Extinction 2: Conservation

https://www.youtube.com/watch?v=W4nFwAvZ0OI

ABC News

Brian O'Meara

EEB464 Fall 2018

Learning objectives

- Understand about phylogenetic diversity as a conservation metric
- Be able to understand how estimates of conservation risk can take into account relatedness
- Use phylogeny to predict extinction risk

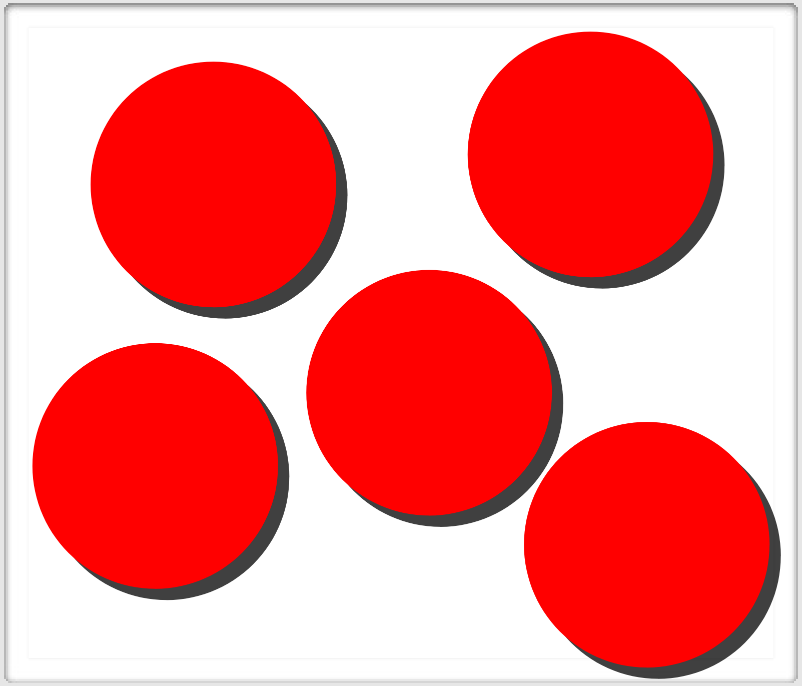
What to save

Causes of risk

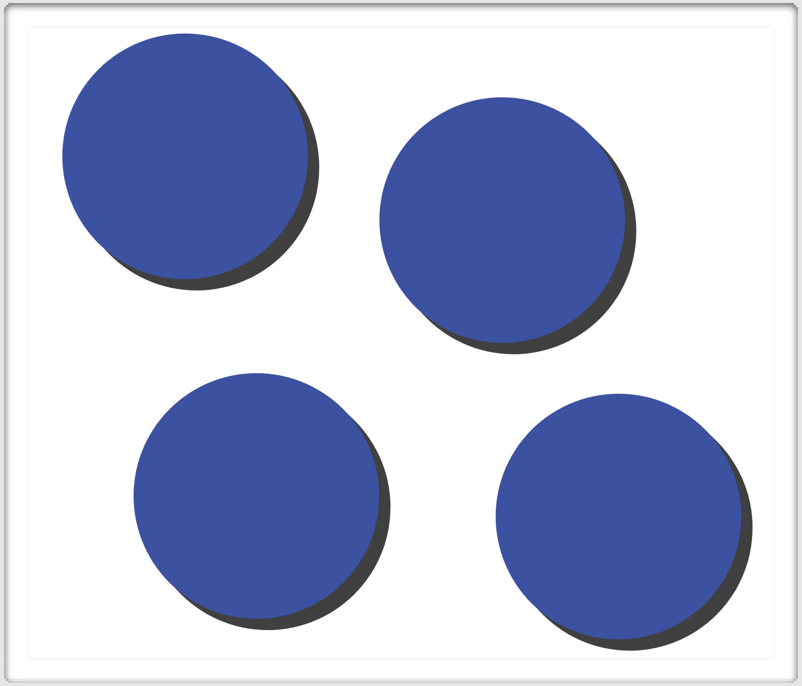
What to save

Causes of risk

Area A



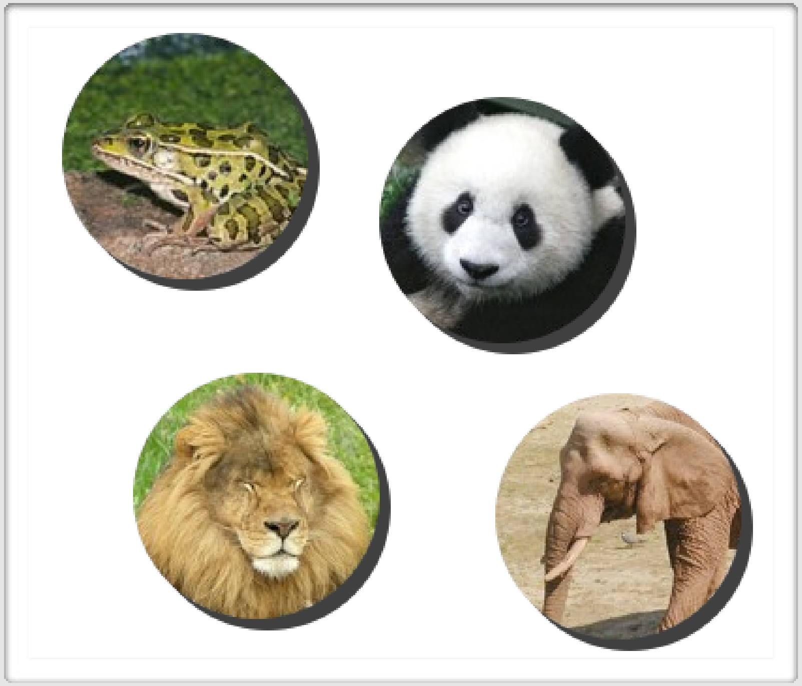
Area B



Which to save?

Area A

Area B



Which to save?

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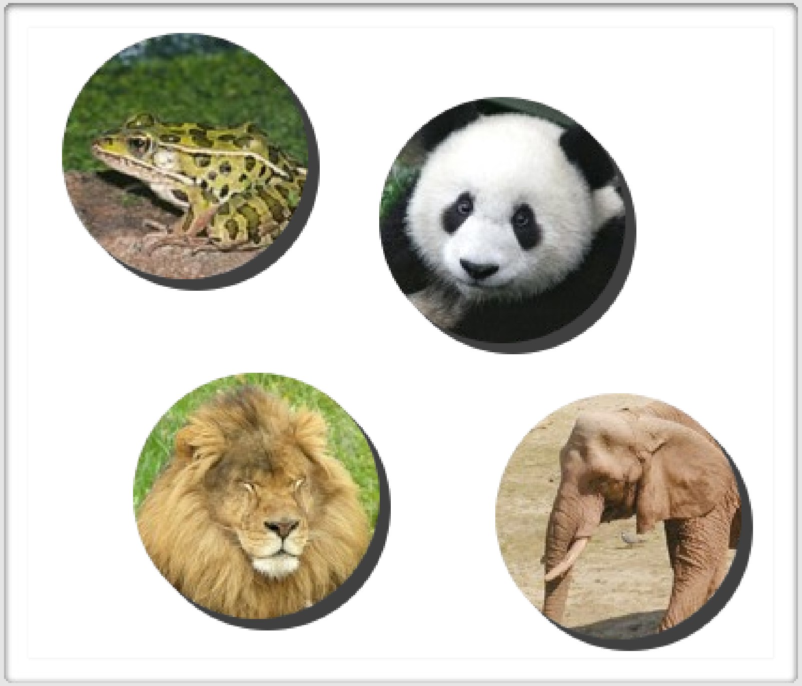
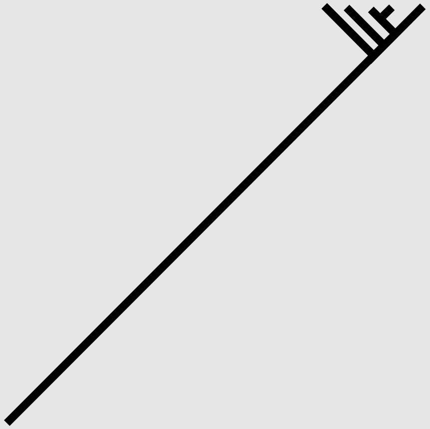
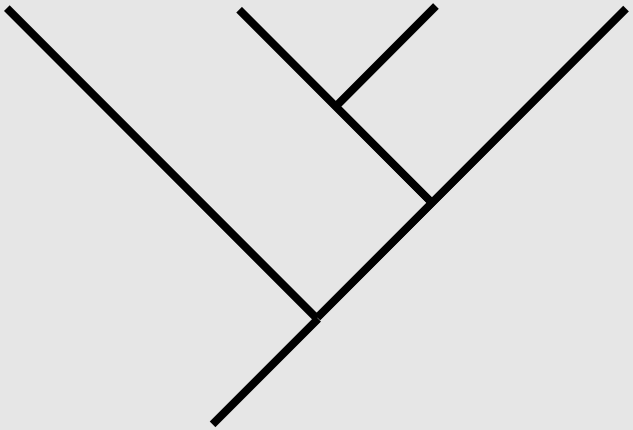
Area A

