



Celebrando la diversidad de la Botánica

TALLER

Análisis de patrones geográficos y evolutivos en Biogeografía y Biología de la Conservación de plantas

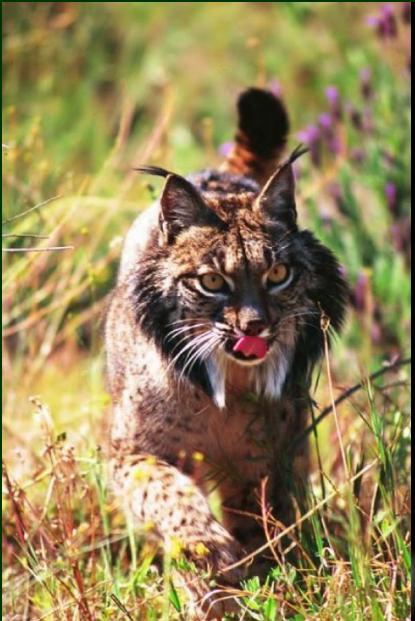
Alberto José Coello Garrido

Ignacio Ramos Gutiérrez

Mario Fernández-Mazuecos

CONSERVACIÓN DE LA BIODIVERSIDAD

(1) ESPECIES



(2) ESPACIOS



ESPECIES *Listas Rojas*

CATEGORÍAS UICN

- Extinta (**EX**)
- Extinta en estado silvestre (**EW**)
- En peligro crítico (**CR**)
- En peligro (**EN**)
- Vulnerable (**VU**)
- Casi amenazada (**NT**)
- Preocupación menor (**LC**)
- Datos insuficientes (**DD**)
- No evaluado (**NE**)



ESPECIES *Listas Rojas*



THE IUCN RED LIST
OF THREATENED SPECIES™

2019-3 | Login / Register | Contact | Terms of Use | English ▾

About

Assessment process

Resources & Publications

Support us

Names - common, scientific, regions etc...



Advanced

AMAZING SPECIES



ANIMALIA - MAMMALIA

Pygmy Slow Loris

Nycticebus pygmaeus

GLOBAL



PLANTAE - MAGNOLIOPSIDA

Nepenthes rigidifolia

↓ Decreasing

GLOBAL



ANIMALIA - AVES

Swan Goose

Anser cygnoid

GLOBAL



PLANTAE - MAGNOLIOPSIDA

Sapele

Entandrophragma cylindricum

feedback

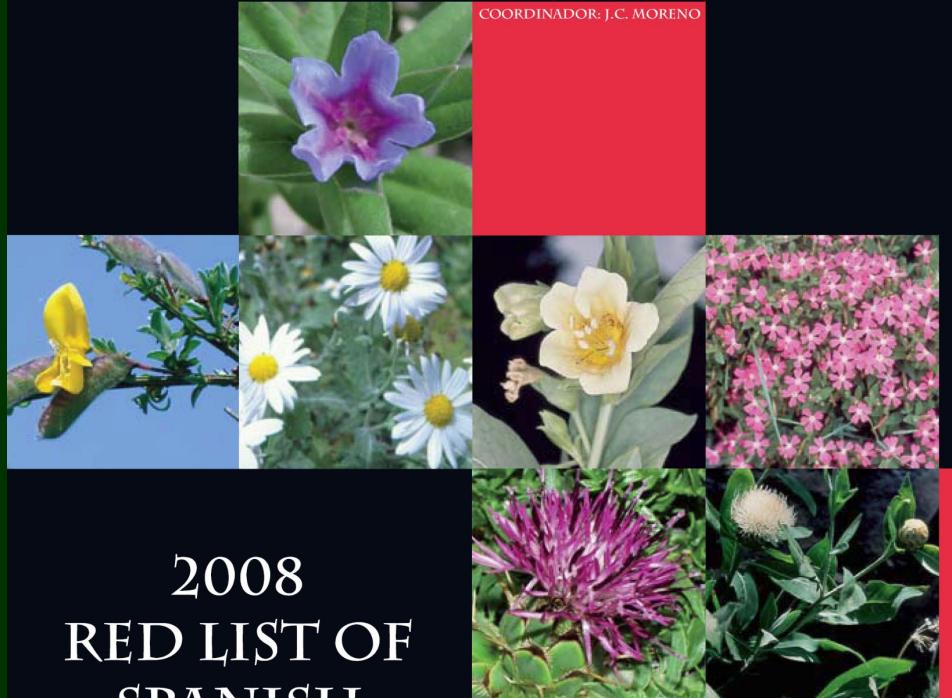


Amazing species

LISTA ROJA 2008

DE LA FLORA VASCULAR ESPAÑOLA

COORDINADOR: J.C. MORENO



2008
RED LIST OF
SPANISH
VASCULAR
FLORA

ESPECIES *Catálogos de Especies Protegidas*

VICEPRESIDENCIA
TERCERA DEL GOBIERNO
MINISTERIO
PARA LA TRANSICIÓN ECOLÓGICA
Y EL RETO DEMOGRÁFICO

Castellano | Q Buscar

Ministerio Energía Medio Ambiente Reto Demográfico Servicios

Home > Biodiversidad y Bosques > Temas > Conservación de especies

Situación actual del Listado de Especies Silvestres en Régimen de Protección Especial y Catálogo Español de Especies Amenazadas

Situación actual del Listado de Especies Silvestres en Régimen de Protección Especial y, en su caso, del Catálogo Español de Especies Amenazadas. (Número de taxones incluidos según el Real Decreto 139/2011, de 4 de febrero y sus modificaciones: Orden AAA/75/2012, de 12 de enero; Orden AAA/1771/2015, de 31 de agosto; Orden AAA/1351/2016, de 29 de julio; Orden TEC/596/2019, de 8 de abril; Orden TED/1126/2020, de 20 de noviembre; Orden TED/980/2021, de 20 de septiembre; Orden TED/339/2023, de 30 de marzo; y Orden TED/452/2025, de 5 de mayo).

Grupos taxonómicos	Listado de Especies Silvestres en Régimen de Protección Especial	Catálogo Español de Especies Amenazadas (categorías)		TOTAL taxones
		Vulnerable	En Peligro de Extinción	
FLORA	191	50	132	373
INVERTEBRADOS	73	17	22	112
PECES	35	3	13	51
ANFIBIOS	19	6	2	27
REPTILES	52	8	8	68
AVES	250	28	24	302
MAMÍFEROS	43	26	8	77
TOTAL nº taxones	663	138	209	1010

NOTA: Los taxones contabilizados incluyen especies, subespecies y poblaciones, tal y como se recoge en los BOE en los que fueron publicados.

Novedades

Listas patrón
El MITECO revisa y actualiza la Lista Patrón de las especies silvestres presentes en España

Preguntas frecuentes...
Acceso a los recursos genéticos y reparto de beneficios

14/08/2025 →
El OAPN y el IEO-CSIC exploran los fondos marinos de las Islas Chafarinas

11/08/2025 →
El MITECO recibe 485 propuestas para proyectos transformadores en el ámbito del empleo verde, la sostenibilidad del sector pesquero, la bioeconomía y la conservación de la biodiversidad marina

Noticias sobre Biodiversidad

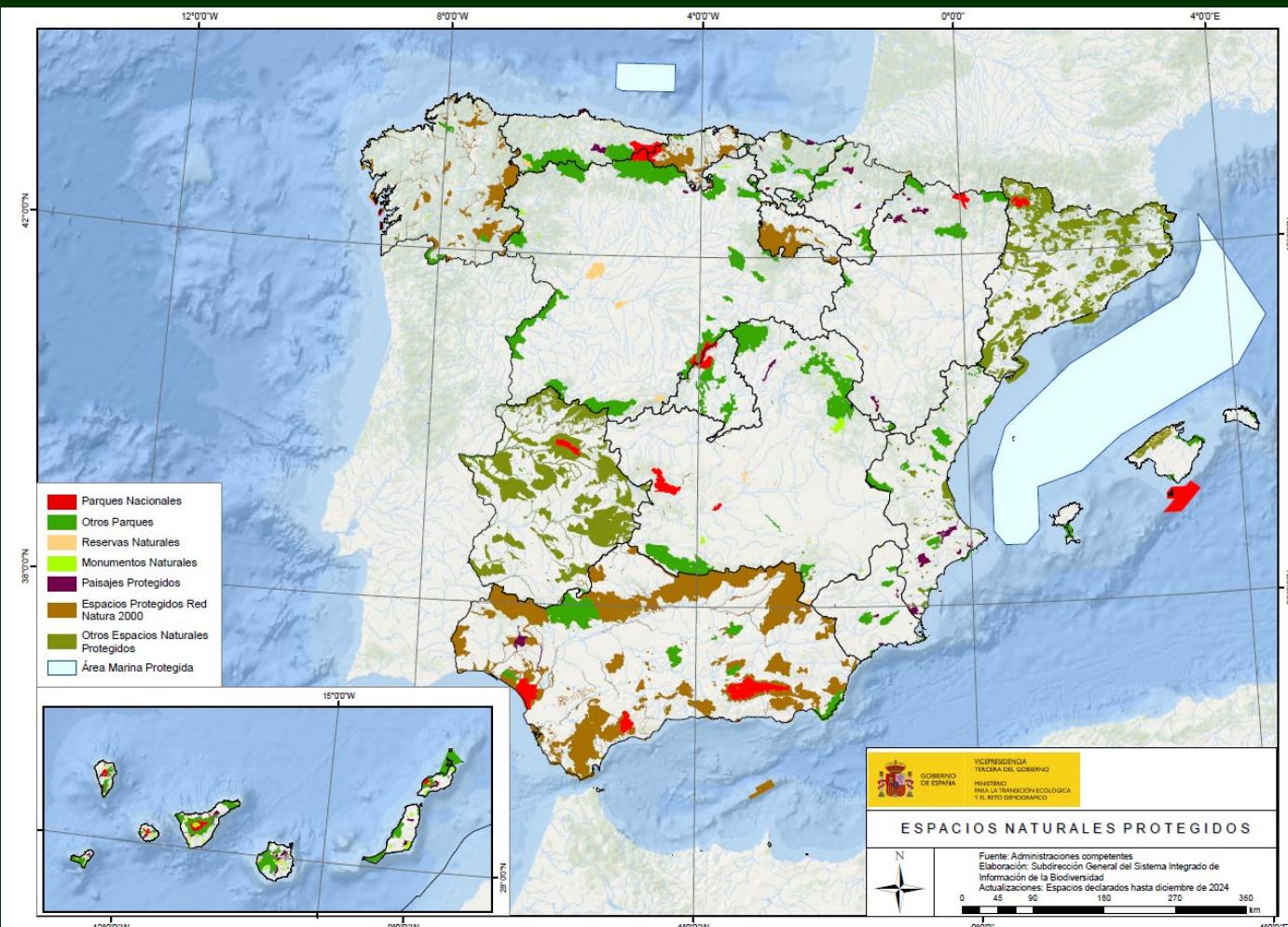
ESPACIOS *Redes de áreas protegidas*

IUCN Protected Area Management Categories

- **Category Ia** – Strict Nature Reserve
- **Category Ib** – Wilderness Area
- **Category II** – National Park
- **Category III** – Natural Monument or Feature
- **Category IV** – Habitat/Species Management Area
- **Category V** – Protected Landscape/Seascape
- **Category VI** – Protected Area with sustainable use of natural resources

ESPACIOS *Redes de áreas protegidas*

The image shows the homepage of the Protected Planet website. At the top, there is a navigation bar with links to 'About', 'News & Stories', 'Resources', 'Update Tracker', 'Thematic Areas', and a search icon. Below the navigation bar, a large banner features the text 'Discover the world's protected and conserved areas' in bold black font. Underneath the banner, a smaller text block reads: 'Protected Planet is the most up to date and complete source of data on protected areas and other effective area-based conservation measures (OECMs), updated monthly with submissions from governments, non-governmental organizations, landowners and communities.' A purple button labeled 'Explore protected areas and OECMs' is located below this text. The main feature is a world map where landmasses are colored according to their protected status, with green representing areas like National Parks and brown representing others like Natura 2000 sites. The map includes labels for major oceans: North Pacific Ocean, Atlantic Ocean, South Pacific Ocean, South Atlantic Ocean, Indian Ocean, and North Pacific Ocean. There are also terrain and satellite view options at the bottom.



“THE AGONY OF CHOICE”





What to Protect?—Systematics and the Agony of Choice

R. I. Vane-Wright, C. J. Humphries & P. H. Williams

Biodiversity Programme, Departments of Botany and Entomology,
The Natural History Museum, Cromwell Road, London SW7 5BD, UK

“THE AGONY OF CHOICE”

Biological Conservation 1992, 61, 11–15



Genetic diversity and the agony of choice

R. H. Crozier

Department of Genetics & Human Variation, La Trobe University, Bundoora, Victoria 3083, Australia



SHORT NOTE

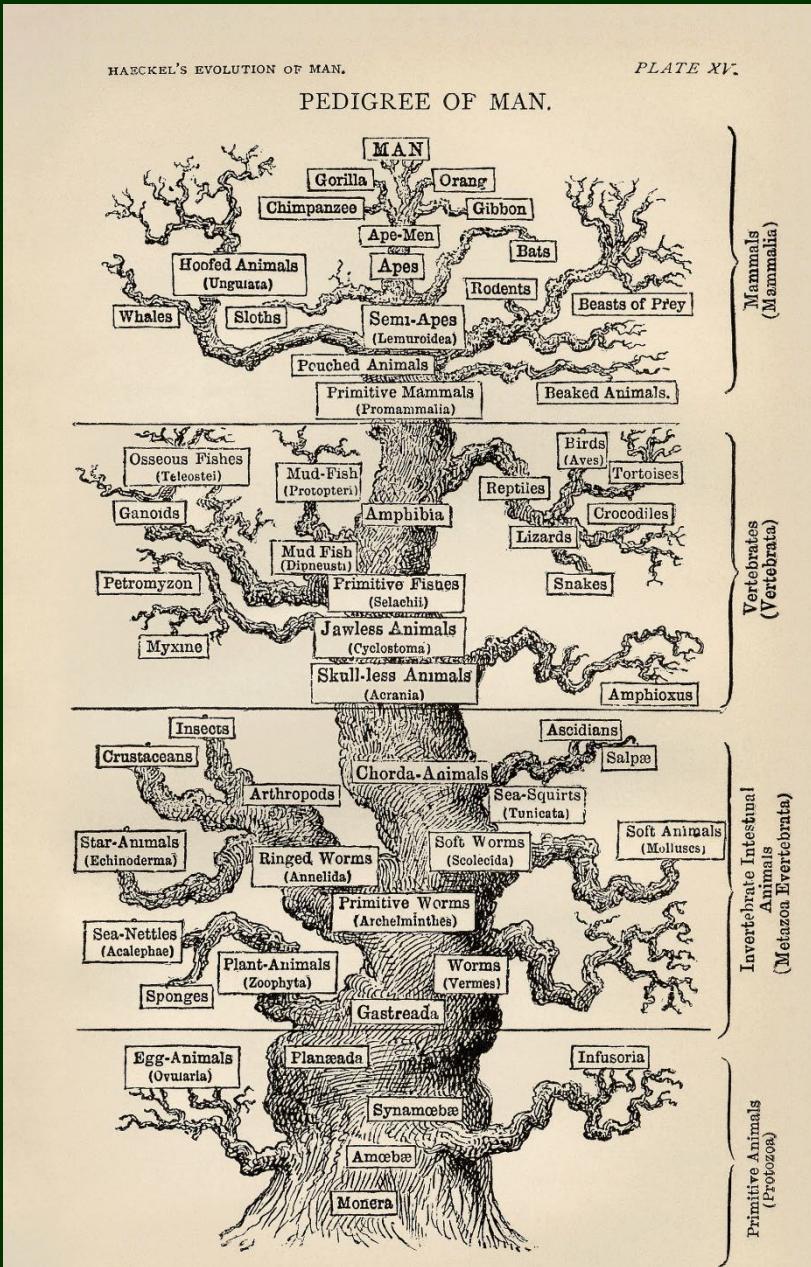
THE OPTIMIZATION OF BIODIVERSITY CONSERVATION

Lars Witting & Volker Loeschke

Department of Ecology and Genetics, University of Aarhus, Ny Munkegade, DK-8000 Aarhus C, Denmark

Biological Conservation 71 (1995) 205–207
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0006-3207/95/\$9.50

