about trait evolution
- 2) Data limitations
- 3) Oversimplification of processes
- 4) Uncertainty in phylogenetic trees
- 5) Scale sensitivity
- 6) Computational challenges

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Phylogenetic niche conservatism



Ecology Letters, (2008) 11: 995–1007

doi: 10.1111/j.1461-0248.2008.01229.x

IDEA AND PERSPECTIVE

Phylogenetic niche conservatism, phylogenetic signal and the relationship between phylogenetic relatedness and ecological similarity among species

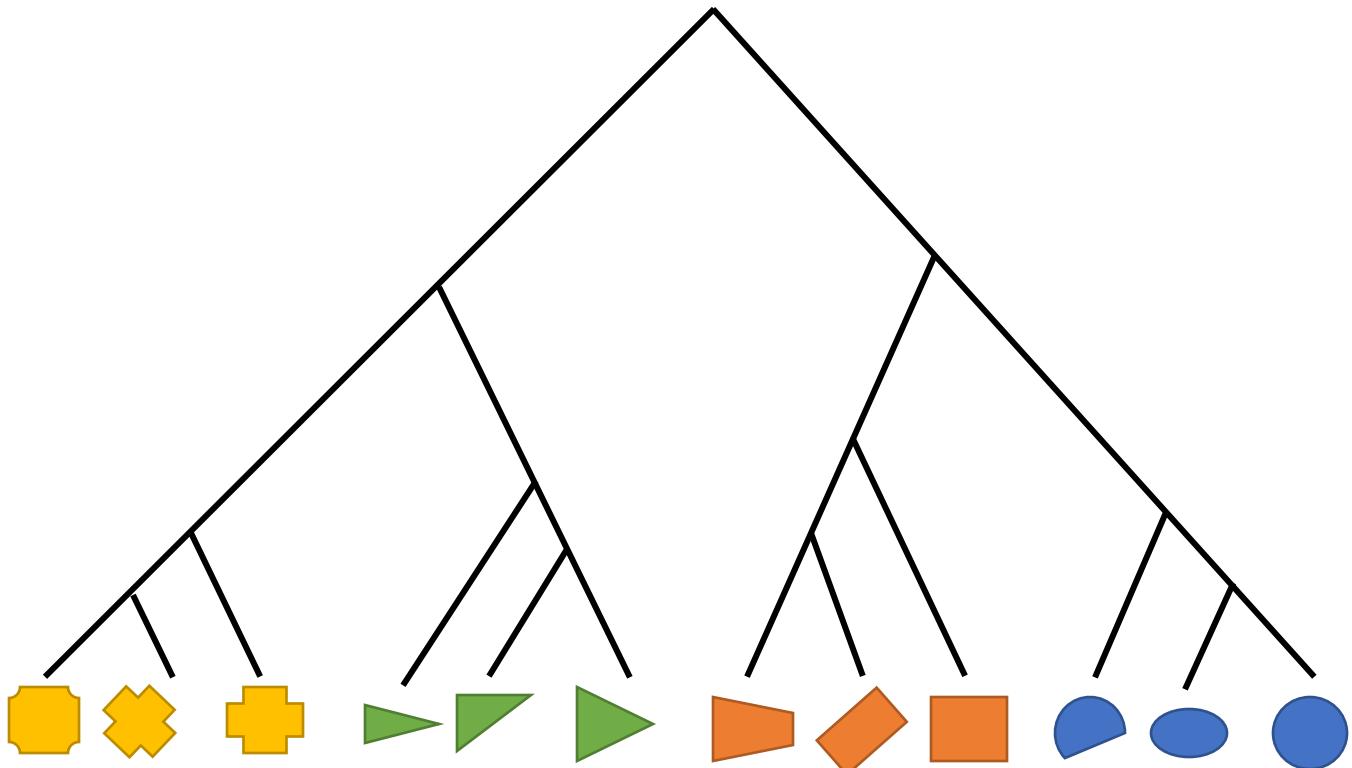
Abstract

Jonathan B. Losos*
Museum of Comparative
Zoology and Department of

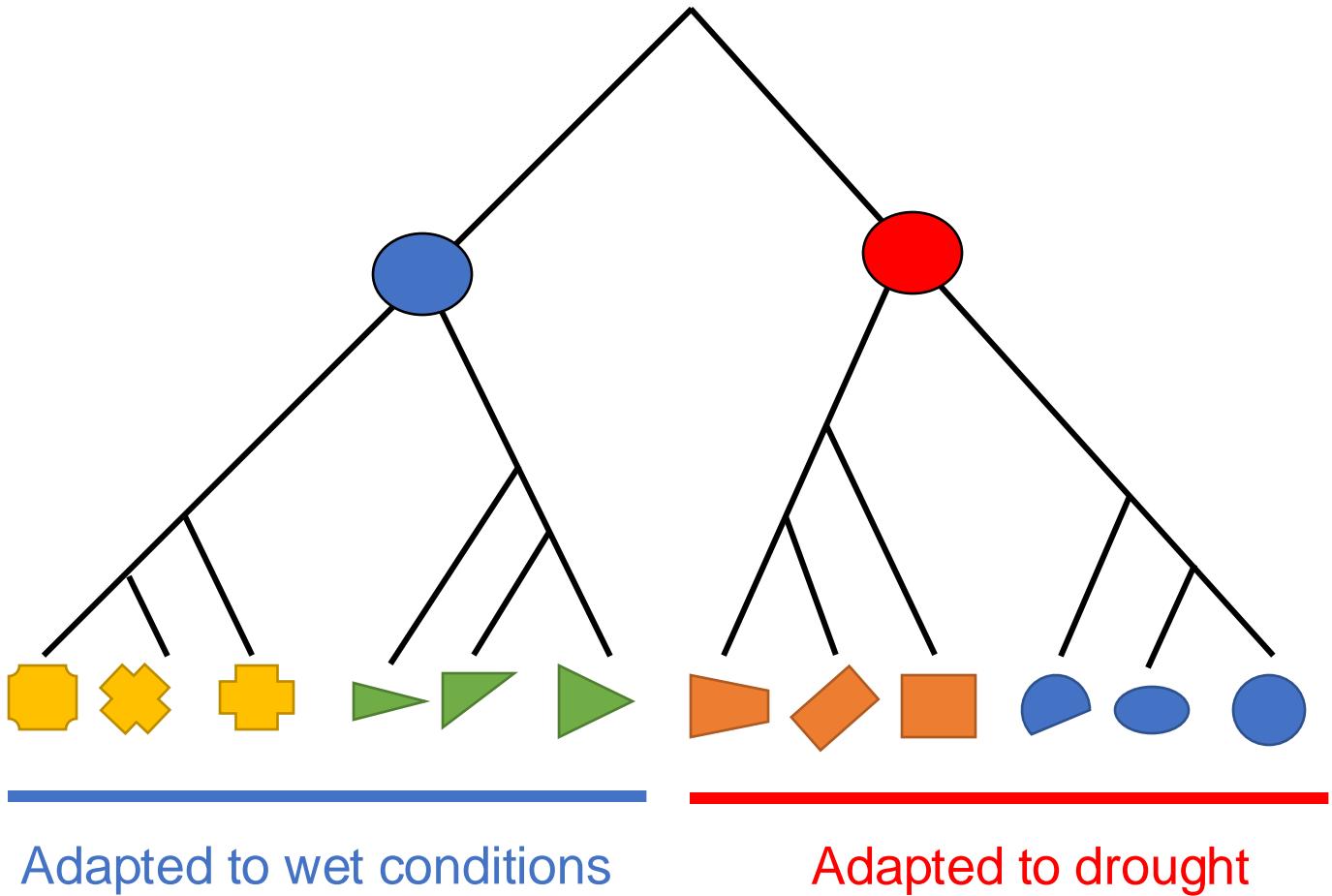
Ecologists are increasingly adopting an evolutionary perspective, and in recent years, the idea that closely related species are ecologically similar has become widespread. In this regard, phylogenetic signal must be distinguished from phylogenetic niche conservatism.

Phylogenetic niche conservatism (PNC) refers to the tendency of related species to retain similar ecological niches over evolutionary time. This concept implies that closely related species often exhibit similar environmental preferences, tolerances, and ecological roles because they inherit traits from a common ancestor.