Area B







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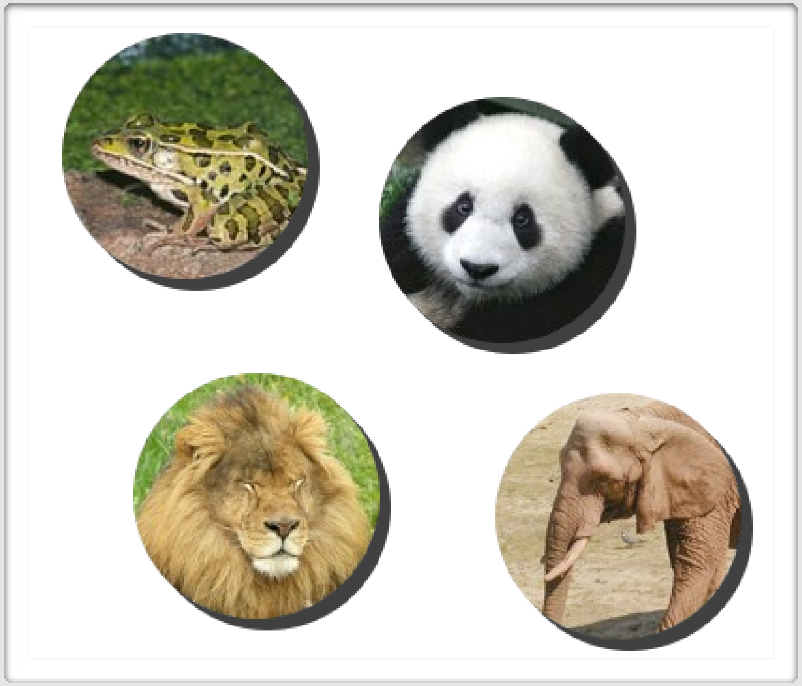
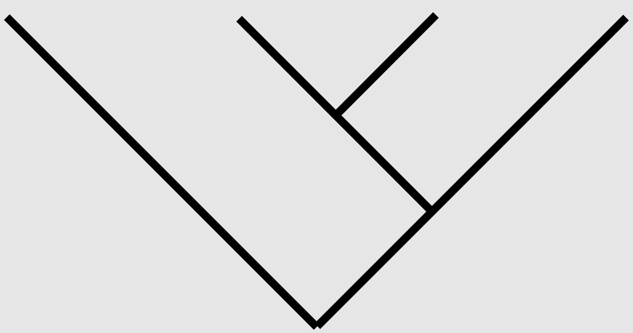
Area A

Area B





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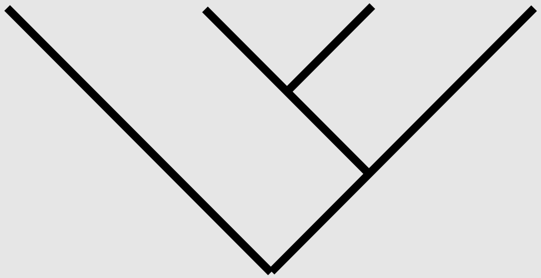
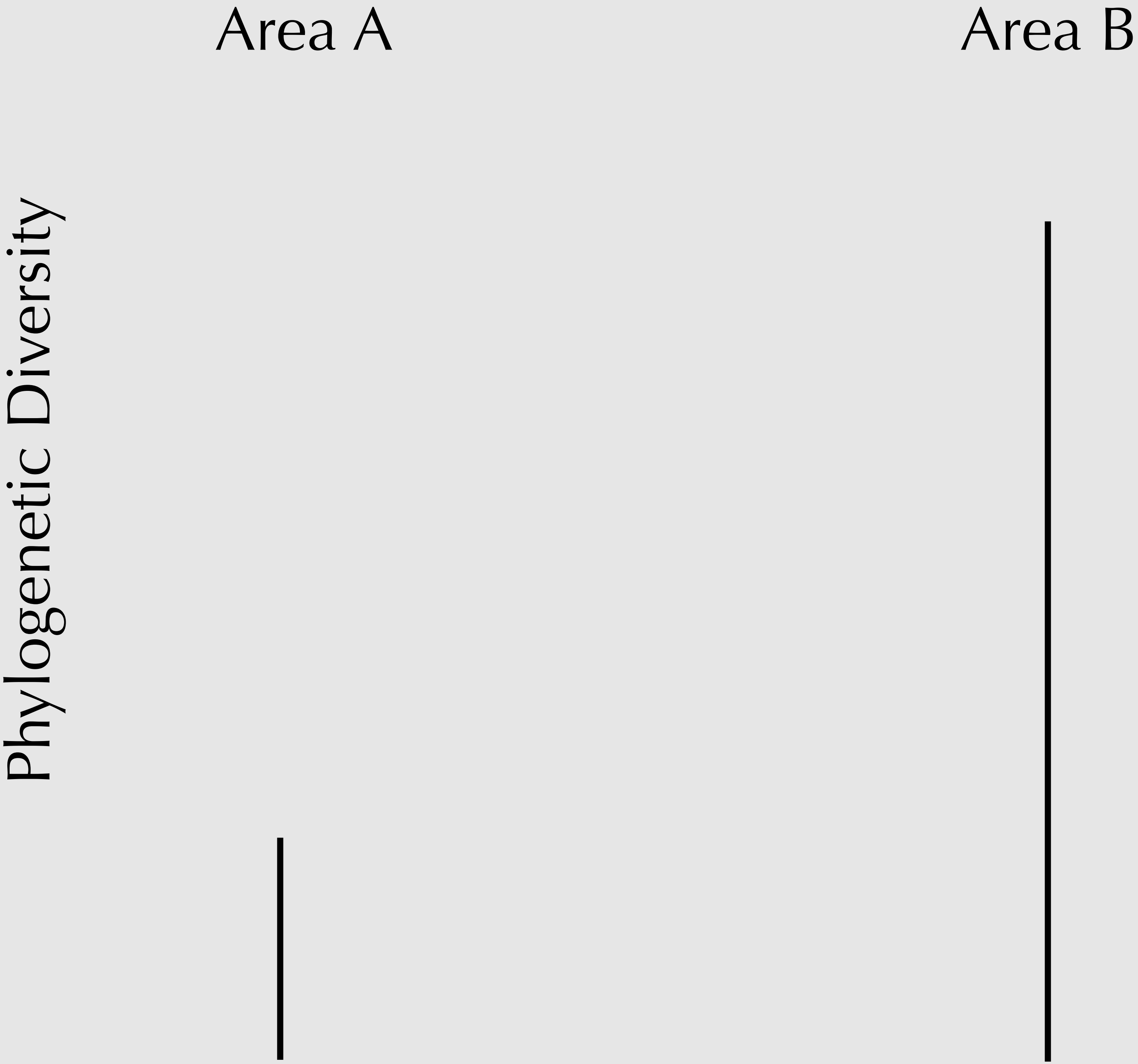
Area A