Historia evolutiva y conservación



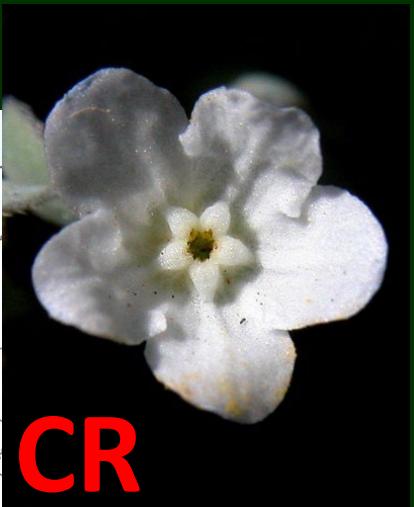
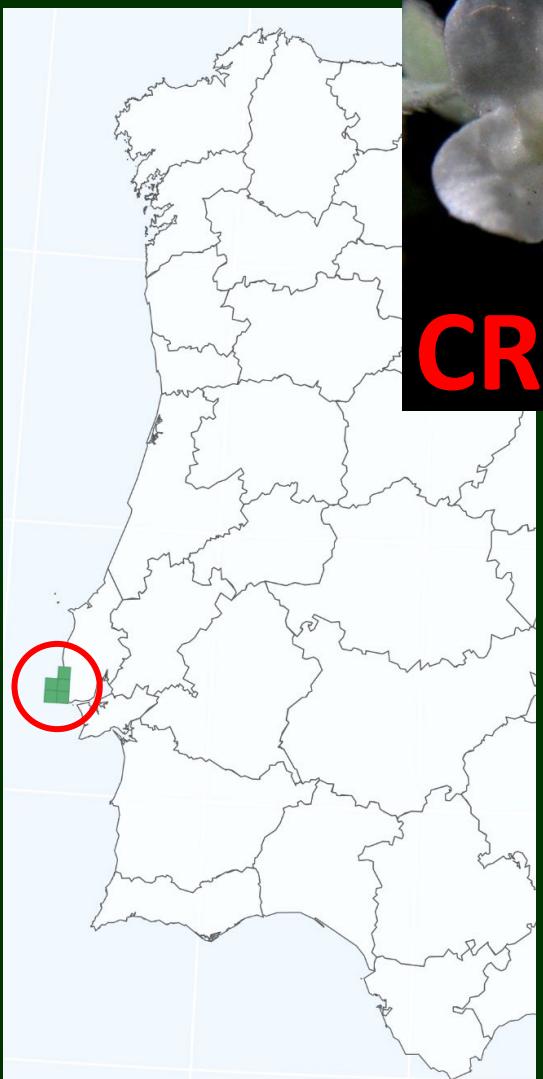
**"THE AGONY
OF CHOICE"**

(1) ESPECIES

(2) ESPACIOS

(1) ESPECIES

(1) ESPECIES



Iberodes kuzinskyana



Gyrocaryum oppositifolium



(1) ESPECIES

Taxonomic treatment

1. ***Iberodes*** M. Serrano, R. Carbalal & S. Ortiz, gen. nov.

Diagnosis: Genus of annual herb species occurring in South-western Europe, mainly in the Iberian peninsula. *Iberodes* is strictly annual

Serrano et al. (2016)



Type species: *Iberodes linifolia* (L.) M. Serrano, R. Carbalal and S. Ortiz

Etiology: The name *Iberodes* refers to the Iberian Peninsula as center of diversification of the genus.

1.1. ***Iberodes linifolia*** (L.) M. Serrano, R. Carbalal and S. Ortiz comb. nov.

Basyonim: *Cynoglossum linifolium* Linnaeus (1753: 134)

≡ *Omphalodes linifolia* (L.) Moench (1794: 419)

≡ *Omphalodes lusitanica* (L.) Schrank (1812: 221)

= *Cynoglossum lusitanicum* Linnaeus (1762: 193)

1.2. ***Iberodes brassicifolia*** (Lag.) M. Serrano, R. Carbalal and S. Ortiz comb. nov.

Basyonim: *Cynoglossum brassicifolium* Lagaasca (1816: 10)

≡ *Omphalodes brassicifolia* (Lag.) Sweet (1826: 293)

= *Omphalodes amplexicaulis* Lehmann (1818: 98)

= *Omphalodes pavoniana* Boissier (1849: 128)

1.3. ***Iberodes commutata*** (G. López) M. Serrano, R. Carbalal and S. Ortiz comb. nov.

Basyonim: *Omphalodes commutata* (López 1980: 83)

1.4. ***Iberodes kuzinskyana*** (Willk.) M. Serrano, R. Carbalal and S. Ortiz comb. nov.

Basyonim: *Omphalodes kuzinskyanae* Willkomm (1889: 318)

≡ *Omphalodes linifolia* (L.) Moench subsp. *kuzinskyana* (Willk.) BRAND (1921: 78)

1.5. ***Iberodes littoralis*** (Lehm.) M. Serrano, R. Carbalal and S. Ortiz comb. nov.

Basyonim: *Omphalodes littoralis* Lehmann (1818: 98)

1.6. ***Iberodes littoralis*** (Lehm.) M. Serrano, R. Carbalal and S. Ortiz subsp. *gallaecica* (M. Lainz) M. Serrano, R. Carbalal and S. Ortiz comb. nov.

Basyonim: *Omphalodes littoralis* Lehm. subsp. *gallaecica* Lainz (1971: 25)

22. ***Gyrocarpum*** Valdés*

[*Gyrocarpum*, -i n. – lat. bot. *Gyrocarpum*, -i n., genero de las *Boraginaceae* creado por B. Valdés Castrillón (1983). En el protólogo se dice: "From the greek «gyros», ring, and «caryos», nut, latinized as a neuter noun [...] the name is formed because the most significant characters of the plant are those of the fruit" –la núcula, ciatiforme, tiene una excavación apical rodeada de un anillo cartilaginoso–; gr. *gîros*, -ou m. = círculo, redondel // anillo, etc.; gr. *káryon*, -ou n.; lat. *caryon*, -i n. = diversos frutos de cáscara ± leñosa, como la nuez del nogal (*Juglans regia* L., *Juglandaceae*), la avellana del avellano (*Corylus Avellana* L., *Betulaceae*) y la castaña del castaño (*Castanea sativa* Mill., *Fagaceae*)]

Hierbas anuales, ligeramente híspidas, sin pelos pluricelulares largos glandulíferos. Hojas enteras, las caulinares opuestas, las medias y superiores sésiles, no decurrentes. Inflorescencia ramificada, paniculiforme, con numerosas cimas multifloras, densas en la floración, laxas en la fructificación. Flores actinomorfas, erectas, bracteadas, pediceladas. Cáliz gamosépalo, dividido hasta el tercio inferior, con lóbulos homomorfos, enteros, laxamente estrigoso, con pelos rectos. Corola rotácea, glabra por la cara externa, con lóbulos patentes; tubo más corto que los lóbulos de la corola, recto, cilíndrico, glabro por la cara interna, sin escamas nectaríferas en la base; garganta con 5 escamas obtusas y papilosas; lóbulos obtusos. Estambres 5, inclusos, adnatos a la misma altura, hacia la mitad del tubo de la corola, con filamentos mucho más cortos que las anteras, cilíndricos, glabros, sin apéndices; anteras no apiculadas, libres, inclusas. Ovario tetralobado; estilo simple, inclusivo, ginobásico; estigma capitado. Fruto pétreo, en tetranúcula. Núculas monospermas, ciatiformes, tuberculadas, con una excavación apical rodeada de un anillo cartilaginoso, sin anillo basal, con la base de inserción anchamente elíptica, plana y carente de apéndice, unidas por su base en el receptáculo plano.

Observaciones.—Género monotípico.

* I. Fernández & S. Talavera

1. ***G. oppositifolium*** Valdés in Willdenowia

13: 108 fig. 1, 109 (1983)

Ind. loc.: “Typus: Sevilla, Constantina, in oppidum Cerro 22.IV.1982, Devesa, Luque & Valdés (SEV 80501, holotipus; H

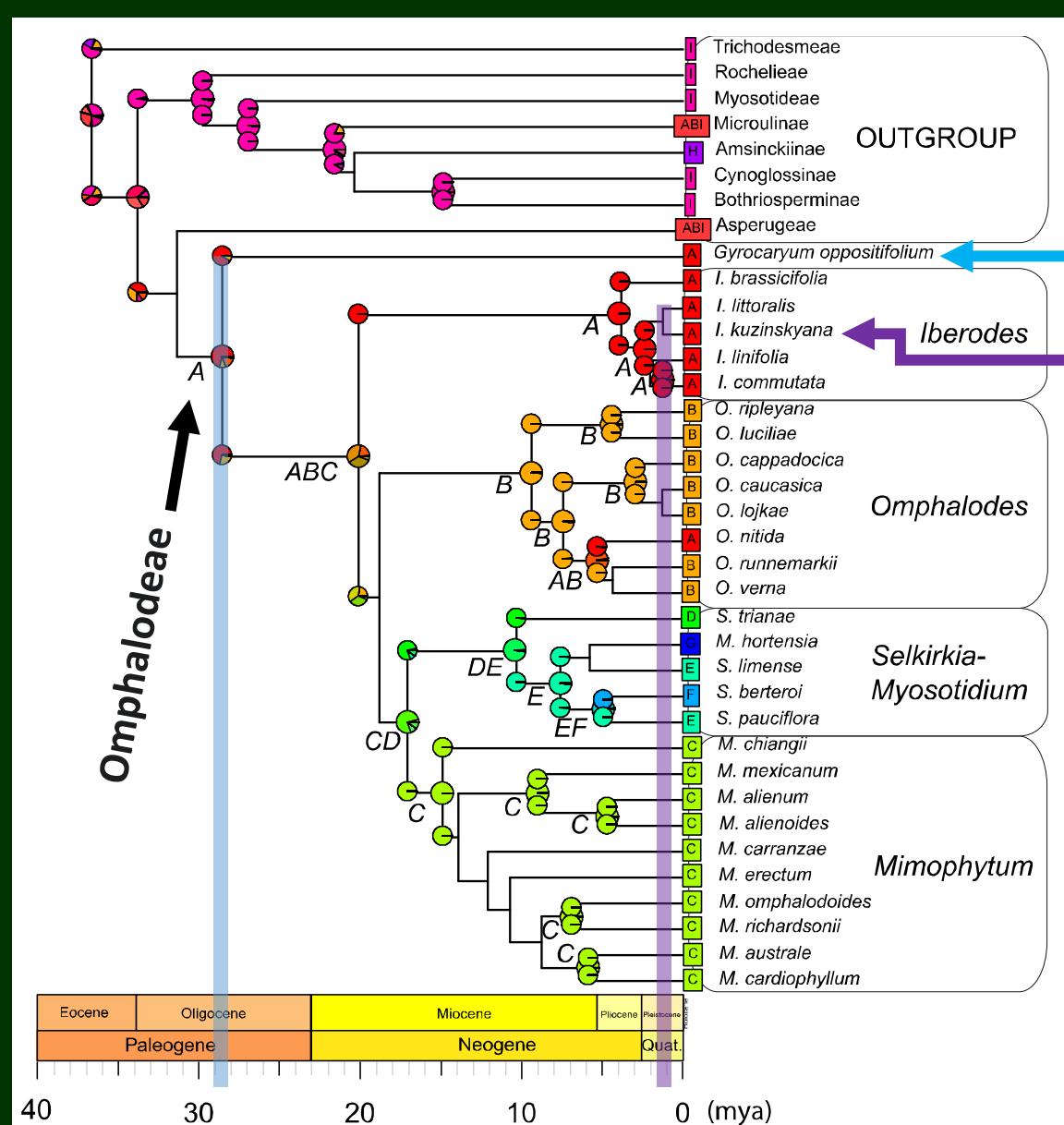
Ic.: Valdés in Willdenowia 13: 108 fig. 1 (1983); Valdés, Andalucía Occid. 2: 401 (1987); lám. 110

Fernández & Talavera (2012)



(1) ESPECIES

Singularidad filogenética

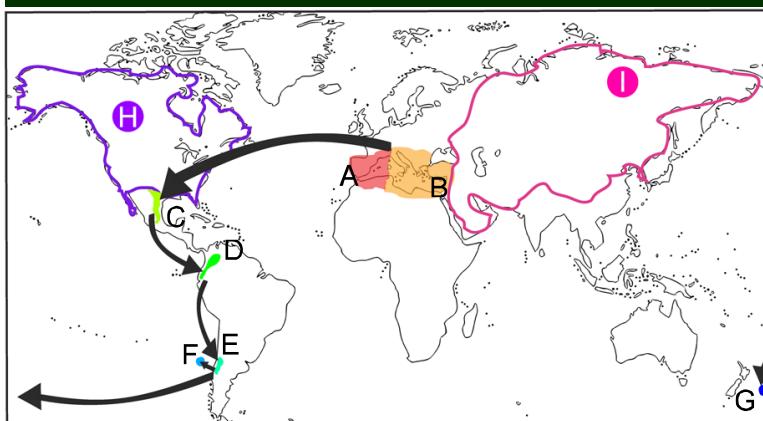


*Gyrocaryum
oppositifolium*
28 Ma



*Iberodes
kuzinskyana*
1 Ma

Otero et al. (2019)



(1) ESPECIES

Singularidad filogenética



Un fósil vivo amenazado

Gyrocarpum opositifolium
Valdés

Environmental and Experimental Botany 170 (2020) 103892



Contents lists available at ScienceDirect

Environmental and Experimental Botany

journal homepage: www.elsevier.com/locate/envexpbot



'Endangered living fossils' (ELFs): Long-term survivors through periods of dramatic climate change[☆]

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^b Universidad Autónoma de Madrid, Department of Biology (Botany), Campus Cantoblanco, 28049, Madrid, Spain

^c Centro de Investigación en Biodiversidad y Cambio Global (CIB-CUAM), Universidad Autónoma de Madrid, 28049, Madrid, Spain

ARTICLE INFO

Keywords:
Ancient lineages
Conservation
EDGE
Endemism
Phylogenetic singularity
Mediterranean floristic regions
Narrow endemics
Relict

ABSTRACT

Geography and climate have been the main drivers of evolution in recent geological epochs. While new lineages of species have been formed in the last millions of years (speciation) and others have vanished as a result of historical climate changes (extinction), some ancient lineages appear to have persisted to the present day without net diversification. In this paper, evolution of ancient lineages is addressed by combining phylogenetic and conservation approaches to test the concept of 'endangered living fossil' (ELF). Using endangered, monospecific genera as starting point, we propose three criteria to identify ELFs (in order): (1) scarcity and narrow distribution of populations, i.e. the species (and thus the genus) is categorised as either 'endangered' or 'critically endangered' using IUCN criteria; (2) evolutionary distinctiveness, i.e. phylogenetic singularity of a single-species lineage as a result of a null net diversification rate; (iii) ancient divergence, i.e. split from the closest extant relatives predating the dramatic climate changes of particular geological epochs (specifically changes since the Miocene-Pliocene boundary). The vascular flora of the Iberian Peninsula offers a suitable study system to reliably test the ELF concept. Indeed, time-calibrated phylogenies revealed that five of the six critically endangered, monospecific genera endemic to the Iberian Peninsula are ELFs. These five genera appear to have diverged from their closest relatives in the Oligocene (*Gyrocarpum*), Miocene (*Avellara*, *Castrilantherum*, *Gadoria*) and around the Miocene-Pliocene boundary (*Naufragia*). This result entails long-term survival (with no net diversification) through at least three dramatic climate changes: the Messinian Salinity Crisis (late Miocene), the establishment of the Mediterranean climate (Pliocene), and the glacial-interglacial cycles (Pleistocene). Using results from the literature, we found examples of ELFs for the Mediterranean floras of California (*Dodecahema*), Chile (*Avellanita*, *Gomortega*, *Legrandia*) and other Mediterranean areas of Europe (*Petagnaea*, *Phitosia*). ELFs are unique and threatened lineages representing an exceptional evolutionary heritage, and therefore they should be prioritised in biodiversity research and conservation programs.