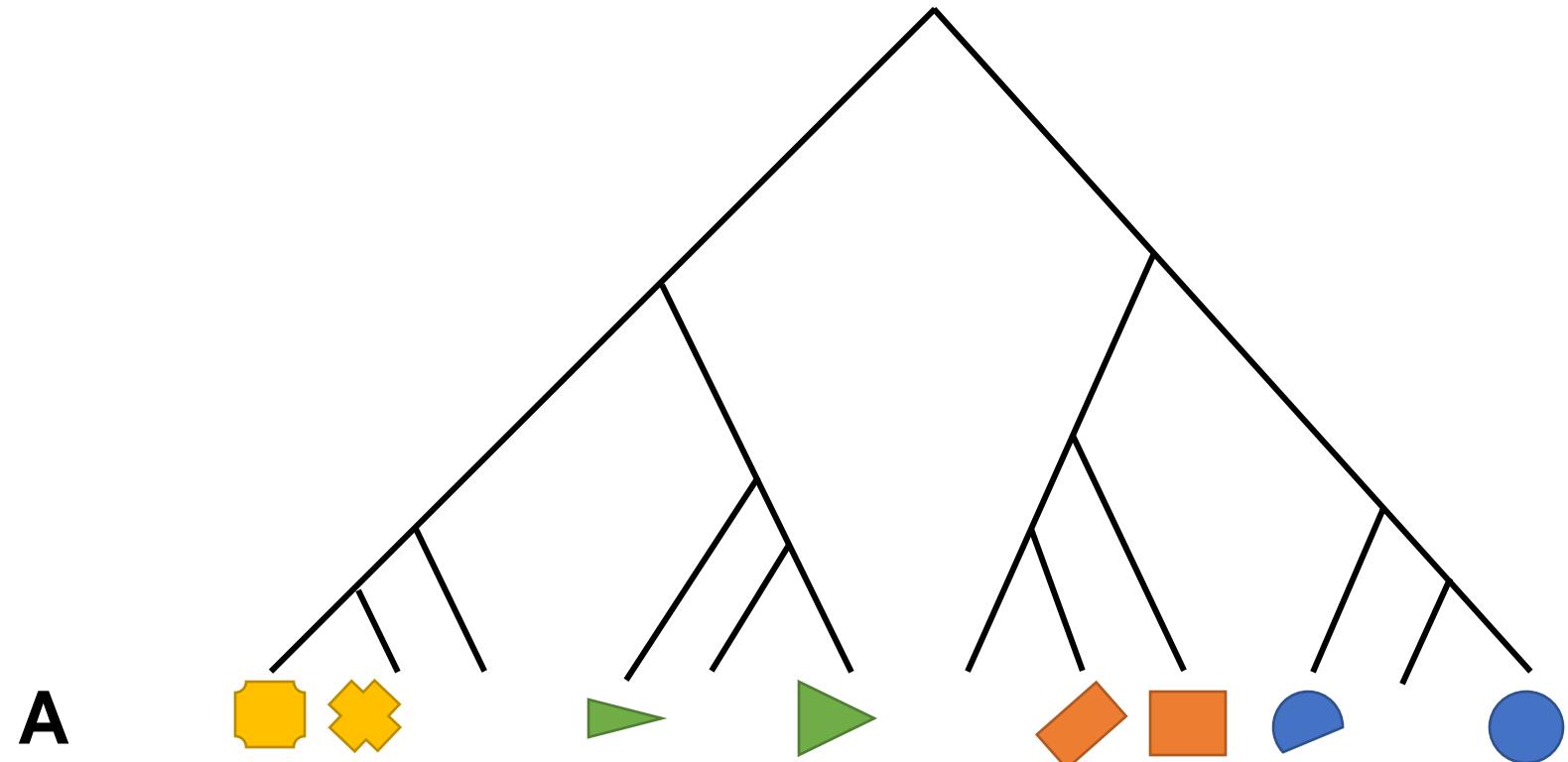
Phylogenetic niche conservatism



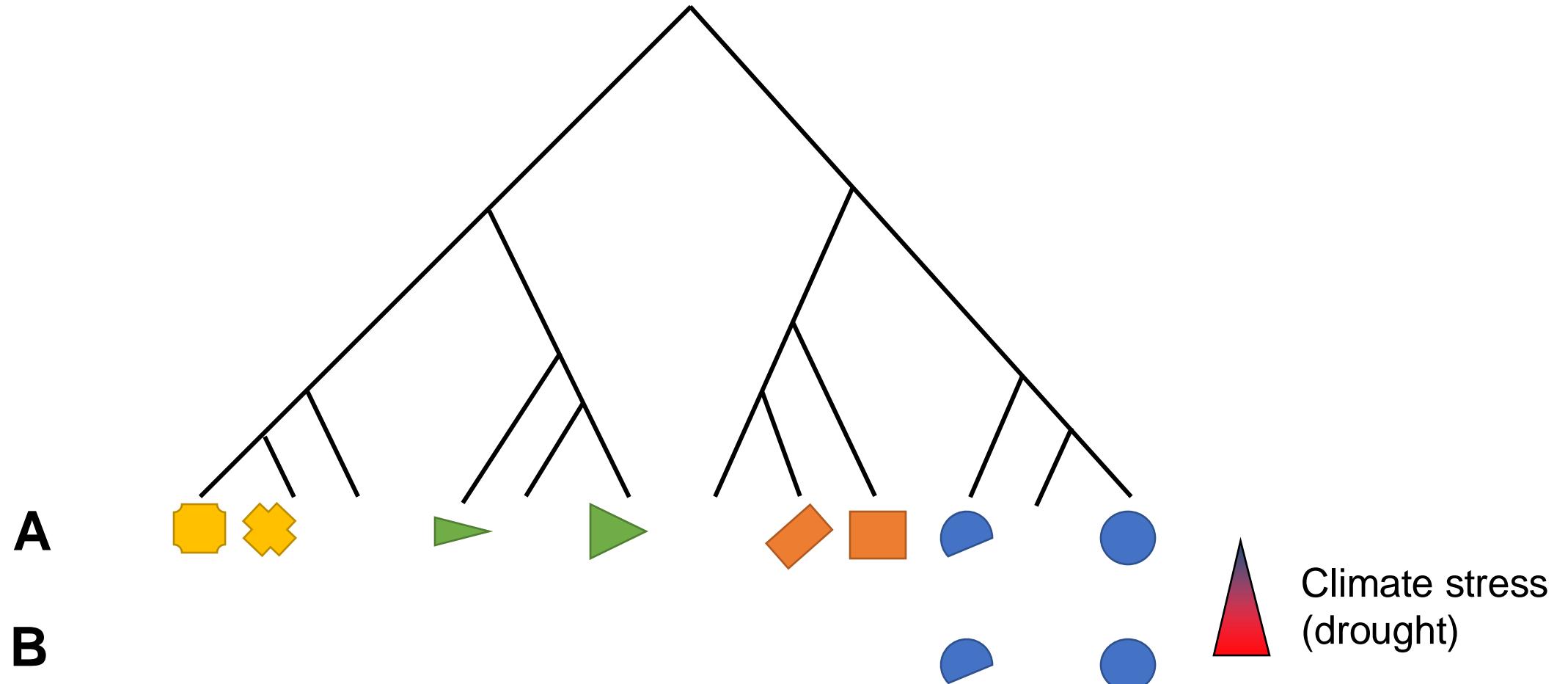
Phylogenetic niche conservatism



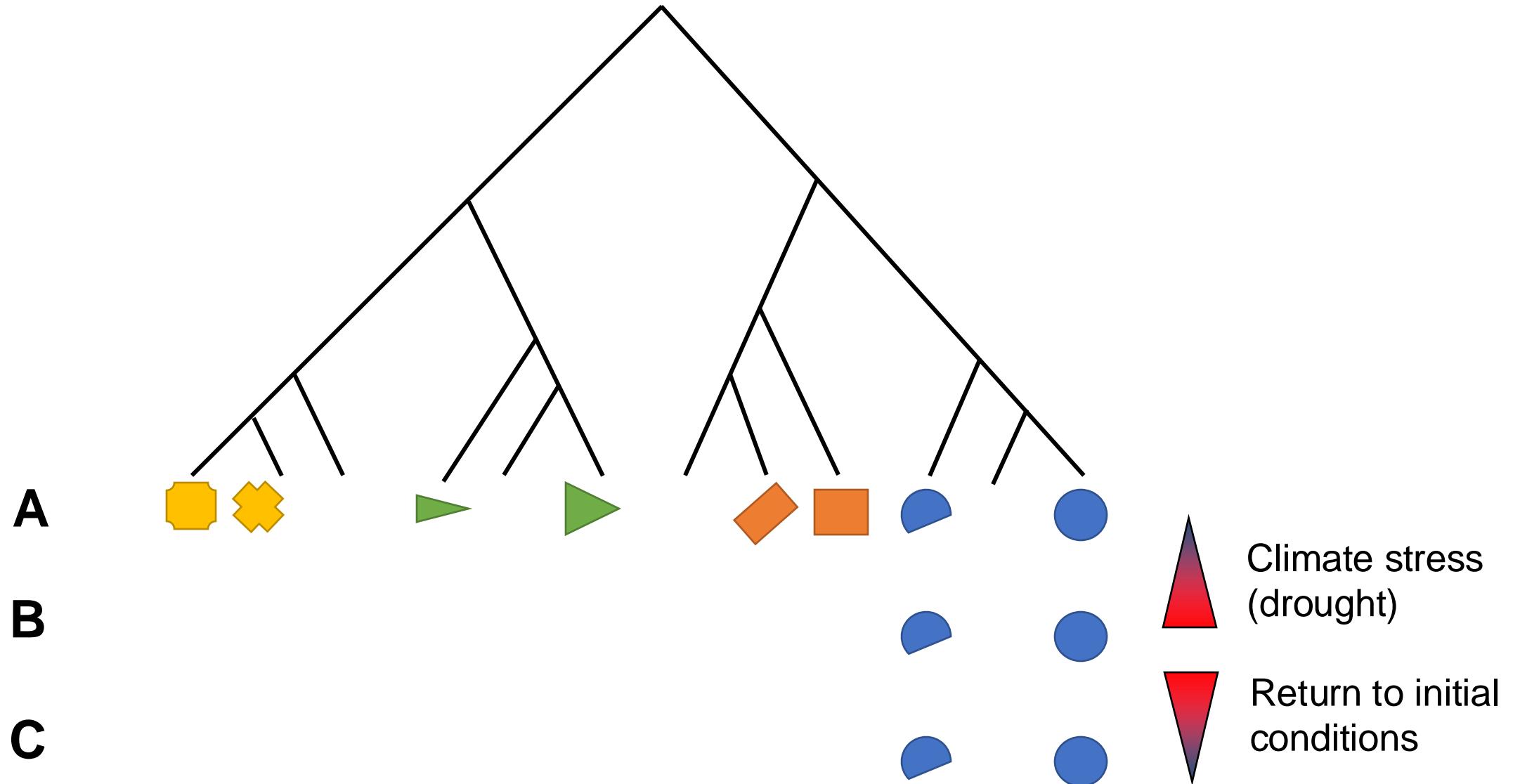
Phylogenetic niche conservatism



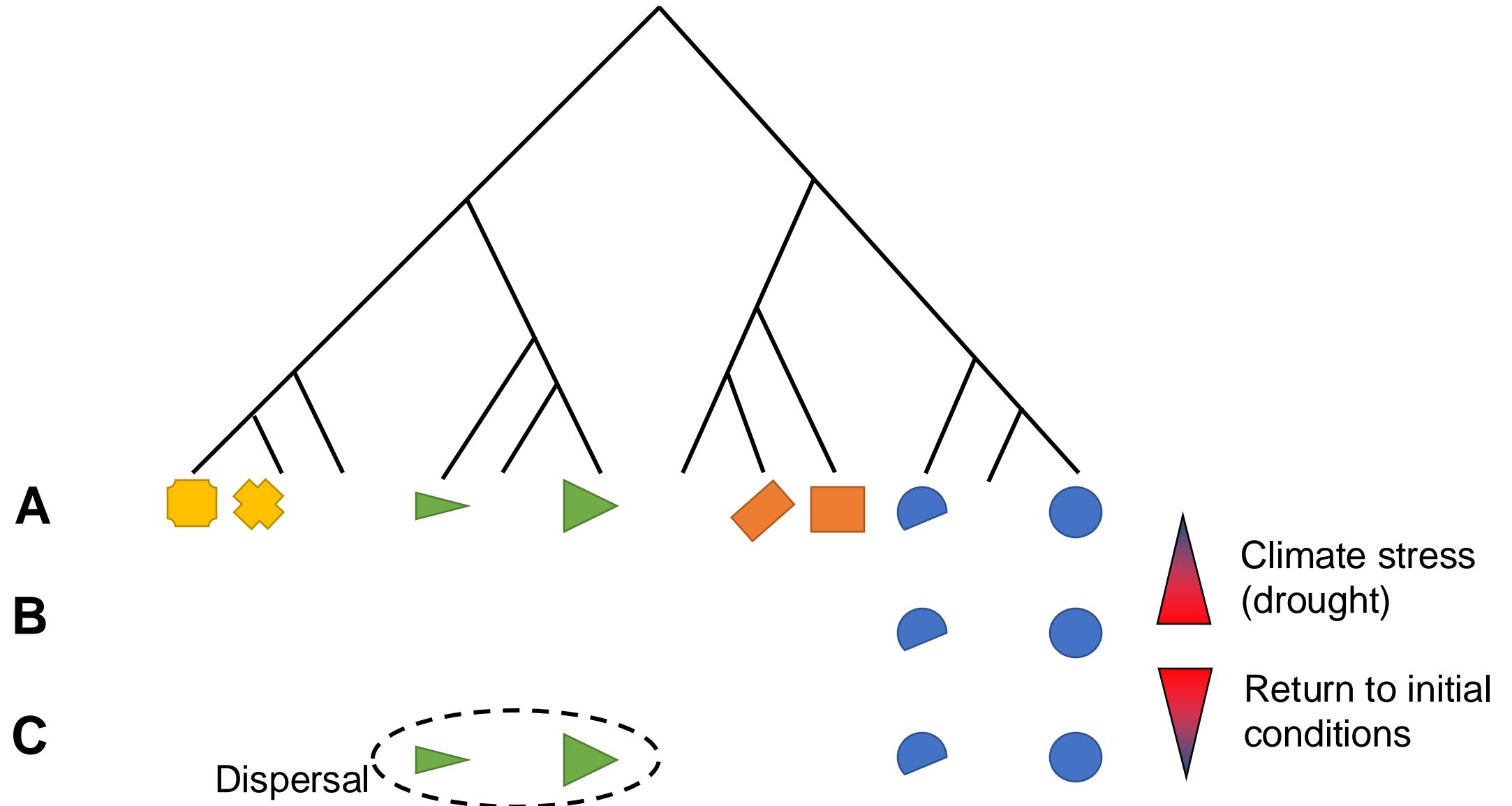
Phylogenetic niche conservatism



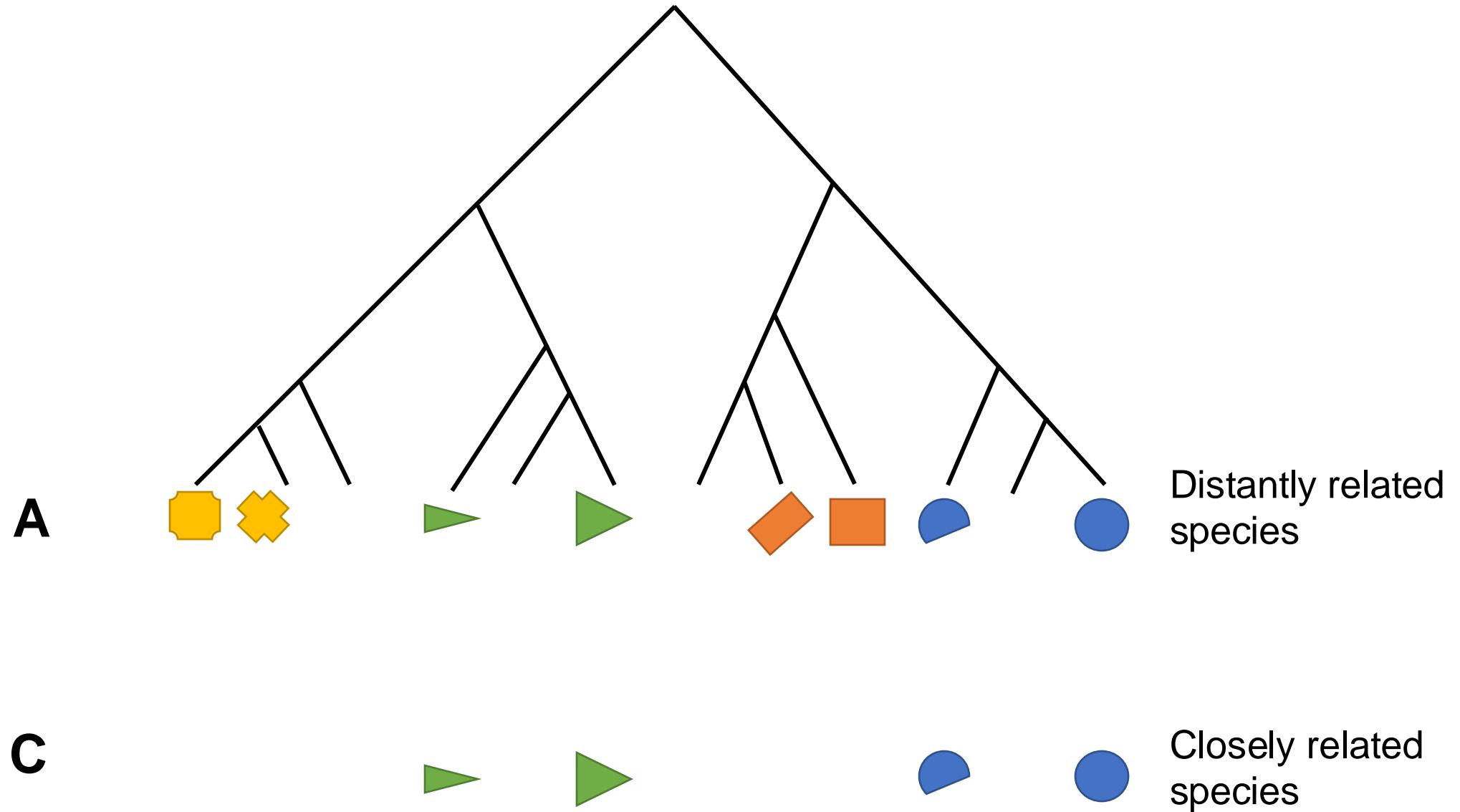
Phylogenetic niche conservatism



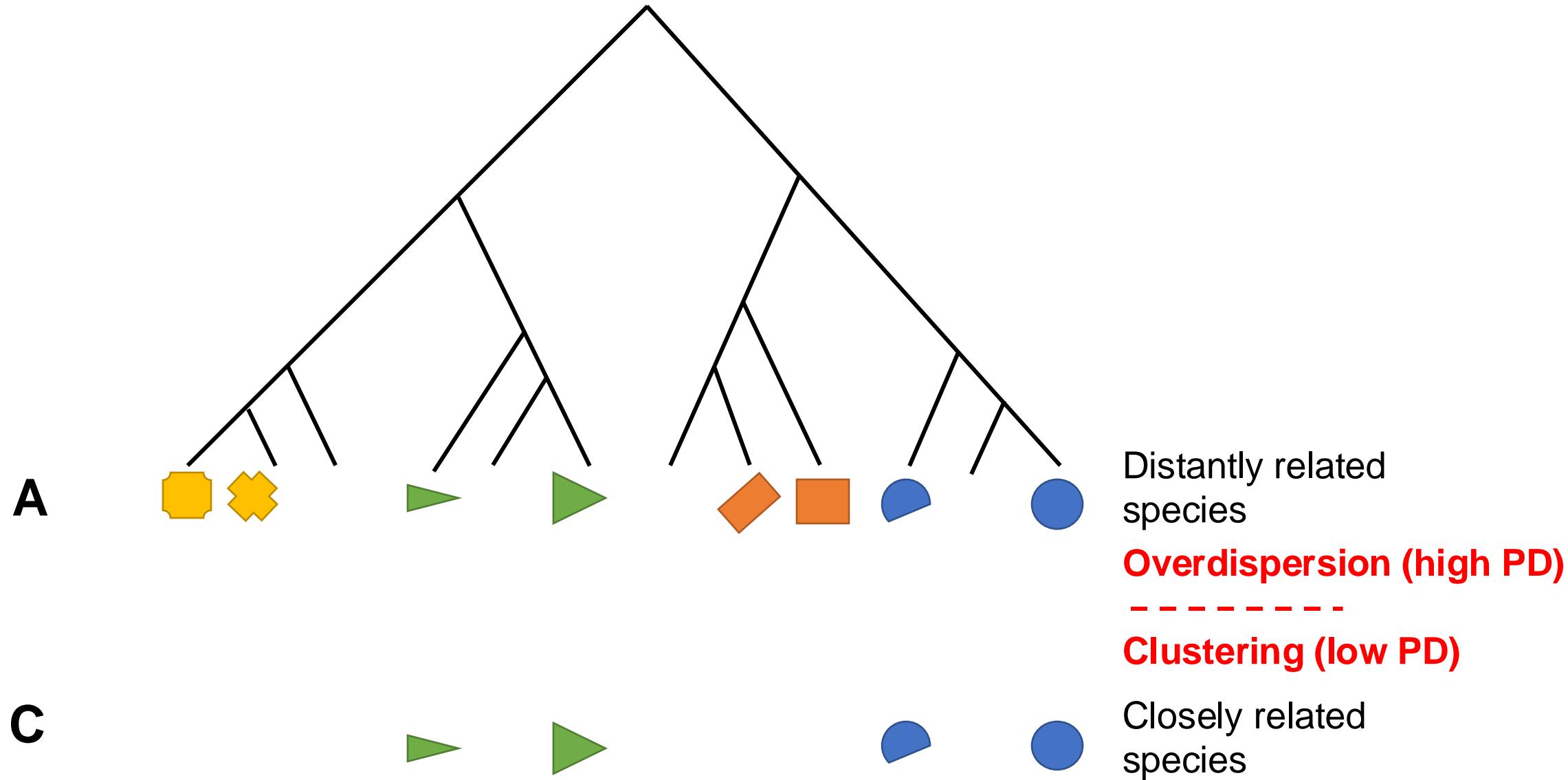
Phylogenetic niche conservatism



Phylogenetic niche conservatism



Phylogenetic niche conservatism



Phylogenetic niche conservatism



Assembly process

Niche conservatism

Niche convergence

Habitat filtering

Clustering

Overdispersion

Competitive exclusion

Overdispersion

Random

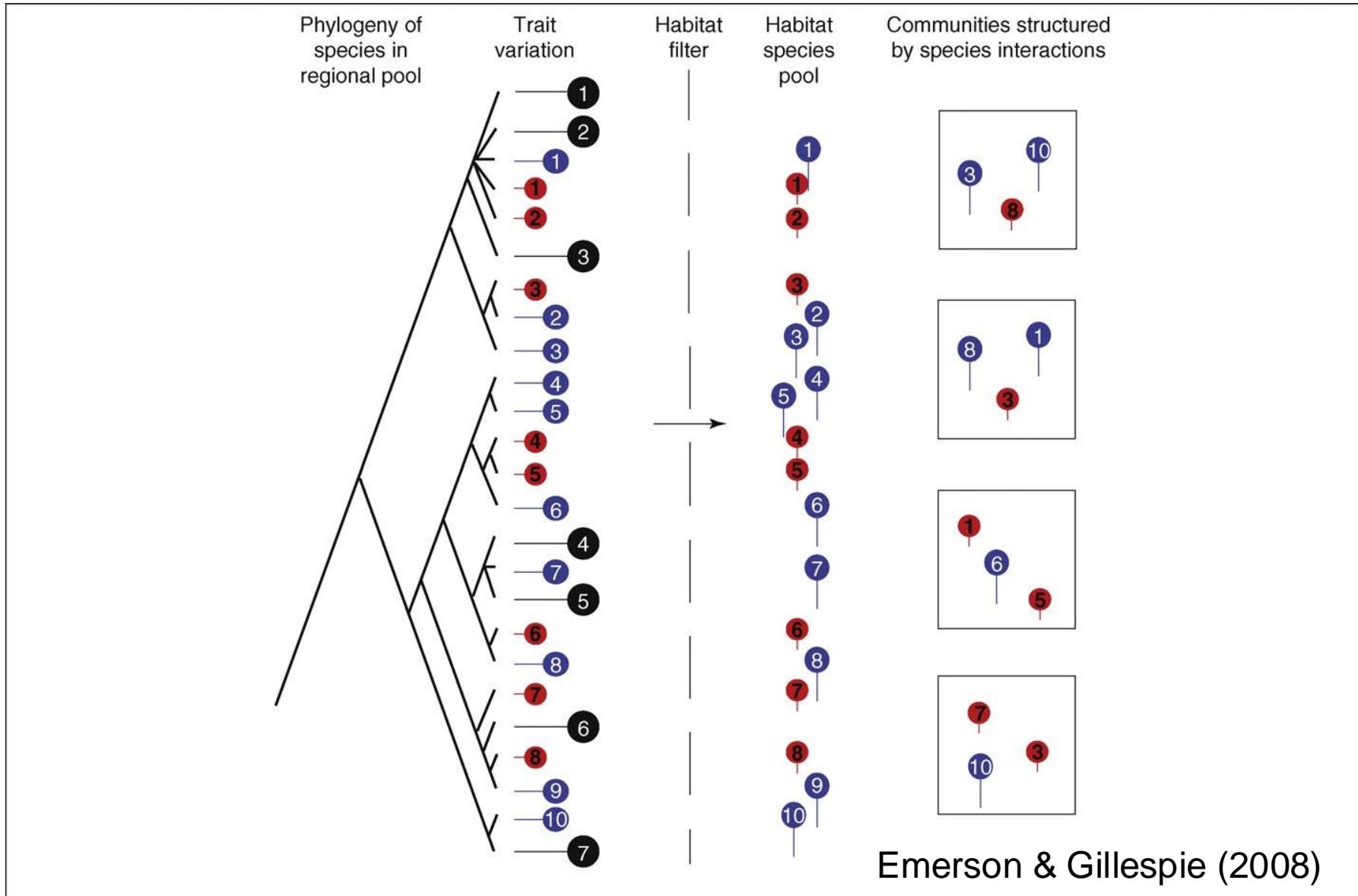
Neutral

Random

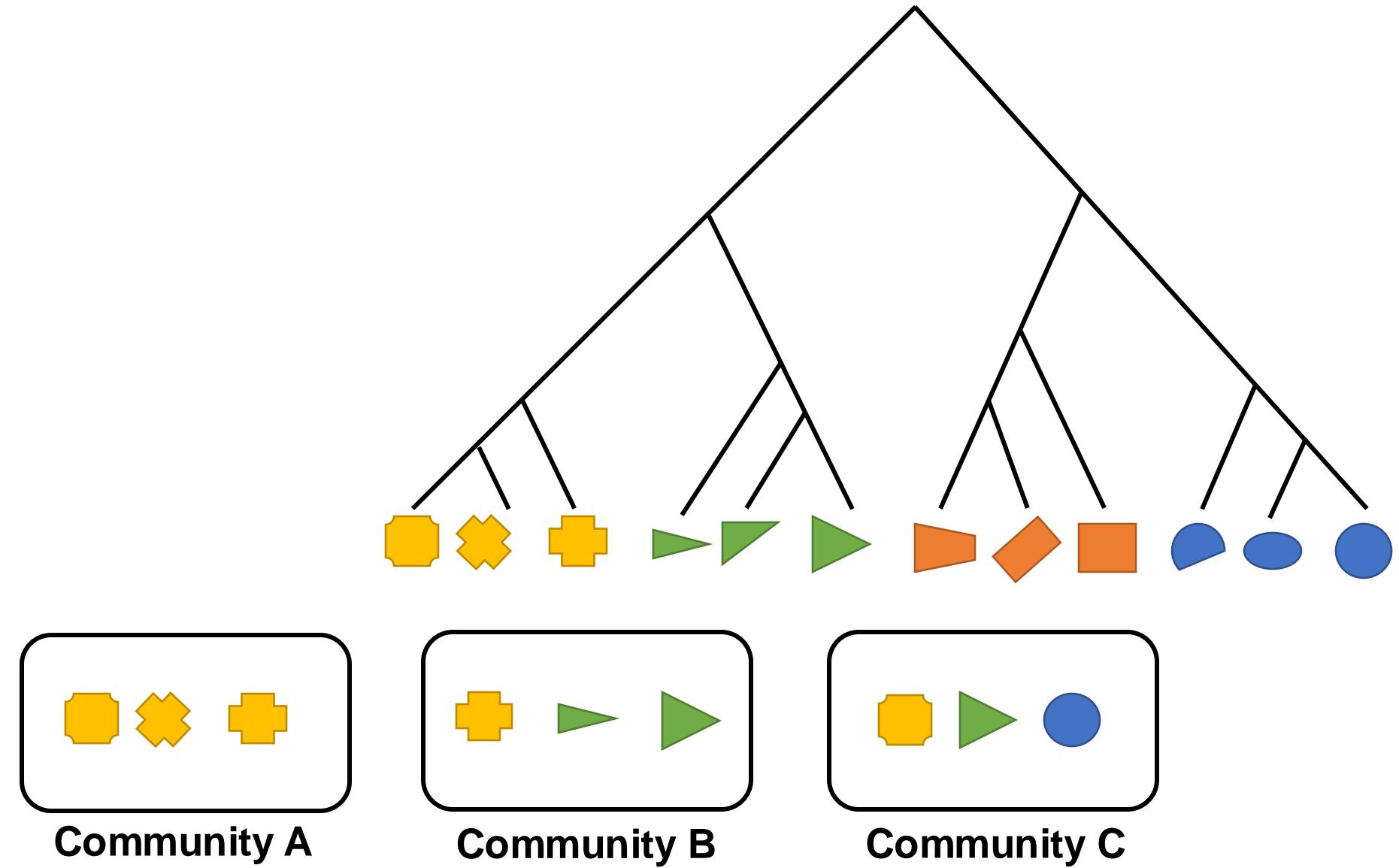
Random

Webb et al., 2002; Hubbell, 2001

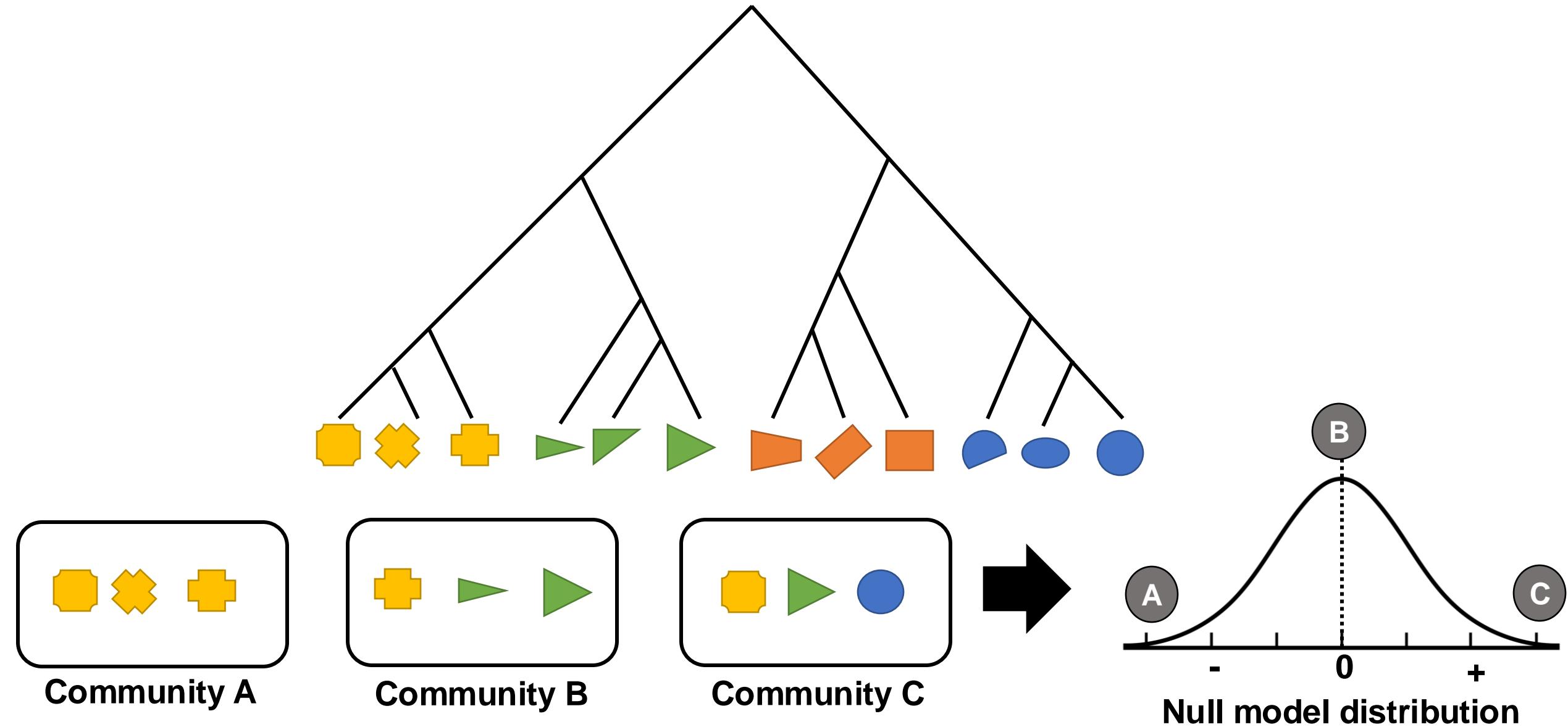
Phylogenetic niche conservatism



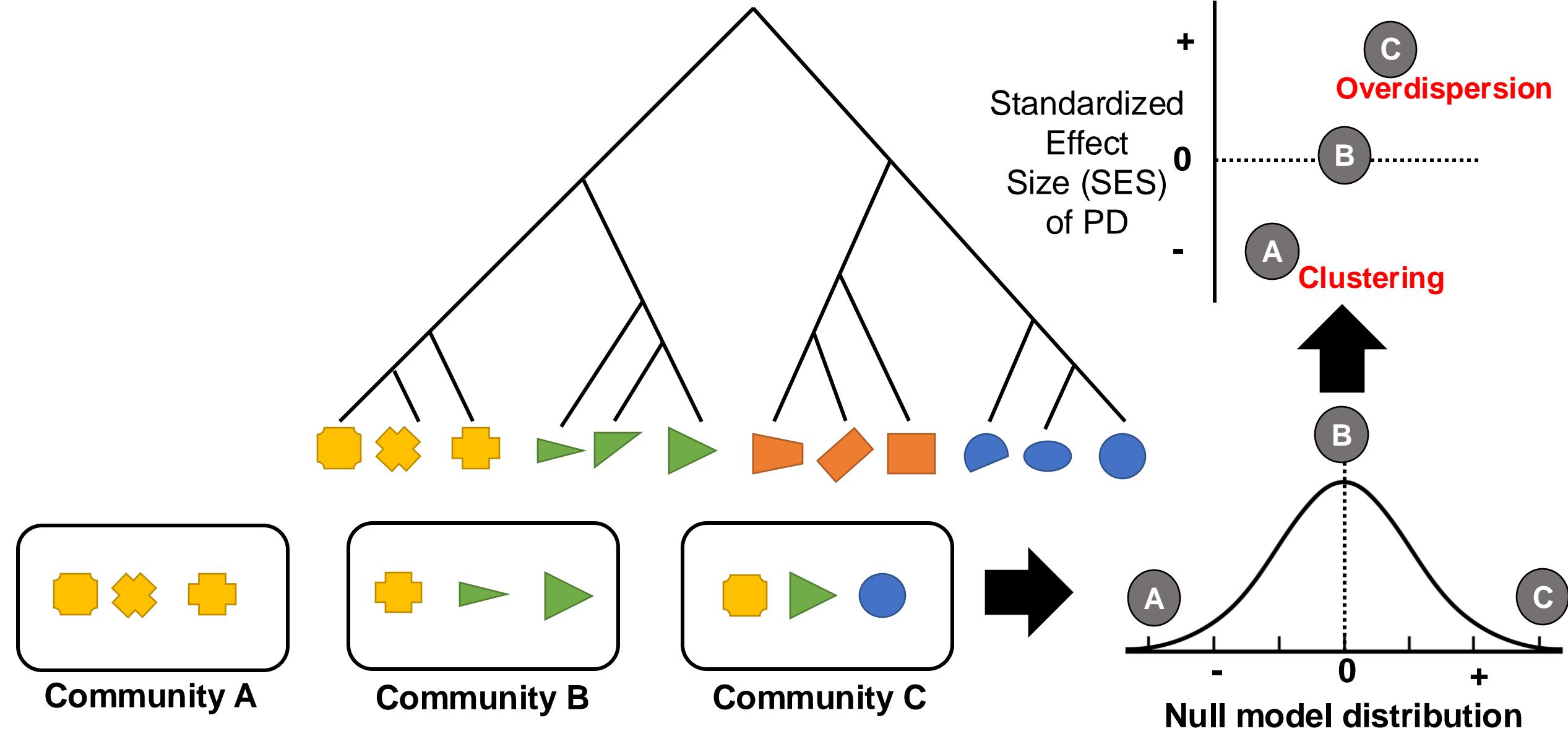
Phylogenetic niche conservatism



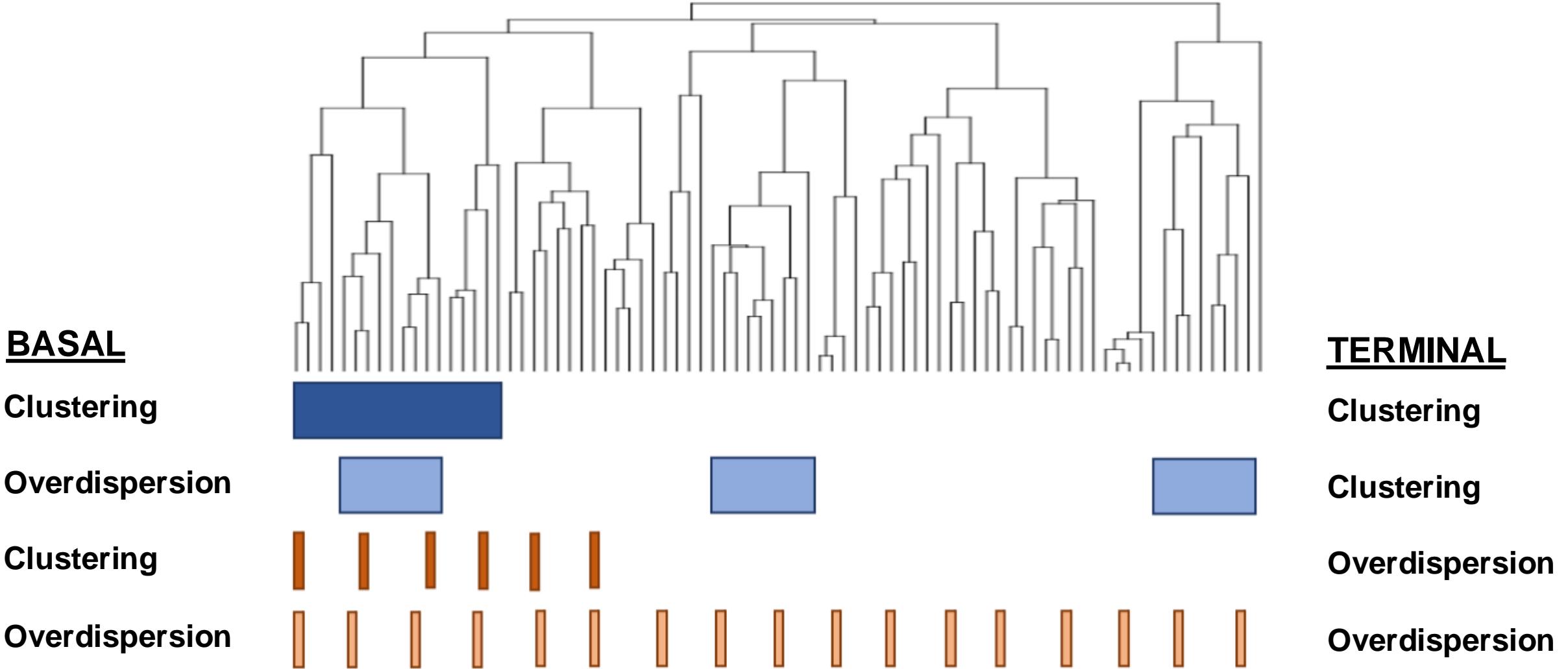
Phylogenetic niche conservatism



Phylogenetic niche conservatism

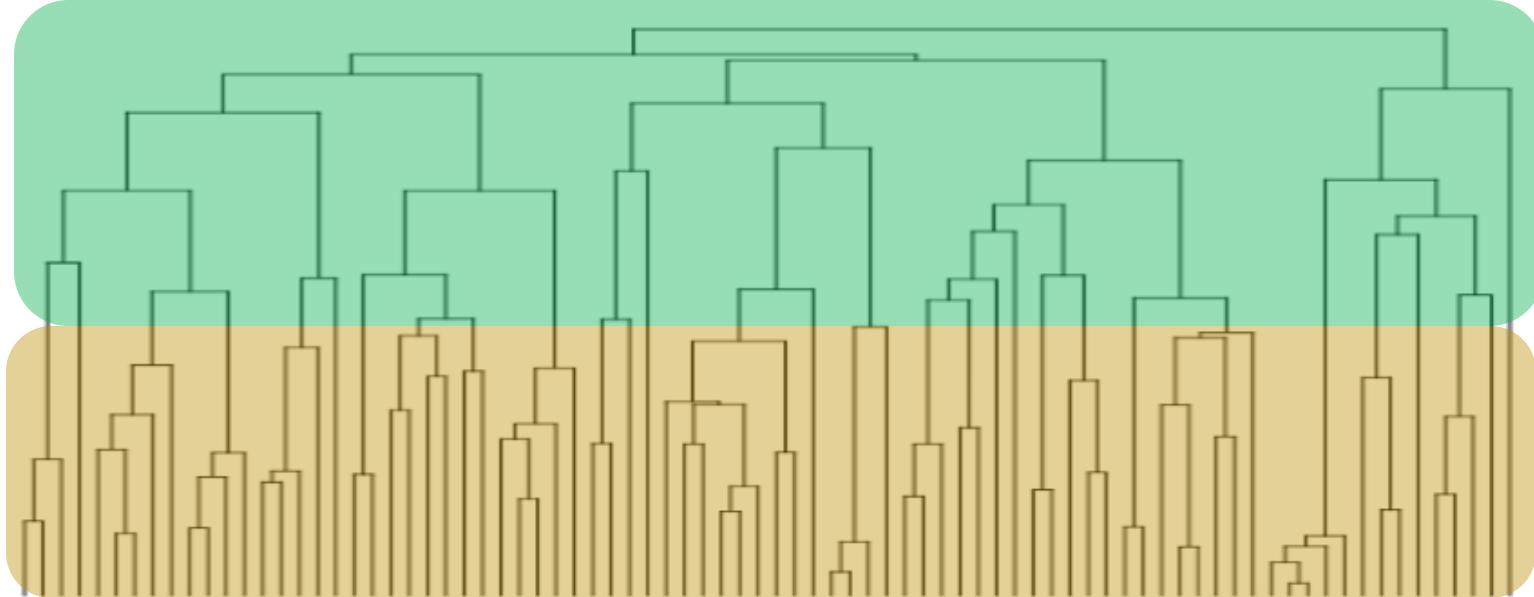


Phylogenetic niche conservatism



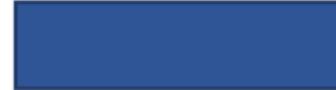
Phylogenetic niche conservatism

BASAL



TERMINAL

Clustering



Clustering

Overdispersion



Clustering

Clustering



Overdispersion

Overdispersion

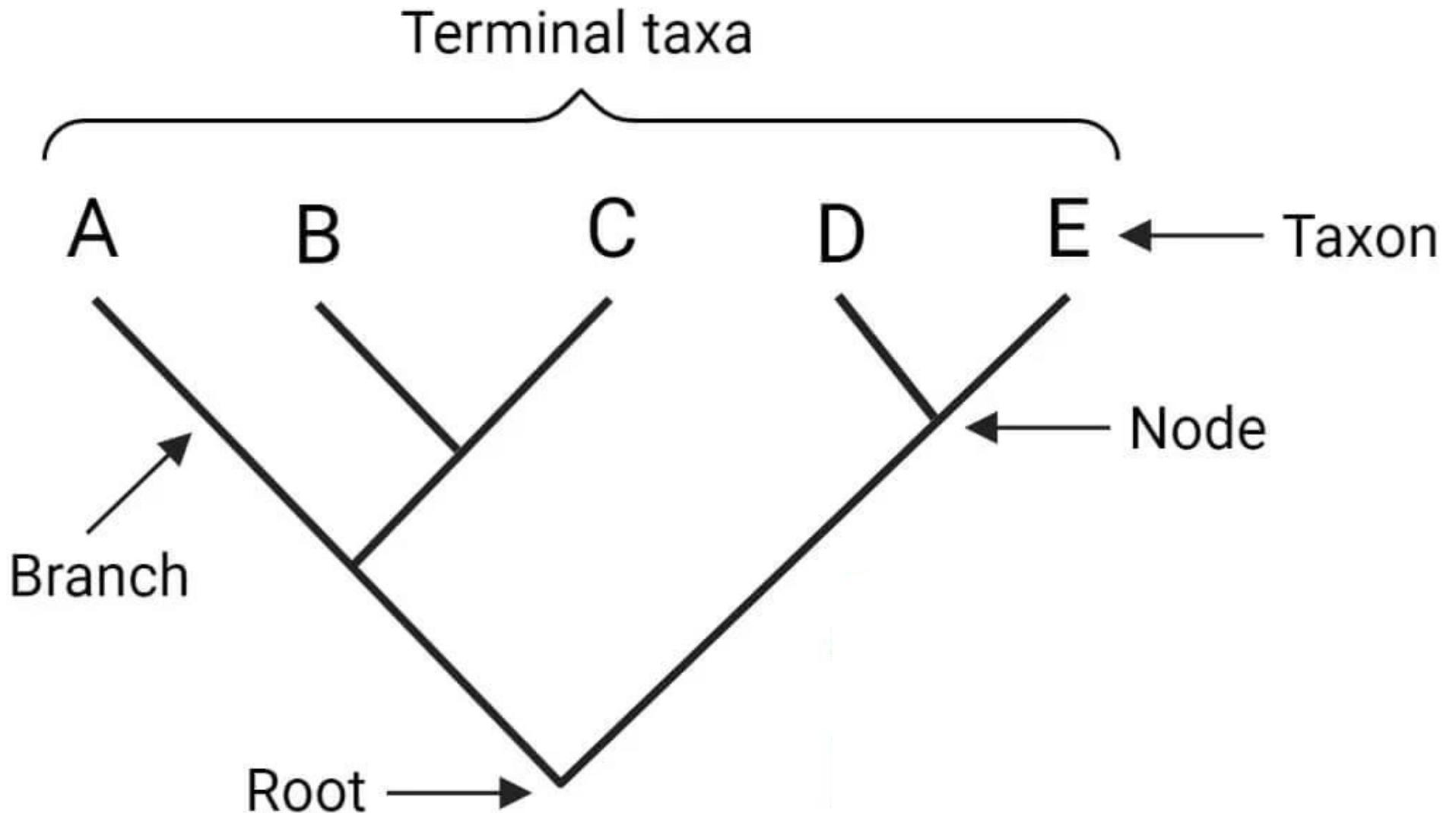


Overdispersion

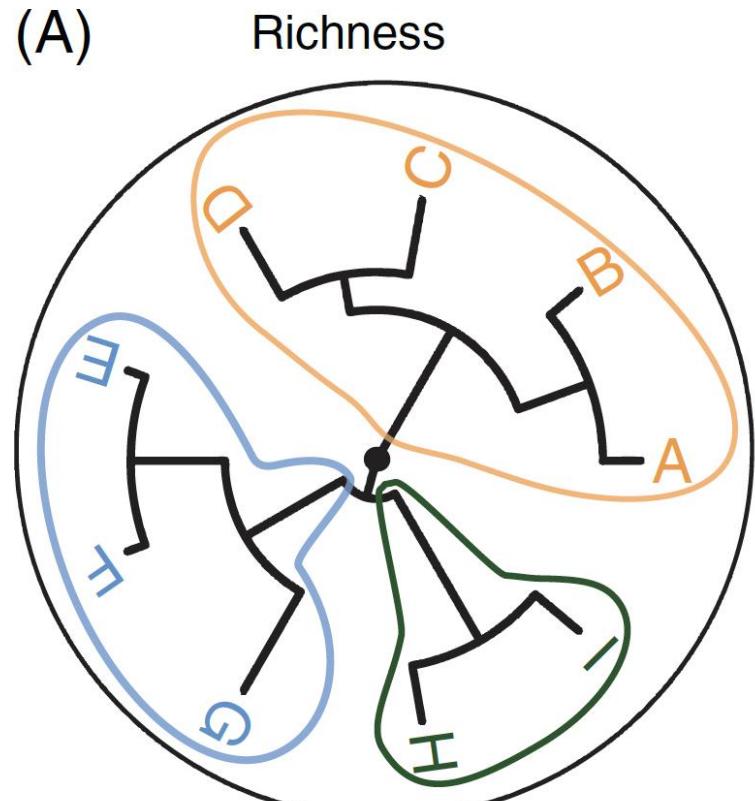
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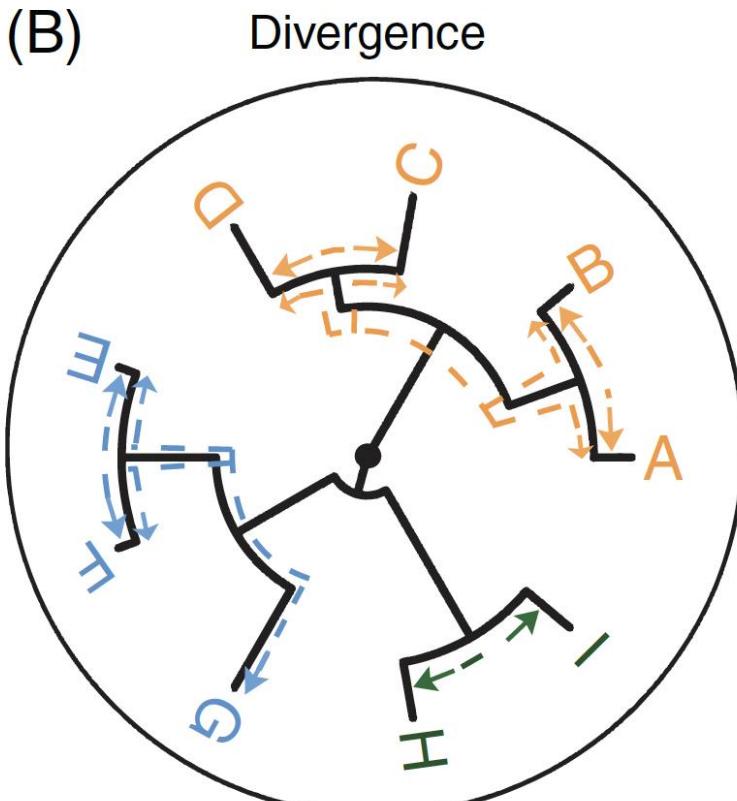
Calculation of phylogenetic diversity



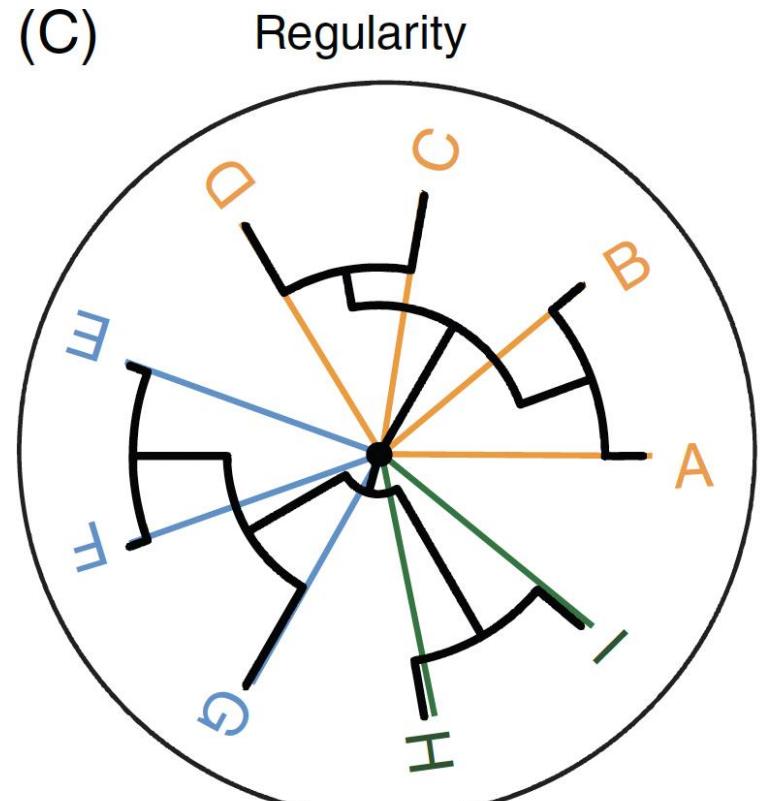
Calculation of phylogenetic diversity



How much?