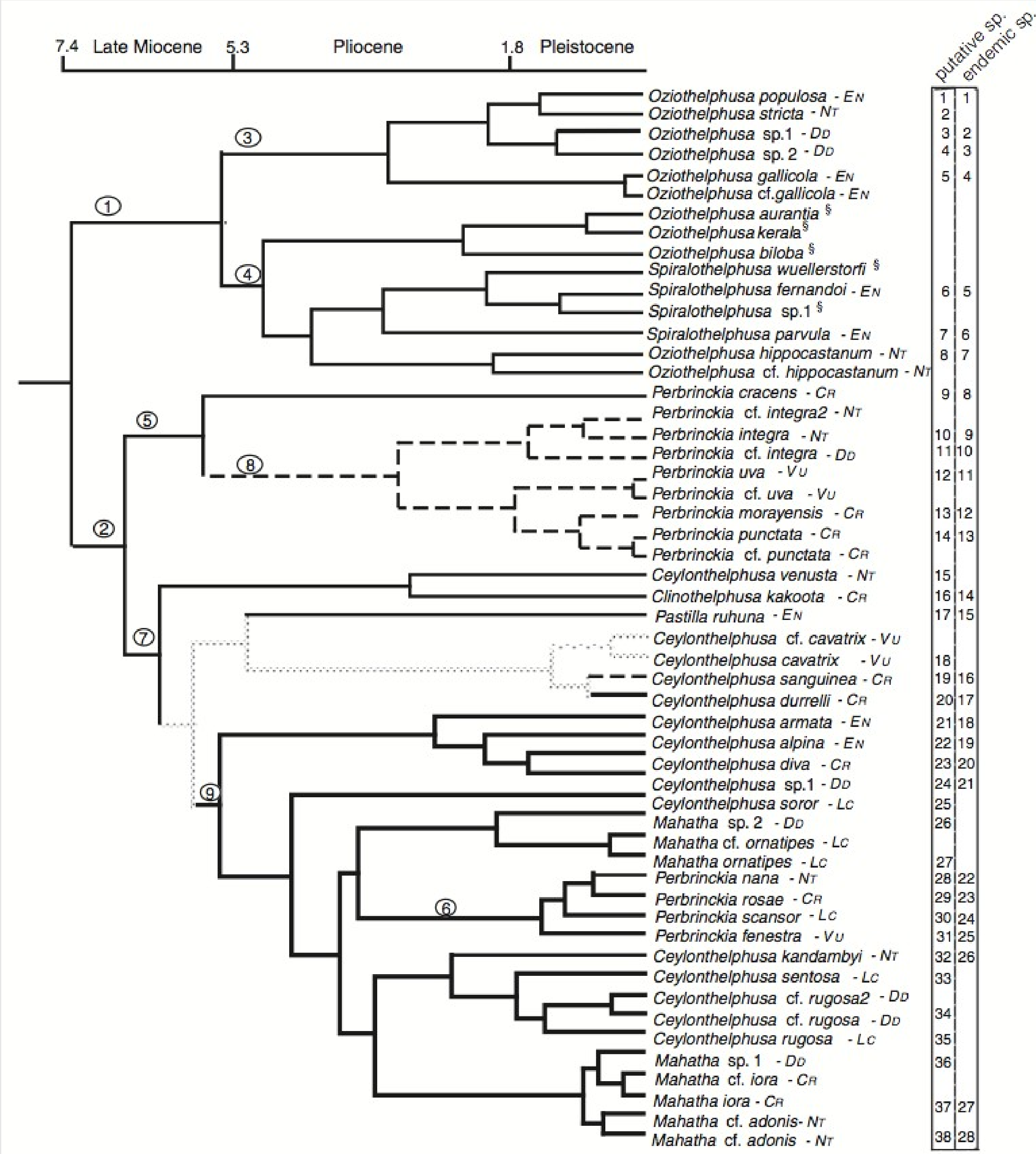
Area B



Area A

Area B


Area A
Area B
Phylogenetic Diversity



http://www.panzerwelten.de/forum/thread-89.html
Oziothelphusa cyclonis, a related species

Beenaerts et al. Phylogenetic diversity of Sri Lankan freshwater crabs and its implications for conservation. Mol Ecol (2010) vol. 19 (1) pp. 183-196

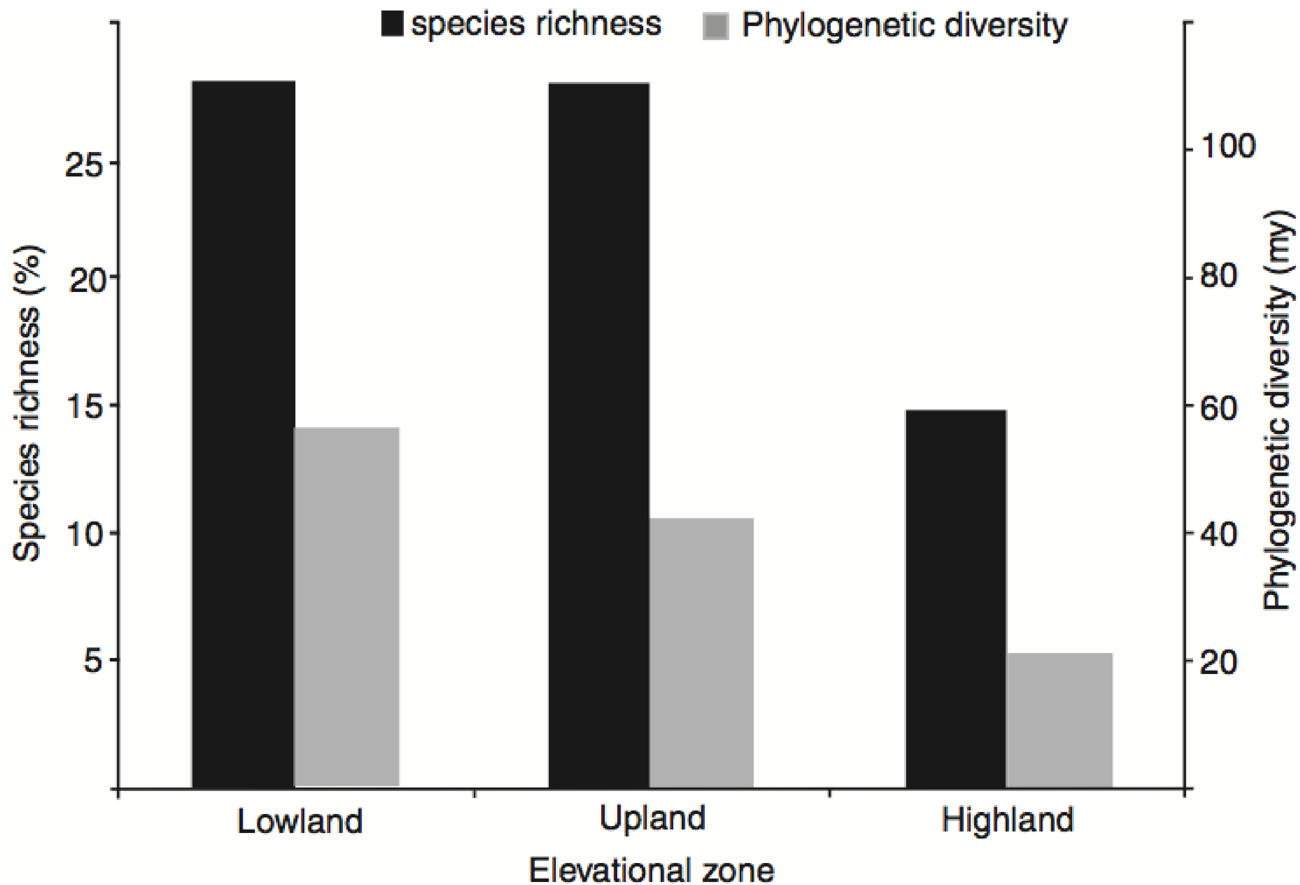


Fig. 4 Species richness and phylogenetic diversity (PD) for the three elevational zones (lowland, upland and highland). The left vertical axis indicates percentage species richness; the right vertical axis indicates PD scores as clade evolutionary history (in million years).

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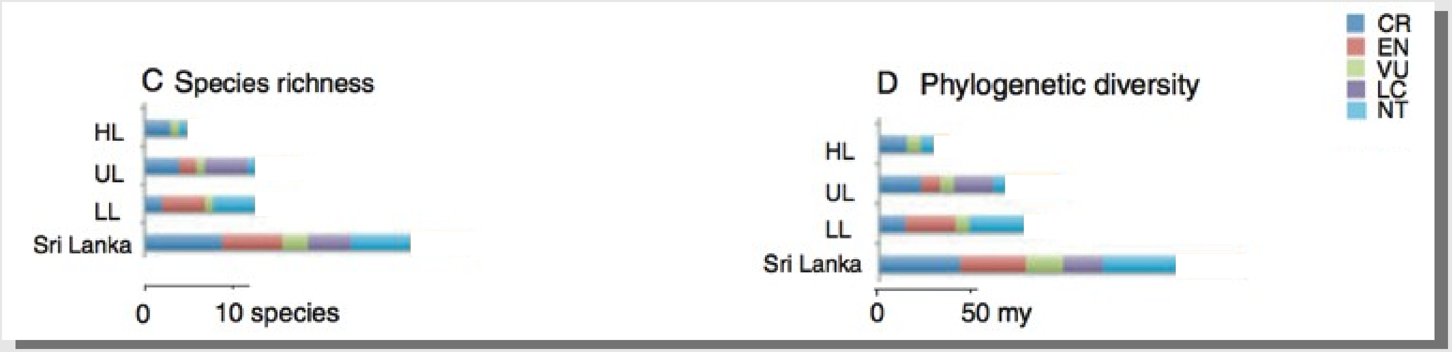