OPEN  ACCESS Freely available online

 PLOS ONE

Mammals on the EDGE: Conservation Priorities Based on Threat and Phylogeny

Nick J. B. Isaac*, Samuel T. Turvey, Ben Collen, Carly Waterman, Jonathan E. M. Baillie

Institute of Zoology, Zoological Society of London, London, United Kingdom

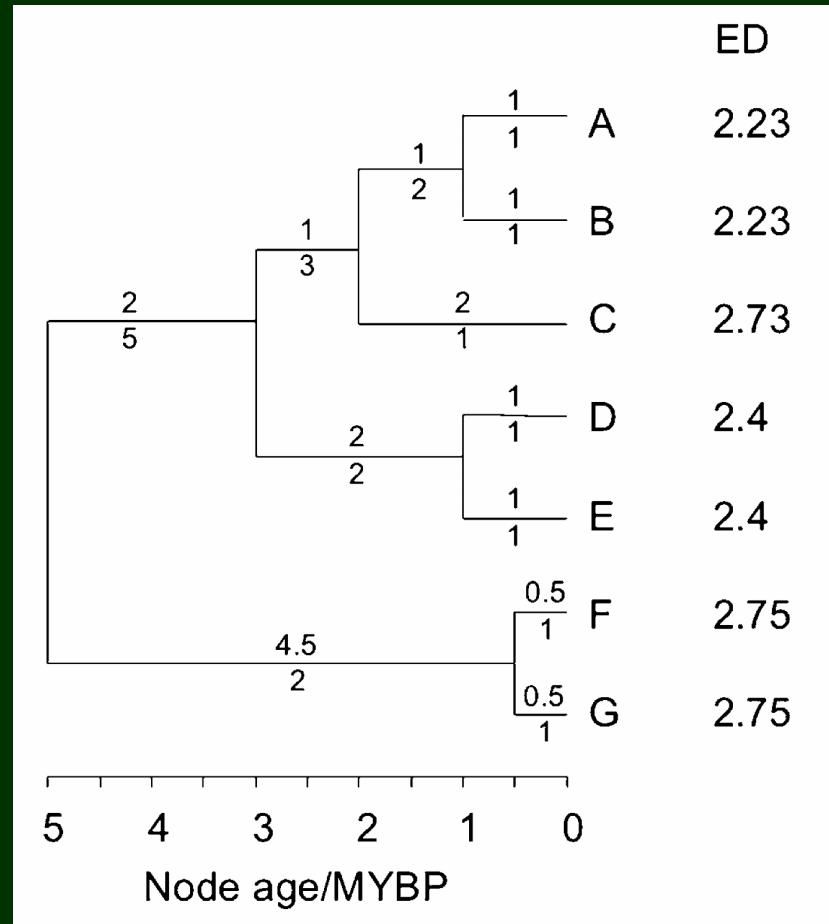
Conservation priority setting based on phylogenetic diversity has frequently been proposed but rarely implemented. Here, we define a simple index that measures the contribution made by different species to phylogenetic diversity and show how the index might contribute towards species-based conservation priorities. We describe procedures to control for missing species, incomplete phylogenetic resolution and uncertainty in node ages that make it possible to apply the method in poorly known clades. We also show that the index is independent of clade size in phylogenies of more than 100 species, indicating that scores from unrelated taxonomic groups are likely to be comparable. Similar scores are returned under two different species concepts, suggesting that the index is robust to taxonomic changes. The approach is applied to a near-complete species-level phylogeny of the Mammalia to generate a global priority list incorporating both phylogenetic diversity and extinction risk. The 100 highest-ranking species represent a high proportion of total mammalian diversity and include many species not usually recognised as conservation priorities. Many species that are both evolutionarily distinct and globally endangered (EDGE species) do not benefit from existing conservation projects or protected areas. The results suggest that global conservation priorities may have to be reassessed in order to prevent a disproportionately large amount of mammalian evolutionary history becoming extinct in the near future.

Citation: Isaac NJB, Turvey ST, Collen B, Waterman C, Baillie JEM (2007) Mammals on the EDGE: Conservation Priorities Based on Threat and Phylogeny. PLoS ONE 2(3): e296. doi:10.1371/journal.pone.0000296

(1) ESPECIES

Evolutionarily Distinct and Globally Endangered (EDGE)

$$EDGE = \ln(1 + ED) + GE * \ln(2)$$



ED: Evolutionary Distinctiveness

$$ED(A) = (2/5) + (1/3) + (1/2) + (1/1) = 2,23$$

$$ED(F) = (4,5/2) + (0,5/1) = 2,75$$

GE: Red List category weight

Least Concern = 0

Near Threatened = 1

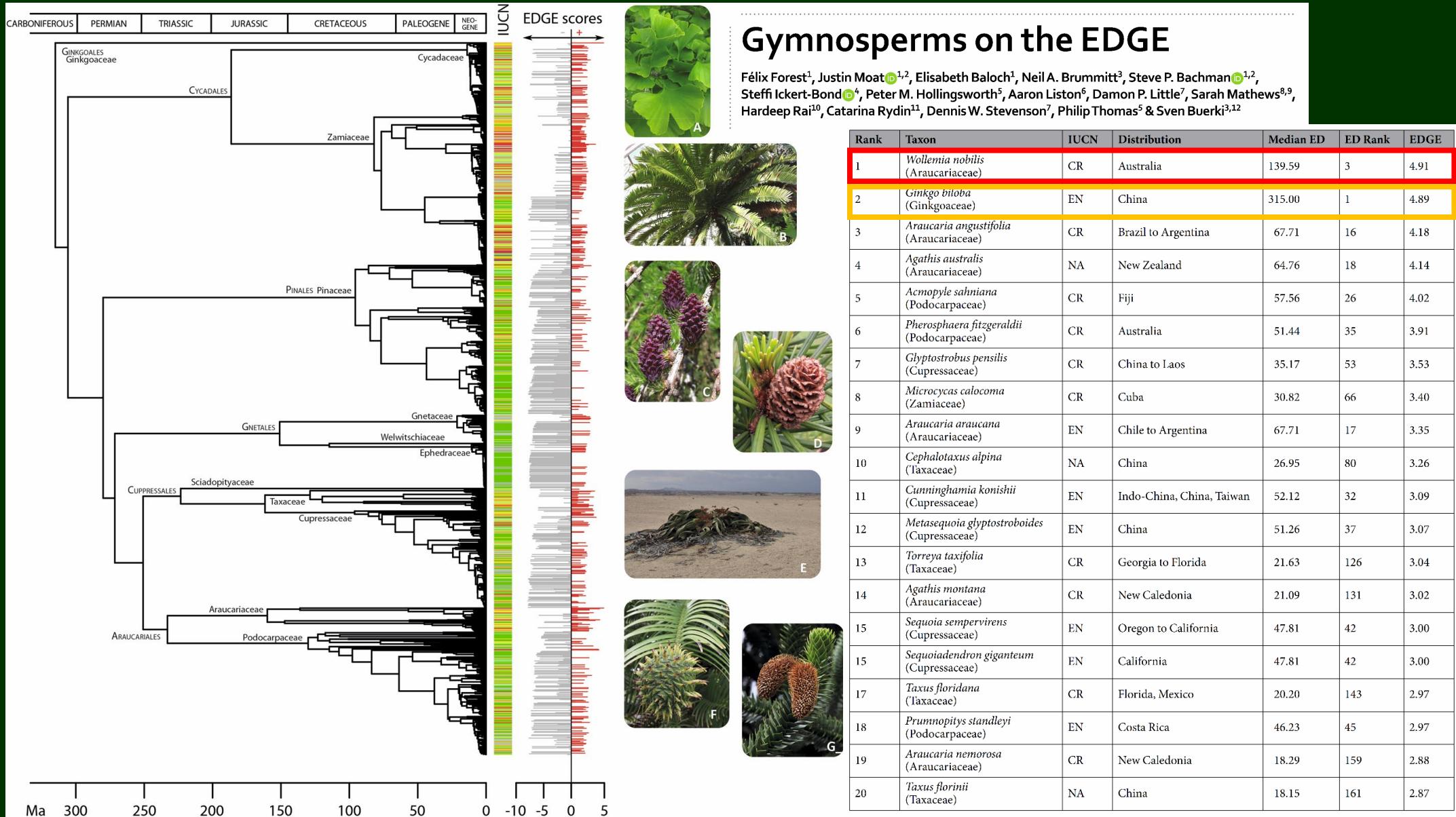
Vulnerable = 2

Endangered = 3

Critically Endangered = 4

(1) ESPECIES

Evolutionarily Distinct and Globally Endangered (EDGE)



(2) ESPACIOS

Biological Conservation 1992, **61**, 1–10



Conservation evaluation and phylogenetic diversity

Daniel P. Faith

Division of Wildlife and Ecology, CSIRO, PO Box 84, Lyneham, ACT, 2602, Australia

(Received 13 May 1991; revised version received 28 September 1991; accepted 11 November 1991)

Protecting biological diversity with limited resources may require placing conservation priorities on different taxa. A system of priorities that reflects the value of taxonomic diversity can be achieved by setting priorities such that the subset of taxa that is protected has maximum underlying feature diversity. Such feature diversity of taxon subsets is difficult to estimate directly, but can be predicted by the cladistic/phylogenetic relationships among the taxa. In this study, a simple measure of phylogenetic diversity is defined based on cladistic information. The measure of phylogenetic diversity, PD, is contrasted with a measure of taxic diversity recently developed by Vane-Wright *et al.* (*Biol. Conserv.*, **55**, 1991). In re-examining reserve-selection scenarios based on a phylogeny of bumble bees (Apidae), PD produces quite different priorities for species conservation, relative to taxic diversity. The potential application of PD at levels below that of the species is then illustrated using a mtDNA phylogeny for populations of crested newts *Triturus cristatus*. Calculation of PD for different population subsets shows that protection of populations at either of two extremes of the geographic range of the group can significantly increase the phylogenetic diversity that is protected.

(2) ESPACIOS

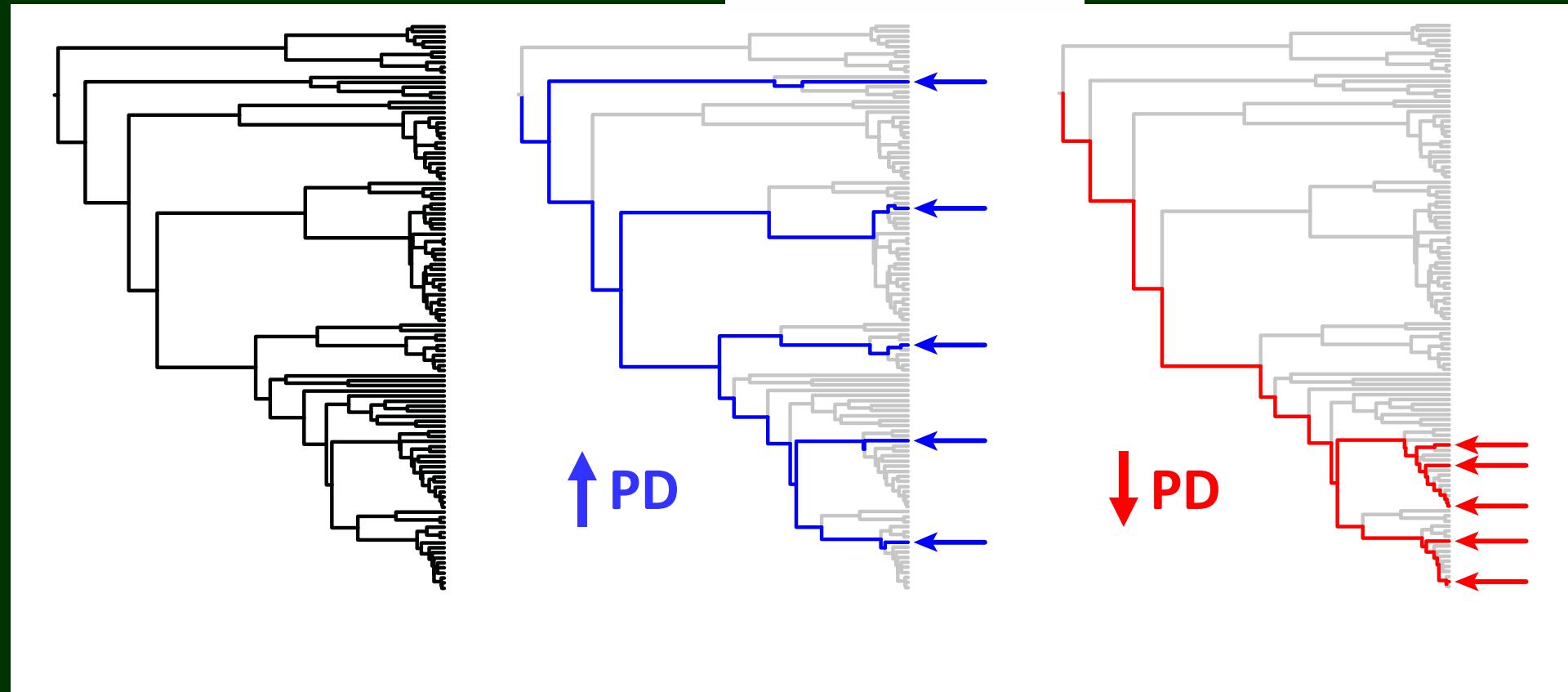
Spatial Phylogenetics

Taxon richness (TR): number of taxa (species, genera).

Phylogenetic diversity (PD): sum of branch lengths spanning a set of taxa in a phylogenetic tree.

$$PD = \sum_{\{c \in C\}} L_c$$

Faith (1992)



(2) ESPACIOS

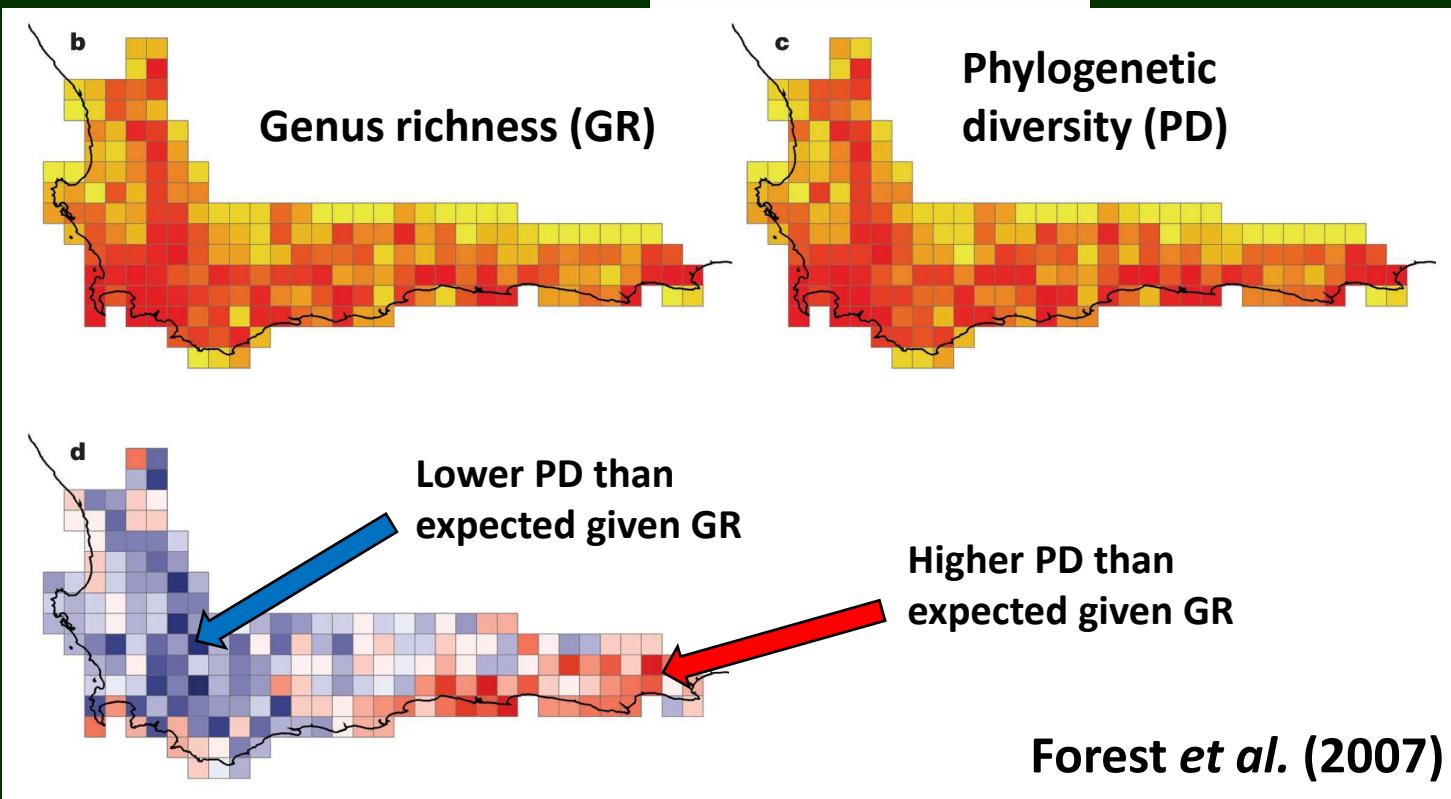
Spatial Phylogenetics

Taxon richness (TR): number of taxa (species, genera).