How different?



How regular?

Calculation of phylogenetic diversity

DIMENSION =>	1. Richness: how much? <i>Sum of . . .</i>			
<=Level of comparison	Unit =>	1.1 Branch lengths	1.2 Pairwise distances	1.3 Phylogenetic isolation
α -diversity (within sets)		1.1a Amount of evolutionary history: <i>Across species</i> PD <i>Across individuals</i> ΔnPD <i>Effective ($q=0$)</i> $^0D(T)^*$, $^0PD(T)^*$ <i>Per species</i> PD_{Ab} <i>Endemic</i> PE	1.2a Sum of pairwise distances: PSR F AED	1.3a Sum of evolutionary distinctiveness: ED

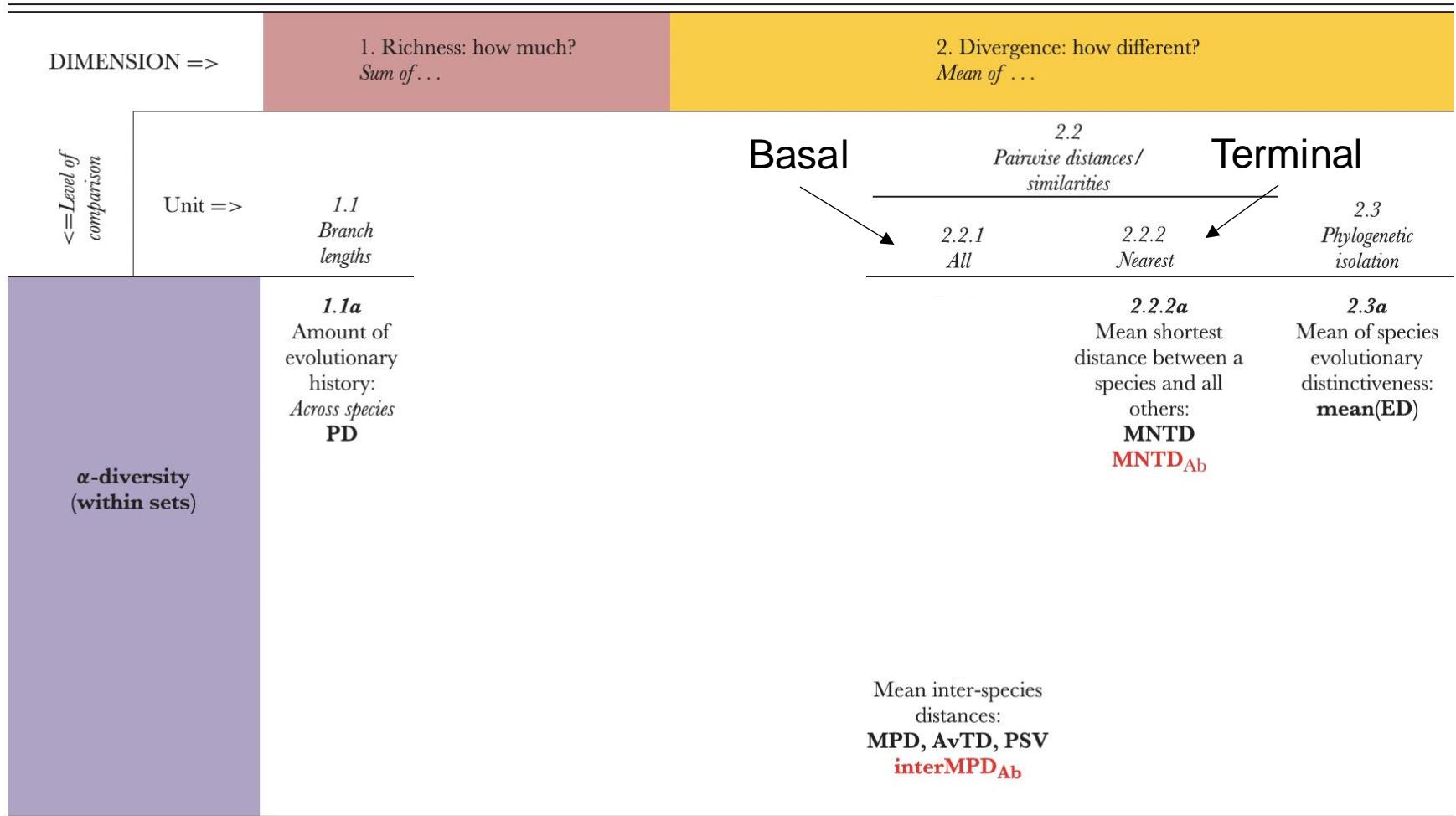
Calculation of phylogenetic diversity

DIMENSION =>		1. Richness: how much? <i>Sum of ...</i>		2. Divergence: how different? <i>Mean of ...</i>			
↓=Level of comparison	Unit =>	2.2 <i>Pairwise distances/ similarities</i>					
		1.1 <i>Branch lengths</i>	1.2 <i>Pairwise distances</i>	1.3 <i>Phylogenetic isolation</i>	2.1 <i>Branch lengths</i>	2.2.1 <i>All</i>	2.2.2 <i>Nearest</i>
α-diversity (within sets)	1.1a Amount of evolutionary history: <i>Across species PD</i> <i>Across individuals ΔnPD</i> <i>Effective (q=0) ⁰D(T)*, ⁰PD(T)*</i> <i>Per species PD_{Ab}</i> <i>Endemic PE</i>	1.2a Sum of pairwise distances: PSR F	1.3a Sum of evolutionary distinctiveness: ED AED	2.1a Sum of branch lengths divided by species richness: avPD avPD_{Ab}	2.2.1a Effective number of species given phylogenetic balance and abundance evenness: $qD^Z(p)^*$	2.2.2a Mean shortest distance between a species and all others: MNTD MNTD_{Ab}	2.3a Mean of species evolutionary distinctiveness: mean(ED)

Calculation of phylogenetic diversity

DIMENSION =>		1. Richness: how much? <i>Sum of ...</i>			2. Divergence: how different? <i>Mean of ...</i>			3. Regularity: how regular? <i>Variance of ...</i>			
↓=Level of comparison	Unit =>	2.2 <i>Pairwise distances / similarities</i>						3.2 <i>Pairwise distances</i>			3.3 <i>Phylogenetic isolation</i>
		1.1 <i>Branch lengths</i>	1.2 <i>Pairwise distances</i>	1.3 <i>Phylogenetic isolation</i>	2.1 <i>Branch lengths</i>	2.2.1 <i>All</i>	2.2.2 <i>Nearest</i>	2.3 <i>Phylogenetic isolation</i>	3.1 <i>Tree topology</i>	3.2.1 <i>All</i>	3.2.2 <i>Nearest</i>
α-diversity (within sets)	1.1a Amount of evolutionary history: <i>Across species</i> PD <i>Across individuals</i> ΔnPD <i>Effective (q=0)</i> ${}^0D(T)^*$, ${}^0PD(T)^*$ <i>Per species</i> PD_{Ab} <i>Endemic PE</i>	1.2a Sum of pairwise distances: PSR F	1.3a Sum of evolutionary distinctiveness: ED AED	2.1a Sum of branch lengths divided by species richness: avPD avPD_{Ab}	2.2.1a Effective number of species given phylogenetic balance and abundance evenness: ${}^qD^Z(p)^*$	2.2.2a Mean shortest distance between a species and all others: MNTD MNTD_{Ab}	2.3a Mean of species evolutionary distinctiveness: mean(ED)	3.1a Branching symmetry and distribution: I_C γ IAC	3.2.1a Variance of pairwise distances: VPD, Λ⁺, VarTD VPD_{Ab} interVPD_{Ab}	3.2.2a Variance of nearest neighbour distances: VNTD VNTD_{Ab} PE_{ve}	3.3a Variance of species isolation metrics: EED HED H_{AED} ${}^qD(P)^*$ ${}^qD(AP)^*$

Calculation of phylogenetic diversity



Calculation of phylogenetic diversity

Where can I find a **plant phylogeny**?

Constructing a broadly inclusive seed plant phylogeny

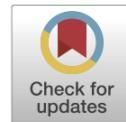
Stephen A. Smith^{1,2}  and Joseph W. Brown¹ 

Three keys to the radiation of angiosperms into freezing environments

Amy E. Zanne^{1,2}, David C. Tank^{3,4}, William K. Cornwell^{5,6}, Jonathan M. Eastman^{3,4}, Stephen A. Smith⁷, Richard G. FitzJohn^{8,9}, Daniel J. McGlinn¹⁰, Brian C. O'Meara¹¹, Angela T. Moles⁶, Peter B. Reich^{12,13}, Dana L. Royer¹⁴, Douglas E. Soltis^{15,16,17}, Peter F. Stevens¹⁸, Mark Westoby⁹, Ian J. Wright⁹, Lonnie Aarssen¹⁹, Robert I. Bertin²⁰, Andre Calaminus¹⁵, Rafaël Govaerts²¹, Frank Hemmings⁶, Michelle R. Leishman⁹, Jacek Oleksyn^{12,22}, Pamela S. Soltis^{16,17}, Nathan G. Swenson²³, Laura Warman^{6,24} & Jeremy M. Beaulieu²⁵

V.PhyloMaker2: An updated and enlarged R package that can generate very large phylogenies for vascular plants

Yi Jin ^{a,*}, Hong Qian ^{b,**}



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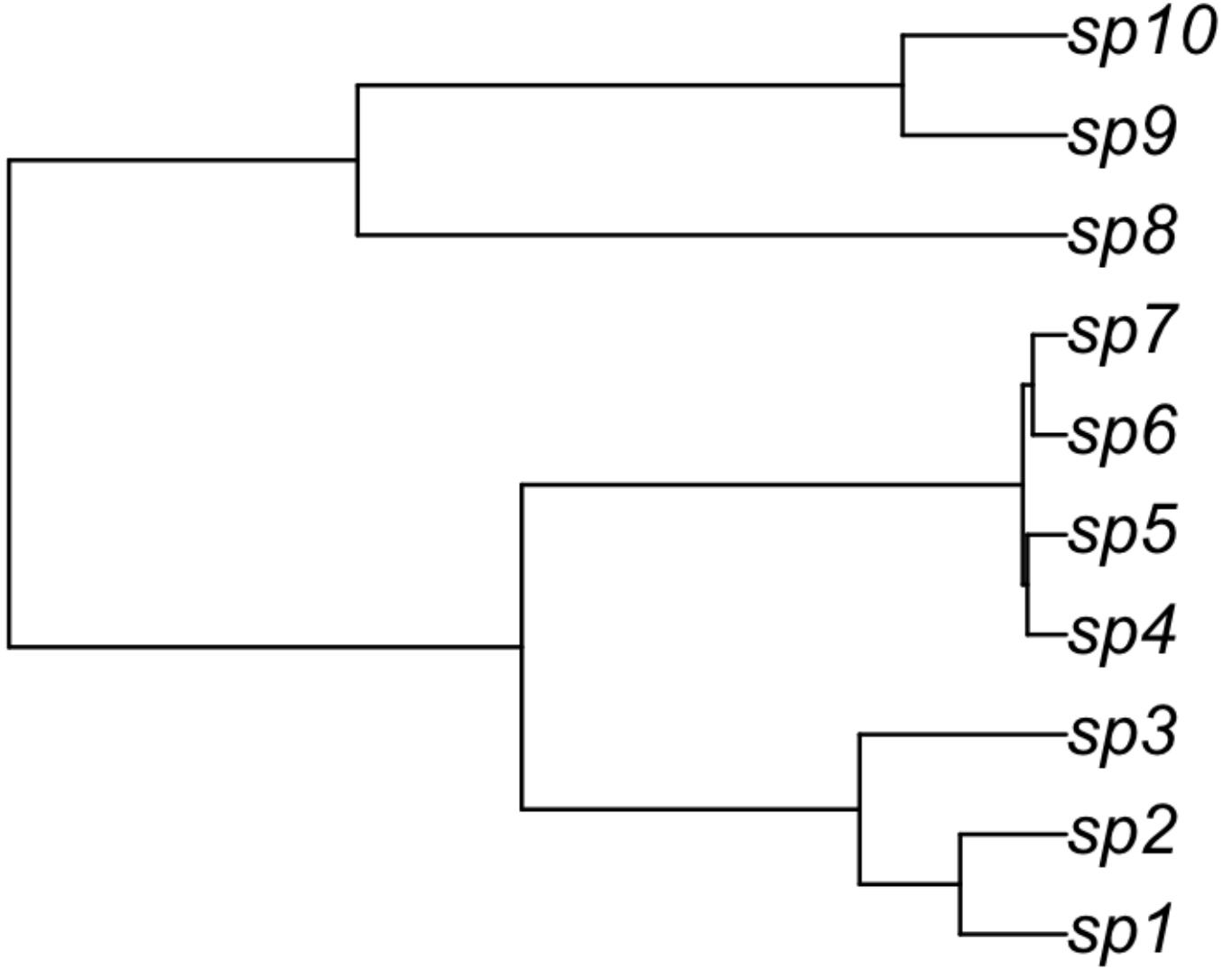
Calculation of phylogenetic diversity

Script to the following examples:

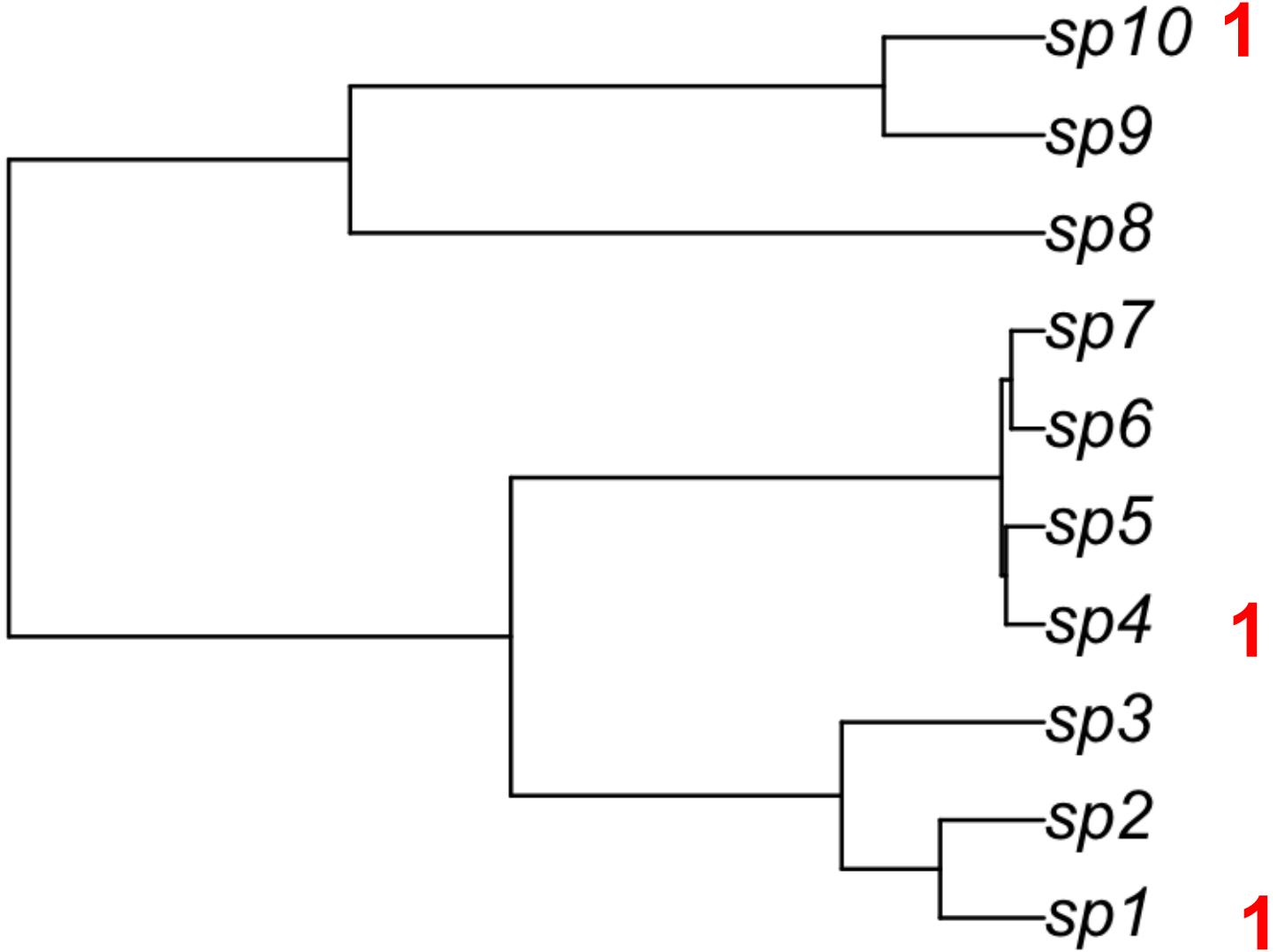


https://github.com/padullesj/IAVS_Ecoinformatics/blob/main/Community_Phylogenetics.R

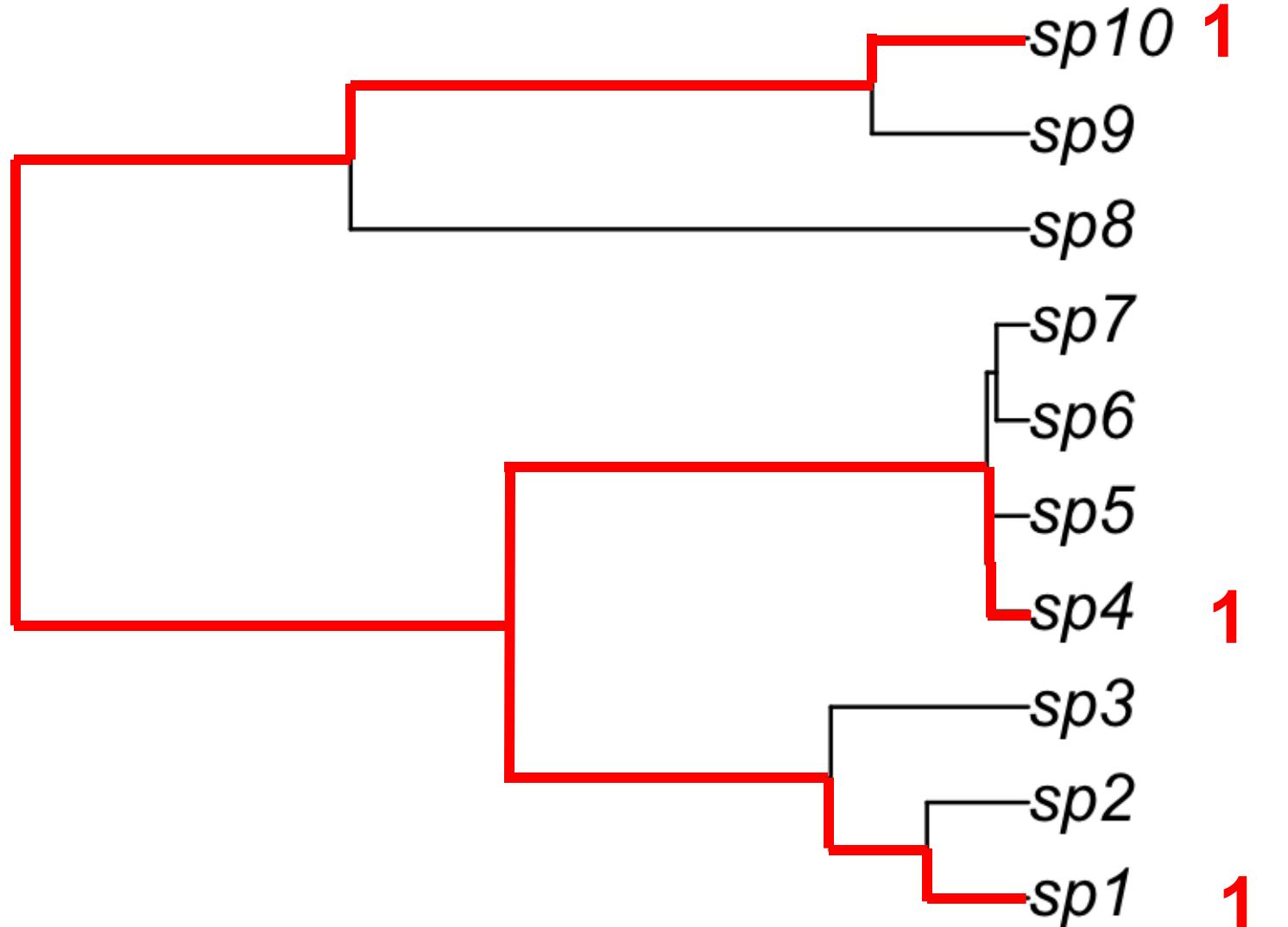
Alpha diversity: Faith's PD



Alpha diversity: Faith's PD



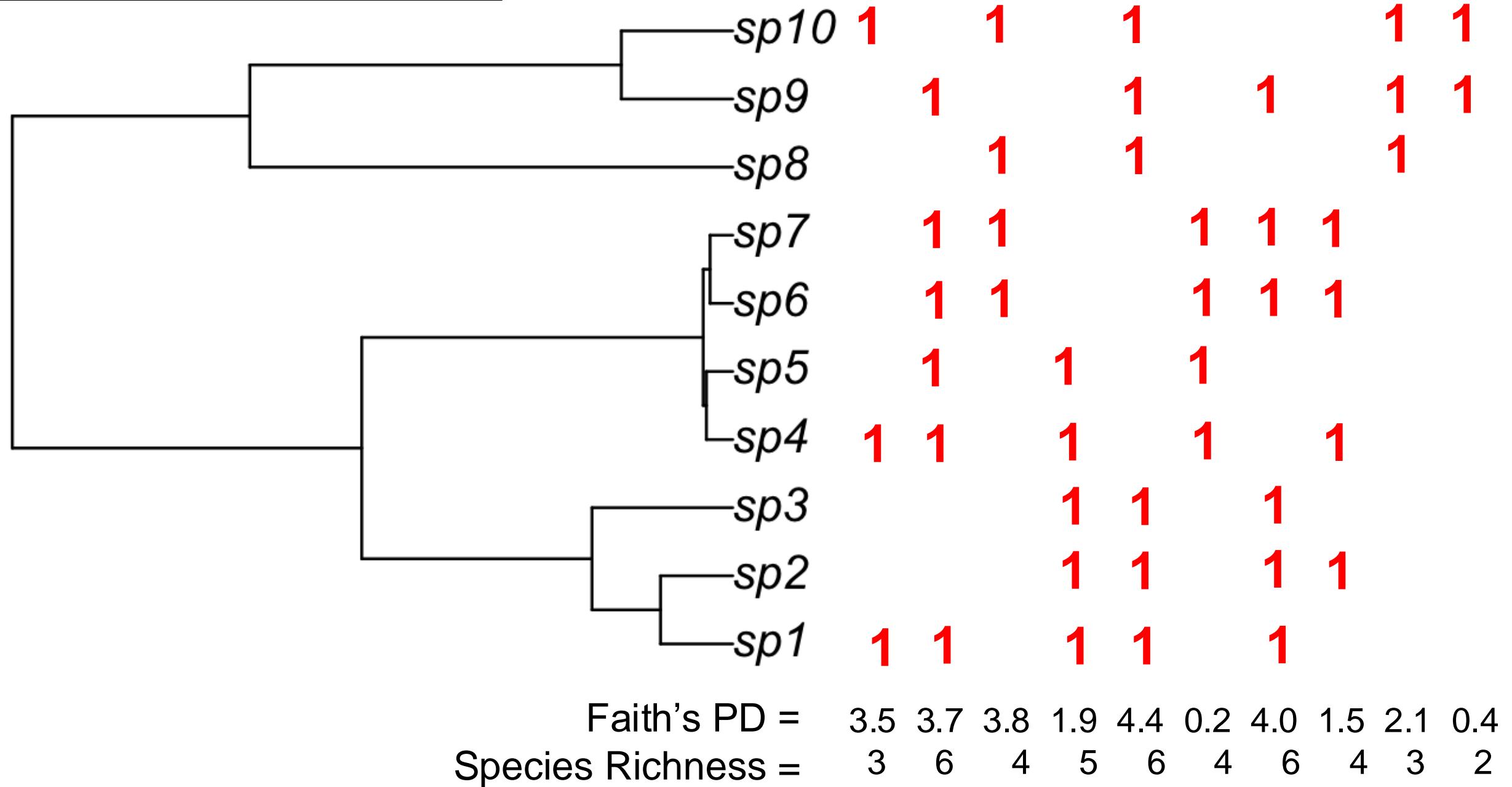
Alpha diversity: Faith's PD



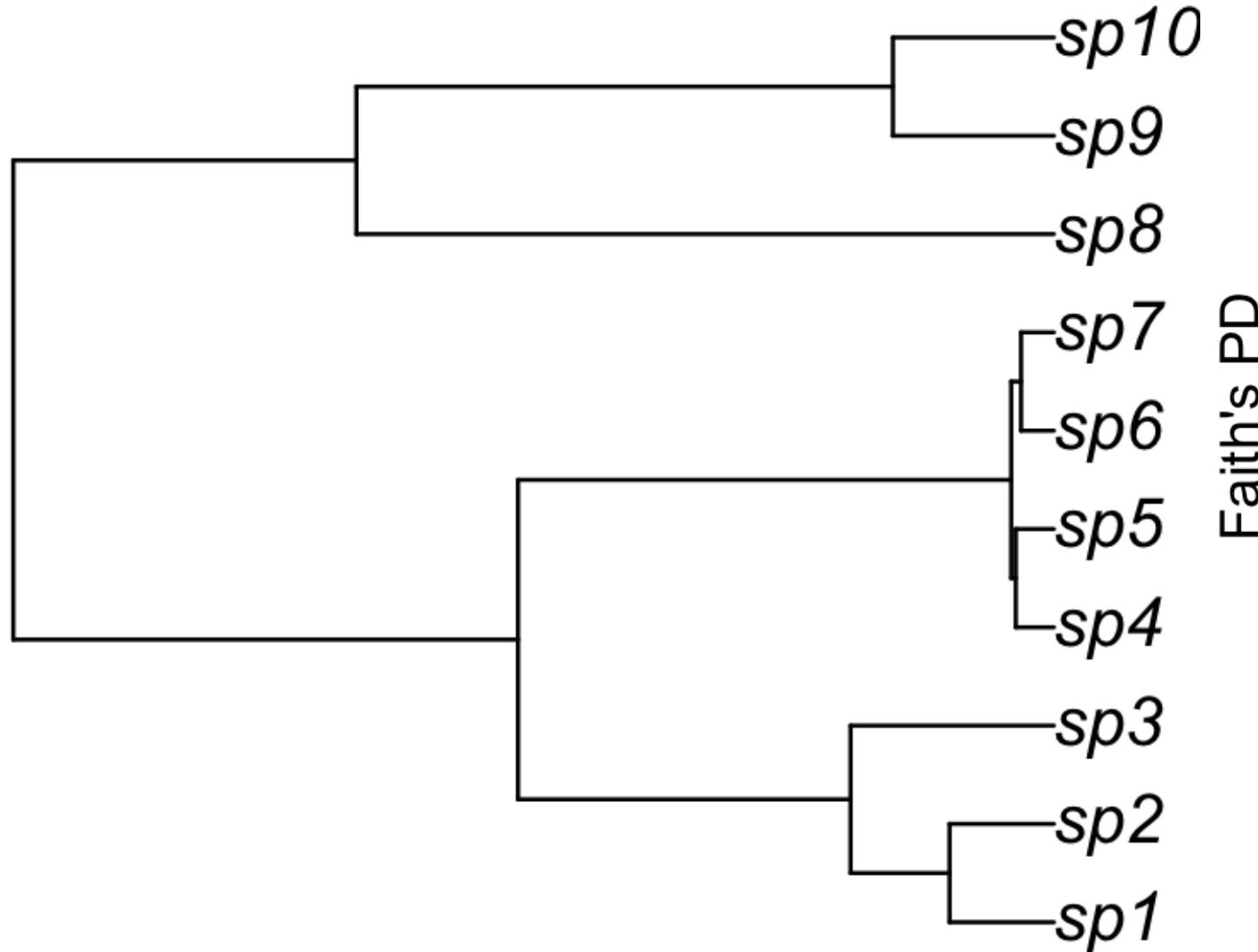
Faith's PD = 3.5

Species Richness = 3

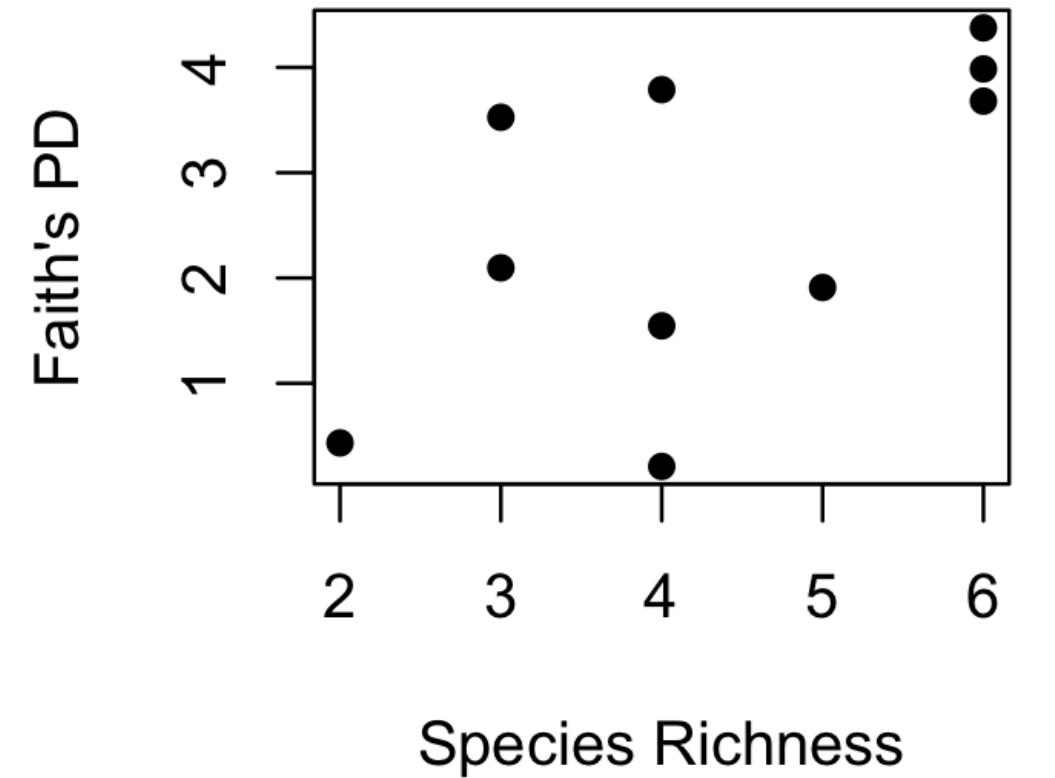
Alpha diversity: Faith's PD



Alpha diversity: Faith's PD



Faith's PD = 3.5 3.7 3.8 4.4 1.9 0.2 4.0 2.1 0.4
Species Richness = 3 6 4 5 6 4 6 4 3 2