As part of a Global Biodiversity Hotspot, the conservation of Sri Lanka's endemic biodiversity warrants special attention. With 51 species (50 of them endemic) occurring in the island, the biodiversity of freshwater crabs is unusually high for such a small area (65 600 km^2). Freshwater crabs have successfully colonized most moist habitats and all climatic and elevational zones in Sri Lanka. We assessed the biodiversity of these crabs in relation to the different elevational zones (lowland, upland and highland) based on both species richness and phylogenetic diversity. Three different lineages appear to have radiated simultaneously, each within a specific elevational zone, with little interchange thereafter. **The lowland and upland zones show a higher species richness than the highland zone while – unexpectedly – phylogenetic diversity is highest in the lowland zone, illustrating the importance of considering both these measures in conservation planning.** The diversity indices for the species in the various IUCN Red List categories in each of the three zones suggest that risk of extinction may be related to elevational zone. **Our results also show that overall more than 50% of Sri Lanka's freshwater crab species** (including several as yet undescribed ones)**, or approximately 72 million years of evolutionary history, are threatened with extinction.**

Beenaerts et al. Phylogenetic diversity of Sri Lankan freshwater crabs and its implications for conservation. Mol Ecol (2010) vol. 19 (1) pp. 183-196

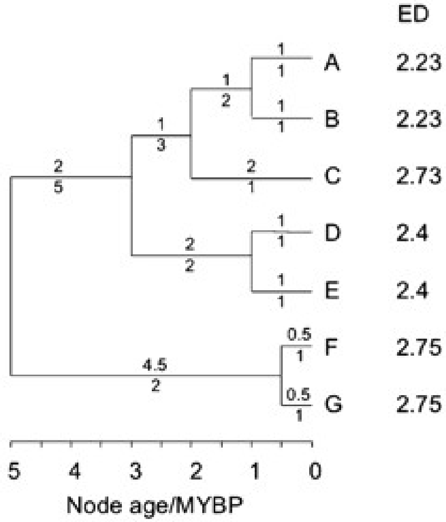


Figure 1. Hypothetical phylogeny of seven species (A–G) with Evolutionary Distinctiveness (ED) scores. Numbers above each branch indicate the length; numbers below show the number of descendent species. MYBP, millions of years before present.
doi:10.1371/journal.pone.0000296.g001

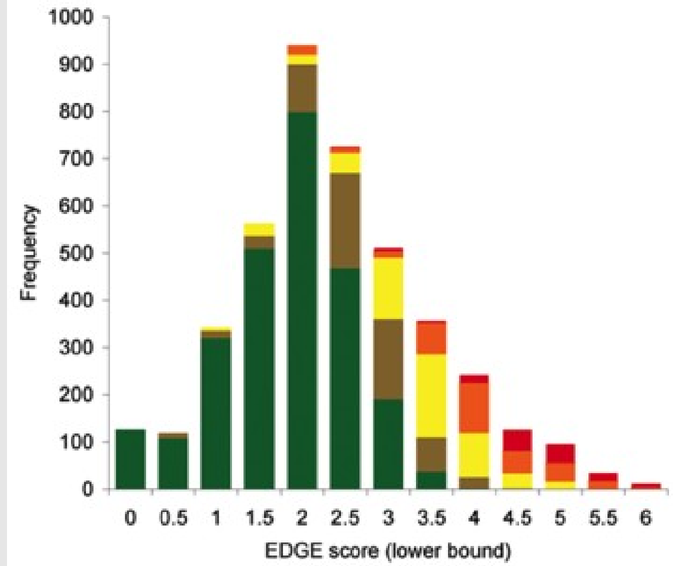
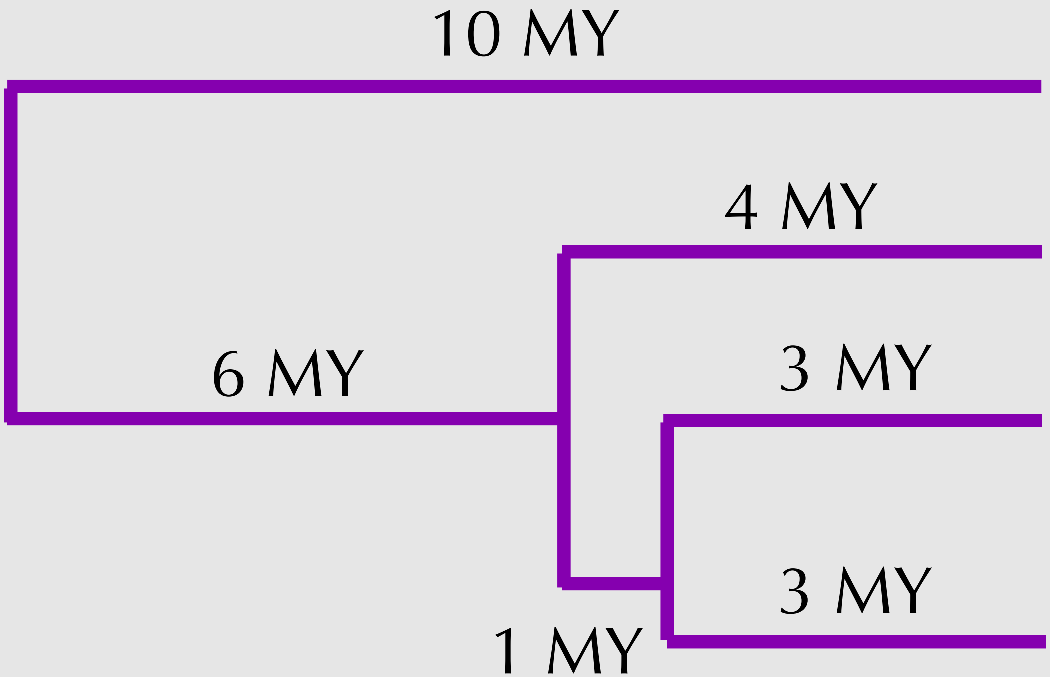


Figure 3. Histogram of EDGE scores for 4182 mammal species, by threat category. Colours indicate the Red List category: Least Concern (green), Near Threatened and Conservation Dependent (brown), Vulnerable (yellow), Endangered (orange) and Critically Endangered (red).
doi:10.1371/journal.pone.0000296.g003

The top 100 EDGE species span all the major mammalian clades and display a comparable range of morphological and ecological disparity, including the largest and smallest mammals, most of the world's freshwater cetaceans, an oviparous mammal and the only species capable of injecting venom using their teeth. However, around three-quarters of species-based mammal conservation projects are specifically aimed at charismatic megafauna, so conventional priority-setting tools may not be sufficient to protect high priority EDGE species. ... [A]n assessment of published conservation strategies and recommendations ... reveals that no species-specific conservation actions have even been suggested for 42 of the top 100 EDGE species. Most of these species are from poorly known regions or taxonomic groups and until now have rarely been highlighted as conservation priorities.

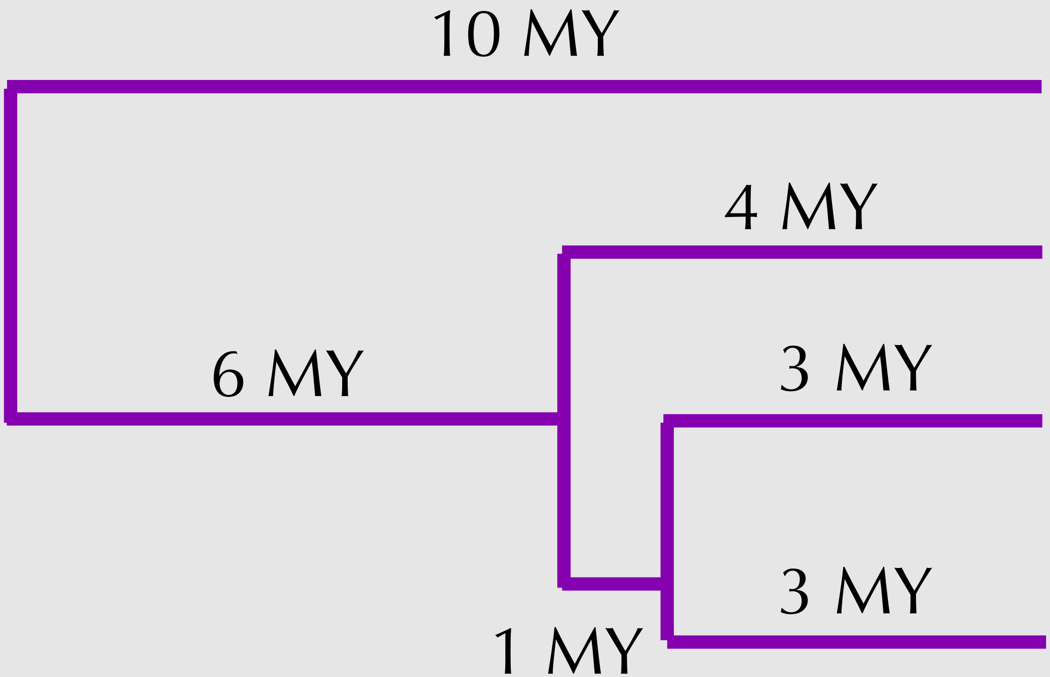
Isaac et al. Mammals on the EDGE: conservation priorities based on threat and phylogeny. PLoS ONE (2007) vol. 2 (3) pp. 296



	A	B	C	D
I: $5M	•		•	•
II: $2M	•	•		•
III: $2M		•		
IV: $3M		•	•	•

You have $8M to save species:

Which combo, A, B, C, or D, saves the most species?