Phylogenetic diversity (PD): sum of branch lengths spanning a set of taxa in a phylogenetic tree.

$$PD = \sum_{\{c \in C\}} L_c$$

Faith (1992)



(2) ESPACIOS

Spatial Phylogenetics

Taxon richness (TR): number of taxa (species, genera).

Phylogenetic diversity (PD): sum of branch lengths spanning a set of taxa in a phylogenetic tree.

$$PD = \sum_{c \in C} L_c \quad \text{Faith (1992)}$$

Phylogenetic endemism (PE): sum of branch lengths spanning a set of taxa in a phylogenetic tree divided by their geographic range.

$$PE = \sum_{c \in C} \frac{L_c}{R_c} \quad \text{Rosauer *et al.* (2009)}$$

Relative phylogenetic diversity (RPD)

*Mishler *et al.* (2014)*

Relative phylogenetic endemism (RPE)

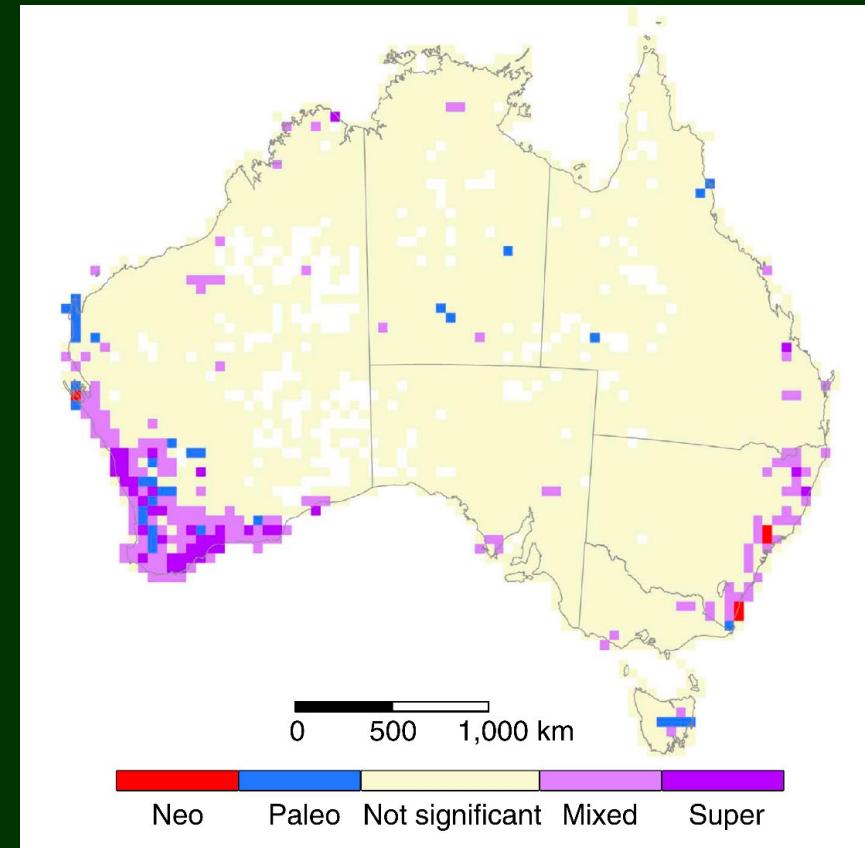
(2) ESPACIOS

Spatial Phylogenetics

Categorical analysis of neo- and paleoendemism (CANAPE):

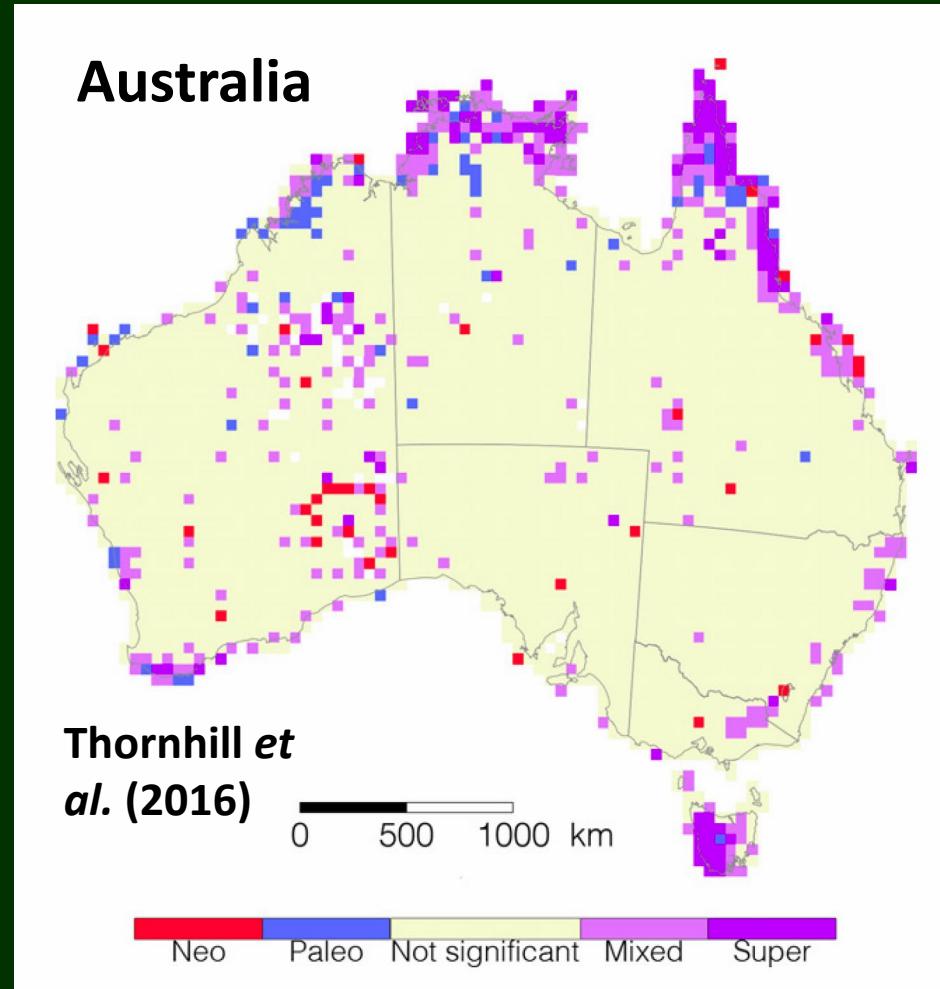
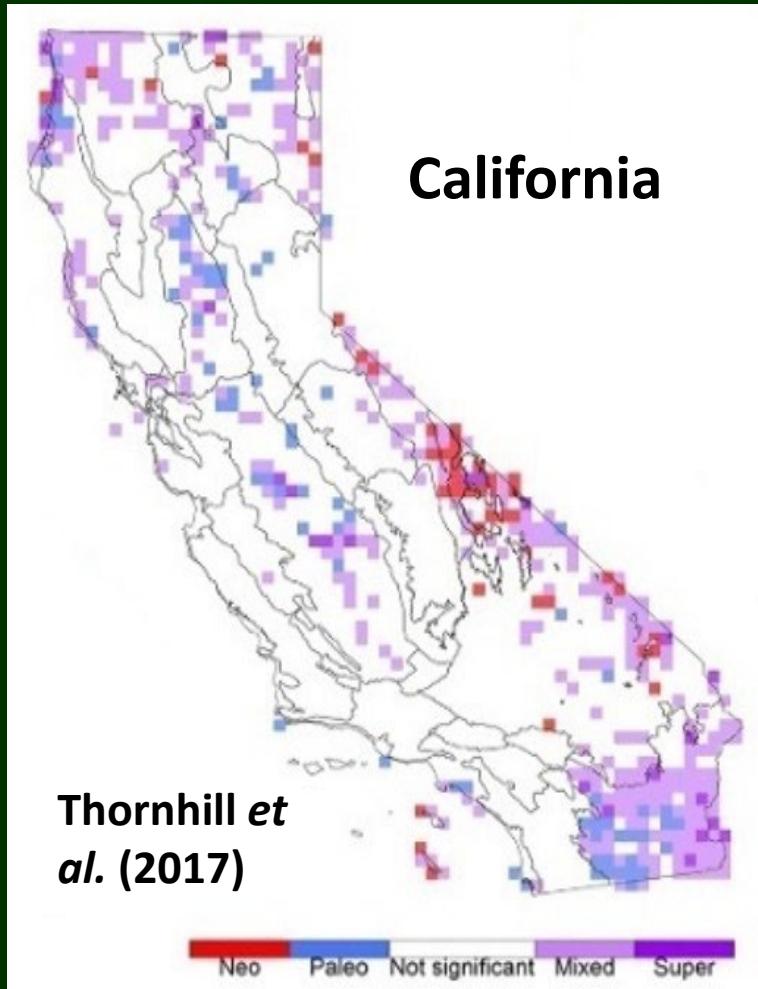
- Centres of paleoendemism: dominated by rare long branches.
- Centres of neoendemism: dominated by rare short branches.
- Centres of mixed endemism: mix of rare long and rare short branches.
- Centres of superendemism: high concentration of both rare long and rare short branches.

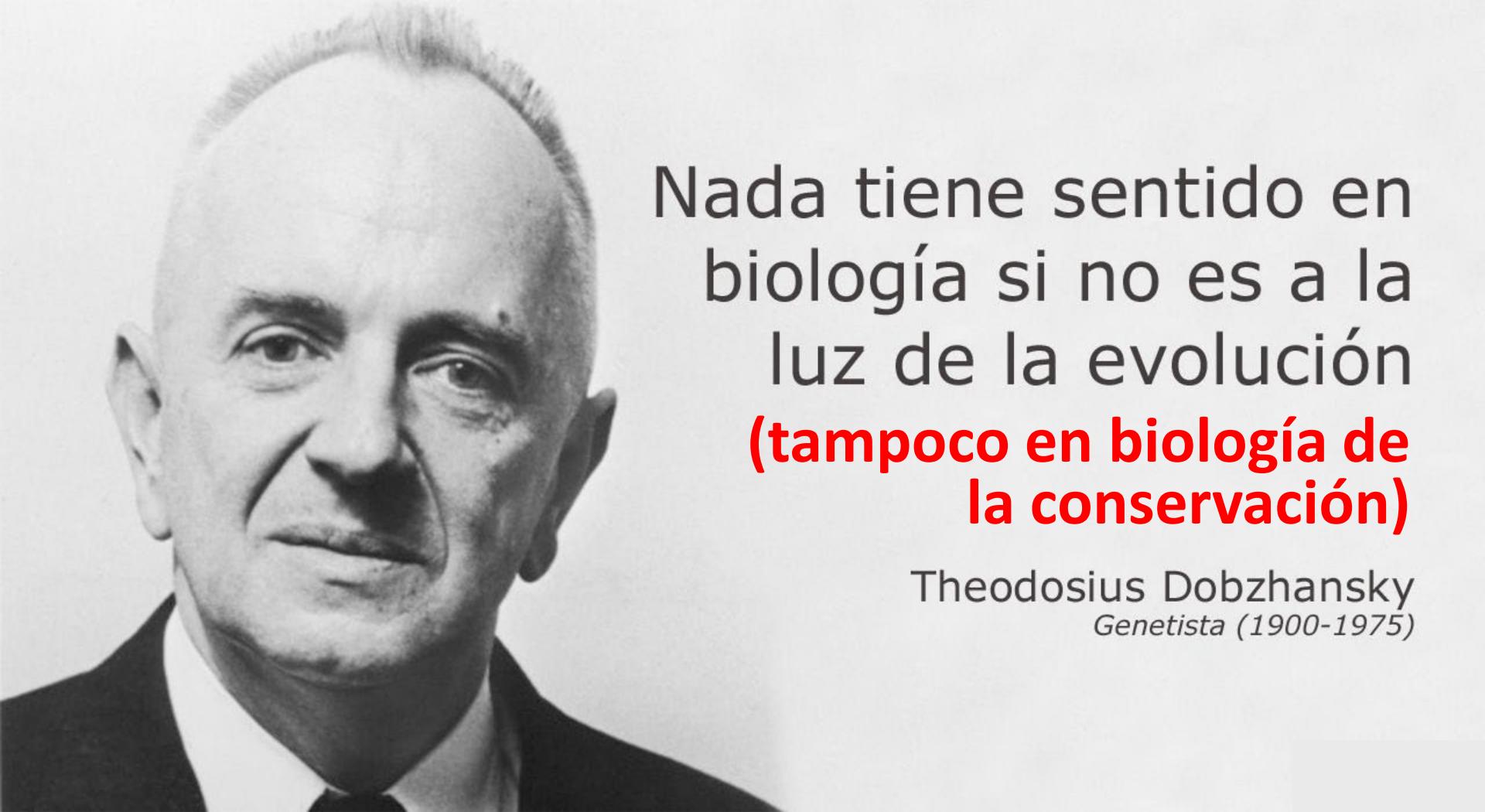
Mishler *et al.* (2014)



(2) ESPACIOS

Spatial Phylogenetics





Nada tiene sentido en
biología si no es a la
luz de la evolución
**(tampoco en biología de
la conservación)**

Theodosius Dobzhansky
Genetista (1900-1975)



Alberto J. Coello



Ignacio Ramos



Ana Otero



Sonia Molino



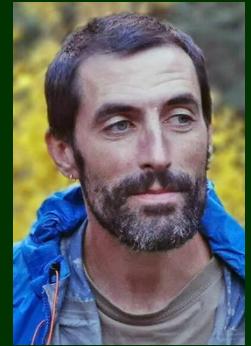
Álex Alonso



Angélica Gallego
Narbón



Carmen Gil



Antoni Buira



Pedro Jiménez
Mejías



Virginia
Valcárcel



Juan Carlos
Moreno Saiz



Llorenç
Sáez



Lisa Pokorny



Santiago
Martín Bravo



Rafael Molina
Venegas



Mónica Míguez



Ricarda Riina



Mario Mairal



Irene Villa
Machío



Carmen
Acedo



Felix Forest



Brent D.
Mishler



Rosa Scherson

¡GRACIAS!