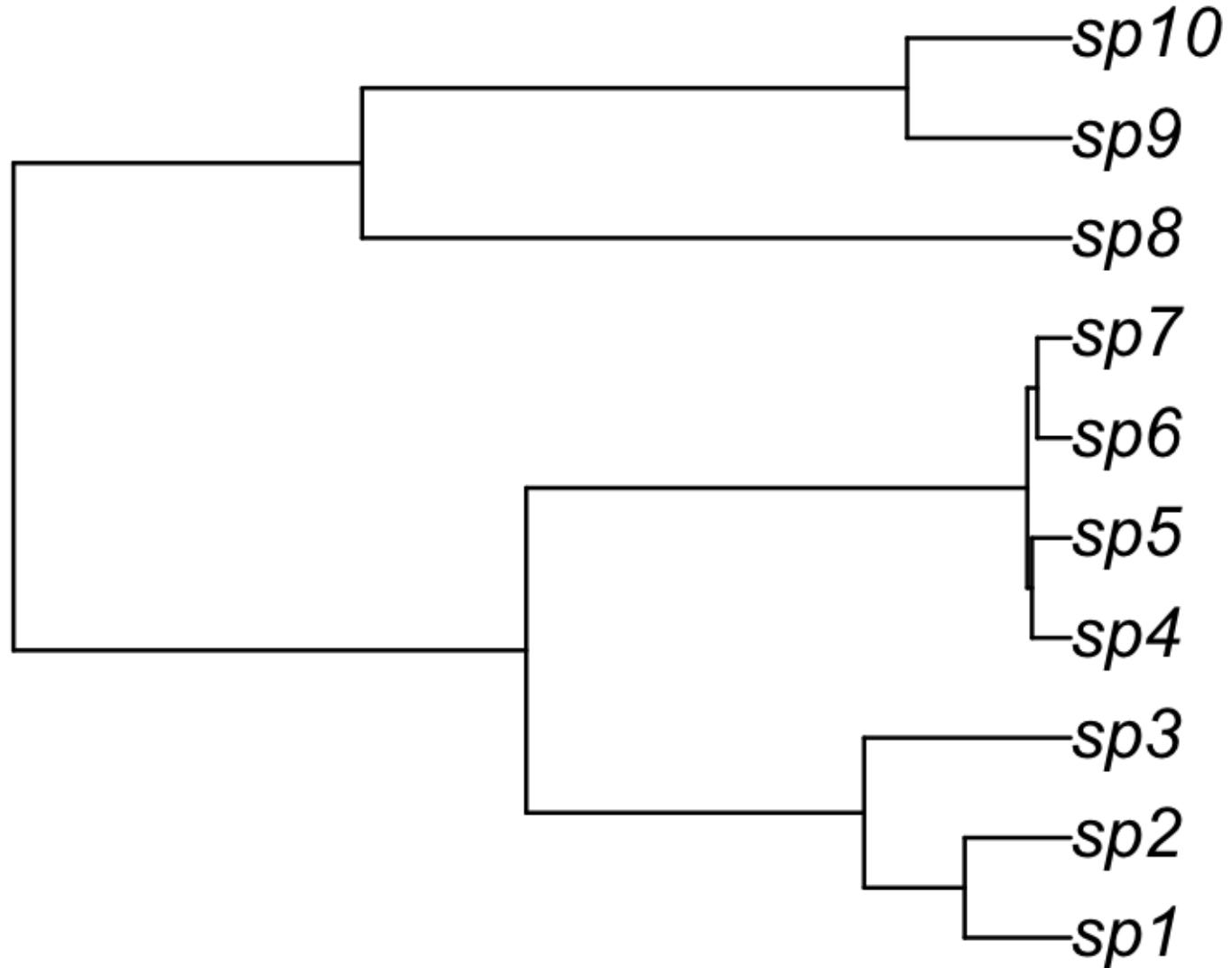


Alpha diversity: Faith's PD

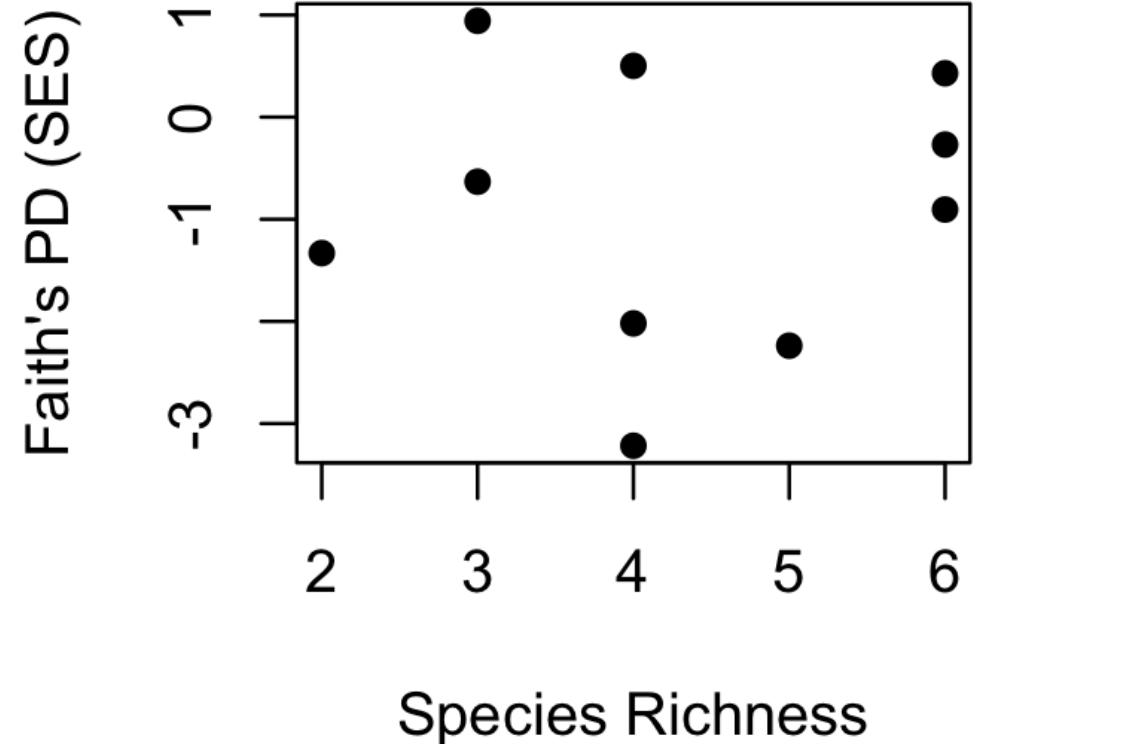
Comparison with a **null model** expectation:

taxa.labels	Shuffle taxa labels across tips of phylogeny (across all taxa included in the phylogeny)
richness	Randomize community data matrix abundances within samples (maintains sample species richness)
frequency	Randomize community data matrix abundances within species (maintains species occurrence frequency)
sample.pool	Randomize community data matrix by drawing species from pool of species occurring in at least one community (sample pool) with equal probability
phylogeny.pool	Randomize community data matrix by drawing species from pool of species occurring in the phylogeny (phylogeny pool) with equal probability
independentswap	Randomize community data matrix with the independent swap algorithm (Gotelli 2000) maintaining species occurrence frequency and sample species richness
trialswap	Randomize community data matrix with the trial-swap algorithm (Miklos & Podani 2004) maintaining species occurrence frequency and sample species richness

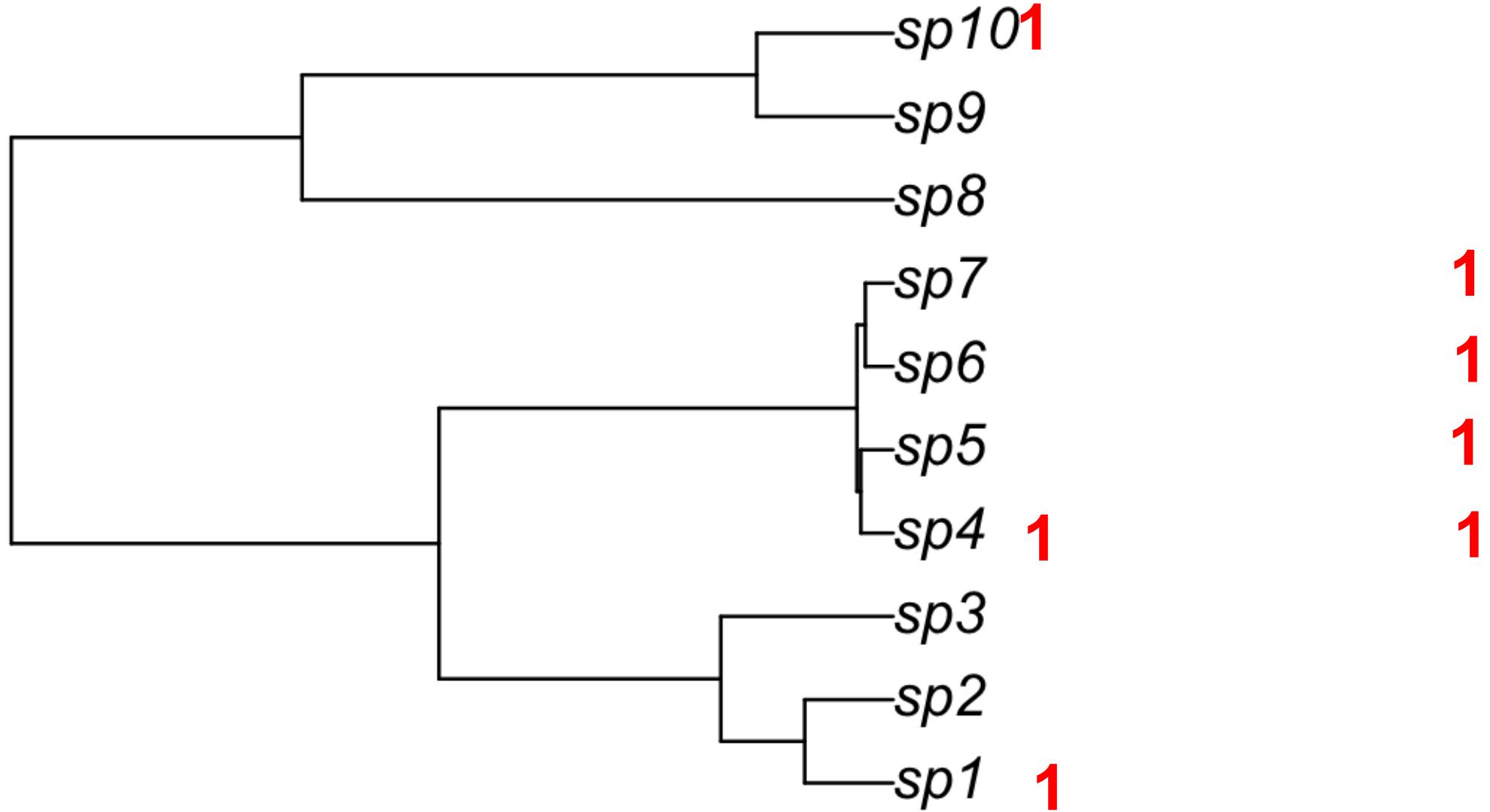
Alpha diversity: Faith's PD



Faith's PD (SES) = 0.9 -1.0 0.6 -2.4 0.4 -3.2 -0.3 -2.0 -0.6 -1.3
Species Richness = 3 6 4 5 6 4 6 4 3 2



Alpha diversity: Faith's PD

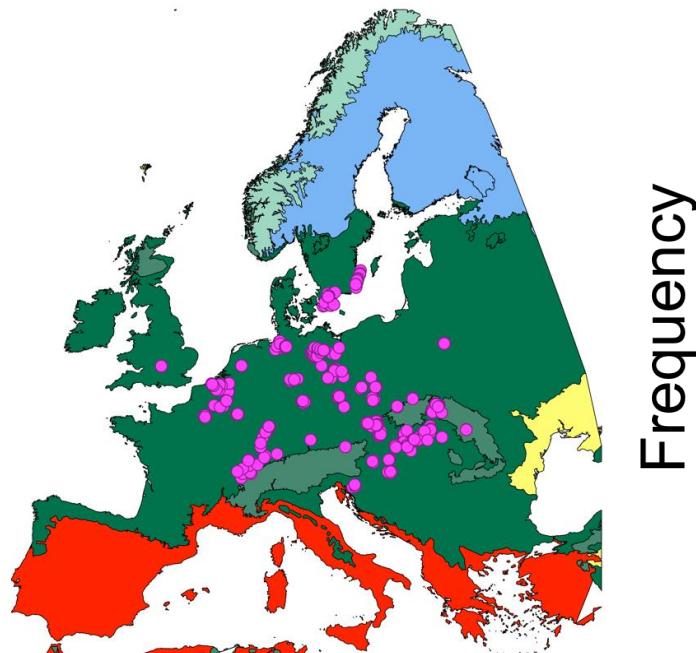


Faith's PD (SES) = 0.9 -1.0 0.6 -2.4 0.4 -3.2 -0.3 -2.0 -0.6 -1.3
 Species Richness = 3 6 4 5 6 4 6 4 3 2

Has there been changes in PD over time?

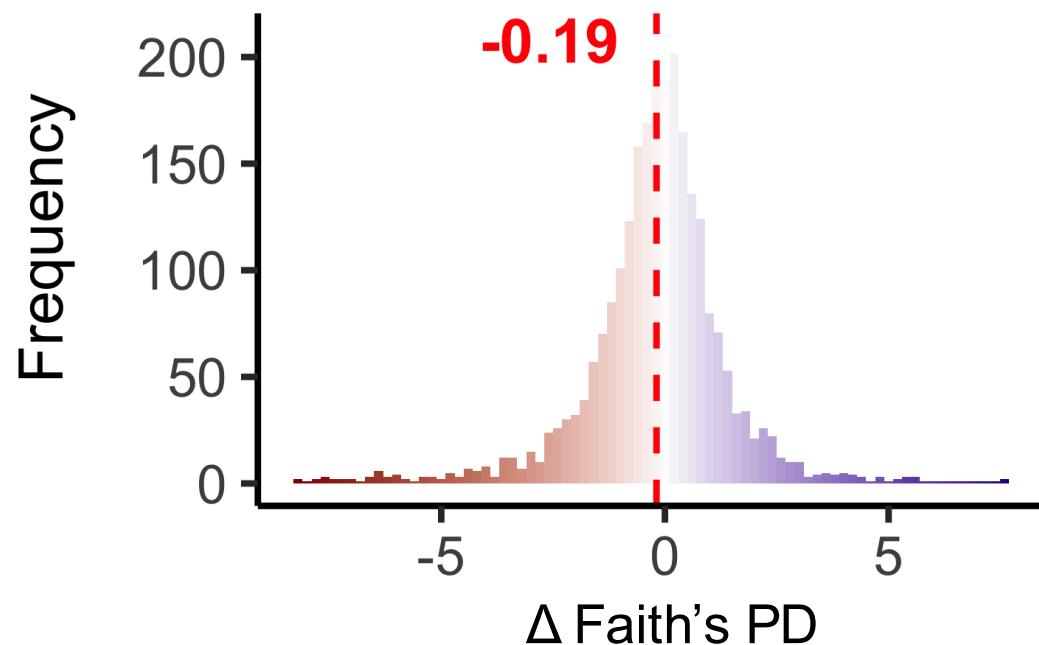
~2600 forest plots

<https://forestreplot.ugent.be>



Baseline survey: 1935-1999

Resurvey: 2001-2020

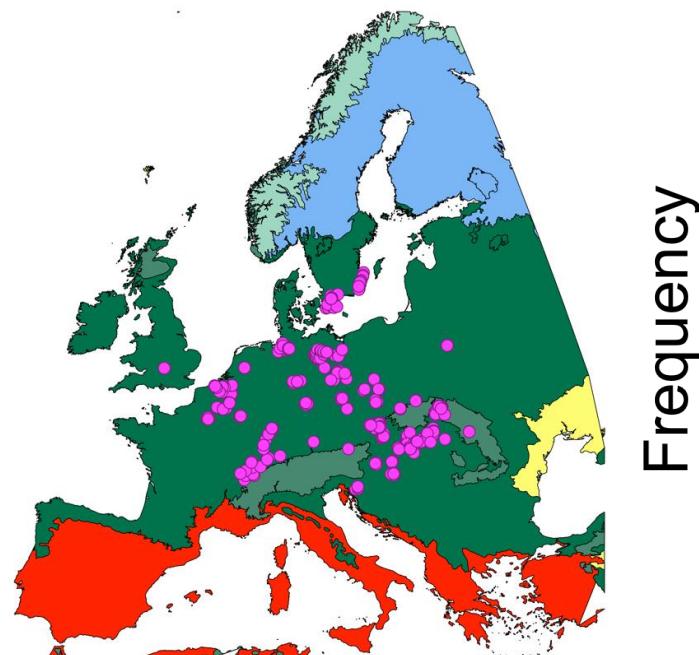


Alpha diversity: Faith's PD

Has there been changes in PD over time?

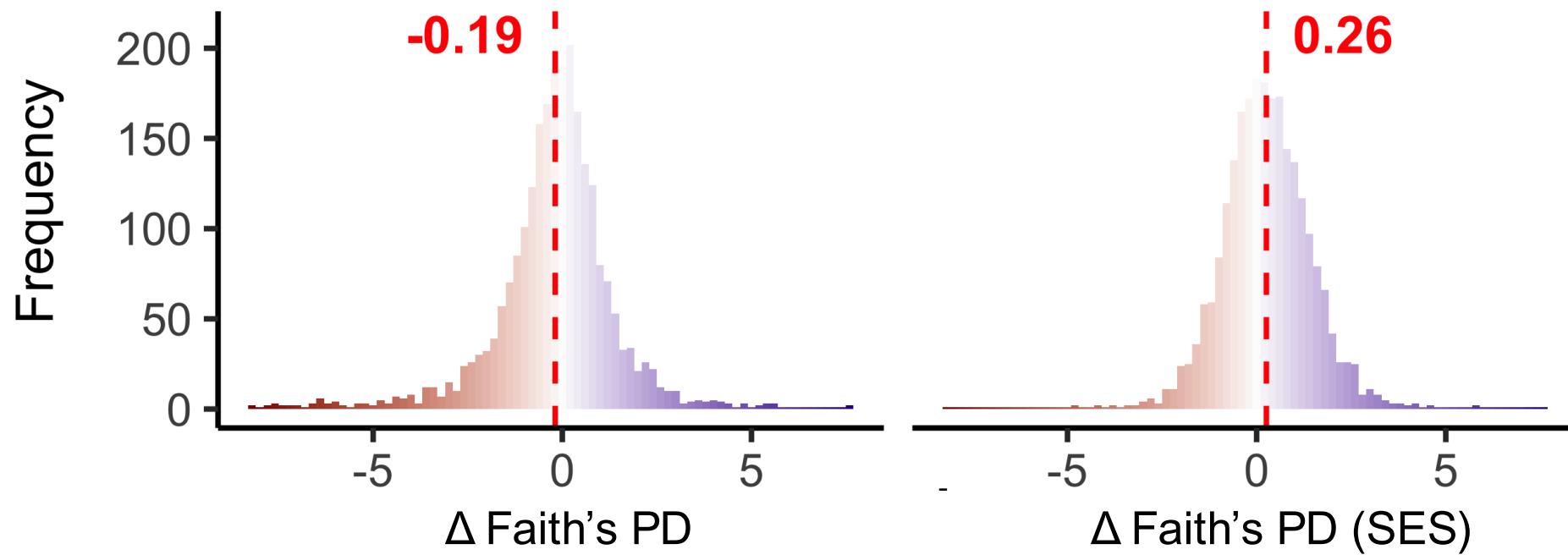
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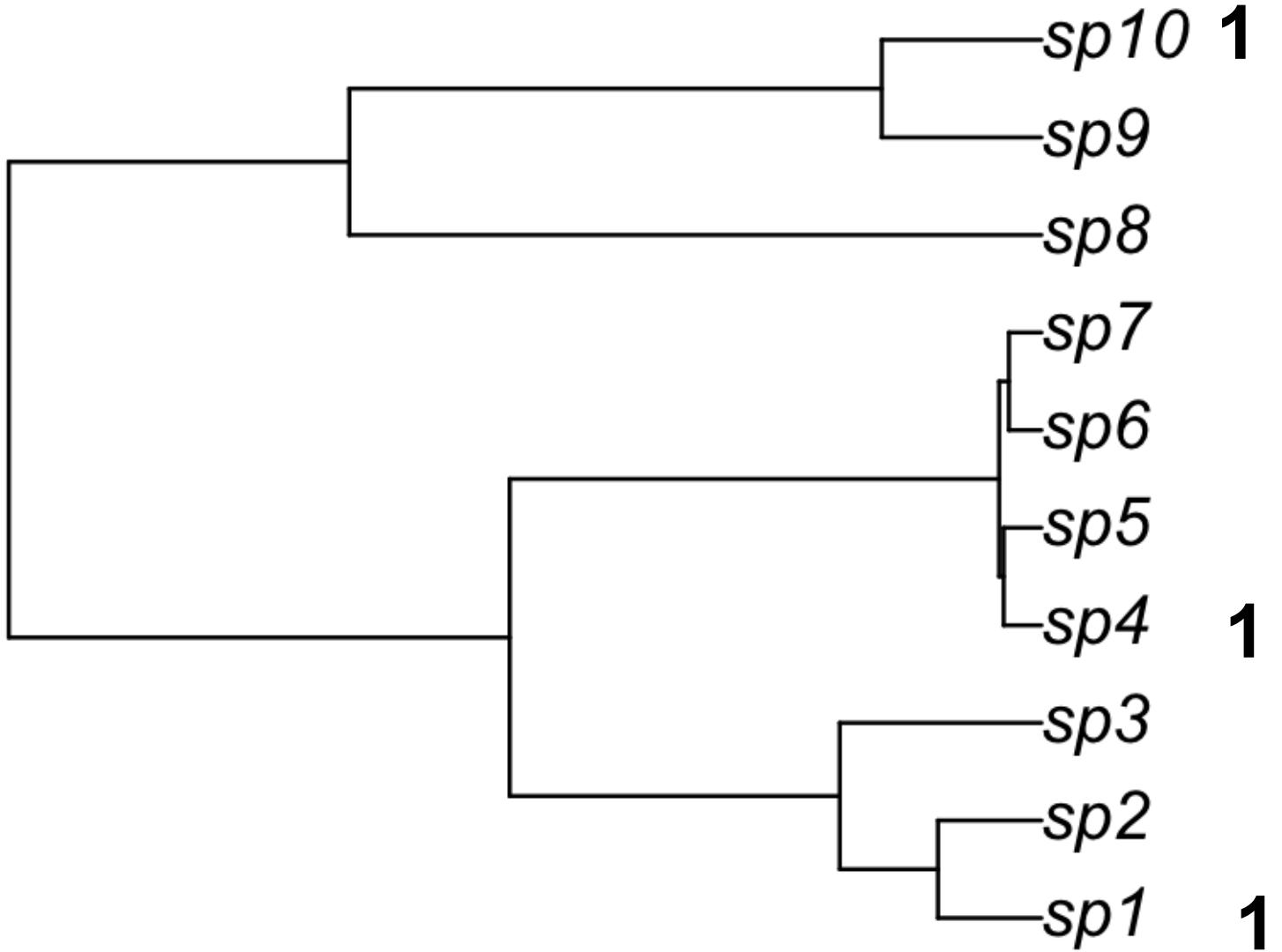


Baseline survey: 1935-1999

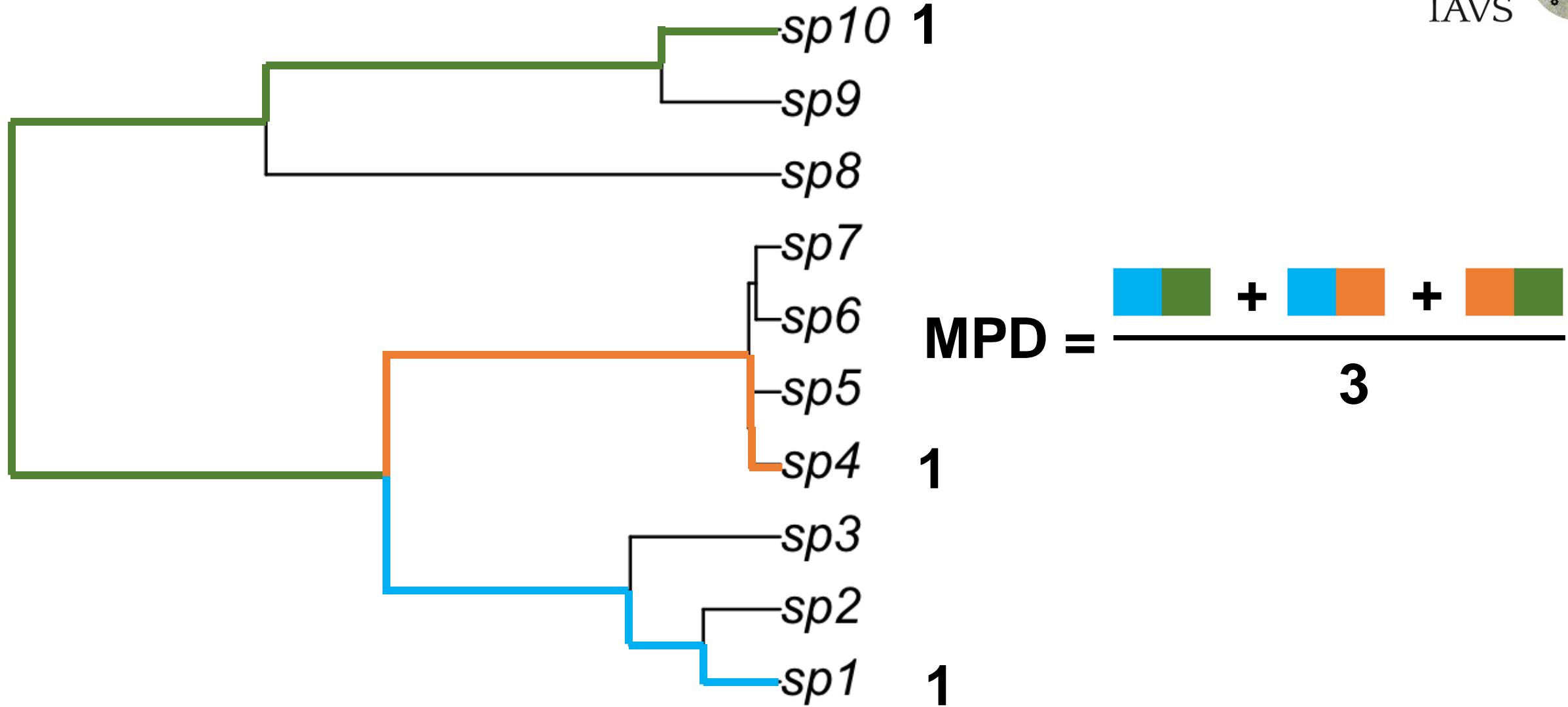
Resurvey: 2001-2020



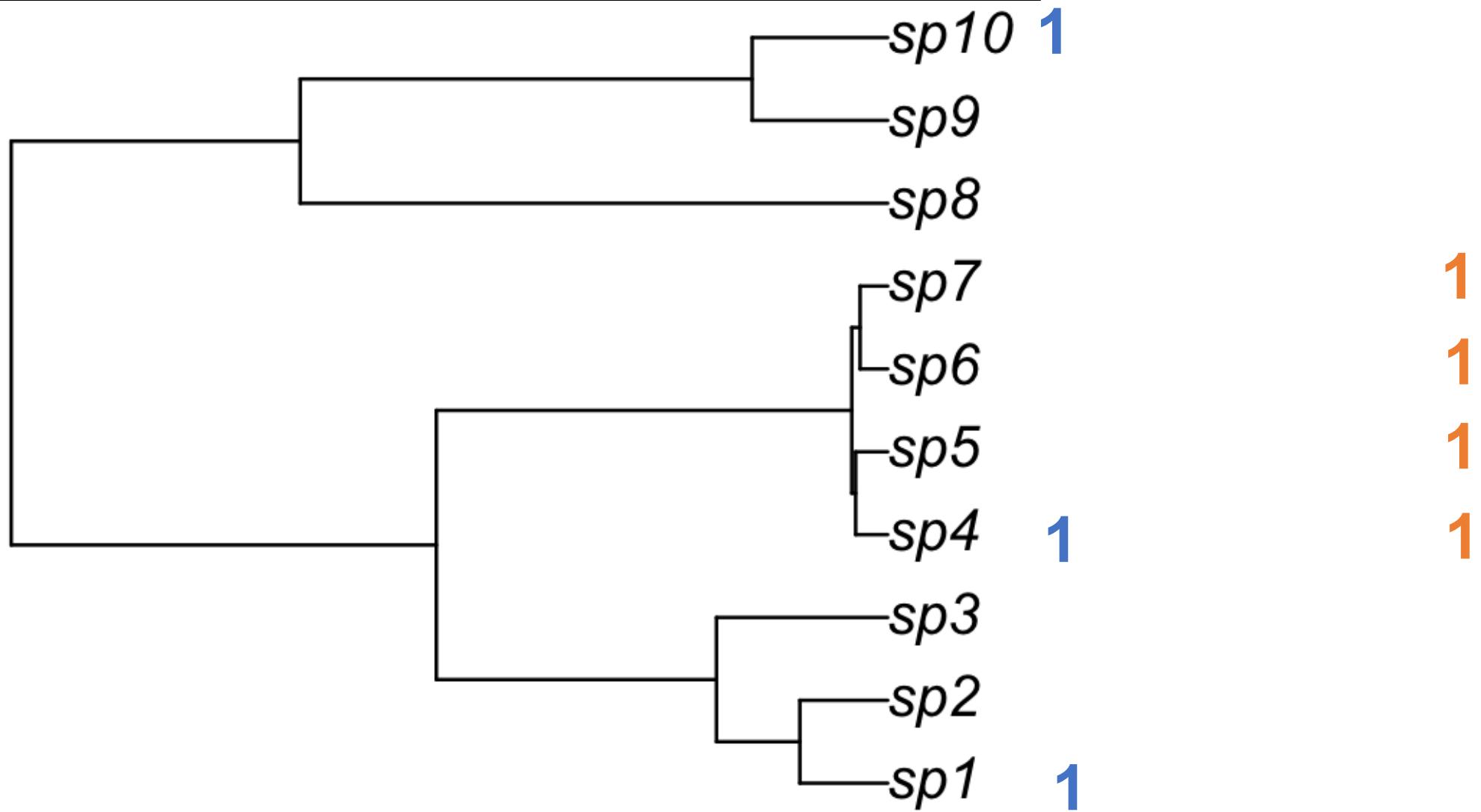
Alpha diversity: Mean Pairwise Distance (MPD)