	A	B	C	D
I: $5M	•		•	•
II: $2M	•	•		•
III: $2M		•		
IV: $3M		•	•	•

You have $8M to save species:

Which combo, A, B, C, or D, saves the most history?

Phylogenies and conservation biology

What to save

Causes of risk

(i) Small populations are more likely to die out than large ones: demographic stochasticity, local catastrophes, slow rates of adaptation, 'mutational meltdown' and inbreeding are all more serious for populations with few individuals (Brown 1995; Lande 1999). Small geographical ranges and low population densities are therefore likely to confer an enhanced extinction risk (Gaston 1994).

(ii) Island endemics are very likely to have small geographical ranges and, hence, small populations. In addition, they may have evolved in isolation from predators and competitors (including humans), perhaps making them particularly vulnerable to the effects of introduced species and over-exploitation (Pimm 1991).

(iii) Species at higher trophic levels are more vulnerable to the cumulative effects of disturbance to species lower down the food chain (e.g. chains of extinction) (Diamond 1984; Crooks & Soulé 1999).

(iv) Species with 'slow' life histories, i.e. small litters, slow growth rates, late sexual maturity, long gestation and long interbirth intervals, are less able to compensate for increased mortality with increased fecundity and are therefore more vulnerable to population extinction (MacArthur & Wilson 1967).

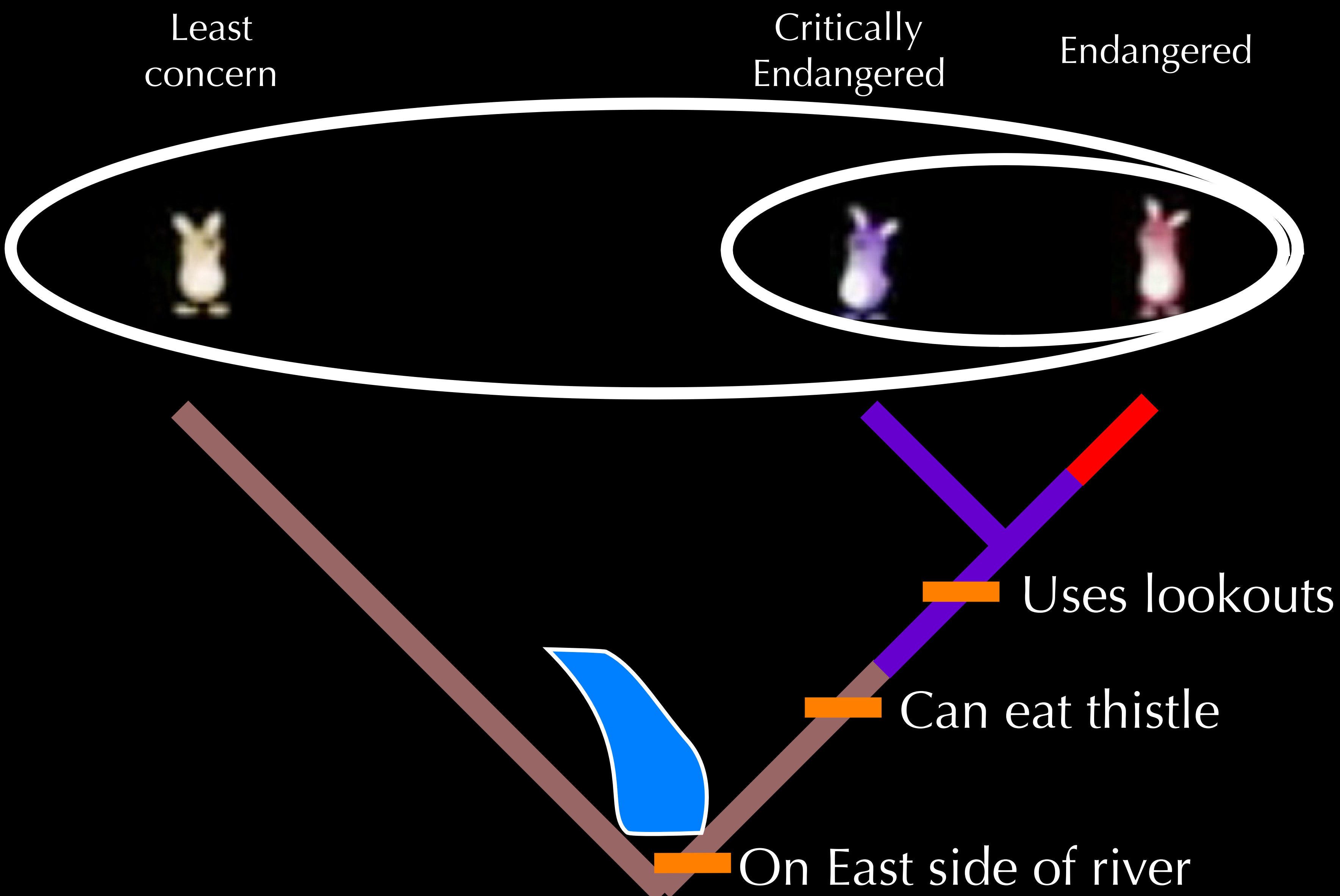
(v) Species with complex social structures for mating, group foraging or group defence are more vulnerable to extinction because persistence depends upon a larger unit than the individual (Allee effects) (Courchamp *et al.* 1999); in addition, social groups are conspicuous which can lead to increased hunting (Soulé 1983).