Financiación: TED2021-131234A-I00 / PID2021-124234NA-I00 / PID2024-158450NB-I00



GOBIERNO
DE ESPAÑA

MINISTERIO
DE CIENCIA, INNOVACIÓN
Y UNIVERSIDADES



Funded by the
European Union
NextGenerationEU



Plan de
Recuperación,
Transformación
y Resiliencia

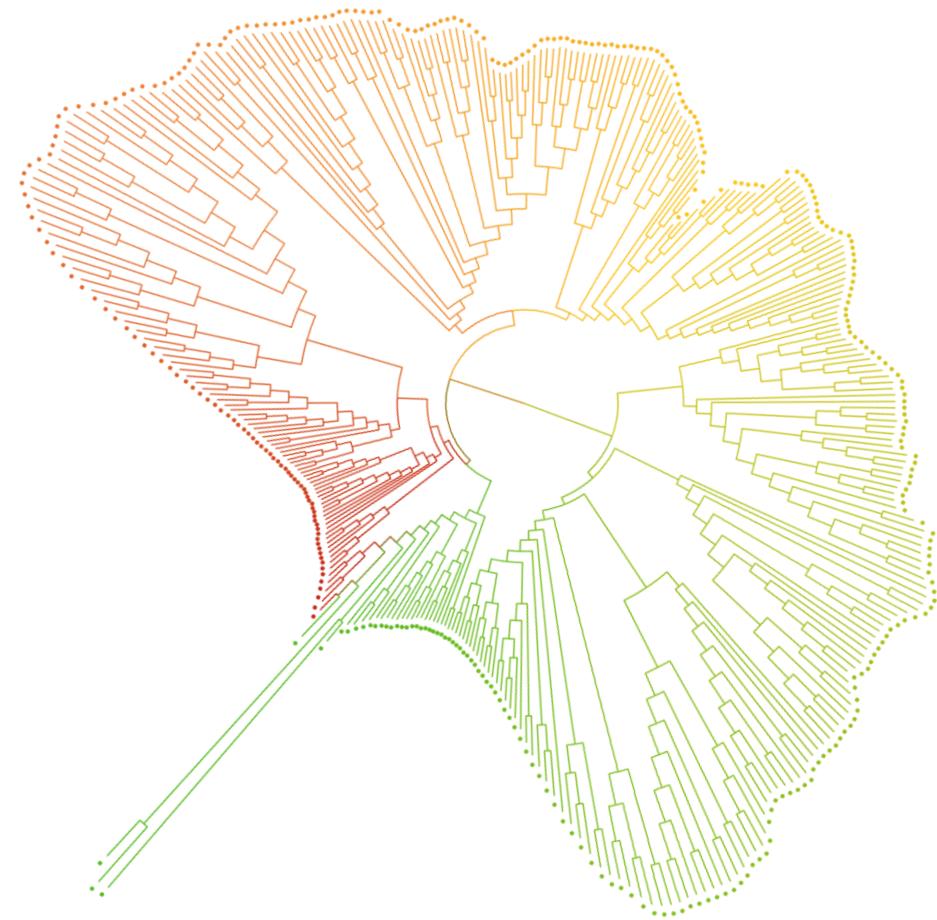


AGENCIA
ESTATAL DE
INVESTIGACIÓN

Taller

Análisis de patrones geográficos y evolutivos en
Biogeografía y Biología de la Conservación en plantas

Pt1. Conservación de Especies:
Especies Amenazadas y Filogenéticamente Singulares
(EDGE)



II CONGRESO DE
BOTÁNICA
SEBOT2025

Celebrando la diversidad de la Botánica

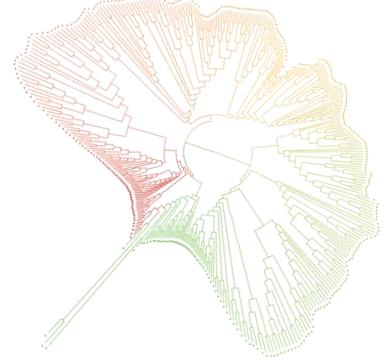


22-25/SEPTIEMBRE2025
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DE OLAVIDE
SEVILLA

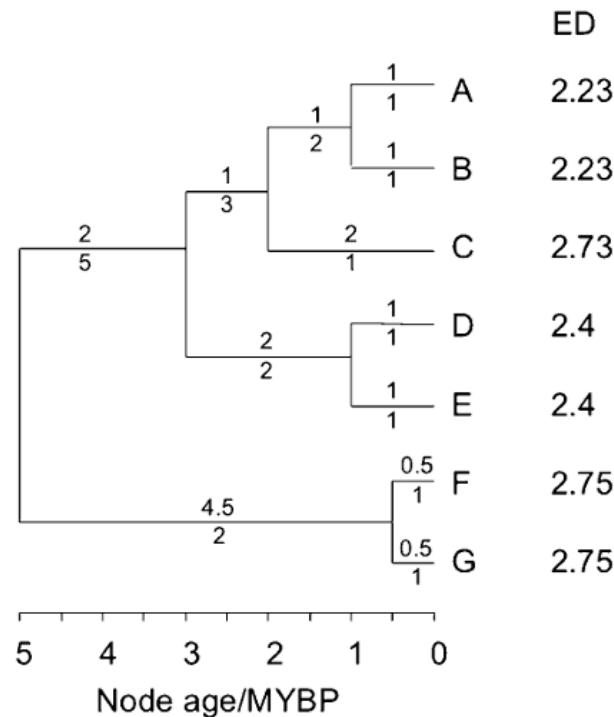


SEBOT
SOCIEDAD BOTÁNICA ESPAÑOLA

Evolutionarily Distinct and Globally Endangered (EDGE)



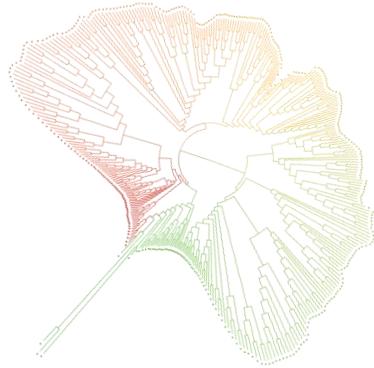
Singularidad evolutiva (filogenética)



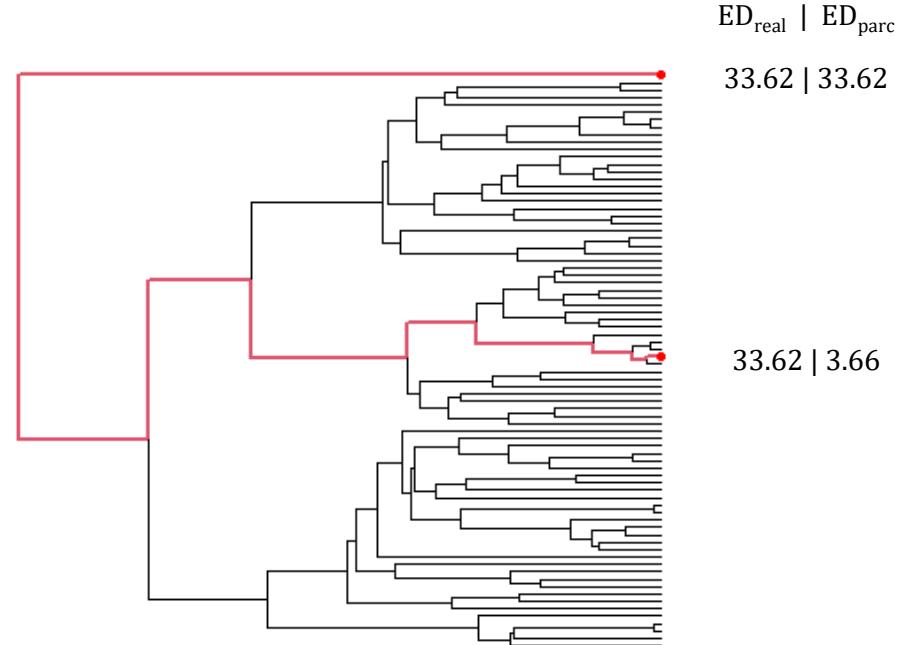
Estado de amenaza

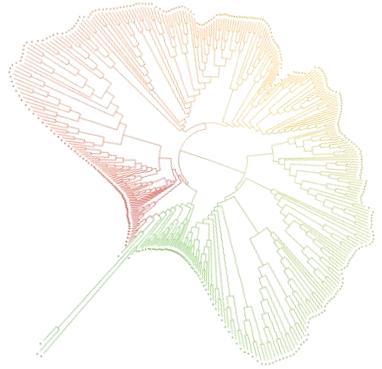


El índice EDGE



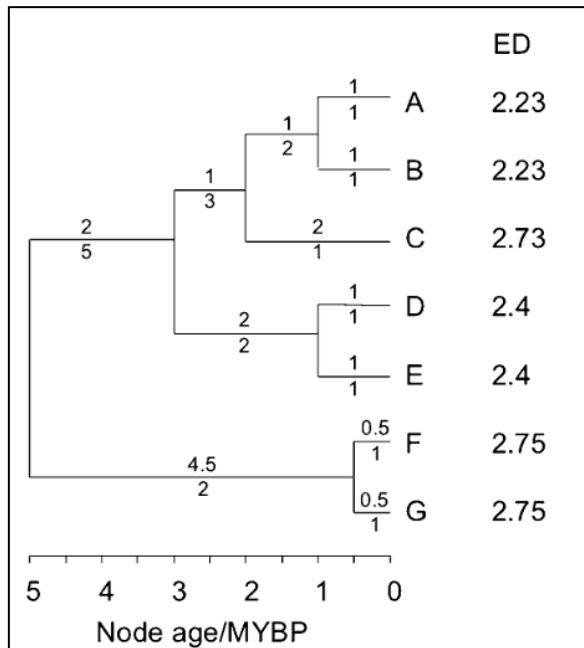
- Actualmente incluido como indicador de monitorización de biodiversidad (*Conv. Biol. Div.*).
- Una métrica **global**: especies poco ED pueden serlo mucho de una región
- Actualmente se está trabajando en cómo desagregar la información para su uso territorial





El índice EDGE*

ED



GE



$$EDGE = \ln(1+ED) + GE * \ln(2)$$

* EDGE clásico/EDGE1

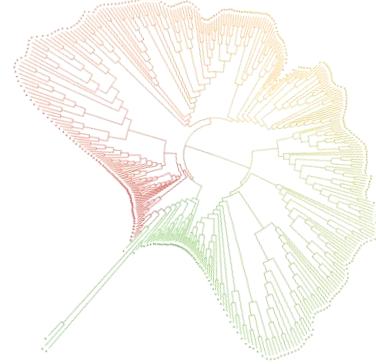
Cómo calcular el índice EDGE1



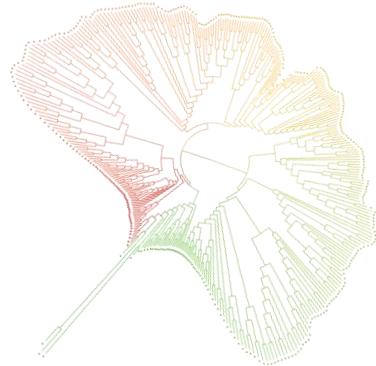
`EDGE_workshop_SEBOT.R`

```
install_github("iramsgutierrez/EDGEcalc")
library(EDGEcalc)
```

```
calculate_EDGE1(tree, table)
```

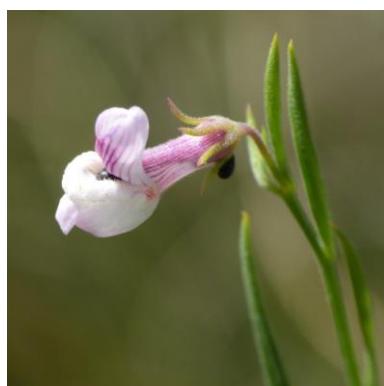


Cómo calcular el índice EDGE1

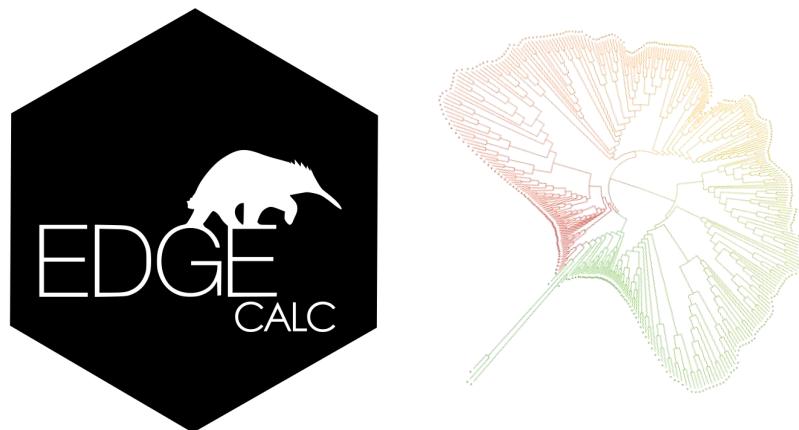


Datos: Antirrinea (Linaria, Antirrhinum...)

- 304 especies
- Filogenia global
- 112 especies evaluadas (192 DD/NE)



Cómo calcular el índice EDGE1

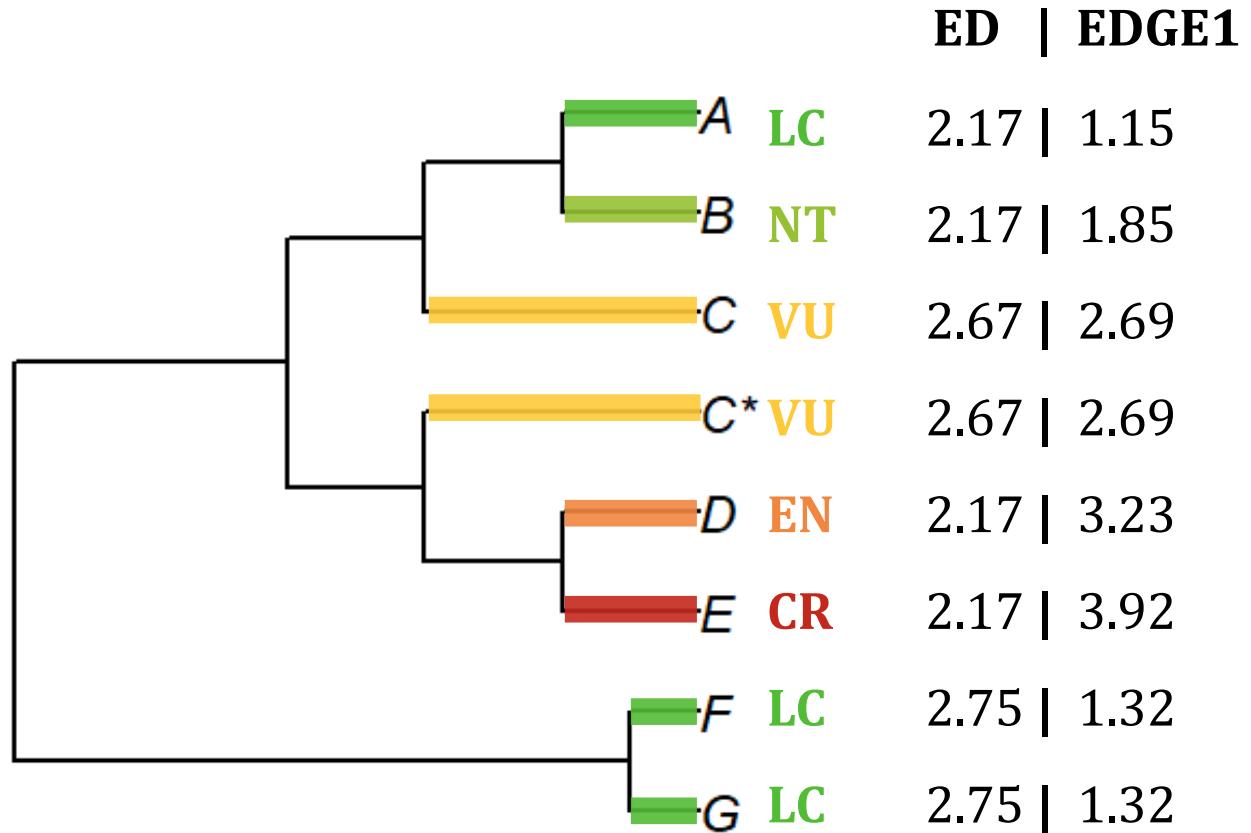
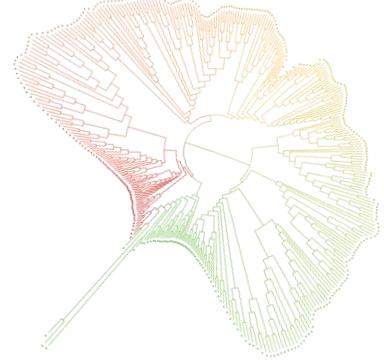


Datos: Antirrineas (*Linaria*, *Antirrhinum*...)