Alpha diversity: Mean Pairwise Distance (MPD)



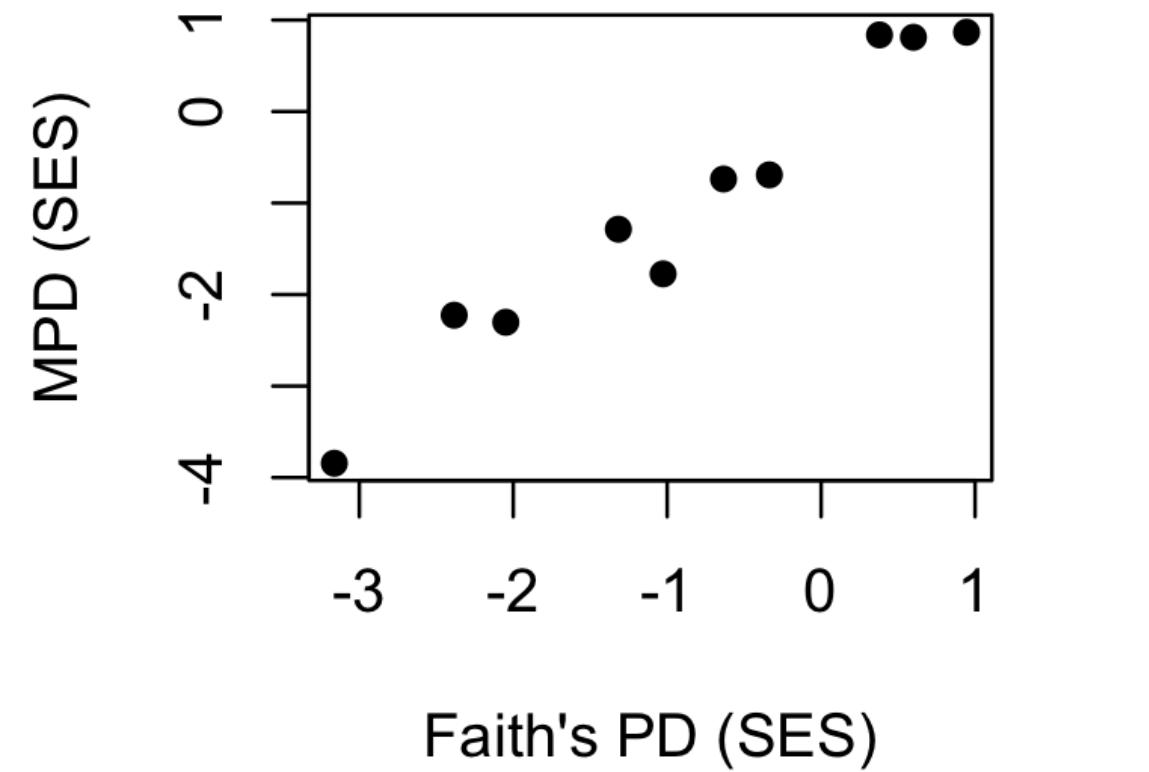
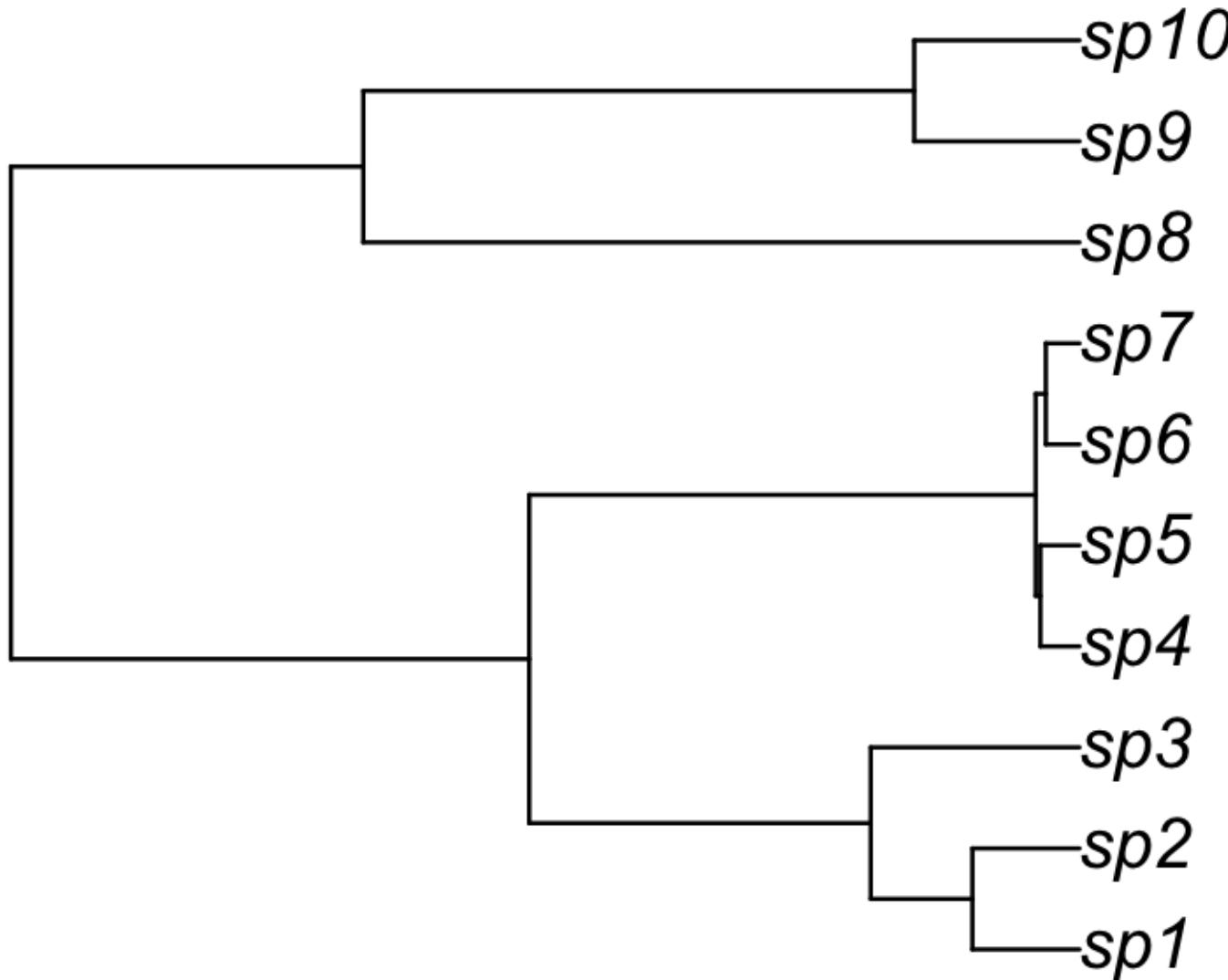
Alpha diversity: Mean Pairwise Distance (MPD)



MPD (SES) = 0.9 -1.8 0.8 -2.2 0.8 -3.8 -0.7 -2.3 -0.7 -1.3

Species Richness = 3 6 4 5 6 4 6 4 3 2

Alpha diversity: Mean Pairwise Distance (MPD)

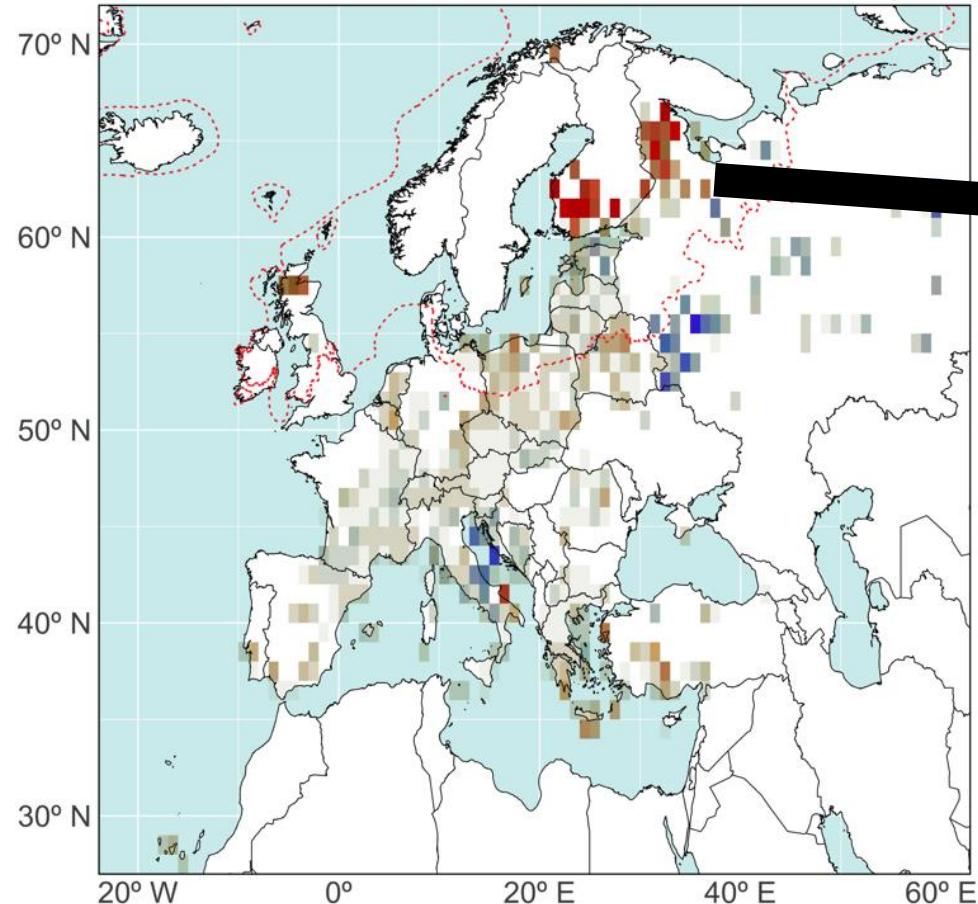


MPD (SES) = 0.9 -1.8 0.8 -2.2 0.8 -3.8 -0.7 -2.3 -0.7 -1.3

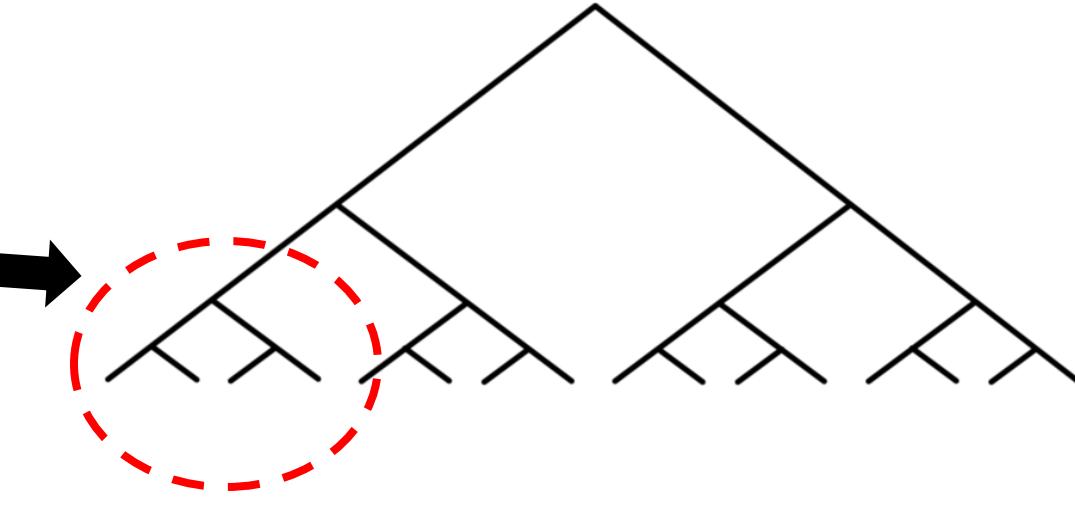
Species Richness = 3 6 4 5 6 4 6 4 3 2

Alpha diversity: Mean Pairwise Distance (MPD)

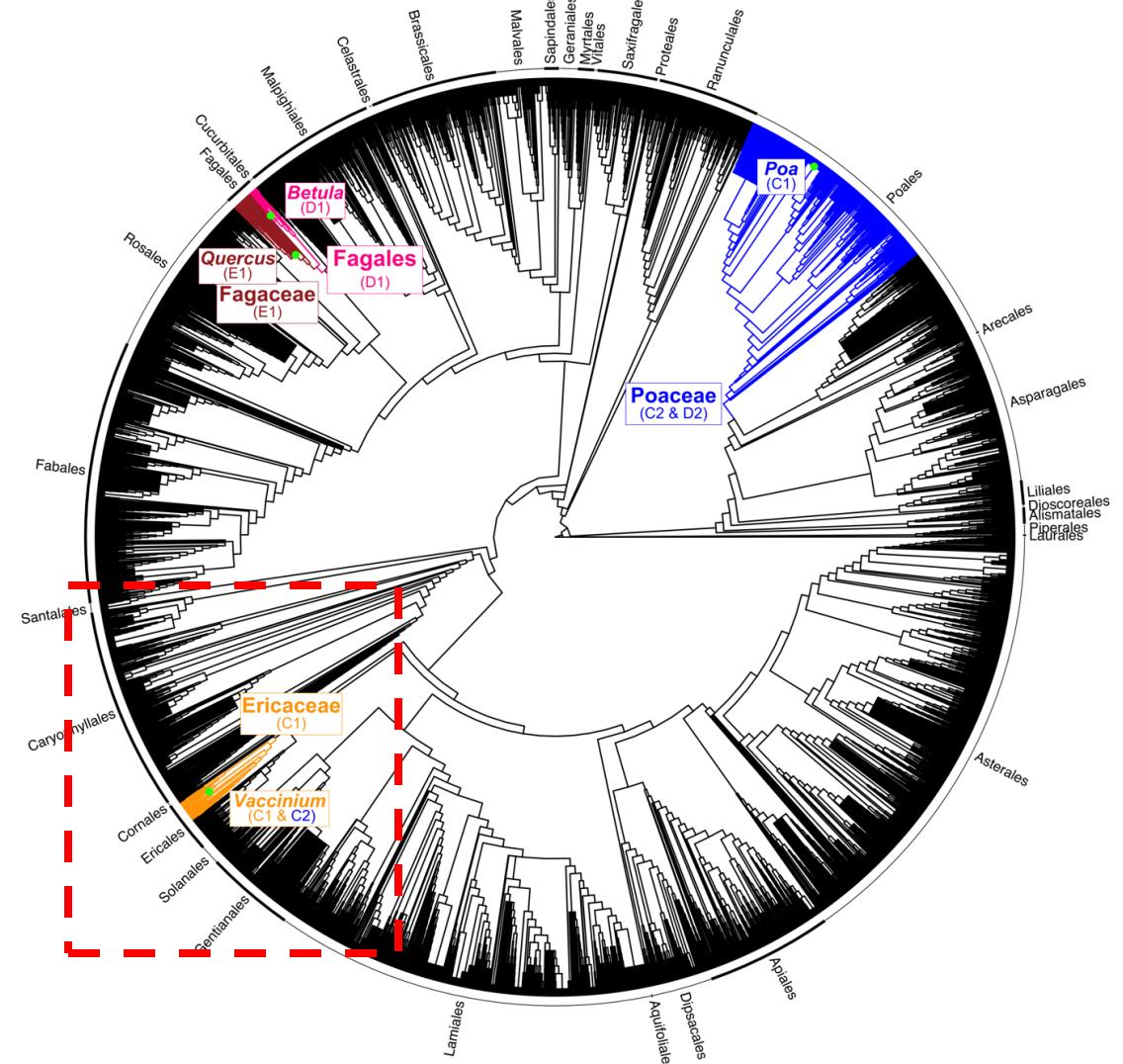
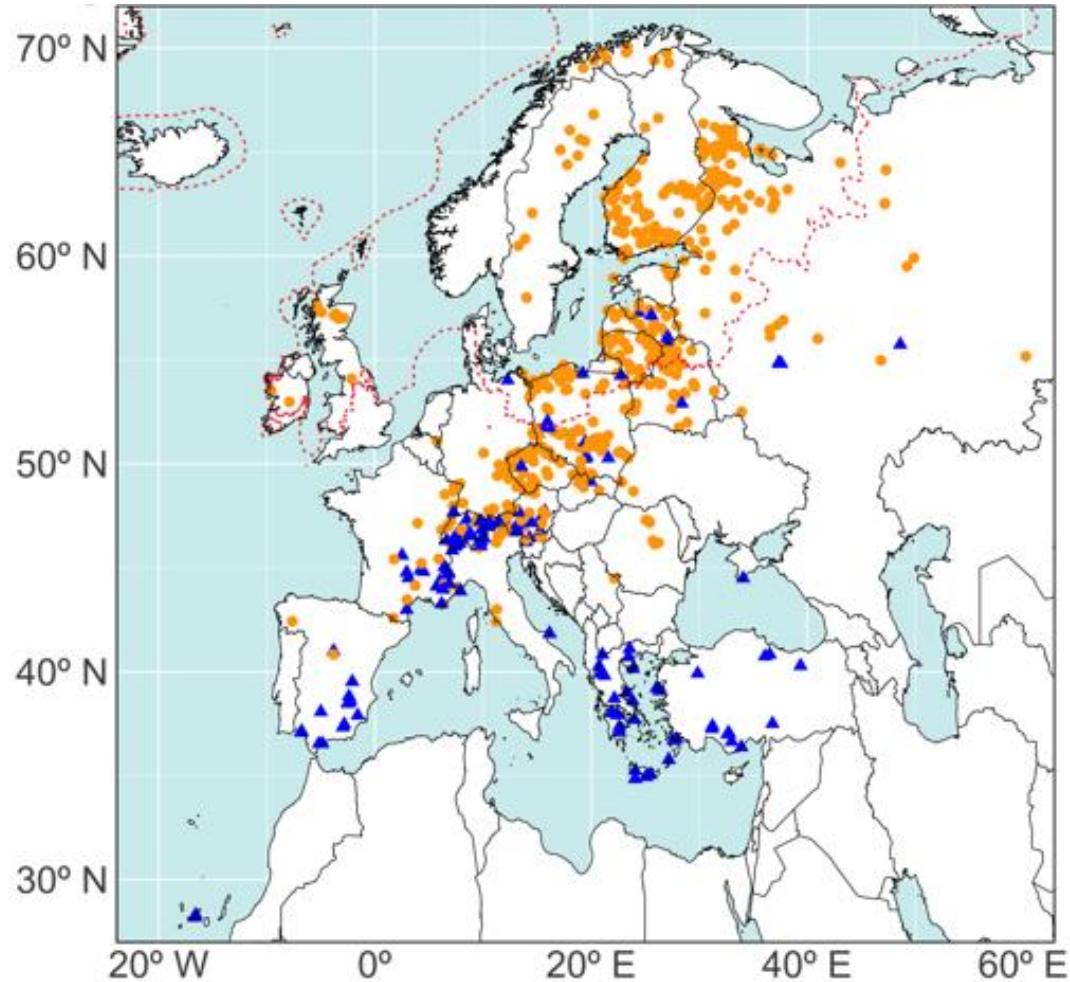
Coniferous forests



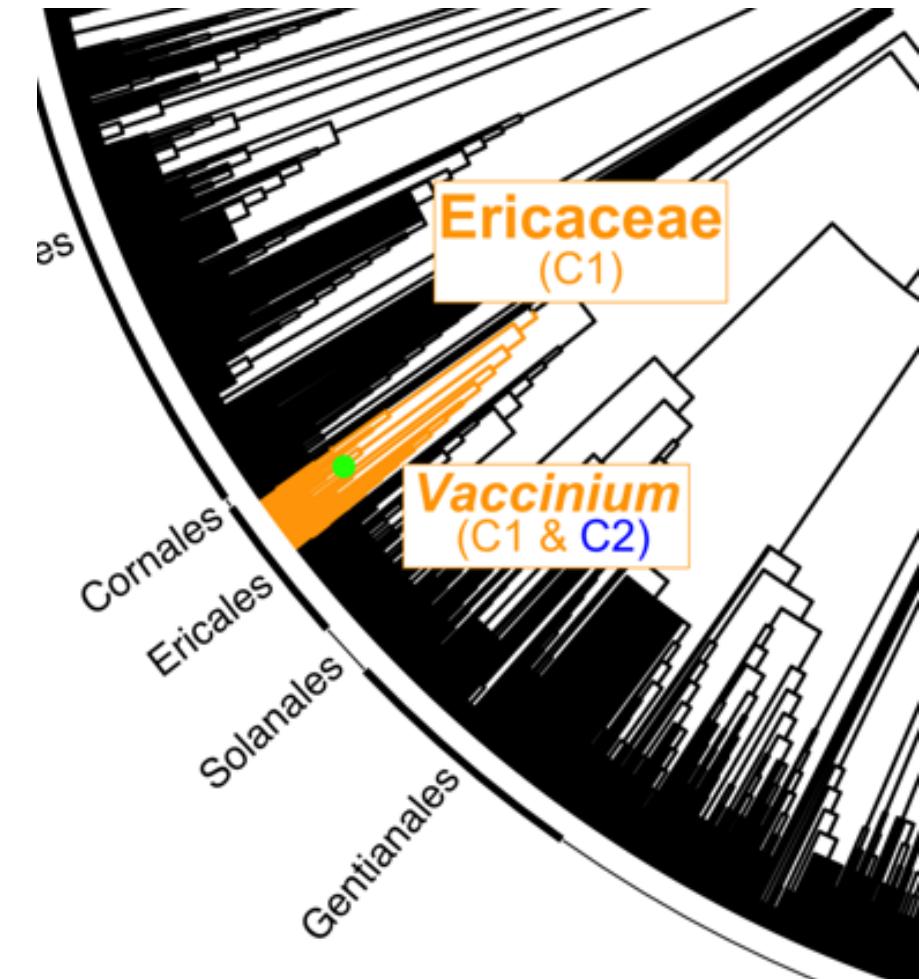
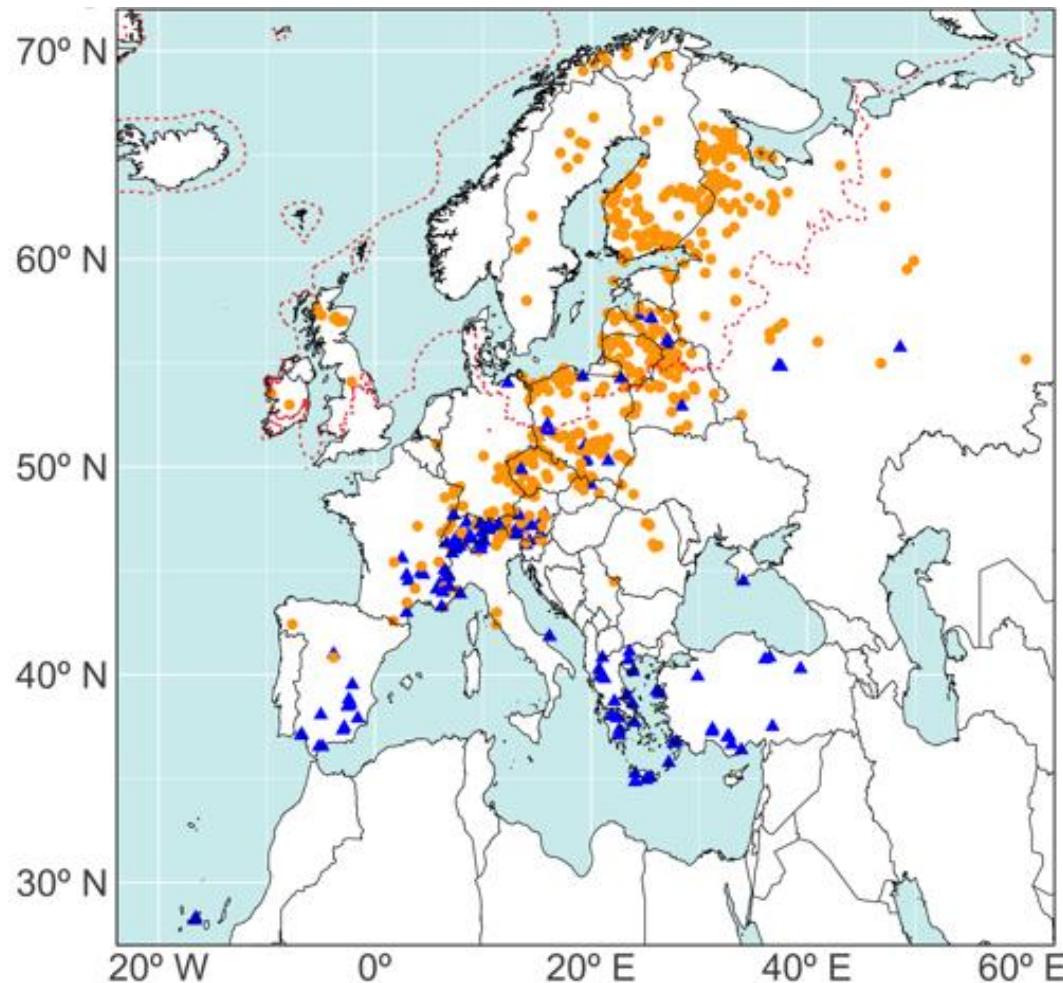
More closely related More distantly related
-1.0 -0.5 0.0 0.5 1.0
MPD (SES)