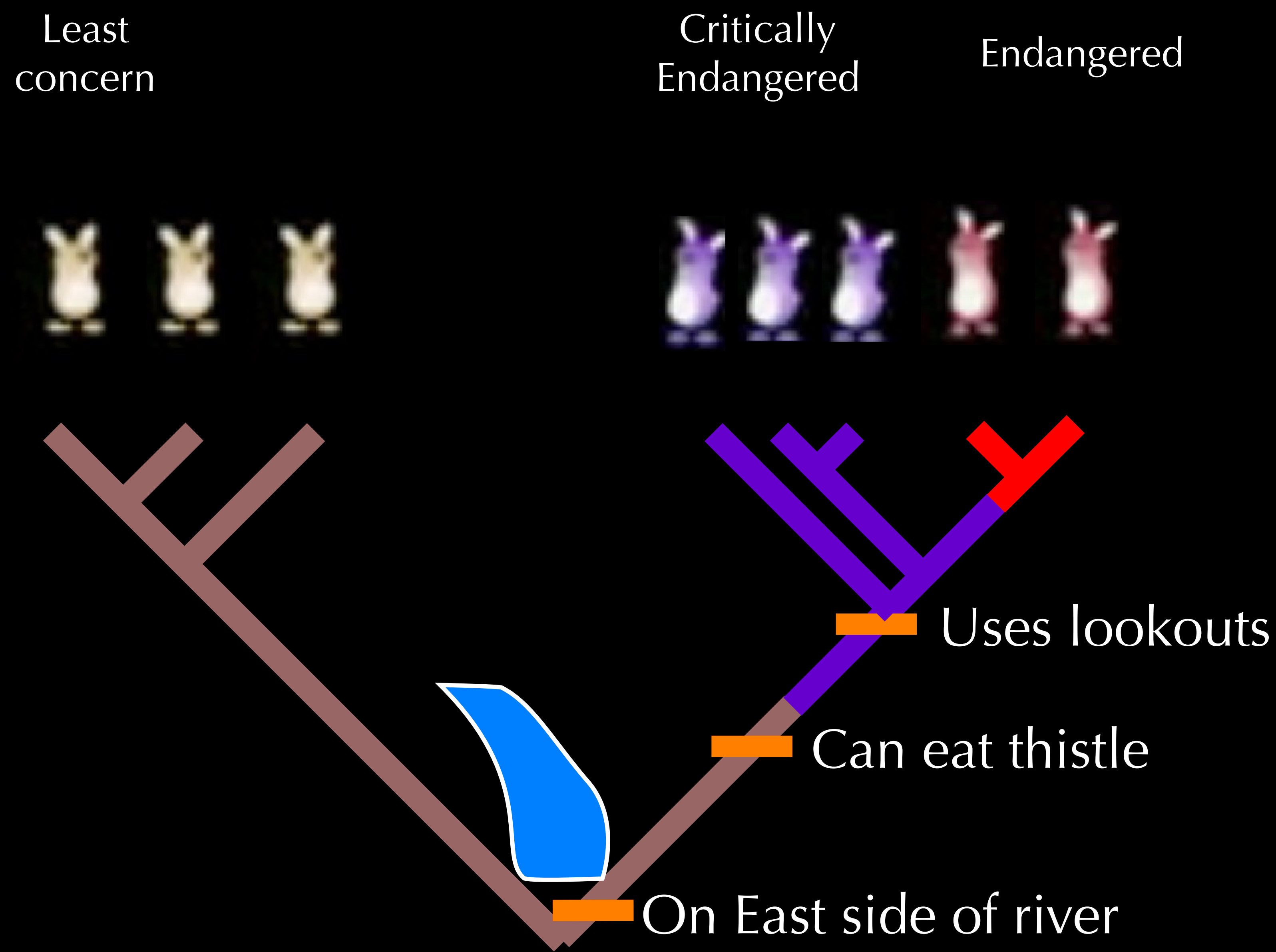
(vi) Species where individuals have large home ranges are particularly vulnerable to habitat loss and degradation and, in particular, to edge effects (Woodroffe & Ginsberg 1998).

(vii) Diurnal species show a suite of characteristics that might make them more vulnerable, e.g. large body size, sociality, high predation rates and large home ranges (Gittleman 1985; Fleagle 1999), as well as being easier to hunt.

(viii) Last but not least, large body size correlates with many of the extinction-promoting traits above (McKinney 1997). Larger species tend to have low population densities, slower life histories and larger home ranges. In addition, humans may be less tolerant of and, thus, more likely to persecute larger carnivores (Weaver *et al.* 1996), and hunters are more likely to target larger primates for food (Cowlishaw & Dunbar 2000).

Purvis et al. Predicting extinction risk in declining species. Proceedings of the Royal Society B: Biological Sciences (2000) vol. 267 (1456) pp. 1947


Least concern
Critically Endangered
Endangered
Uses lookouts
Can eat thistle
On East side of river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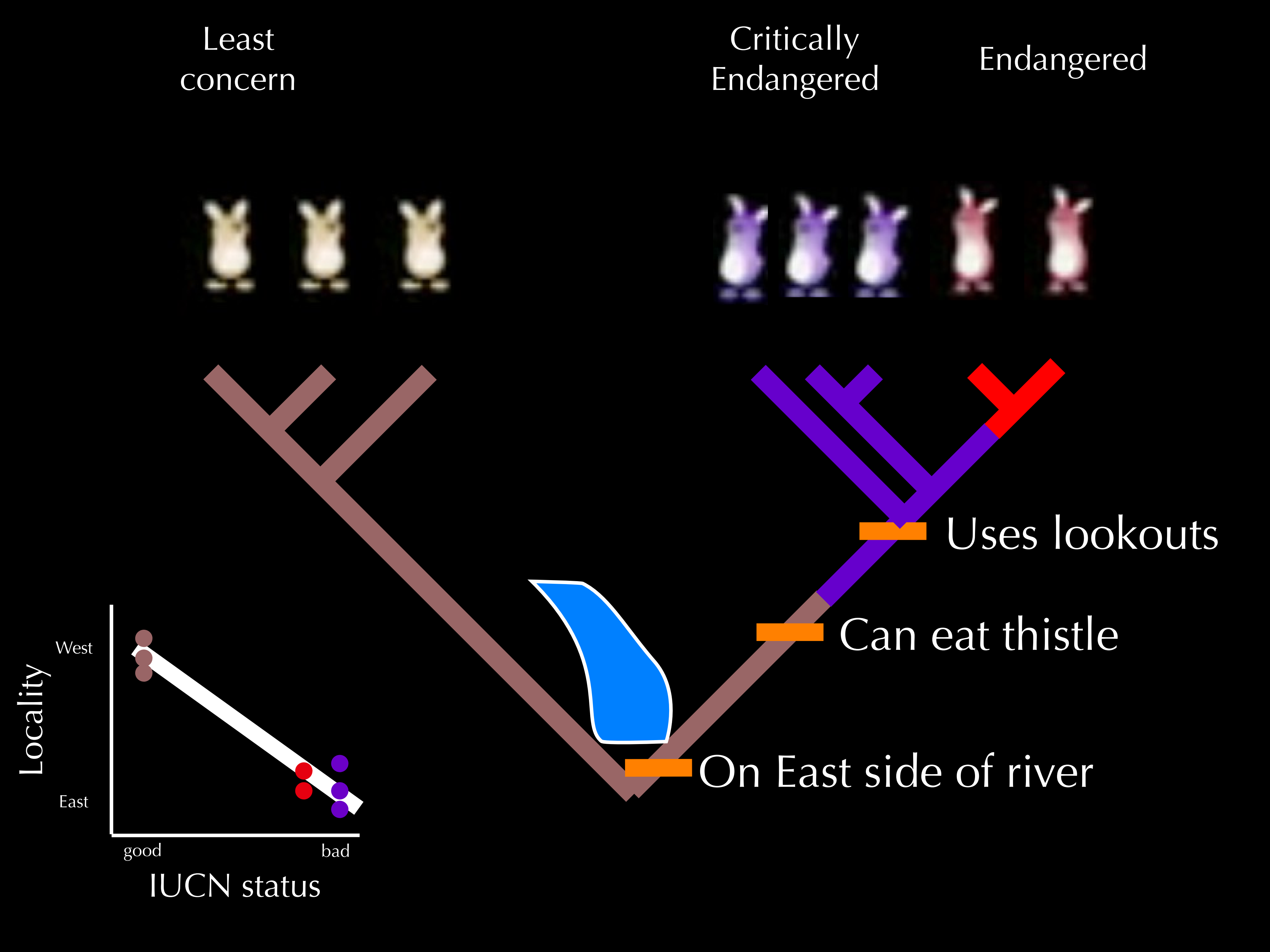

Least concern
Critically Endangered
Endangered
Uses lookouts
Can eat thistle
On East side of river
West
East
Locality
good
bad
IUCN status