- 304 especies
- Filogenia global
- 112 especies evaluadas (192 DD/NE)

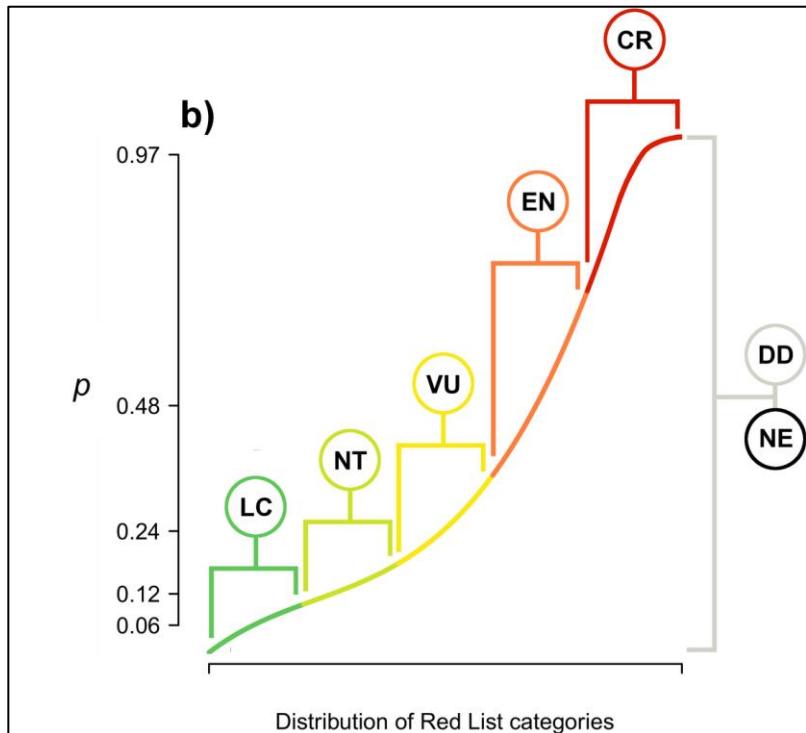
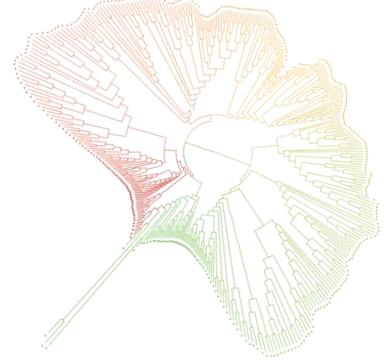
		species	RL.cat	ED	EDGE
74		Gadoria_falukei	CR	13.829567	5.469212
285	Pseudomisopates_rivas-martinezii		CR	7.816204	4.949180
7		Anarrhinum_fruticosum	CR	5.520645	4.647562
190		Linaria_nigricans	EN	10.123149	4.488470
64		Cymbalaria_fragilis	CR	4.458574	4.469776
106		Linaria_arenaria	CR	3.407741	4.255951
13		Antirrhinum_charidemi	CR	3.003122	4.159663
197		Linaria_orbensis	EN	5.572050	3.962267
37		Asarina_procumbens	NT	16.708348	3.567183
29		Antirrhinum_pertegasi	EN	3.096731	3.489631
34		Antirrhinum_subbaeticum	EN	2.875421	3.434096
237		Linaria_tursica	VU	6.703071	3.427913
...					
101		Linaria_amethystea	LC	1.453099	0.8973519
219		Linaria_saxatilis	LC	1.453099	0.8973519
241		Linaria_verticillata	LC	1.343784	0.8517667
1	Acanthorhinum_ramosissimum		NE	7.816204	NA
2		Albraunia_foveopilosa	NE	7.703761	NA
4		Anarrhinum_corsicum	NE	5.834951	NA
6		Anarrhinum_forskaohlii	NE	5.520645	NA
10		Anarrhinum_pedatum	NE	5.834951	NA
31		Antirrhinum_rothmaleri	NE	1.926068	NA
...					

El índice EDGE1

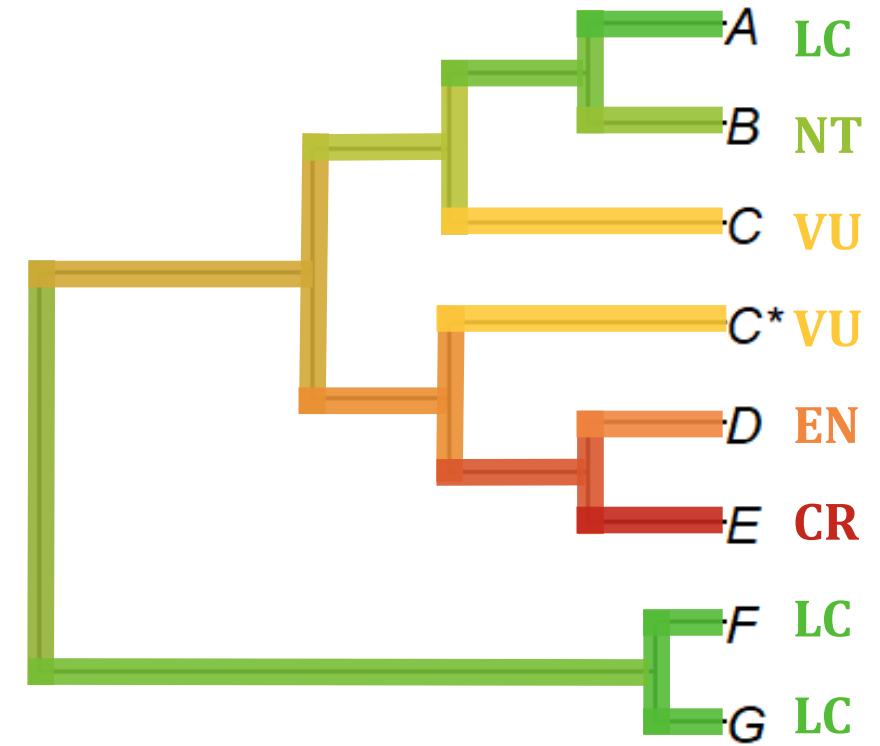


- Contexto-independiente
- Requiere evaluación (no DD / NE):
factible para grupos reducidos

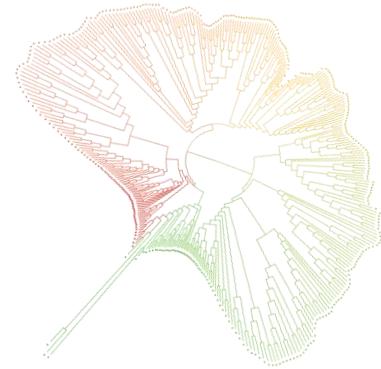
El índice EDGE2



- prob extinción muestreada
- ED dependiente de p_{ext}
“probabilidad de quedarte solo en un clado”
- Incl. DD y NE: grupos grandes



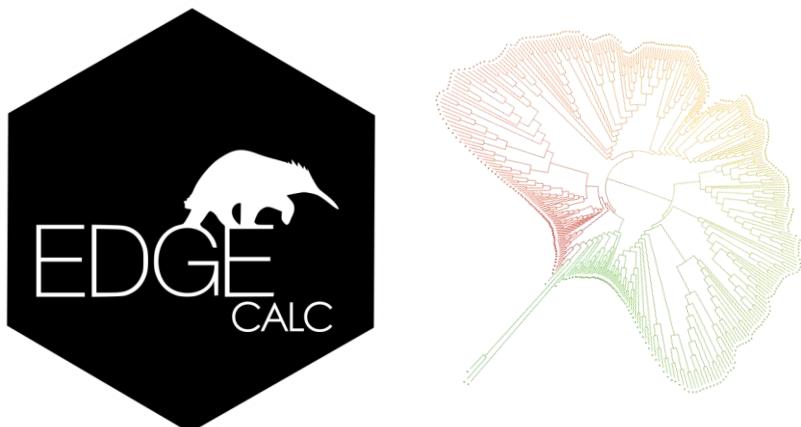
Cómo calcular el índice EDGE2



```
calculate_EDGE2(tree, table)
```



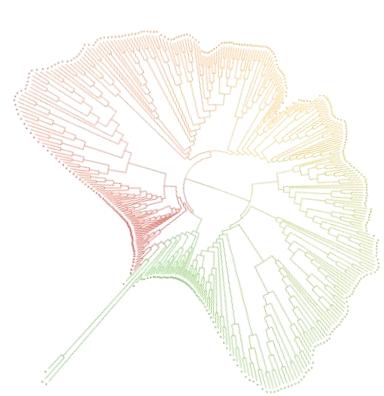
Cómo calcular el índice EDGE2



`calculate_EDGE2(tree, table)`

```
> print(EDGE2list, max = 100)
      species RL.cat     TBL     pext      ED      EDGE
35          Gadoria_falukei CR 12.113434 0.9158702 12.113435 11.094334
107         Sairocarpus_cornutus NE 7.022450 0.7606250 7.022470 5.341467
101        Pseudomisopates_rivas-martinezii CR 4.618680 0.8659967 6.088920 5.272984
81          Albraunia_foveopilosa NE 5.110476 0.6929860 5.125372 3.551811
253         Linaria_microsepala NE 3.929060 0.5576304 5.627242 3.137921
46          Epixiphium_wislizeni NE 16.058292 0.1952968 16.058292 3.136133
75 chaenorhinum_litorale_subsp_pterosporum NE 2.487980 0.9385356 3.307190 3.103915
100         Acanthorrhinum_ramosissimum NE 4.618680 0.3727807 8.034154 2.994977
254         Linaria_peloponnesiaca NE 3.929060 0.5116803 5.779743 2.957381
295         Linaria_lineolata NE 3.266409 0.8491973 3.266410 2.773827
49          Maurandya_barclaiana NE 5.124398 0.4154875 6.198303 2.575317
181         Linaria_armeniaca NE 3.812653 0.4994294 4.869042 2.431743
84          chaenorhinum_spicatum NE 2.216932 0.9160586 2.618745 2.398924
19          Nanorrhinum_elegans NE 2.950230 0.8101799 2.950354 2.390318
50          Lophospermum_breedlovei NE 2.515007 0.7681269 3.058088 2.348999
69          schweinfurthia_pterosperma NE 1.360590 0.8717602 2.621632 2.285435
```

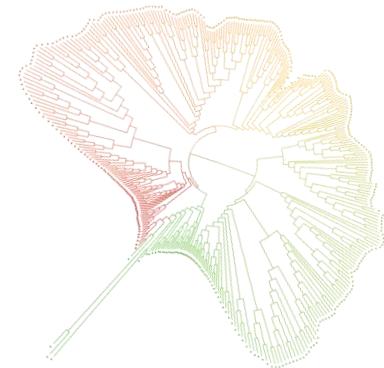
Cómo calcular el índice EDGE2



```
calculate_EDGE2_multiple(tree, table, n.iter)
```



Cómo calcular el índice EDGE2



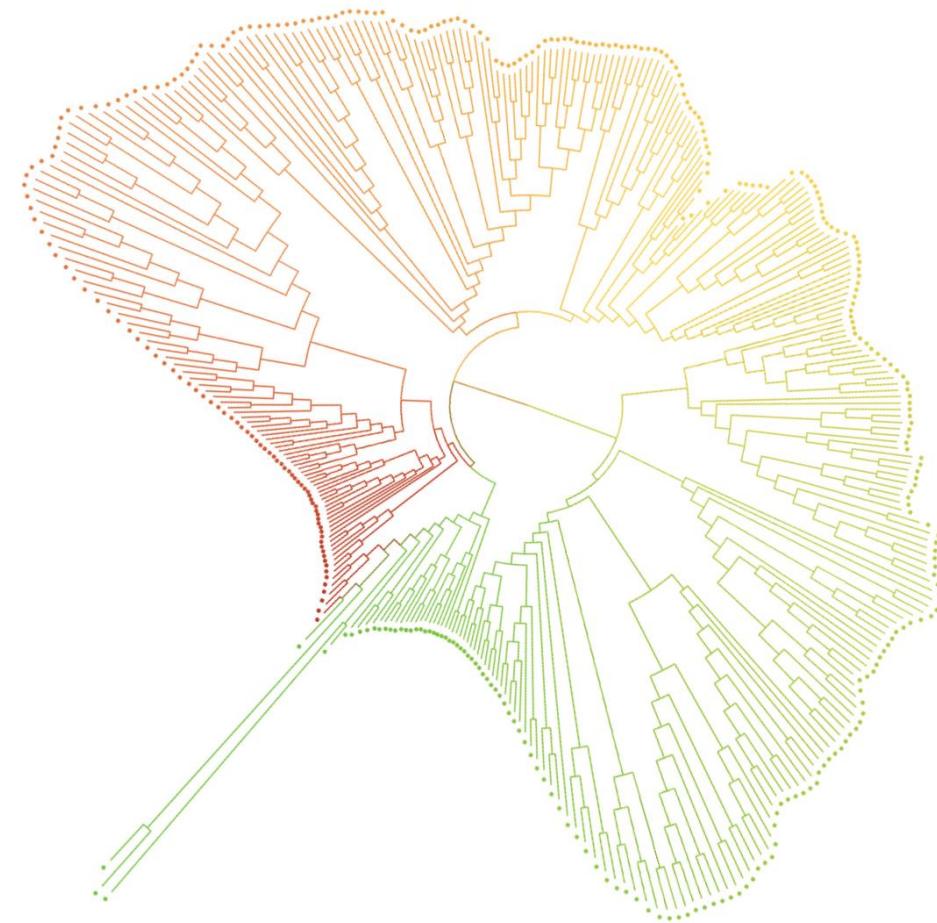
```
calculate_EDGE2_multiple(tree, table, n.iter)
```

```
> print(EDGE2list_summ, n = 15)
# A tibble: 304 × 6
  species      RL.cat meanTBL meanpext meanED meanEDGE
  <chr>        <chr>    <dbl>   <dbl>   <dbl>   <dbl>
1 Gadoria_falukei CR       12.1    0.930   12.1    11.3 
2 Pseudomisopates_rivas-martinezii CR       4.62    0.925   5.77    5.34 
3 Epixiphium_wislizeni   NE       16.1    0.310   16.1    4.97 
4 Holmgrenanthe_petrophila NE       10.8    0.292   10.9    3.17 
5 Linaria_nigricans    EN       5.00    0.513    5.54    2.84 
6 Linaria_orbensis     EN       4.95    0.504    4.95    2.50 
7 Acanthorrhinum_ramosissimum NE       4.62    0.291   8.27    2.41 
8 Sairocarpus_cornutus   NE       7.02    0.342   7.02    2.40 
9 Maurandya_barclaiana  NE       5.12    0.345   6.70    2.39 
10 Anarrhinum_fruticosum CR       2.13    0.888   2.54    2.26 
11 Sairocarpus_kingii    NE       6.46    0.339   6.46    2.19 
12 Pseudorontium_cyathiferum NE       7.89    0.271   7.91    2.15 
13 Maurandella_antirrhiniflora NE       5.12    0.269   7.16    2.00 
14 Asarina_procumbens    NT       15.3    0.127   15.3    1.94 
15 Linaria_ventricosa    NE       5.70    0.334   5.70    1.90
```

Taller

Análisis de patrones geográficos y evolutivos en
Biogeografía y Biología de la Conservación en plantas

Pt 2. Conservación de espacios:
Análisis de Categorización de Neo- Y Paleo-Endemismos
(CANAPE)



II CONGRESO DE
BOTÁNICA
SEBOT2025

Celebrando la diversidad de la Botánica



22-25/SEPTIEMBRE2025
UNIVERSIDAD PABLO
DE OLAVIDE
SEVILLA



SEBOT
SOCIEDAD BOTÁNICA ESPAÑOLA

Diversidad filogenética

Biological Conservation 1992, 61, 1–10



Conservation evaluation and phylogenetic diversity

Daniel P. Faith

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(Received 13 May 1991; revised version received 28 September 1991; accepted 11 November 1991)

- La diversidad filogenética (PD) es una medida de la diversidad de linajes en un área

Protecting biological diversity with limited resources may require placing conservation priorities on different taxa. A system of priorities that reflects the value of taxonomic diversity can be achieved by setting priorities such that the subset of taxa that is protected has maximum underlying feature diversity. Such feature diversity in taxa subsets is difficult to estimate directly, but can be predicted by calculating phylogenetic diversity (PD). In this study, a simple measure of phylogenetic diversity is defined based on cladistic information. The measure of phylogenetic diversity, PD, is contrasted with a measure of taxic diversity recently developed by Vane-Wright *et al.* (*Biol. Conserv.*, **55**, 1991). In re-examining reserve-selection scenarios based on a phylogeny of bumble bees (Apidae), PD produces quite different priorities for species conservation, relative to taxic diversity. The potential application of PD at levels below that of the species is then illustrated using a mtDNA phylogeny for populations of crested newts *Triturus cristatus*. Calculation of PD for different population subsets shows that protection of populations at either of two extremes of the geographic range of the group can significantly increase the phylogenetic diversity that is protected.

INTRODUCTION

The goal of conserving biological diversity will not be met without addressing the gap that exists between basic conceptual representations of biological diversity and the actual requirements for practical, working definitions of biological diversity for conservation evaluation. One difficulty in working with biological diversity in practice is that the accepted units of diversity (usually species) may be hard to identify and their geographic distribution hard to estimate (the 'assessment' problem, McNeely *et al.*, 1990). Another difficulty is that limited resources for conservation may impose practical limitations on the conservation of these units of diversity (the 'resources' problem, McNeely *et al.*, 1990).