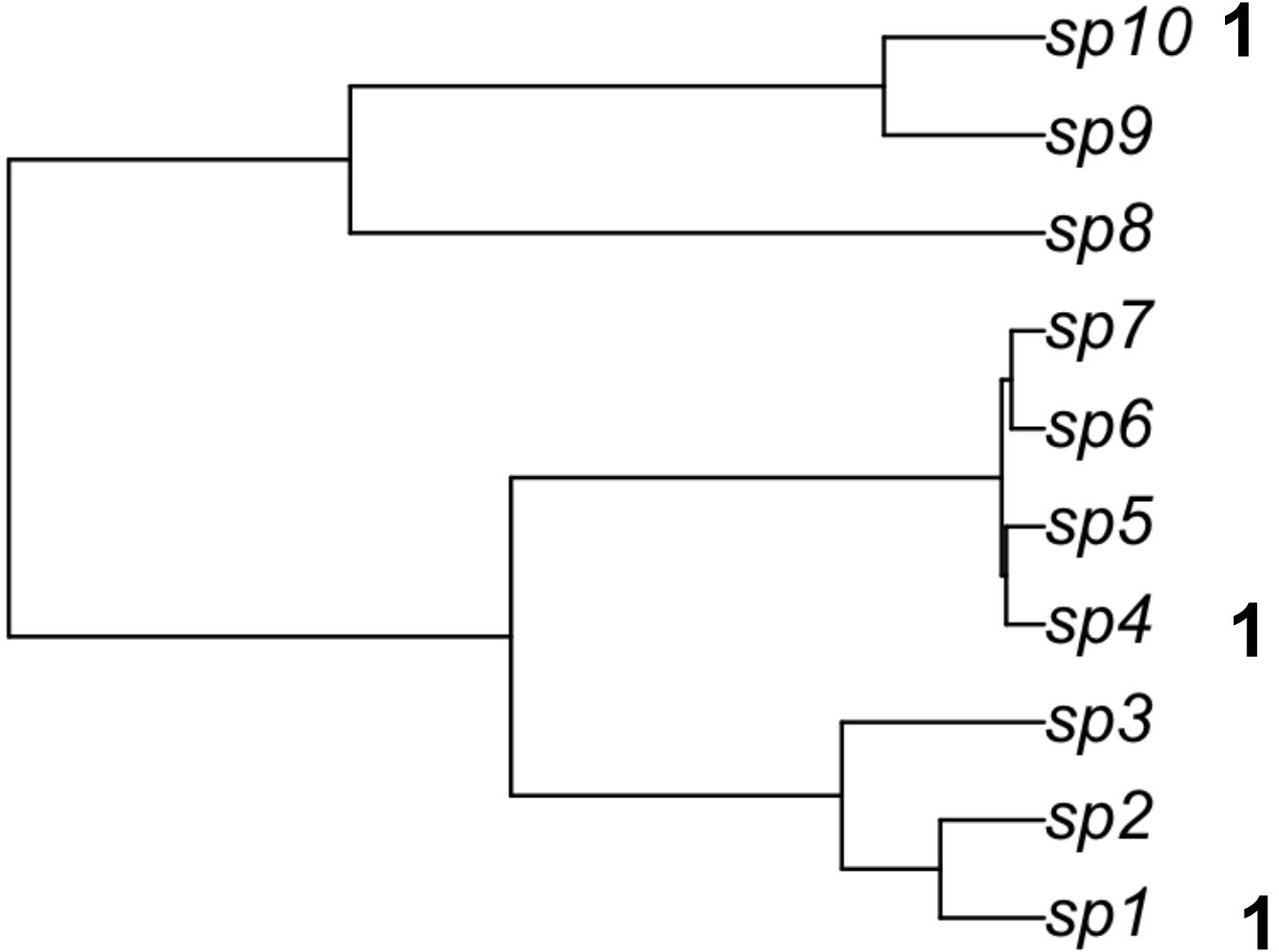
Coniferous forests



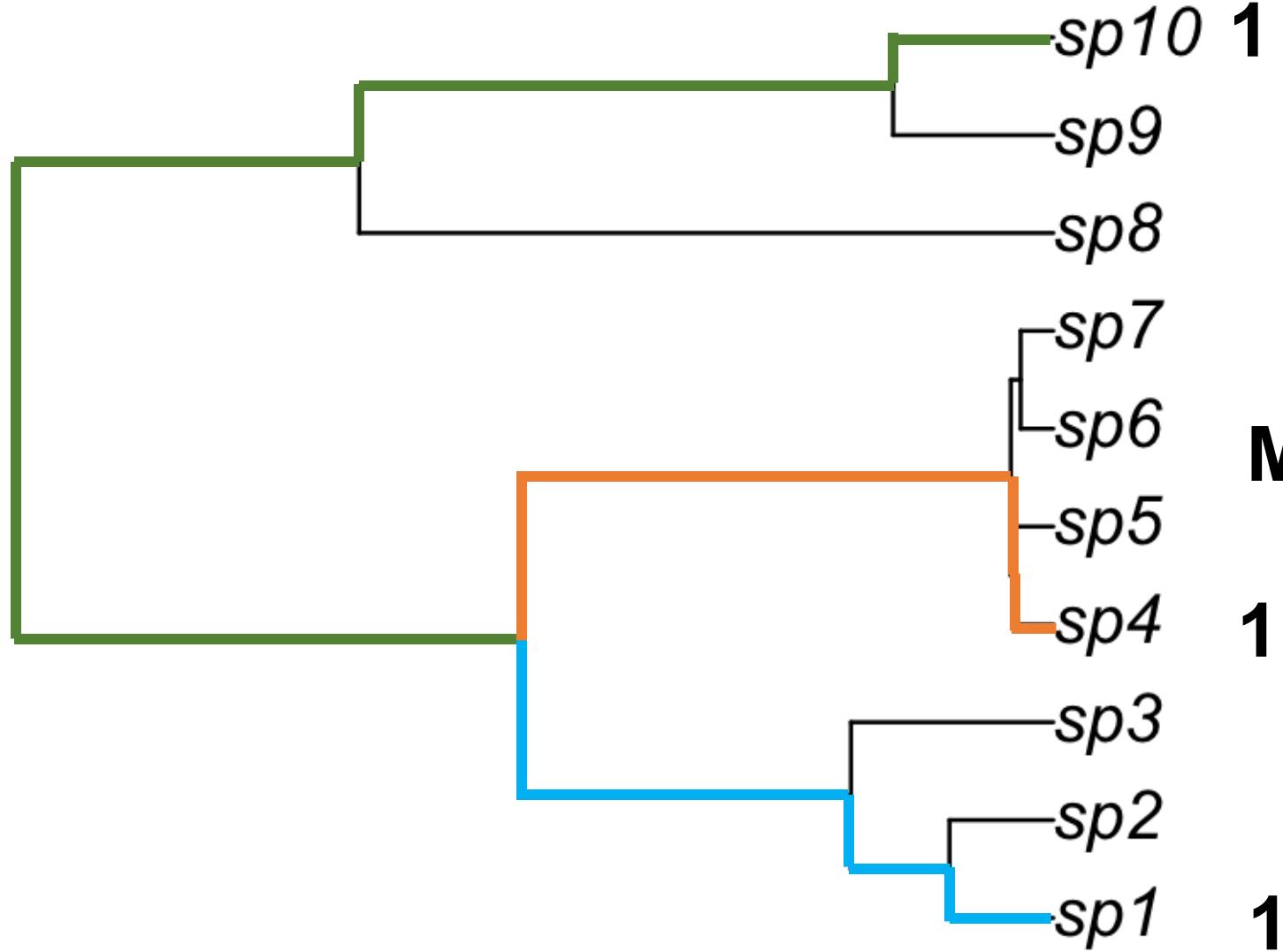
Coniferous forests



Alpha diversity: Mean Nearest Taxon Distance (MNTD)

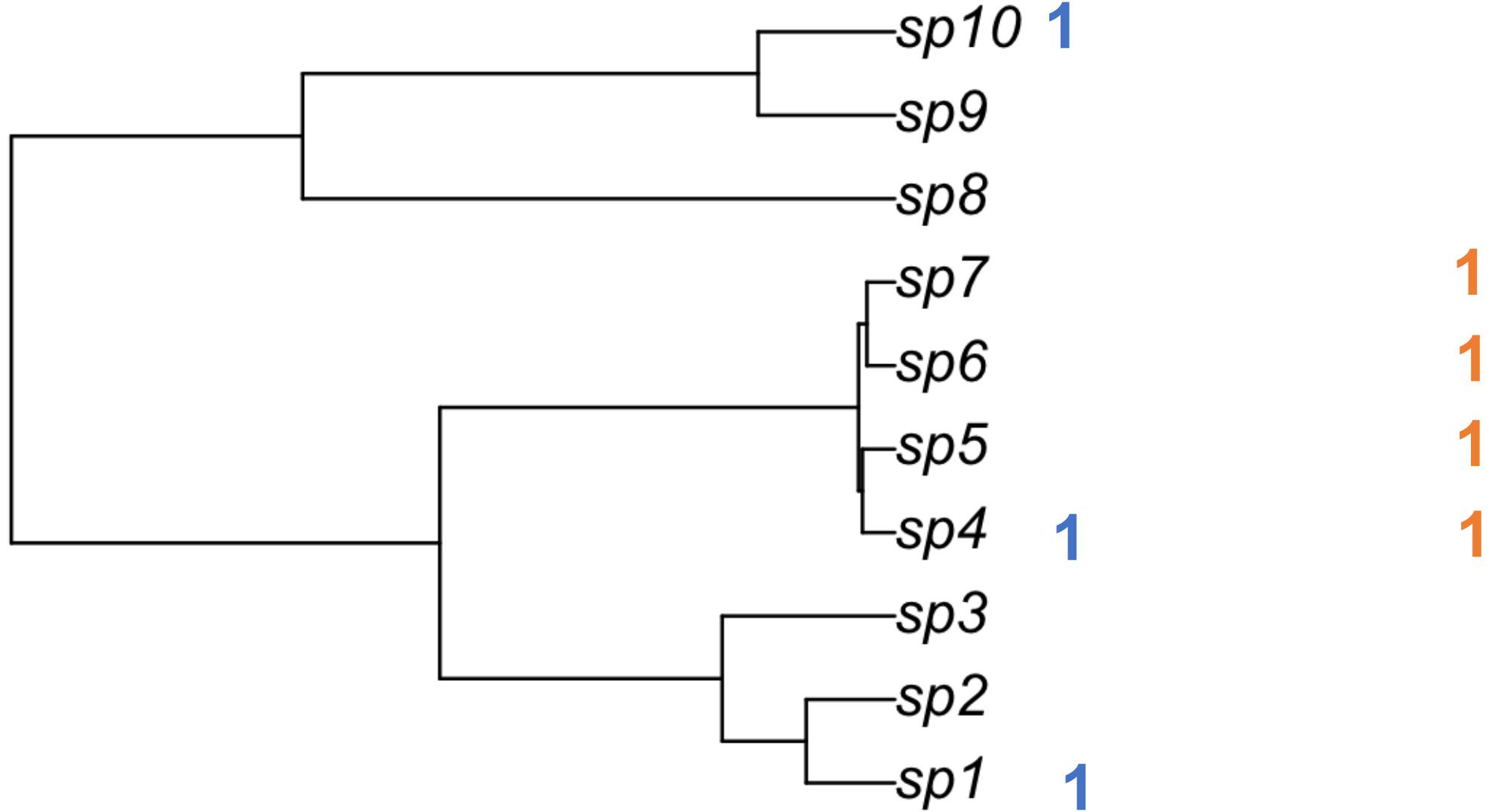


Alpha diversity: Mean Nearest Taxon Distance (MNTD)



$$\text{MNTD} = \frac{\text{orange distance} + \text{green distance} + \text{blue distance}}{3}$$

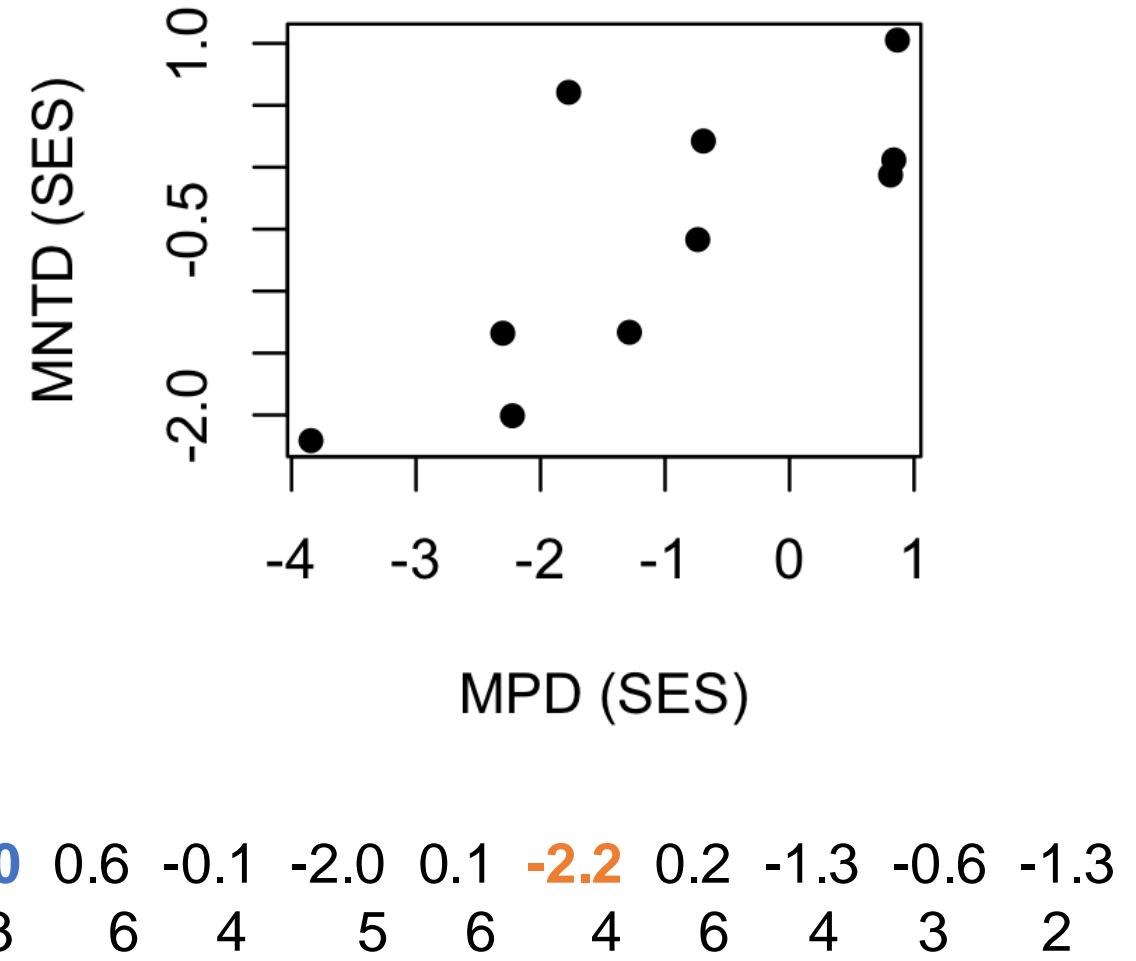
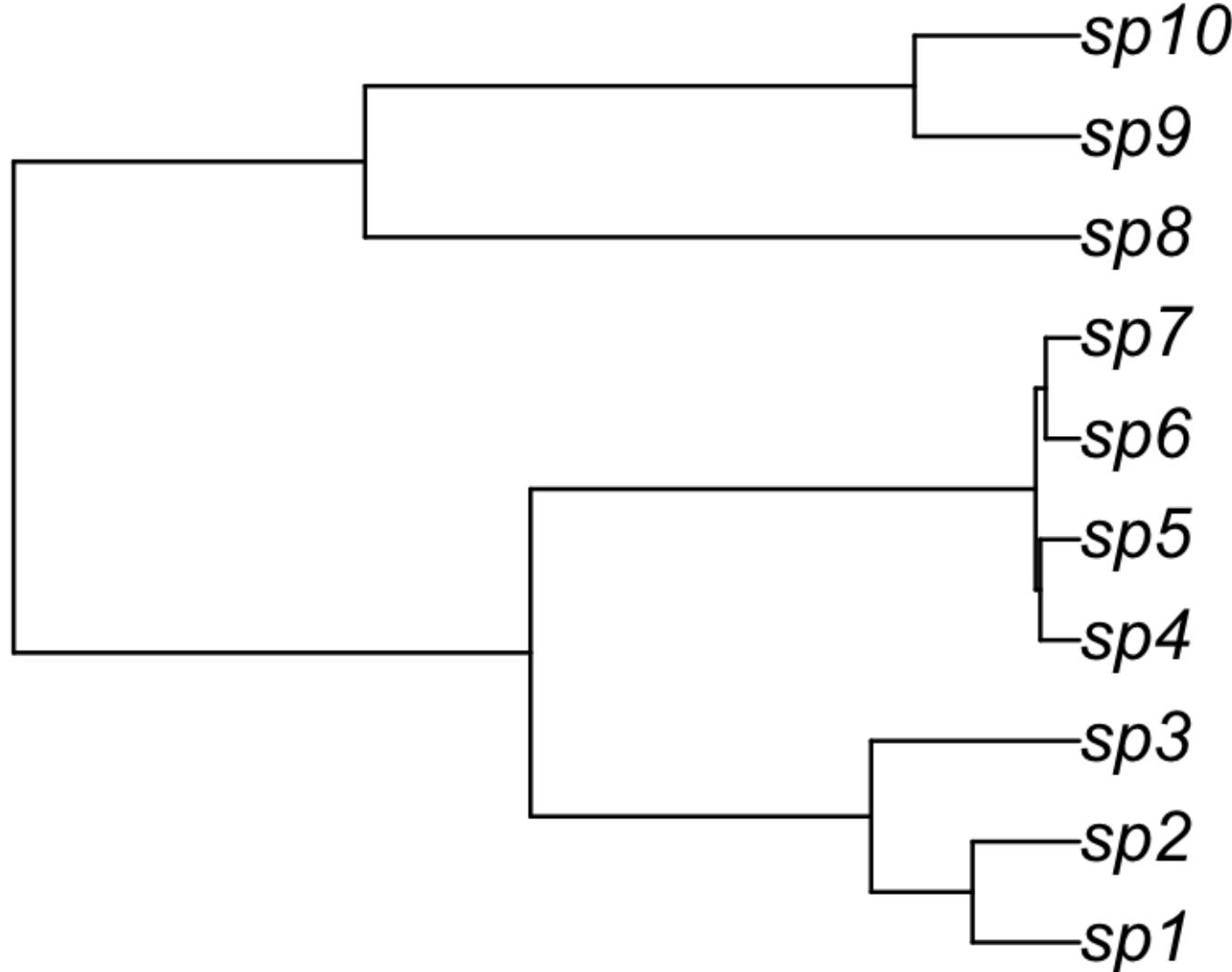
Alpha diversity: Mean Nearest Taxon Distance (MNTD)



MNTD (SES) = 1.0 0.6 -0.1 -2.0 0.1 -2.2 0.2 -1.3 -0.6 -1.3

Species Richness = 3 6 4 5 6 4 6 4 3 2

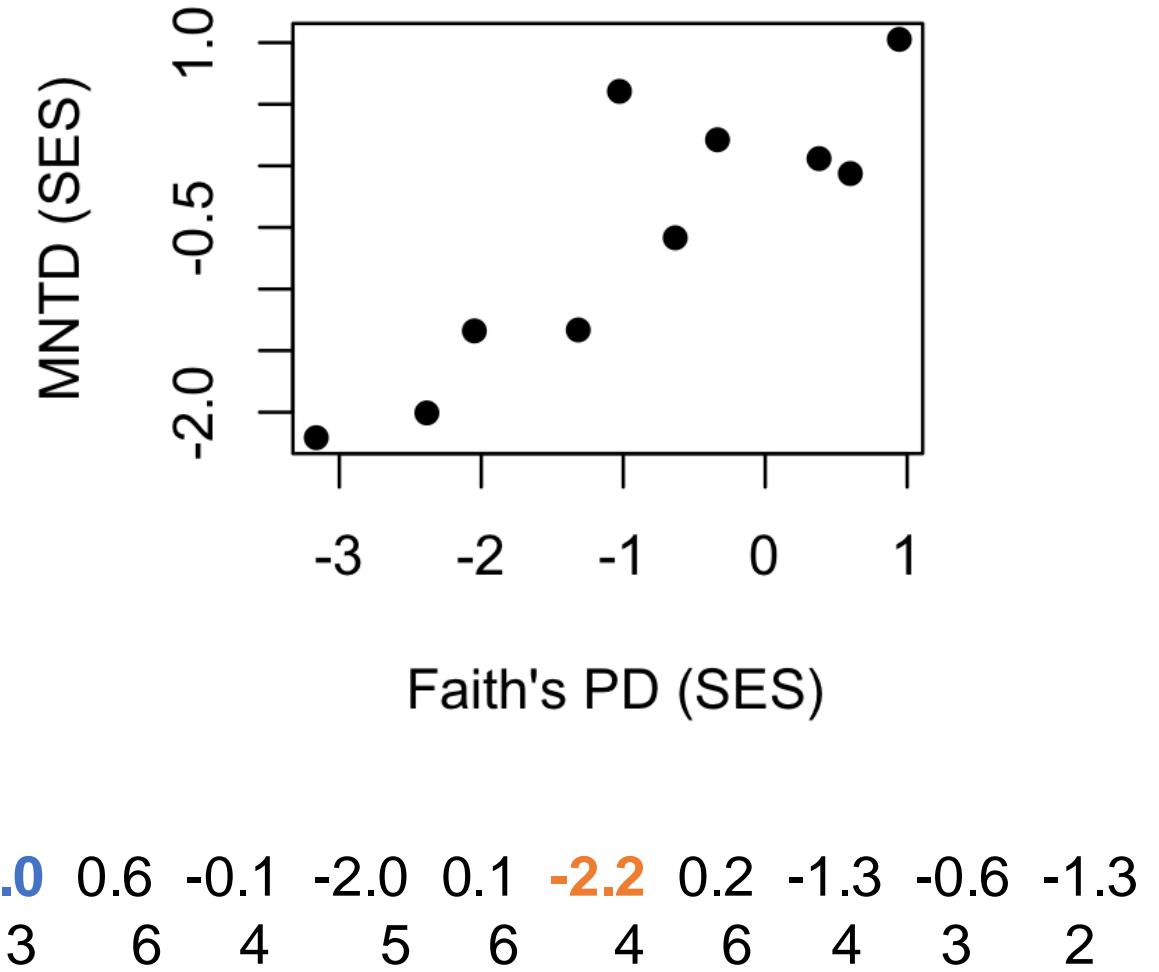
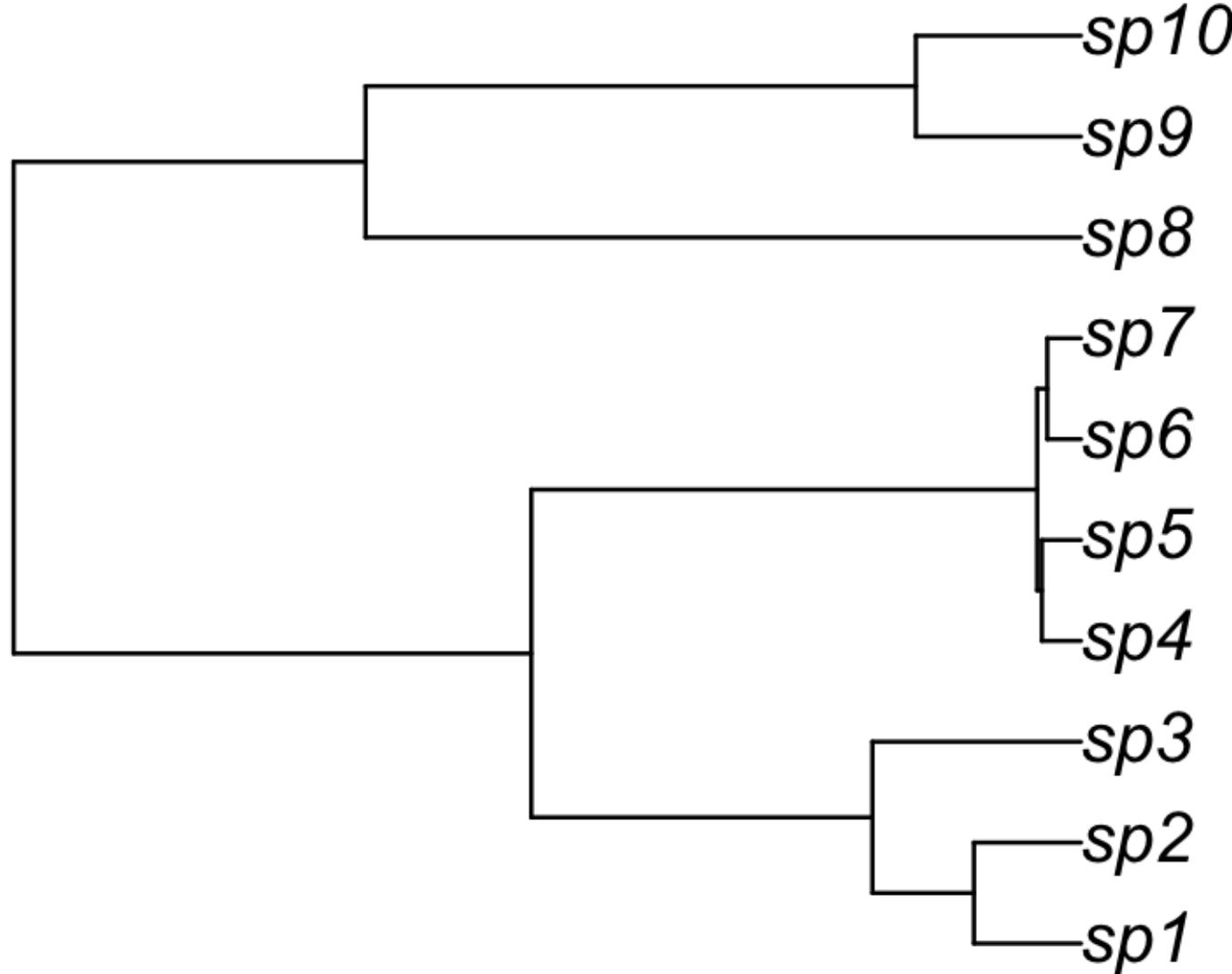
Alpha diversity: Mean Nearest Taxon Distance (MNTD)



MNTD (SES) = 1.0 0.6 -0.1 -2.0 0.1 -2.2 0.2 -1.3 -0.6 -1.3

Species Richness = 3 6 4 6 4 6 4 3 2

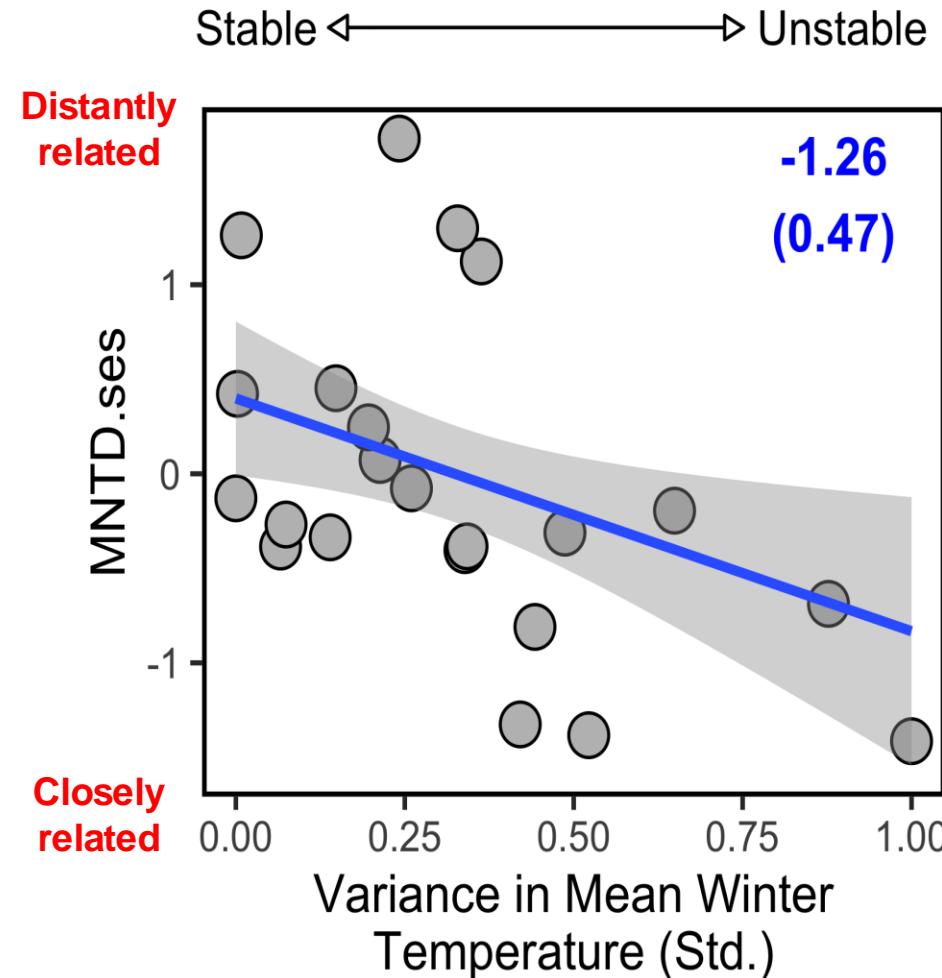
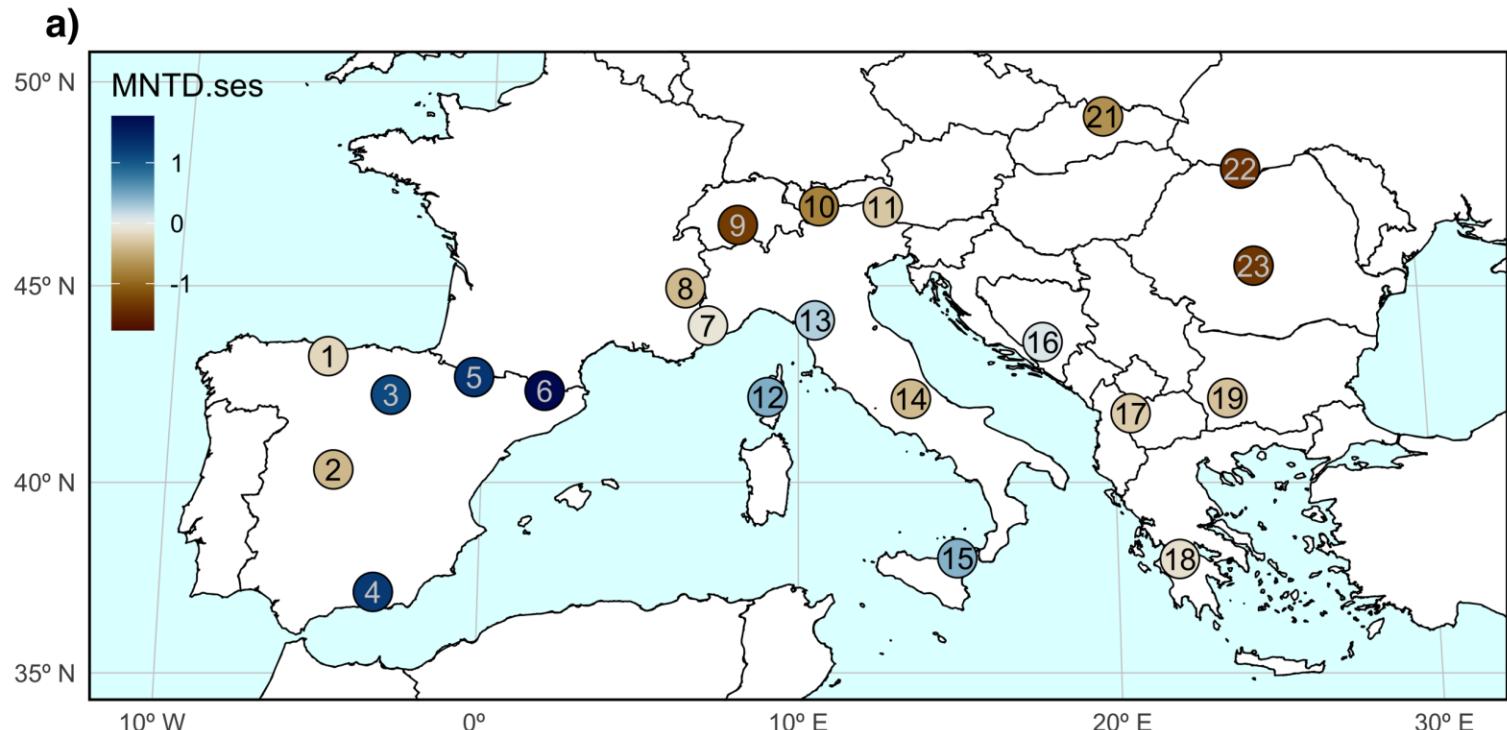
Alpha diversity: Mean Nearest Taxon Distance (MNTD)