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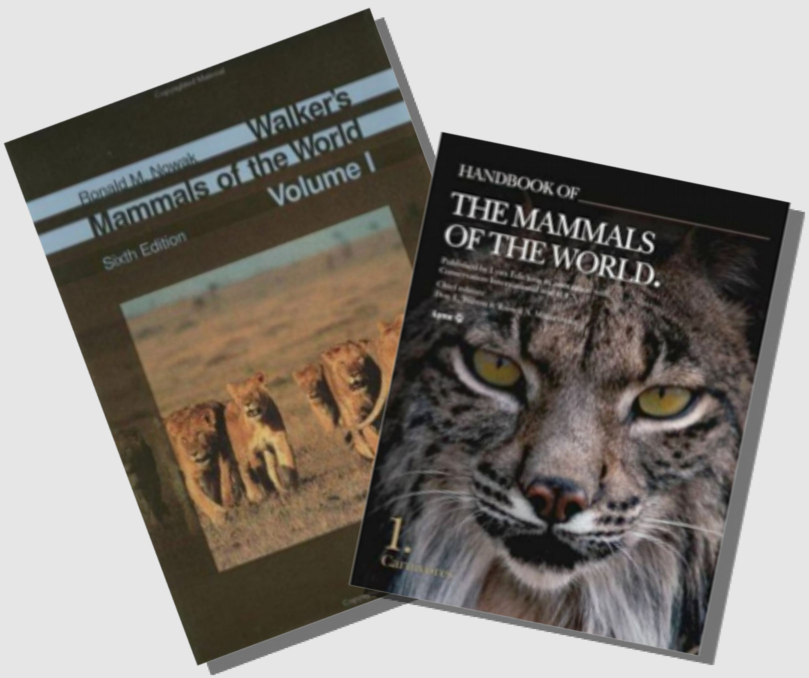
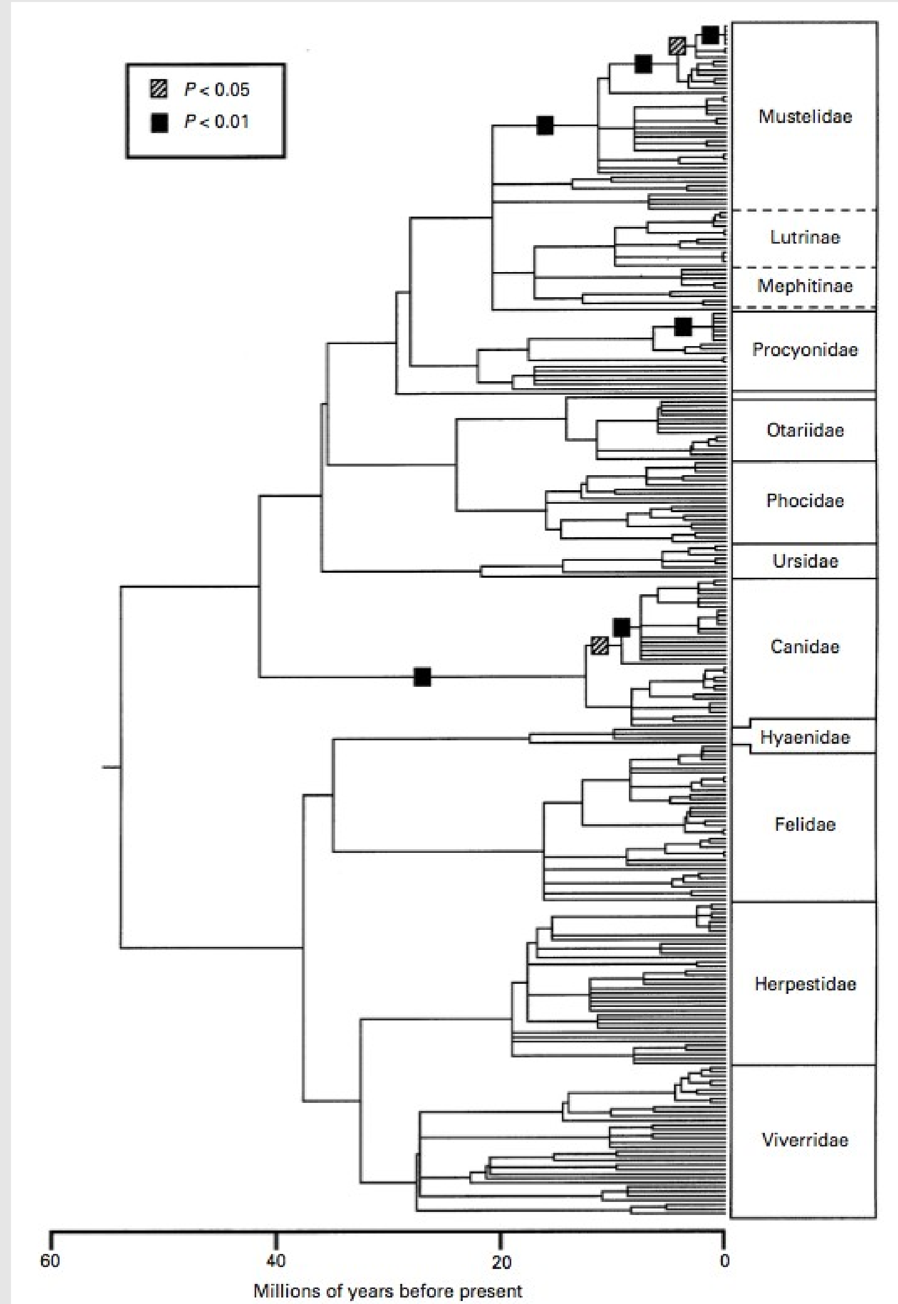
IUCN RED LIST