Research on biological diversity has begun to respond to these challenges. In response to the difficulties of assessing biological diversity at the

species level (both because of limits of taxonomic knowledge and problems in estimating the number of species in any particular place), other biological units or attributes have been identified that can be used in place of species. Units based on environmental types or community types mean that biological diversity is more generally represented by some measure of the number of different biological 'attributes' present (Pressey & Nicholls, 1989). Similarly, Noss (1990) recommends that the vague concept of biological diversity be replaced in practice by the use of a number of measurable *indicators* of biodiversity, defined at various levels of biological organisation (landscape, community, population, or genome).

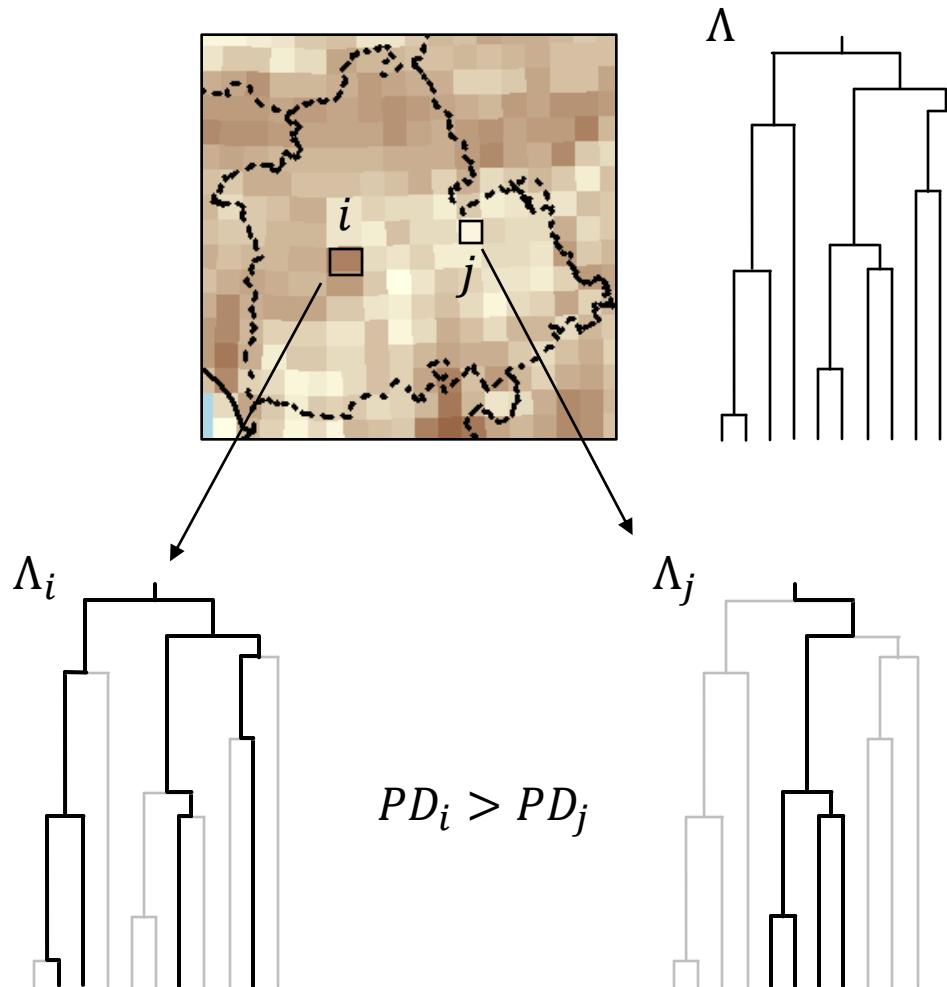
The resources problem has prompted research relating to optimal strategies for conservation evaluation, including procedures for the design of nature reserves. For example, the minimum number of areas can be found which, as a set, meets the requirement that each species (or other attribute) is represented a fixed number of times (Margules *et al.*, 1988). When limited resources

Biological Conservation 0006-3207/92/S05.00 © 1992 Elsevier Science Publishers Ltd, England. Printed in Great Britain

1

Diversidad filogenética

$$PD_i = \sum_{\lambda_i \in \Lambda_i} l_{\lambda_i}$$



Endemismo ponderado

Journal of Biogeography, 28, 183–198



Endemism in the Australian flora

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and ³Department of Botany, University of Cape Town, Rondebosch 7700, South Africa

Abstract

Aim To detect centres of vascular plant endemism at a continental scale by analysis of specimen-based distributional data and to relate any pattern to environmental factors and history.

Location Australia.

Methods Presence of 8468 seed plant species-level taxa throughout continental Australia and Tasmania was mapped on a 1° grid to visualize the pattern of species richness. This sample comprises half the known flora. Three indices of endemism were calculated but we preferred one that is unrelated to species richness, so that these two concepts could be distinguished in practice. Centres of endemism were detected by simple mapping and by spatial autocorrelation analysis (SAC). Linear regression was used to examine the relationship of the patterns of species richness and endemism to latitude, topography and climate.

Results Both species richness and endemism vary greatly across the continent but in most cases the same centres were high in both richness and endemism. Twelve distinct centres were identified. The major centres of both diversity and endemism are south-western Australia, the Border Ranges between New South Wales and Queensland, the Wet Tropics near Cairns, Tasmania and the Iron-McLwraith Range of eastern Cape York Peninsula. The last centre appears to be more significant than recognized by past authors. Whether this is a true Australian centre of endemism, or is largely an outlier of the flora of Papua New Guinea, is explored. Another centre, in the Adelaide-Kangaroo Island region, has been overlooked altogether by previous authors. Regression analysis did not find a simple climatic explanation of the observed patterns. There was a suggestion that topographic variation within the 1° cells may be positively correlated with endemism, which is consistent with mountainous regions functioning as refugia. One clear result is that all the major centres of endemism are near-coastal. A likely explanation is that Pleistocene expansions of the central desert have been a powerful limitation on the viability of refugia for narrowly endemic species. All the centres of endemism lie outside the estimated limits of the expanded arid zone at the last glacial maximum (18,000 yr bp). In particular, the 'Central Australian Mountain Ranges' centre of plant diversity and endemism' of Boden & Given (1995) is detected as a strong centre of species richness, but not at all as a centre of endemism. This is despite good sampling of this region.

Main conclusions Endemism can be distinguished from species richness by using an appropriate index and mapping of such indices can detect centres of endemism. This study demonstrates the value of specimen based distributional data, such as is held in state herbaria and museums.

Keywords

Biodiversity, endemism, species richness, Australia, Pleistocene, refugia, extinction, climate.

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Endemismo ponderado

$$WE_i = \sum_{s_i \in S_i} \frac{1}{r_{s_i}}$$

Area_i (una especie)



Gyrocarpum oppositifolium
(distribución muy reducida)

↓ r_{s_i}

$$WE_i > WE_j$$

Area_j (una especie)



Capsella bursa-pastoris
(distribución paleártica)

↑ r_{s_j}

Endemismo filogenético

- El endemismo filogenético (PE) mide cómo de rica es un área en taxones filogenéticamente aislados y de distribución reducida

$$PE_i = PD_i \cdot WE_i$$

$$PE_i = \sum_{\lambda_i \in \Lambda_i} l_{\lambda_i} \cdot \frac{1}{r_{\lambda_i}}$$

MOLECULAR ECOLOGY

Molecular Ecology (2009) 18, 4061–4072

doi: 10.1111/j.1365-294X.2009.04311.x

Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history

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Abstract

We present a new, broadly applicable measure of the spatial restriction of phylogenetic diversity, termed *phylogenetic endemism* (PE). PE combines the widely used phylogenetic diversity and weighted endemism measures to identify areas where substantial components of phylogenetic diversity are restricted. Such areas are likely to be of considerable importance for conservation. PE has a number of desirable properties not combined in previous approaches. It assesses endemism consistently, independent of taxonomic status or level, and independent of previously defined political or biological regions. The results can be directly compared between areas because they are based on equivalent spatial units. PE builds on previous phylogenetic analyses of endemism, but provides a more general solution for mapping endemism of lineages. We illustrate the broad applicability of PE using examples of Australian organisms having contrasting life histories: pea-flowered shrubs of the genus *Daviesia* (Fabaceae) and the Australian species of the Australo-Papuan tree frog radiation within the family Hylidae.

Keywords: *Daviesia*, endemism, Hylidae, phylogenetic diversity, phylogenetic endemism, weighted endemism

Received 18 February 2009; revision received 14 May 2009; accepted 1 June 2009

Introduction

Measures of endemism are central to characterizing and mapping the distribution of biological diversity, whether to understand the spatial component in evolution or to identify areas of priority for conservation, such as global biodiversity hotspots (Myers *et al.* 2000). However, because diversity, or evolutionary history, is distributed unequally between taxa (Vane-Wright *et al.* 1991) as well as between areas, assessing endemism of species alone may not be sufficient to identify concentrations of spatially restricted evolutionary diversity (Sechrest *et al.* 2002; Mooers & Atkinson 2003). Biodiversity metrics can better reflect spatial diversity patterns for biogeography and conservation planning by incor-

porating evolutionary history through phylogenetic relationships. These benefits have been recognized widely, and a range of techniques have been developed to do this (Vane-Wright *et al.* 1991; Crozier 1992; Faith & Cranston 1992; Solow *et al.* 1993).

Phylogenetic diversity (PD; Faith 1992; Moritz & Faith 1998) is a simple and widely used measure which takes the length of branches in a phylogenetic tree as a surrogate for unique or shared features represented by the taxa in the tree. By counting the length of the branches linking a set of taxa through the root of the tree, PD elegantly accounts for shared evolutionary history to reflect the combined contribution made by these taxa to the overall diversity of the group. A strength of the PD method is that by shifting the measure of diversity from species or nodes to units of phylogenetic variation, it becomes relatively robust to taxonomic uncertainty and change (Mace *et al.* 2003). For example, the collapse of

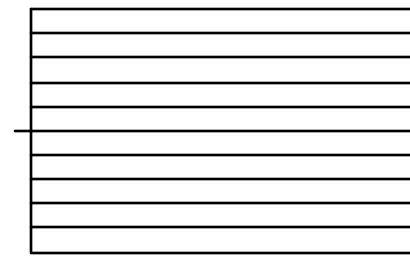
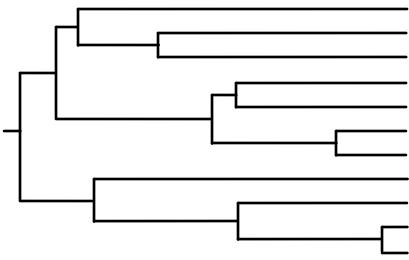
Correspondence: Dan Rosauer, Fax: 61-2-6246-5249;
E-mail: dan.rosauer@csiro.au

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Rosauer *et al.* (2009) Mol. Ecol. 18(19): 4061–4072

WE vs PE

- El WE puede ser entendido como un PE sin longitudes de rama



$$l_{\lambda_i} = 1 \quad \forall \lambda_i \in \Lambda_i$$

$$PE_i = \sum_{\lambda_i \in \Lambda_i} l_{\lambda_i} \cdot \frac{1}{r_{\lambda_i}}$$

$$PE_i = \sum_{\lambda_i \in \Lambda_i} l_{\lambda_i} \cdot \frac{1}{r_{\lambda_i}} = \sum_{\lambda_i \in \Lambda_i} \frac{1}{r_{\lambda_i}} = WE_i$$

Métricas relativas

- Diseñadas sobre PD y PE
- Mientras PD y PE están altamente correlationados con la riqueza, la PD relativa (RPD) y el PD relativo (RPE) son más robustos
- RPD y RPE comparan los valores de PD o PE del árbol real con los calculados sobre un árbol sin longitudes de rama



ARTICLE

Received 20 Apr 2014 Accepted 20 Jun 2014 Published 18 Jul 2014

Phylogenetic measures of biodiversity and neo- and paleo-endemism in Australian *Acacia*

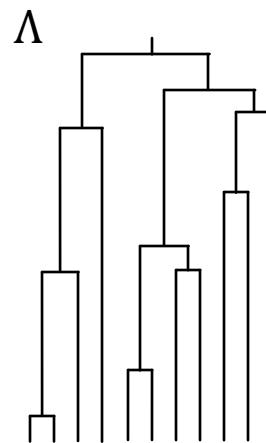
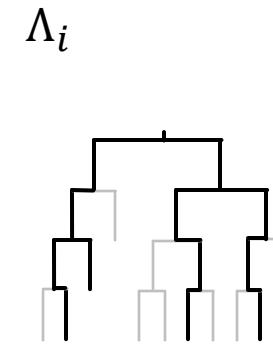
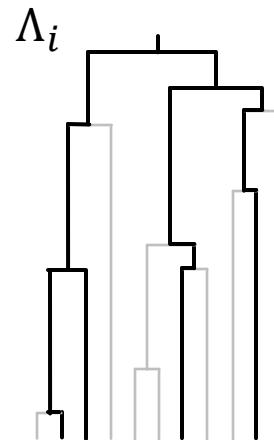
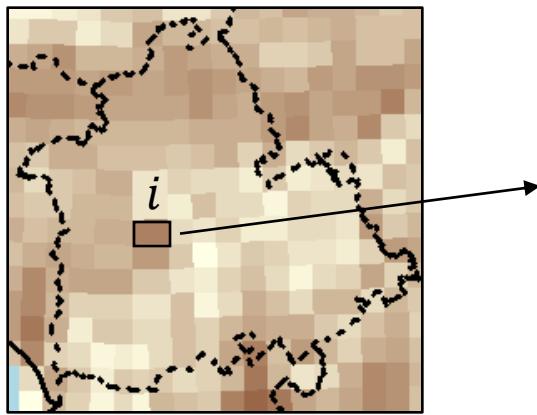
Brent D. Mishler^{1,2}, Nunzio Knerr¹, Carlos E. González-Orozco^{1,3}, Andrew H. Thornhill^{1,4}, Shawn W. Laffan⁵ & Joseph T. Miller¹

Understanding spatial patterns of biodiversity is critical for conservation planning, particularly given rapid habitat loss and human-induced climatic change. Diversity and endemism are typically assessed by comparing species ranges across regions. However, investigation of patterns of species diversity alone misses out on the full richness of patterns that can be inferred using a phylogenetic approach. Here, using Australian *Acacia* as an example, we show that the application of phylogenetic methods, particularly two new measures, relative phylogenetic diversity and relative phylogenetic endemism, greatly enhances our knowledge of biodiversity across both space and time. We found that areas of high species richness and species endemism are not necessarily areas of high phylogenetic diversity or phylogenetic endemism. We propose a new method called categorical analysis of neo- and paleo-endemism (CANAPE) that allows, for the first time, a clear, quantitative distinction between centres of neo- and paleo-endemism, useful to the conservation decision-making process.

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⁴Australian Tropical Herbarium, James Cook University, Cairns, Queensland 4870, Australia.
⁵Centre for Ecosystem Science, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, New South Wales 2052, Australia. Correspondence and requests for materials should be addressed to B.D.M. (email: bmishler@berkeley.edu).

15:4473 | DOI: 10.1038/ncomms5473 | www.nature.com/naturecommunications
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Diversidad filogenética relativa

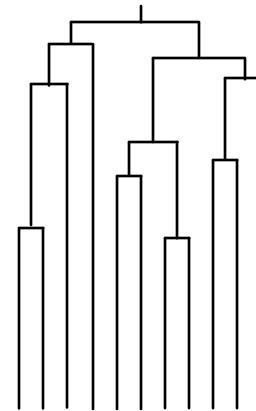


$$PD_{orig_i} = \sum_{\lambda_i \in \Lambda_i} l_{\lambda_i} \quad \text{---} \quad PD_{alt_i} = \sum_{\lambda'_i \in \Lambda'_i} l_{\lambda'_i}$$

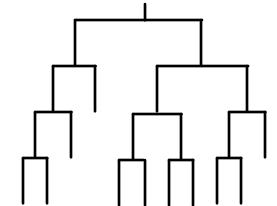
$$RPD_i = \frac{PD_{orig_i}}{PD_{alt_i}}$$

Interpretación de RPD

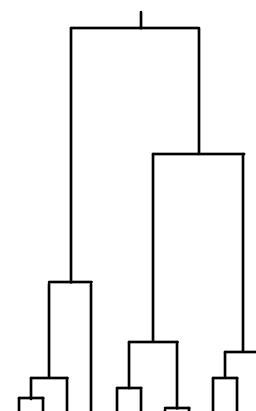
- $RPD > 1 \Rightarrow$ Sobrerepresentación de ramas largas (refugios, competencia entre parientes cercanos...)