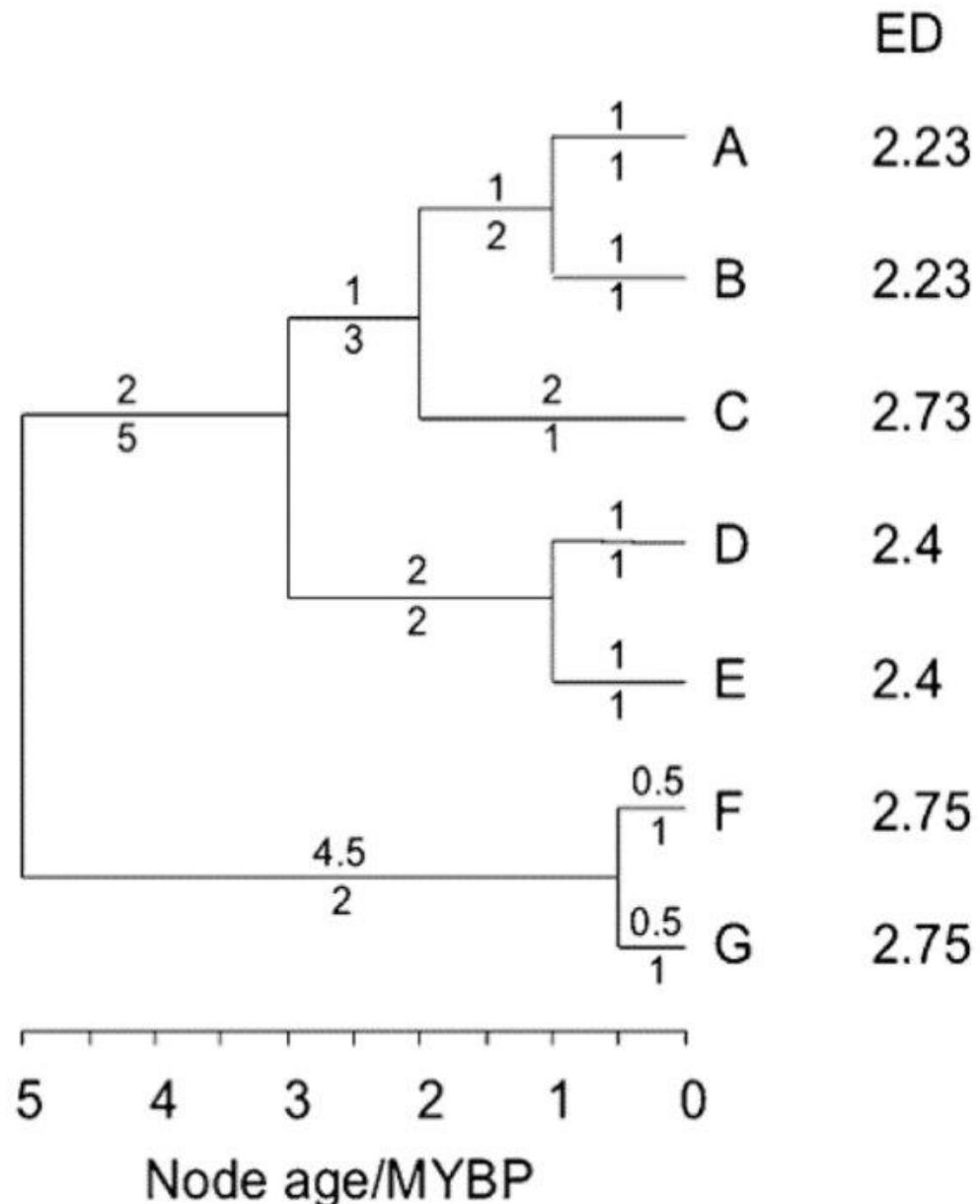
MNTD (SES) = 1.0 0.6 -0.1 -2.0 0.1 -2.2 0.2 -1.3 -0.6 -1.3

Species Richness = 3 6 4 5 6 4 6 4 3 2

Alpha diversity: Mean Nearest Taxon Distance (MNTD)



Alpha diversity: Community Evolutionary Distinctiveness (CED)



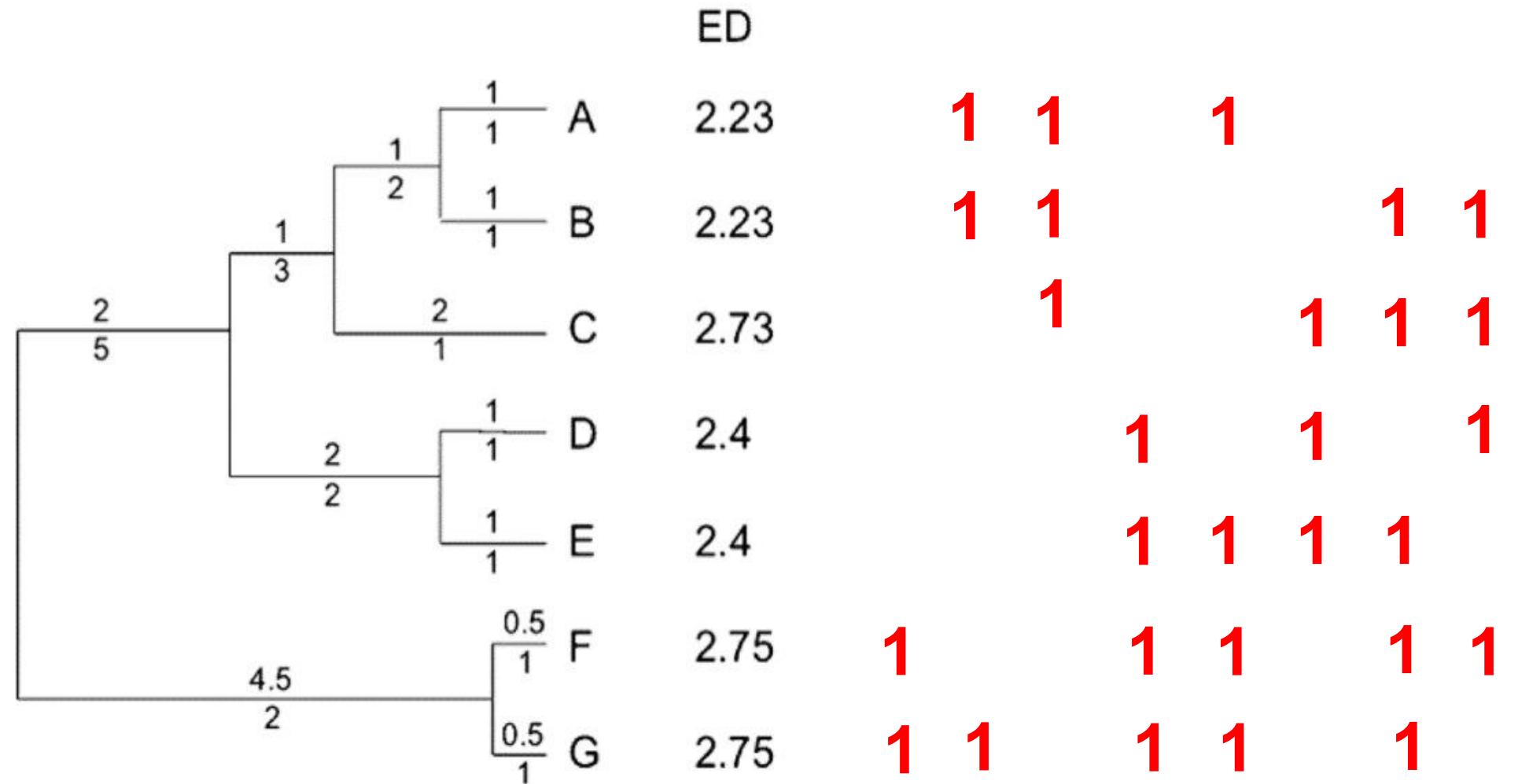
ED is a measure of how isolated a species or groups of species are in a phylogenetic tree.

$$ED_A = (1/1) + (1/2) + (1/3) + (2/5)$$

CED = Mean ED of all species in a community

Isaac et al. (2007)

Alpha diversity: Community Evolutionary Distinctiveness (CED)



5
4
3
2
1
0

Node age/MYBP

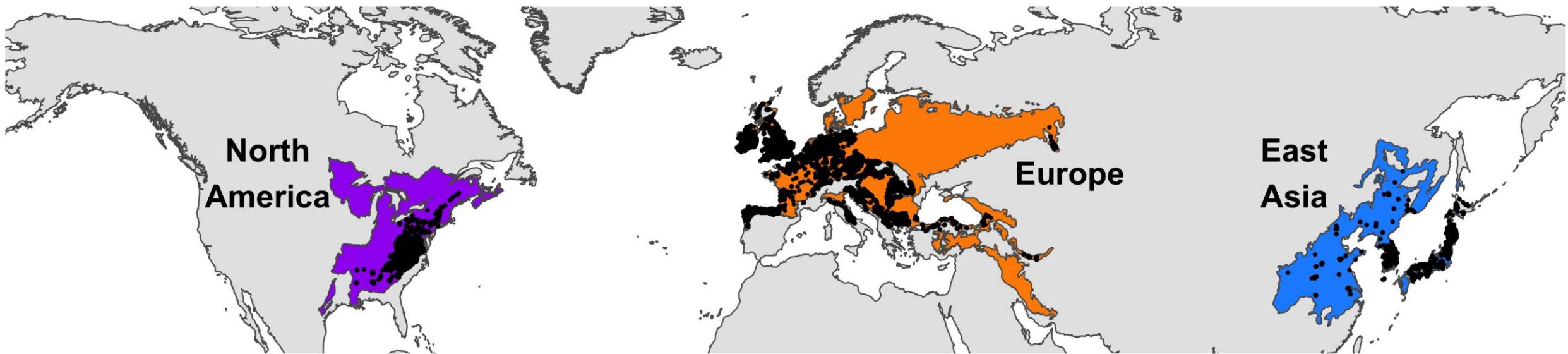
CED =
SR =

2.8 2.4 2.4 2.6 2.5 2.6 2.5
2 3 3 4 4 3 5 4

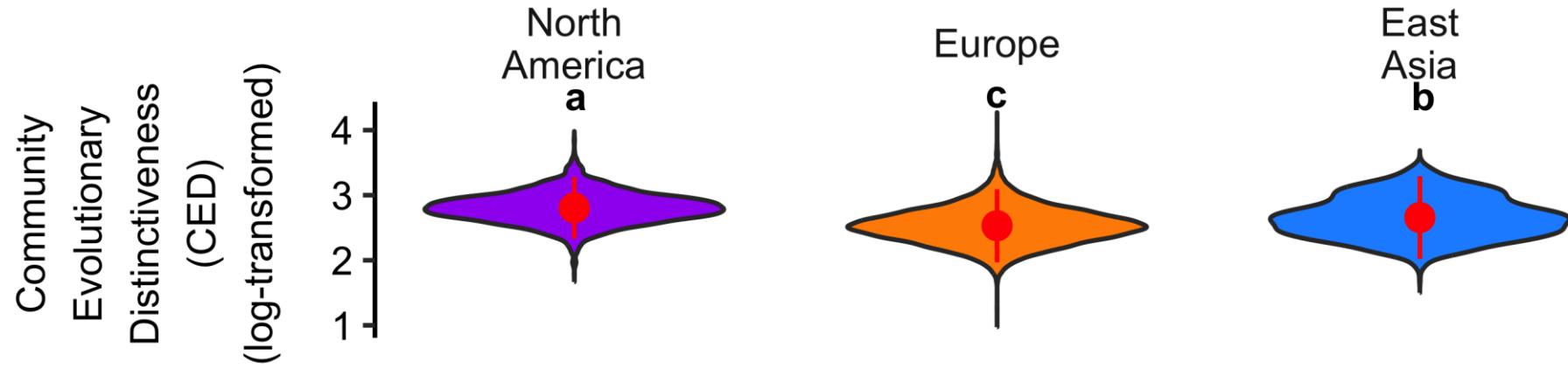
Isaac et al. (2007)

Alpha diversity: Community Evolutionary Distinctiveness (CED)

Vegetation plots from temperate deciduous forests in the northern hemisphere

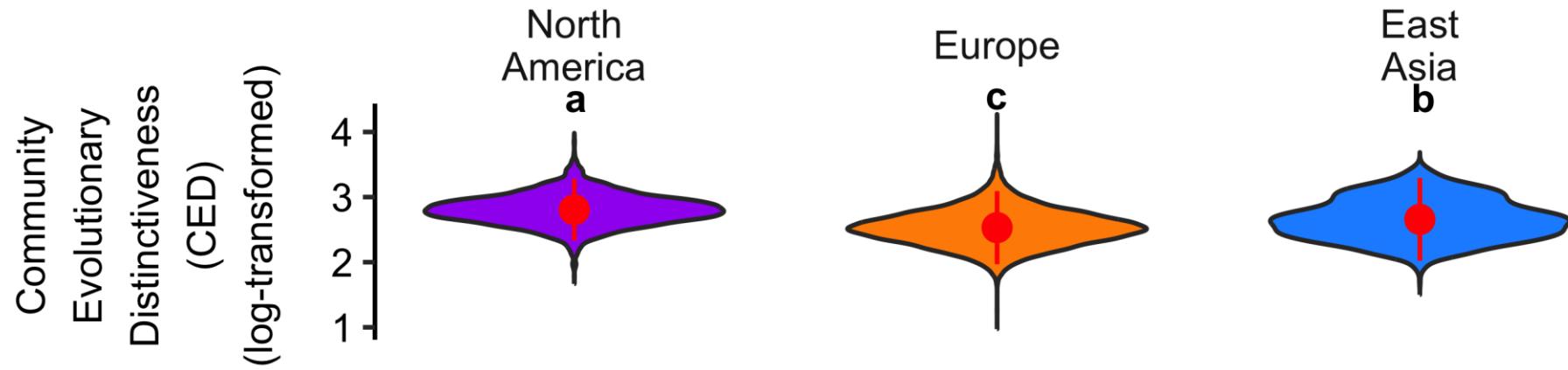


Alpha diversity: Community Evolutionary Distinctiveness (CED)

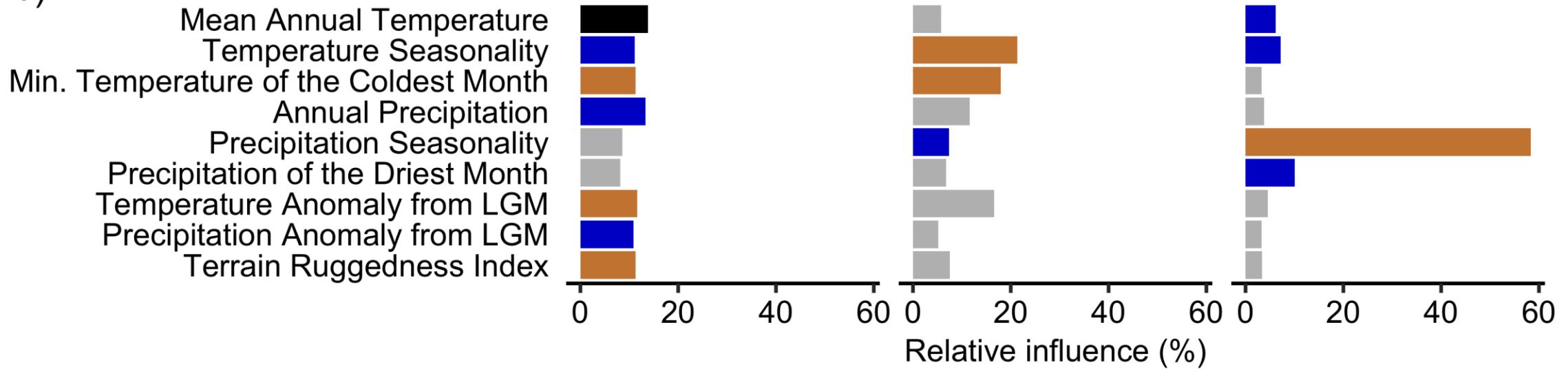


Alpha diversity: Community Evolutionary Distinctiveness (CED)

a)



b)



Scheme of the presentation

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Beta diversity

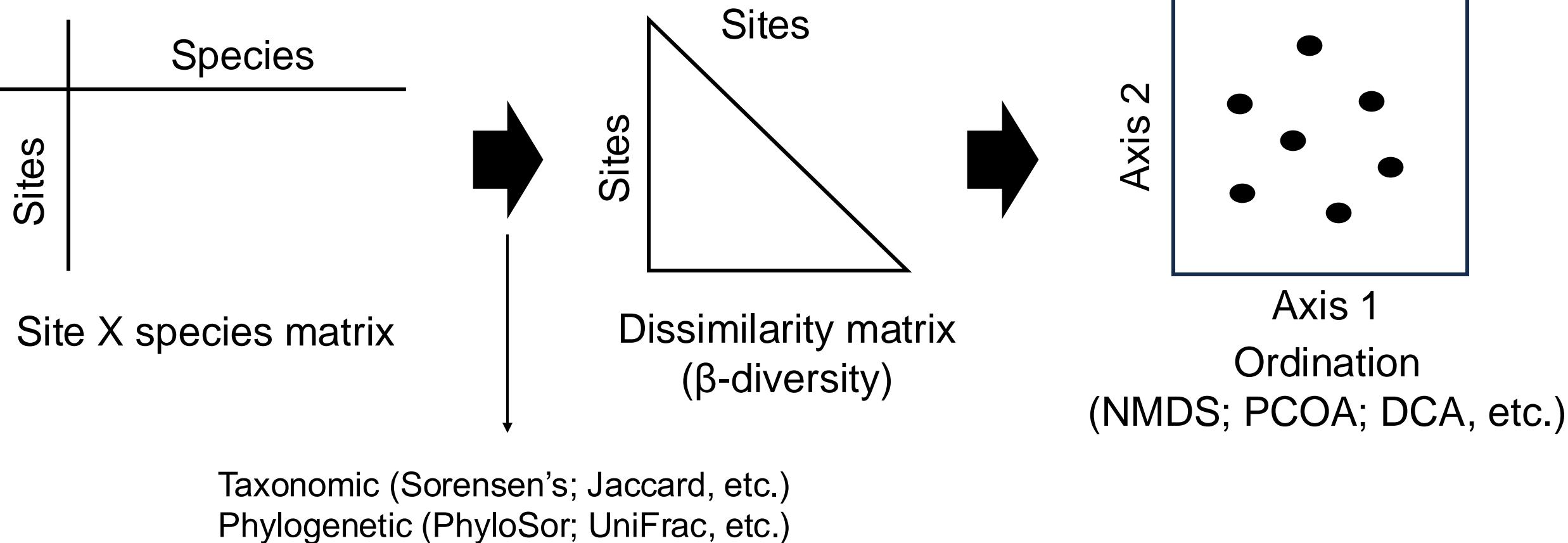
DIMENSION =>		1. Richness: how much? <i>Sum of ...</i>			2. Divergence: how different? <i>Mean of ...</i>				3. Regularity: how regular? <i>Variance of ...</i>			
<=Level of comparison	Unit =>	1.1 Branch lengths	1.2 Pairwise distances	1.3 Phylogenetic isolation	2.1 Branch lengths	2.2 Pairwise distances / similarities		2.3 Phylogenetic isolation	3.1 Tree topology	3.2 Pairwise distances		3.3 Phylogenetic isolation
		2.2.1 All	2.2.2 Nearest	3.2.1 All	3.2.2 Nearest							
β -diversity (between sets)	1.1b Amount of (un)shared evolutionary history: Phylosor Phylosor_{Ab} Unifrac Unifrac_{Ab} Faith's PDβ	1.2b Sum of inter-set distances relative to intra-set distances: S_Jaccard S_Sokal-Sneath S_Sorensen S_Ochial Sβ (with absolute abundances)	NA	2.1b Effective number of sets: ${}^qD_\beta(T)^*$ Amount of entropy gained on average by merging the sets: H$_\beta^*$ I$_{q\beta}^*$	2.2.1b Average inter-set relative to intra-set distances: S_Jaccard S_Sokal-Sneath S_Sorensen S_Ochial Sβ (with relative abundances) Average inter-set distances conditionally to intra-set (dis)similarities: PCD Amount of average distances gained on average by merging the sets: Rao's DISC Proportion of average distances gained on average by merging the sets: P_{ST} Proportion of average inter-species distances gained on average by merging the sets: B_{ST} Π_{ST} Average inter-set distances: COMDIST , Rao's D, D_{pw} COMDIST_{Ab} , Rao's D_{Ab} , D_{pw}_{Ab}	2.2.2b Average minimum distance between a species of a set and all species in another set: COMDISTNT , D_{nn} COMDISTNT_{Ab} , D_{nn}_{Ab}	NA	NA	NA	NA	NA	

Beta diversity

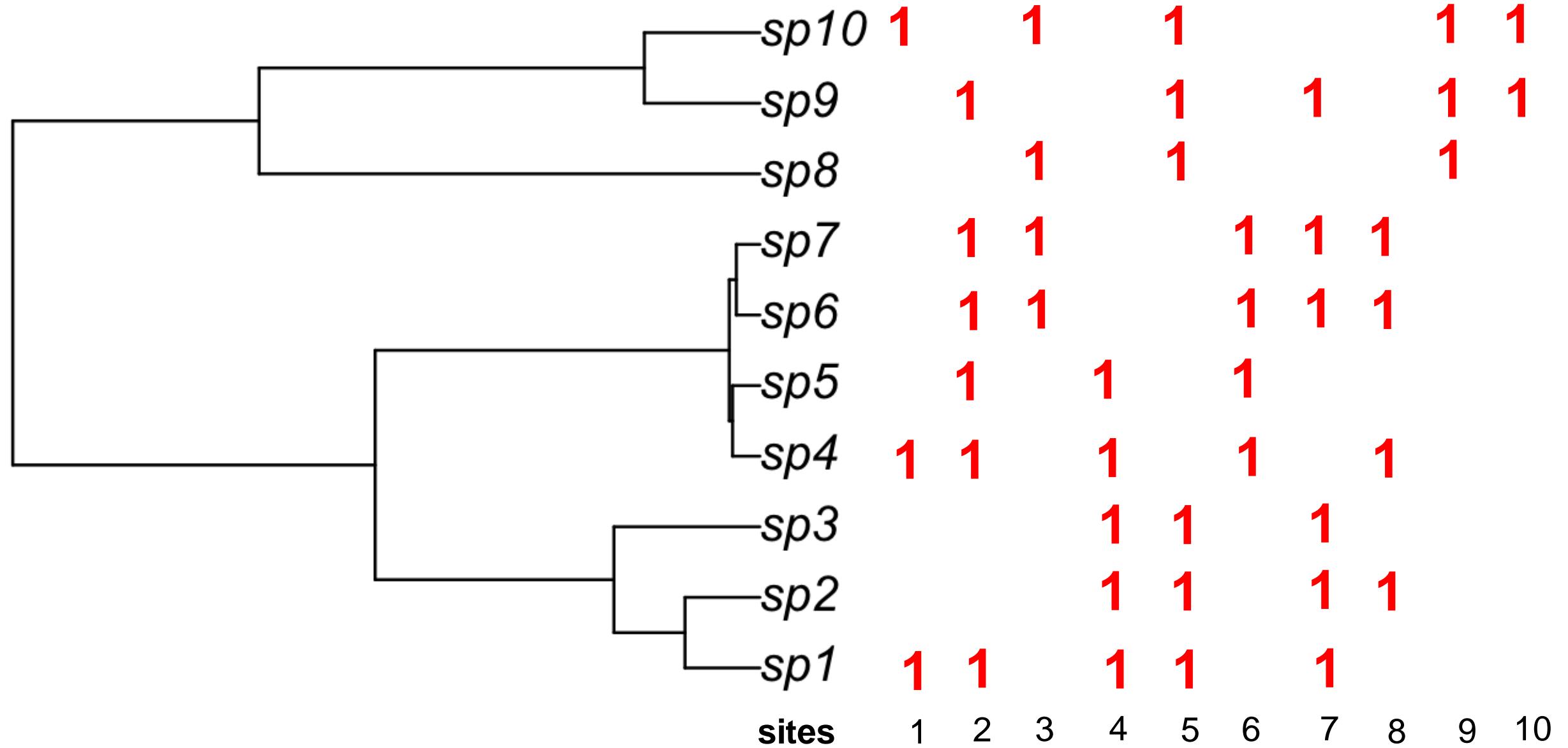
DIMENSION =>	1. Richness: how much? <i>Sum of ...</i>			2. Divergence: how different? <i>Mean of ...</i>				3. Regularity: how regular? <i>Variance of ...</i>				
<=Level of comparison	2.2 Pairwise distances/ similarities								3.2 Pairwise distances			3.3 Phylogenetic isolation
	Unit =>	1.1 Branch lengths	1.2 Pairwise distances	1.3 Phylogenetic isolation	2.1 Branch lengths	2.2.1 All	2.2.2 Nearest	2.3 Phylogenetic isolation	3.1 Tree topology	3.2.1 All	3.2.2 Nearest	3.3 Phylogenetic isolation
		1.1b Amount of (un)shared evolutionary history: Phylosor						2.2.2b Average minimum distance between a species of a set and all species in another set: COMDISTNT, Dnn COMDISTNT_{Ab}, Dnn_{Ab}				
β -diversity (between sets)								Average inter-set distances: COMDIST, Rao's D, Dpw COMDIST_{Ab}, Rao's D_{Ab}, Dpw_{Ab}				

Beta diversity: PhyloSor

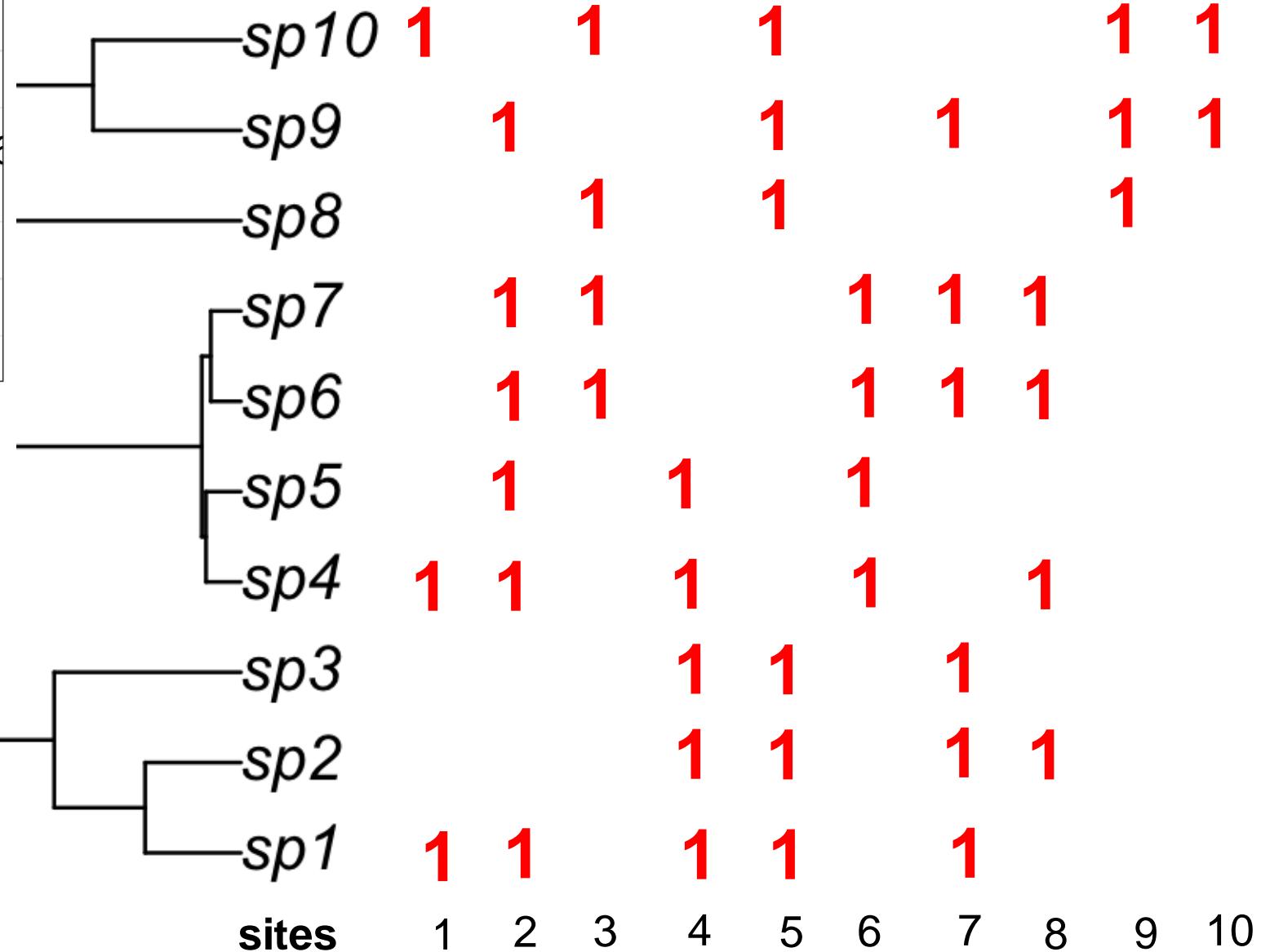
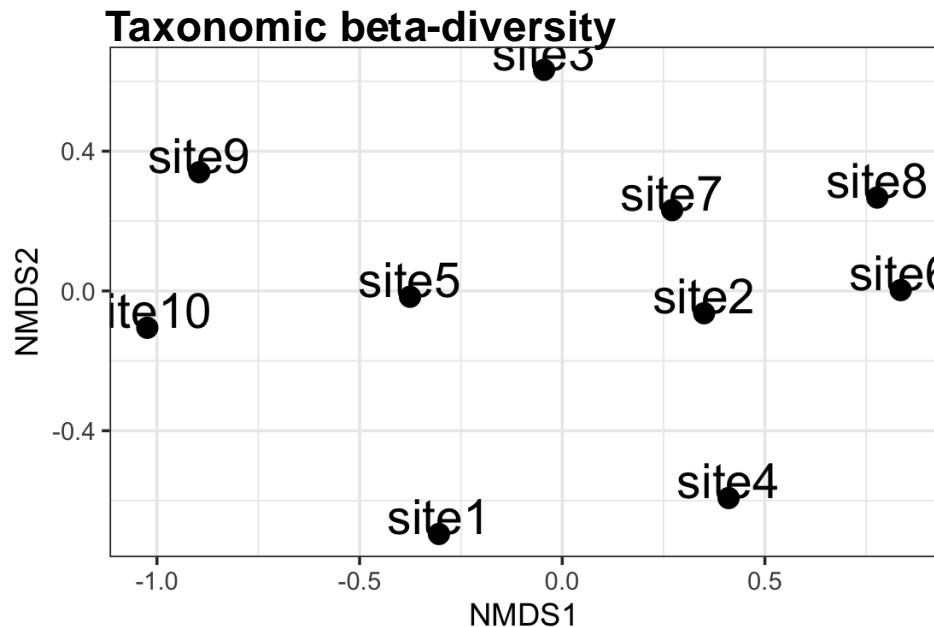
Phylosor = Phylogenetic Sorenson's Similarity