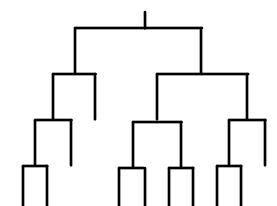
$$PD_{org} > PD_{alt}$$



- $RPD < 1 \Rightarrow$ Sobrerepresentación de ramas cortas (divergencia reciente, filtrado de rasgos conservados filogenéticamente...)



$$PD_{org} < PD_{alt}$$



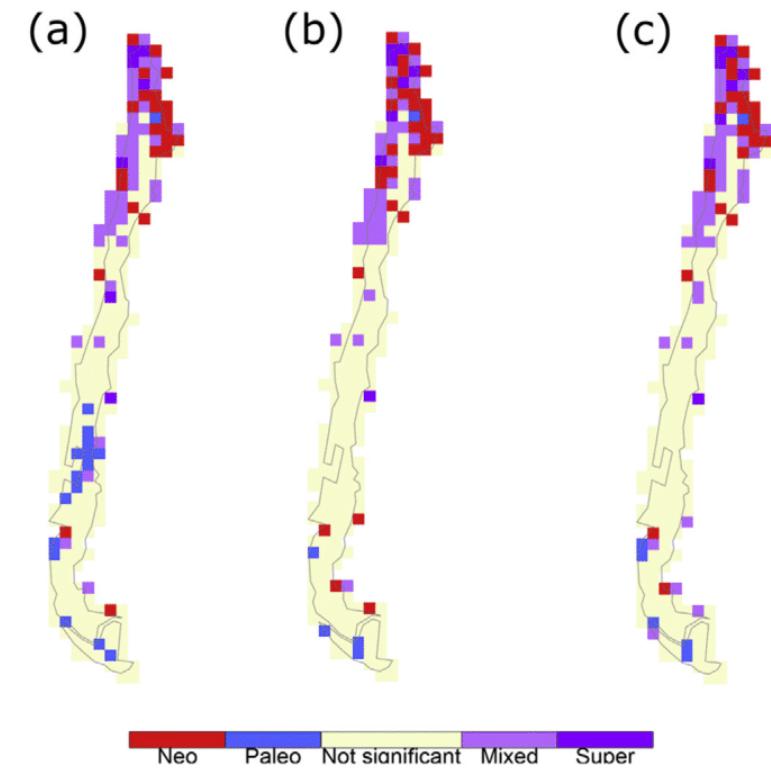
Endemismo filogenético relativo

- RPE es matemáticamente equivalente al RPD, pero para el PE
- $RPE > 1 \Rightarrow$ Sobrerepresentación de ramas largas de distribución reducida (paleo-endemismos)
- $RPE < 1 \Rightarrow$ Sobrerepresentación de ramas cortas (neo-endemismos)

$$RPE_i = \frac{PE_{ori_i}}{PE_{alt_i}}$$

CANAPE

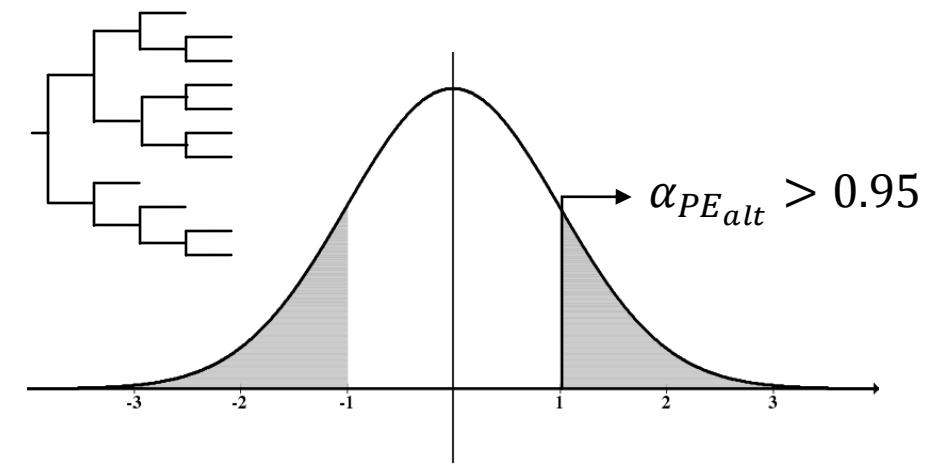
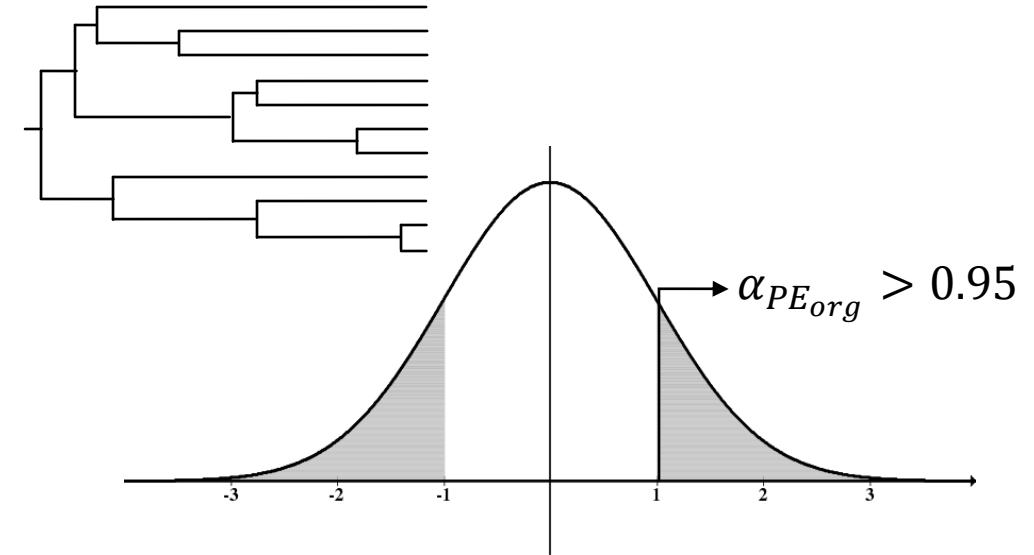
- Análisis de Categorización de Neo- Y Paleo-Endemismos
- Análisis en dos pasos para categorizar centros de endemismo
- Tipos:
 - Neo-endemismo
 - Paleo-endemismo
 - Endemismo-mixto
 - Super-endemismo



Scherson *et al.* (2017) *Mol. Phylogenet. Evol.* 112: 88-95

CANAPE (paso 1)

- Detectar centros de endemismo
- Análisis de una cola del PE
- El árbol alternativo se utiliza para detectar los taxones raros de ramas cortas

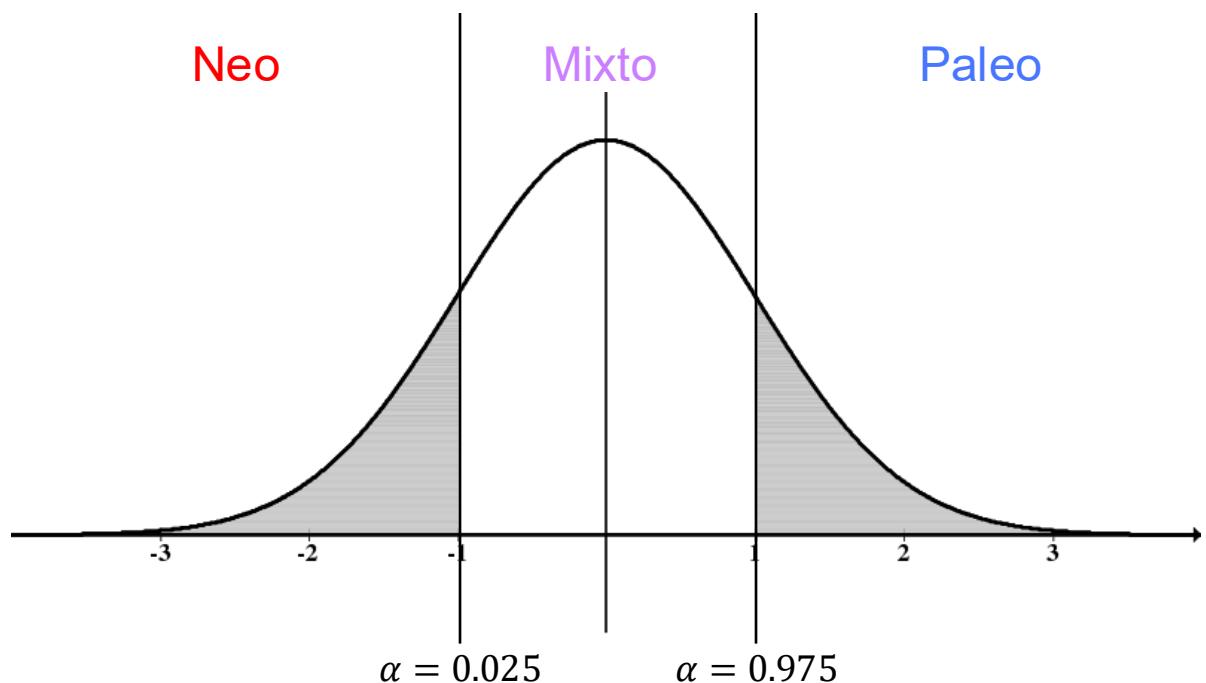


CANAPE (paso 2)

- Sólo se aplica a los centros de endemismos detectados en el paso 1

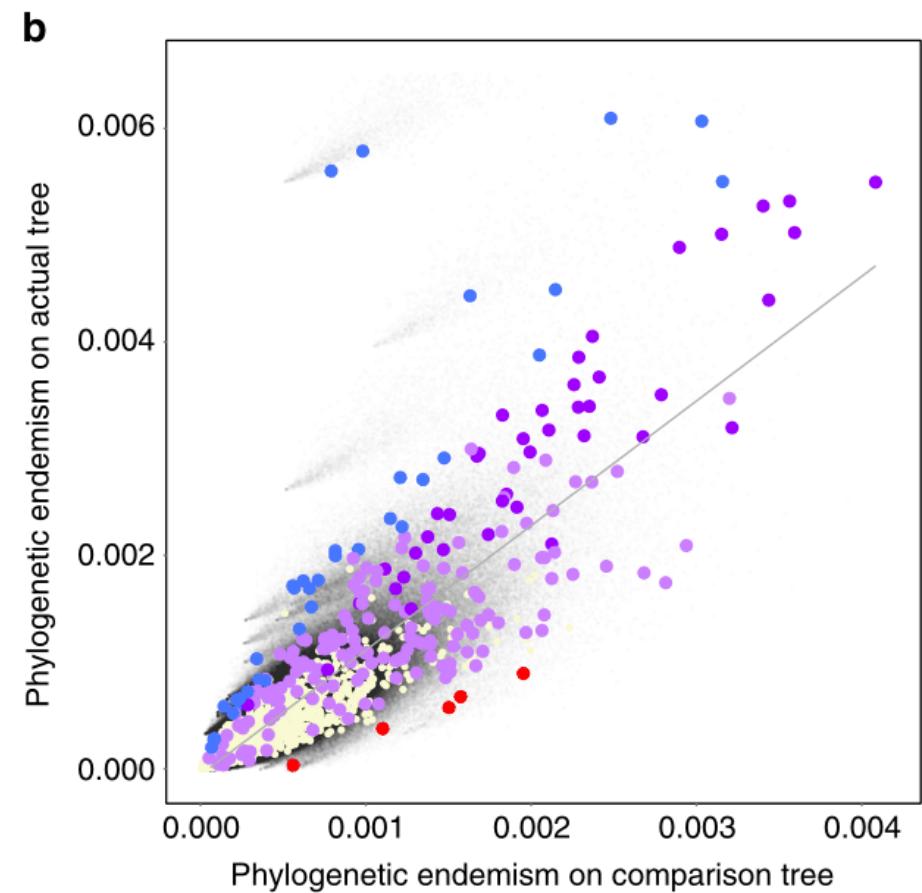
$$\alpha_{PE_{org}} > 0.95 \vee \alpha_{PE_{alt}} > 0.95$$

- Análisis de dos colas sobre el RPE para clasificar los centros de endemismo:
 - $\alpha_{RPE} < 0.025 \Rightarrow$ Neo-endemismo
 - $0.025 < \alpha_{RPE} < 0.975 \Rightarrow$ Endemismo-mixto
 - $\alpha_{RPE} > 0.975 \Rightarrow$ Paleo-endemismo



CANAPE (paso dos)

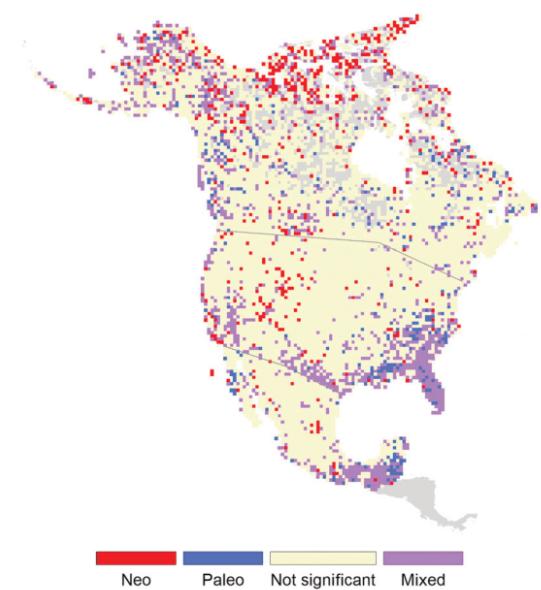
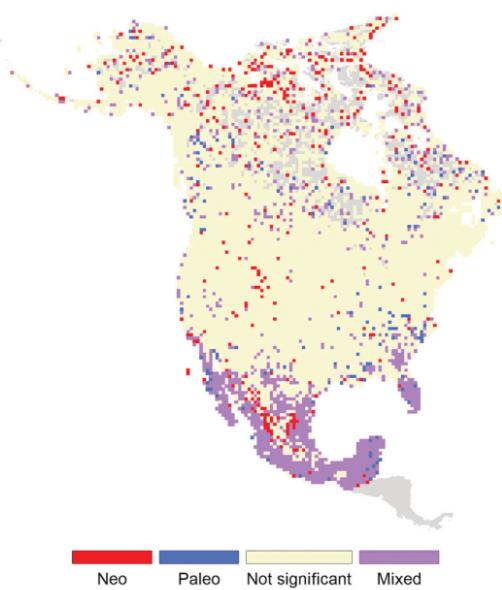
- Super-endemismo: subcategoría del endemismo mixto
- Condiciones (todas):
 - $0.025 < \alpha_{RPE} < 0.975$ (Endemismo-mixto)
 - $\alpha_{PE_{org}} > 0.99$
 - $\alpha_{PE_{alt}} > 0.99$



Mishler *et al.* (2014) *Nat. Commun.* 5(1): 4473

Limitaciones y problemas

- Intenso factor borde
- Parientes fuera del área de estudio
- Requiere filogenias muy completas
- Requiere distribuciones precisas



Mishler *et al.* (2020) *J. Syst. Evol.* 58(4): 393-405

Cómo calcular CANAPE y otras métricas de filogenia espacial

R scripts/canape.R



canaper

The goal of `canaper` is to enable [categorical analysis of neo- and paleo-endemism \(CANAPE\)](#) in R.

- For [tutorials](#), see the [canaper website](#).

Installation

The stable version can be installed from [CRAN](#):

```
install.packages("canaper")
```



Links

[View on CRAN](#)

[Browse source code](#)

[Report a bug](#)

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[Full license](#)

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Community

[Contributing guide](#)

Citation

[Citing canaper](#)

Developers

Joel H. Nitta

The development version can be installed from [r-universe](#) or [github](#):

```
# r-universe
options(repos = c(
  ropensci = "https://ropensci.r-universe.dev/",
  CRAN = "https://cran.rstudio.com/"))
```