Beta diversity: PhyloSor

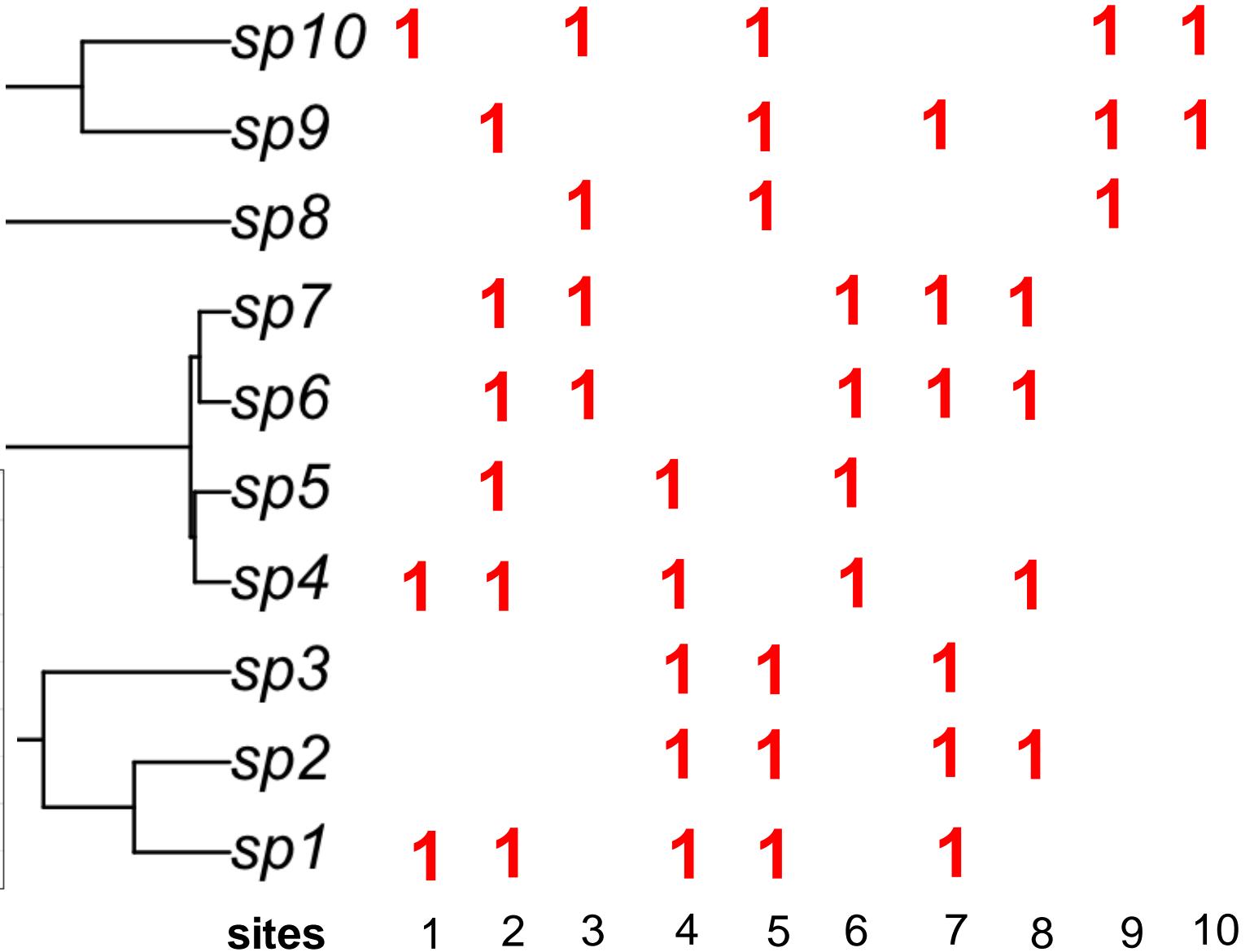
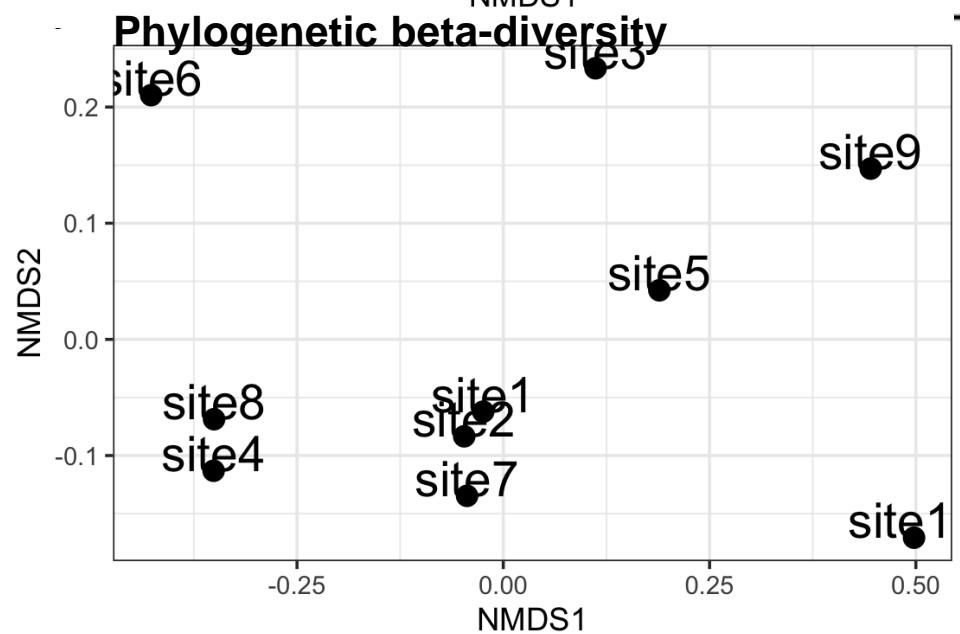
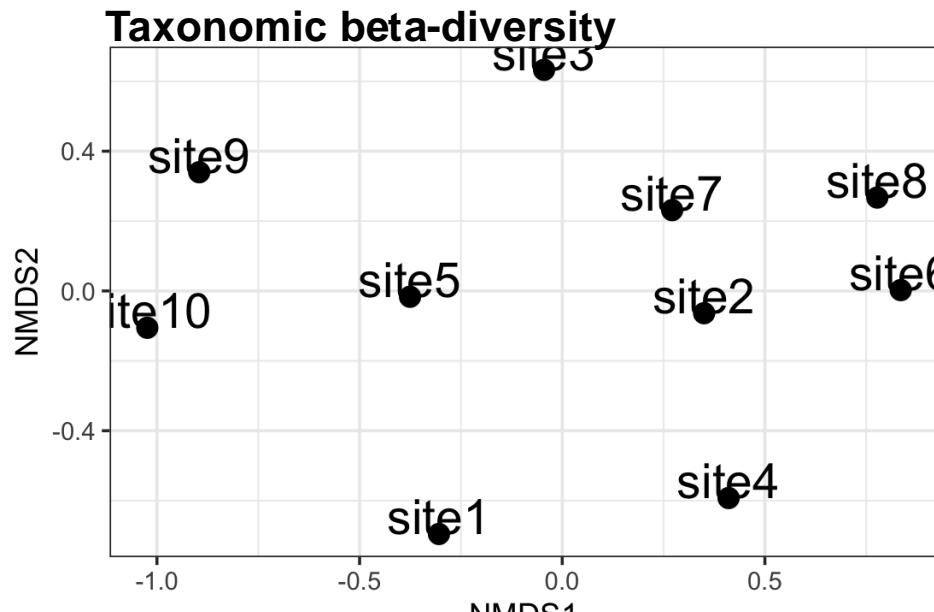


Beta diversity: PhyloSor

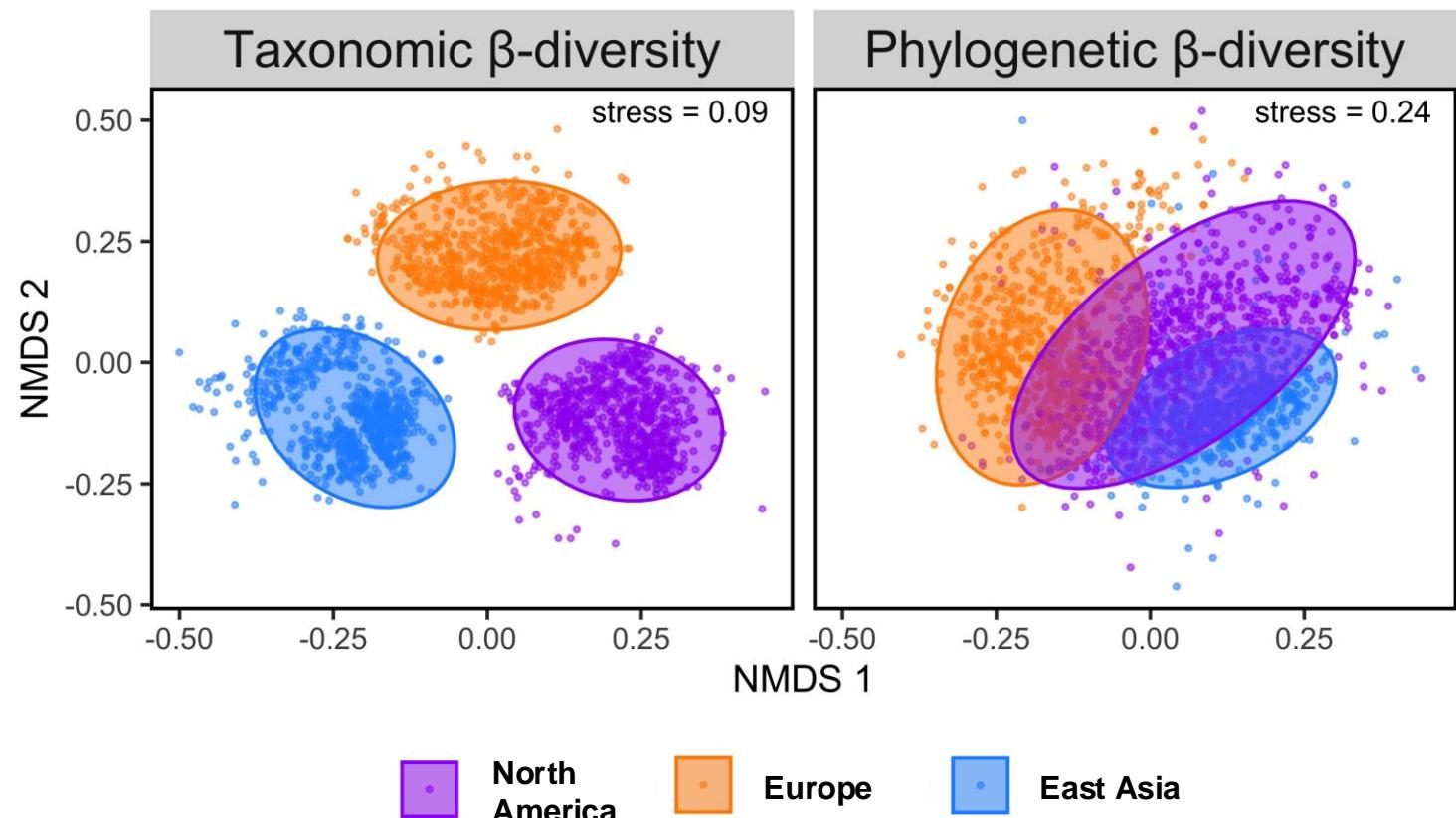
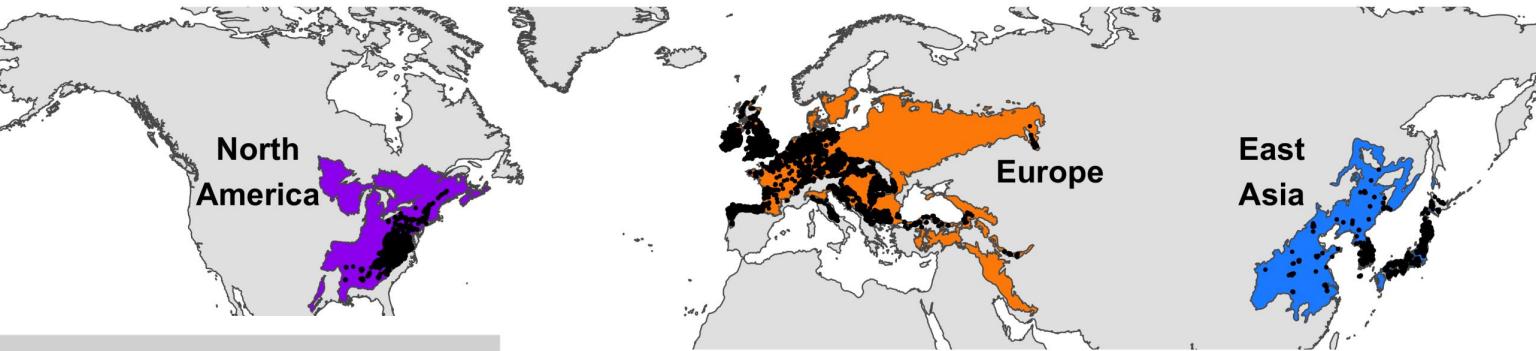


Beta diversity: PhyloSor

Mantel $r = 0.71$



Vegetation plots from temperate deciduous forests in the northern hemisphere



Beta diversity: D_{pw}/D_{nn}

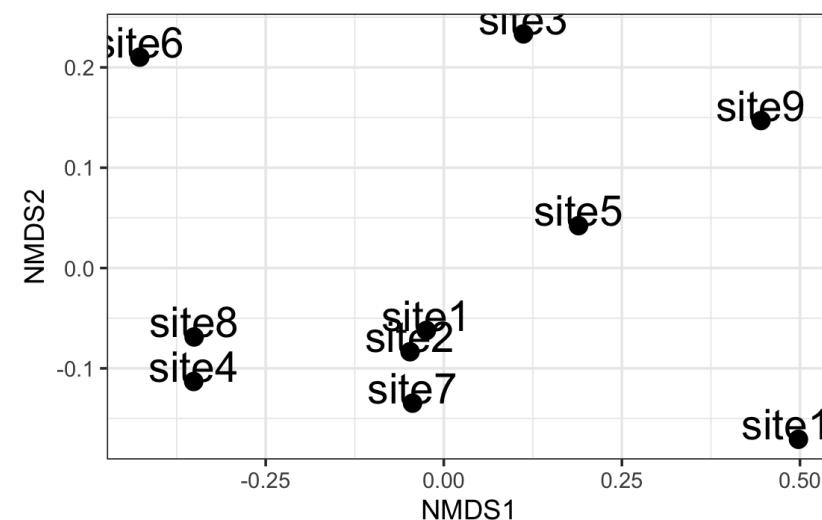
D_{pw} = inter-community mean pairwise distance (MPD)

Mantel r (PhyloSor vs. D_{pw})= 0.70

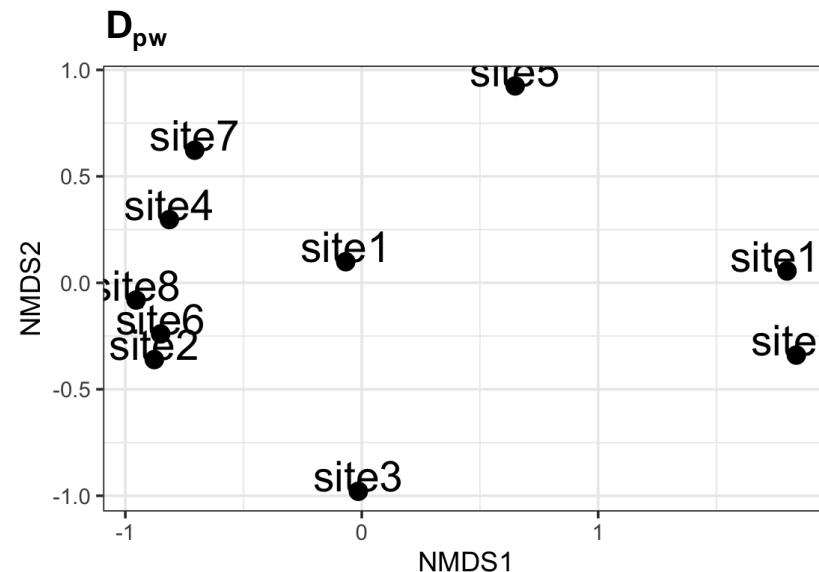
D_{nn} = inter-community mean nearest taxon distance (MNTD)

Mantel r (PhyloSor vs. D_{nn})= 0.89

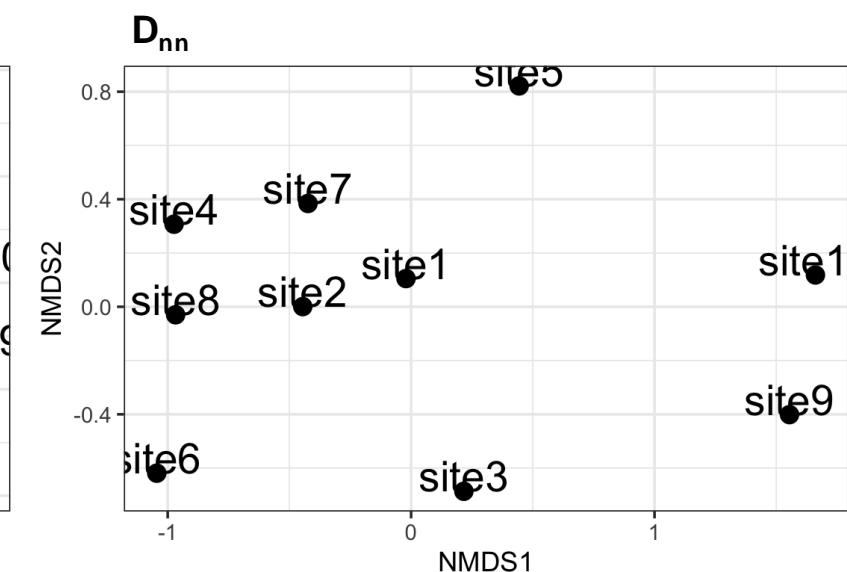
Phylogenetic beta-diversity (PhyloSor)



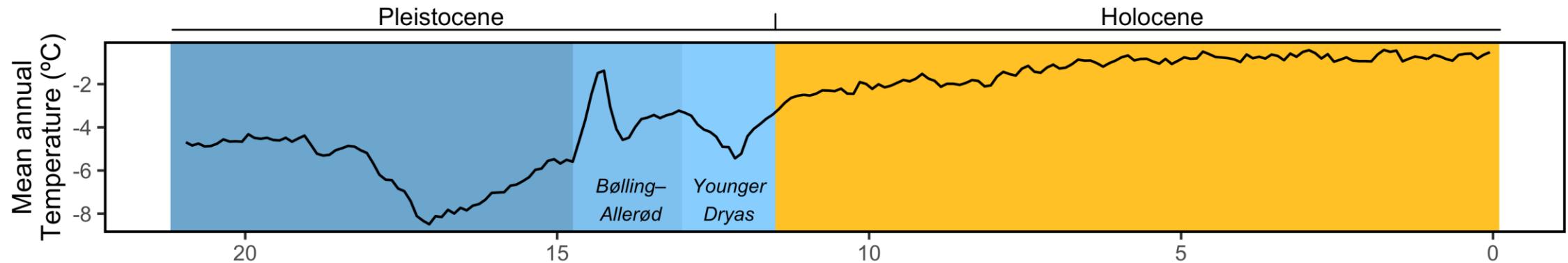
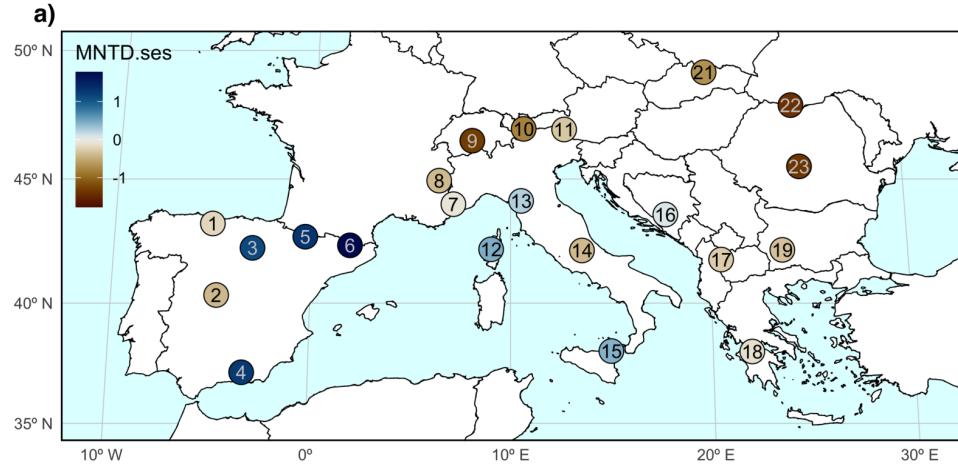
D_{pw}



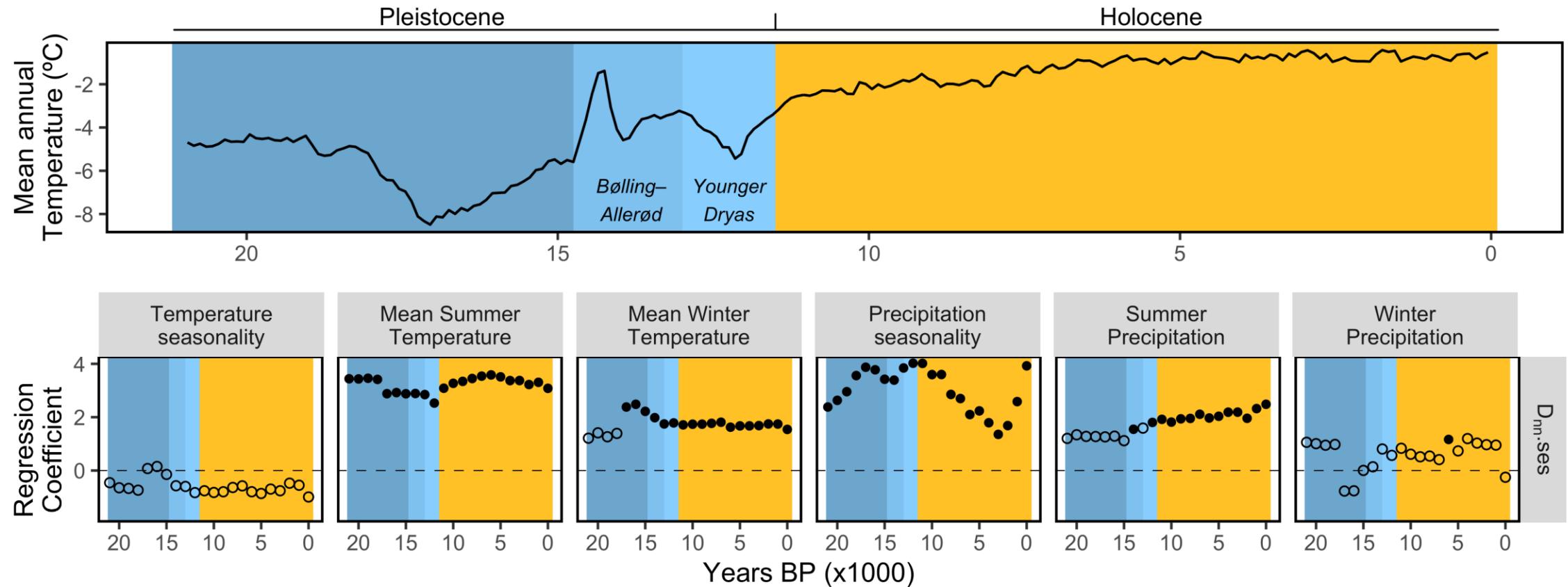
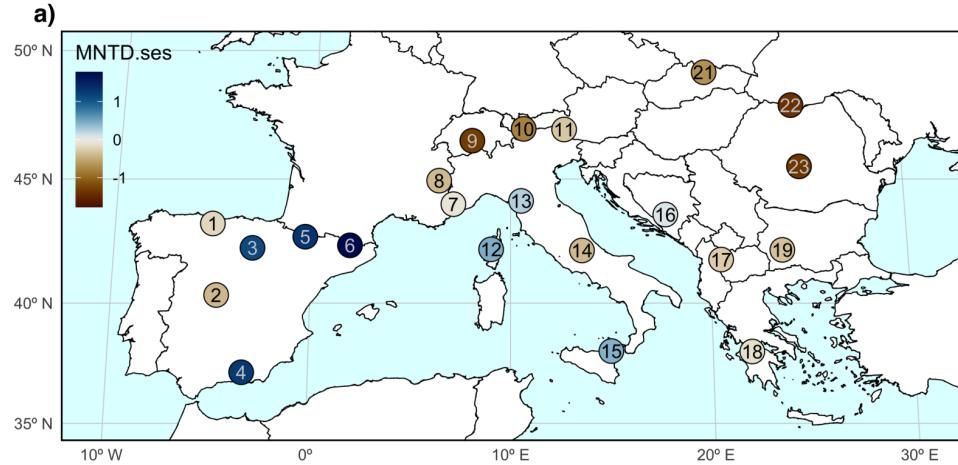
D_{nn}



Beta diversity: D_{pw}/D_{nn}



Beta diversity: D_{pw}/D_{nn}



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R packages to calculate PD metrics

Some examples:

- “**ape**” Functions for handling phylogenetic trees.
- “**picante**” Specialized in community phylogenetics: PD, MPD (SES), MNTD (SES), CED, PhyloSor, Dpw, Dnn, etc.
- “**phylocomr**” PD, PhyloSor, Rao’sQE, etc. Some functionality will be faster here than in “picante”.
- “**pez**” PD, MPD (SES), MNTD (SES), CED, PhyloSor, D_{pw} , D_{nn} , and many others. Phylogenetic tree manipulations.
- “**phyloregions**” Appropriate for biogeographic studies. Usually faster than “picante” and “pez”. PD, CED, PhyloSor, etc.
- “**betapar**” Phylogenetic beta-diversity.

R packages to calculate PD metrics

Additional useful packages:

- “**vegan**” Community ecology. Basic functions. Toy data.
- “**phytools**” Techniques for visualizing, analyzing, manipulating, reading, writing, and inferring phylogenetic trees.
- “**ggTree**” Visualization of phylogenetic trees.

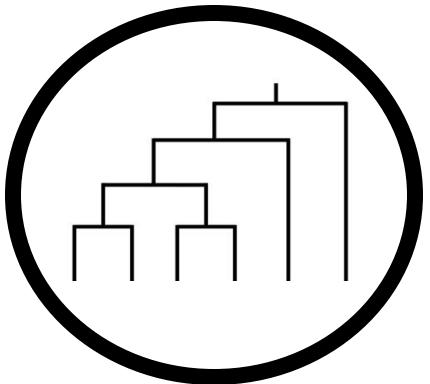
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Conclusions

- Phylogenetic diversity (PD) metrics **complement taxonomic and functional diversity** metrics by incorporating information about species' evolutionary relationships.
- PD metrics have been widely used to infer **community assembly processes**, though such interpretations can often be complex and context-dependent.
- A **wide range of alpha and beta PD metrics** is available, so it is important to carefully evaluate which metrics best align with your research questions.
- **Numerous R packages, functions, and null models** are available for calculating PD metrics. Select them thoughtfully, considering your data characteristics and computational requirements.

Community phylogenetics: Metrics and applications



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