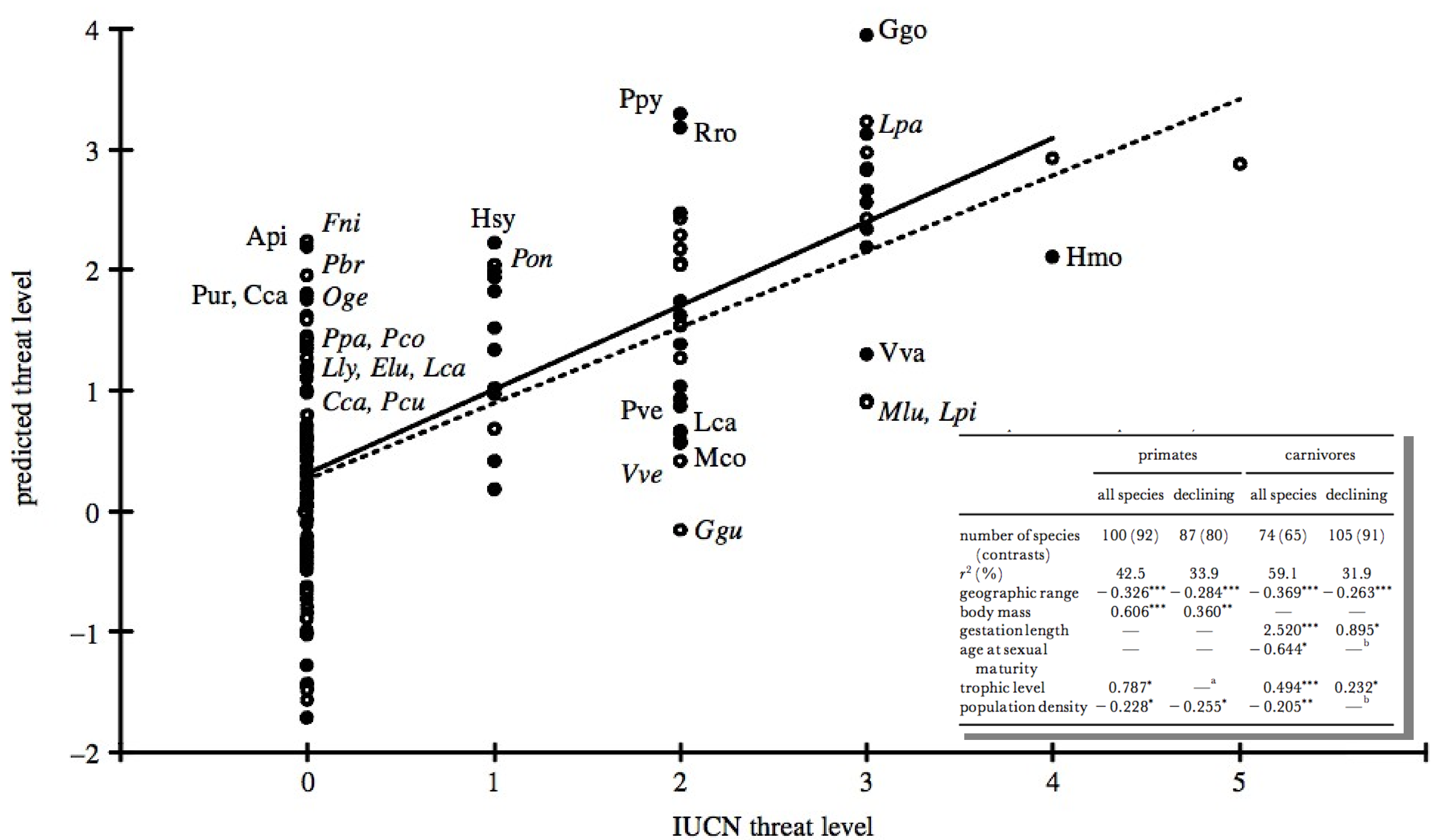




Bininda-Emonds et al. Biological Reviews (1999) vol. 74 (2) pp. 143-175

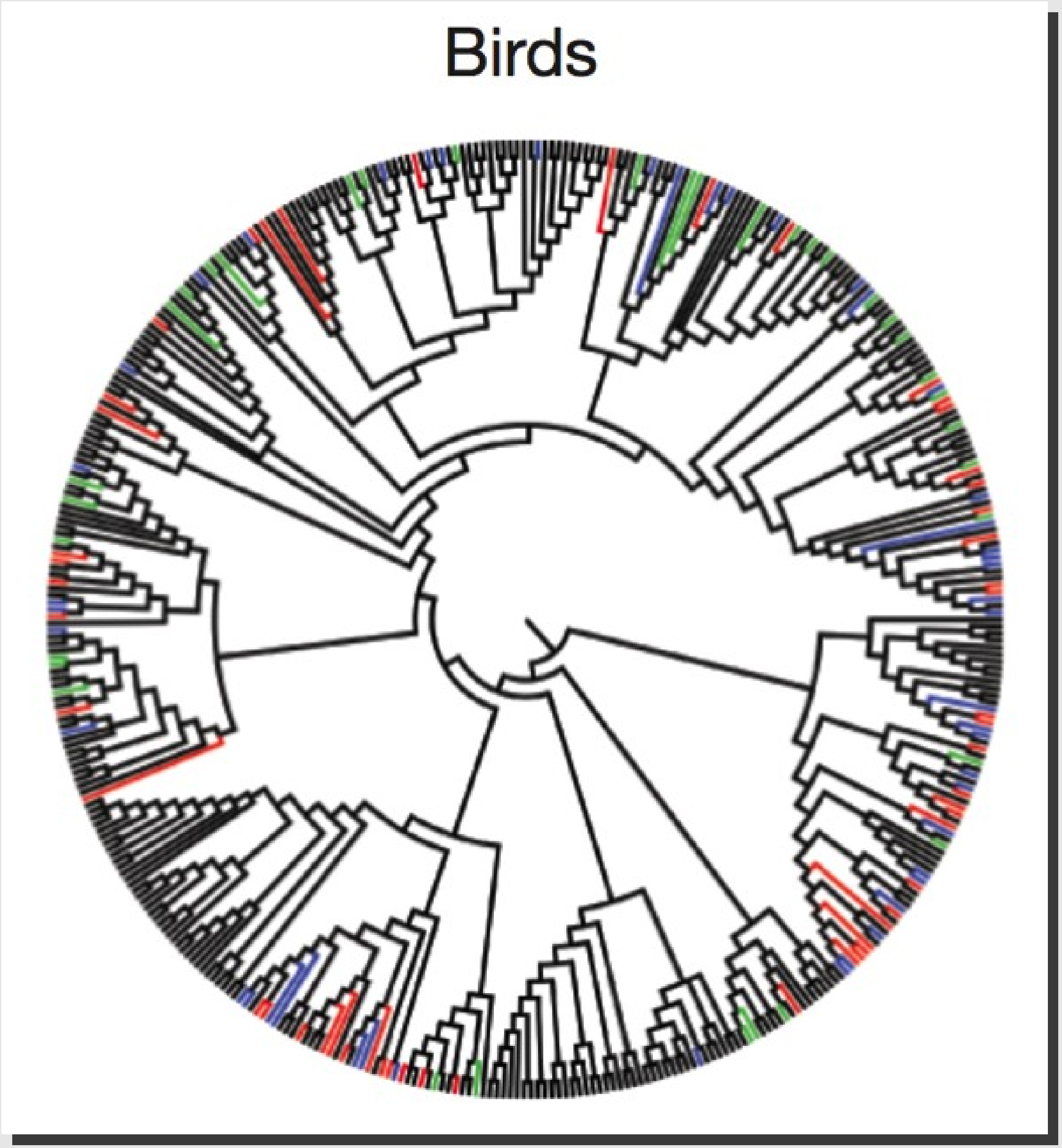
variable	N_s	N_c	as sole predictor	with geographical range
geographical range	355	292	-11.73^{***}	—
island status	355	292	3.82^{***}	0.24
body mass	317	266	0.91	2.23^{*}
gestation length	219	197	2.11^{*}	2.22^{*}
litter size	284	245	-3.24^{***}	-1.32
age at sexual maturity	172	156	1.64	0.86
interbirth interval	175	161	0.86	0.93
trophic level	321	270	1.57	1.54
activity timing	327	274	2.10^{*}	0.77
home range size	197	174	-0.22	1.81
population density	162	147	-2.07^{*}	-2.82^{**}
group size	237	202	-0.08	0.19

Purvis et al. Predicting extinction risk in declining species. Proceedings of the Royal Society B: Biological Sciences (2000) vol. 267 (1456) pp. 1947



	primates		carnivores	
	all species	declining	all species	declining
number of species (contrasts)	100 (92)	87 (80)	74 (65)	105 (91)
r^2 (%)	42.5	33.9	59.1	31.9
geographic range	-0.326^{***}	-0.284^{***}	-0.369^{***}	-0.263^{***}
body mass	0.606^{***}	0.360^{**}	—	—
gestation length	—	—	2.520^{***}	0.895^{*}
age at sexual maturity	—	—	-0.644^{*}	—[b]
trophic level	0.787^{*}	—[a]	0.494^{***}	0.232^{*}
population density	-0.228^{*}	-0.255^{*}	-0.205^{**}	—[b]

Purvis et al. Predicting extinction risk in declining species. Proceedings of the Royal Society B: Biological Sciences (2000) vol. 267 (1456) pp. 1947



Thuiller et al. 2011

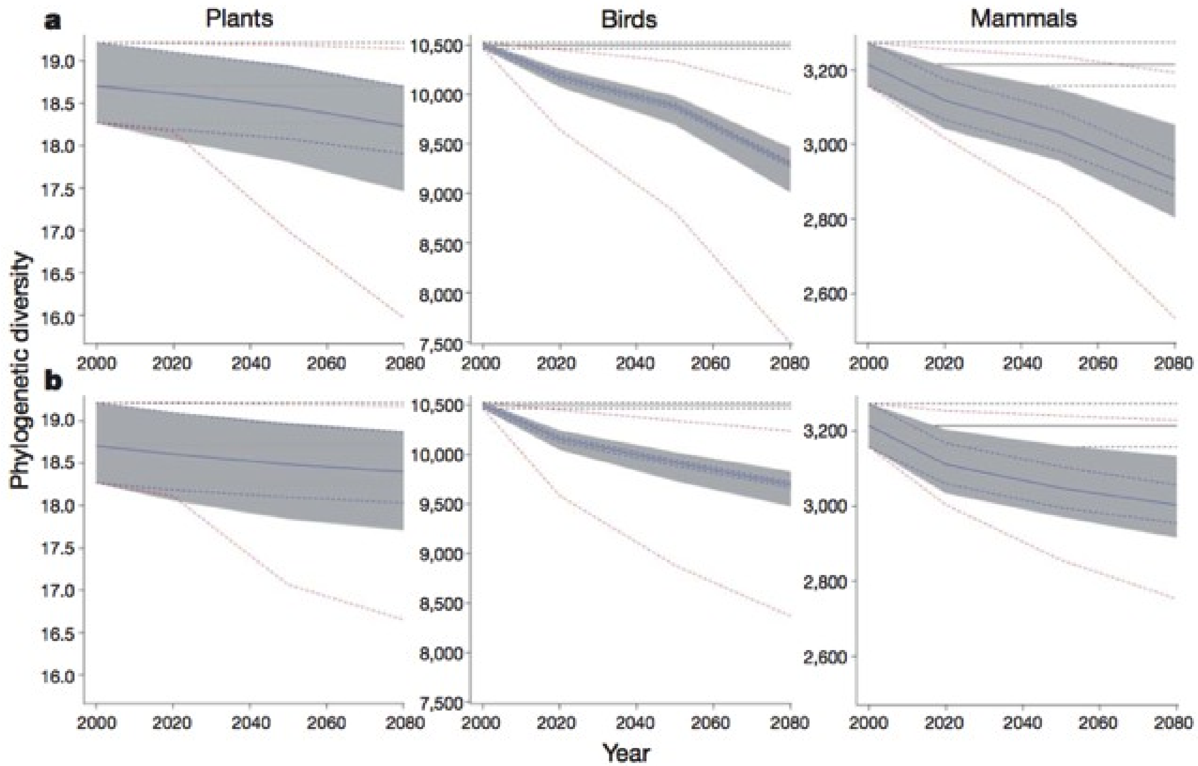


Figure 2 | Changes in phylogenetic diversity versus scenarios of random extinction for plants, birds and mammals. **a**, Emission scenario A1F1; **b**, emission scenario B1. Black solid and dashed lines depict the median, maximum and minimum current phylogenetic diversities across the sample of trees. Blue solid and dashed lines represent the median, maximum and minimum projected phylogenetic diversities due to range change across the sample of trees. The grey area is the quantile range of projected phylogenetic diversity due to range contraction (from 2020 onward), randomly scattered across the sample of trees. The red lines are the remaining phylogenetic diversity when the risk of extinction is positively (lower line) or negatively (upper line) related to the evolutionary distinctiveness of the taxa.

Thuiller et al. 2011

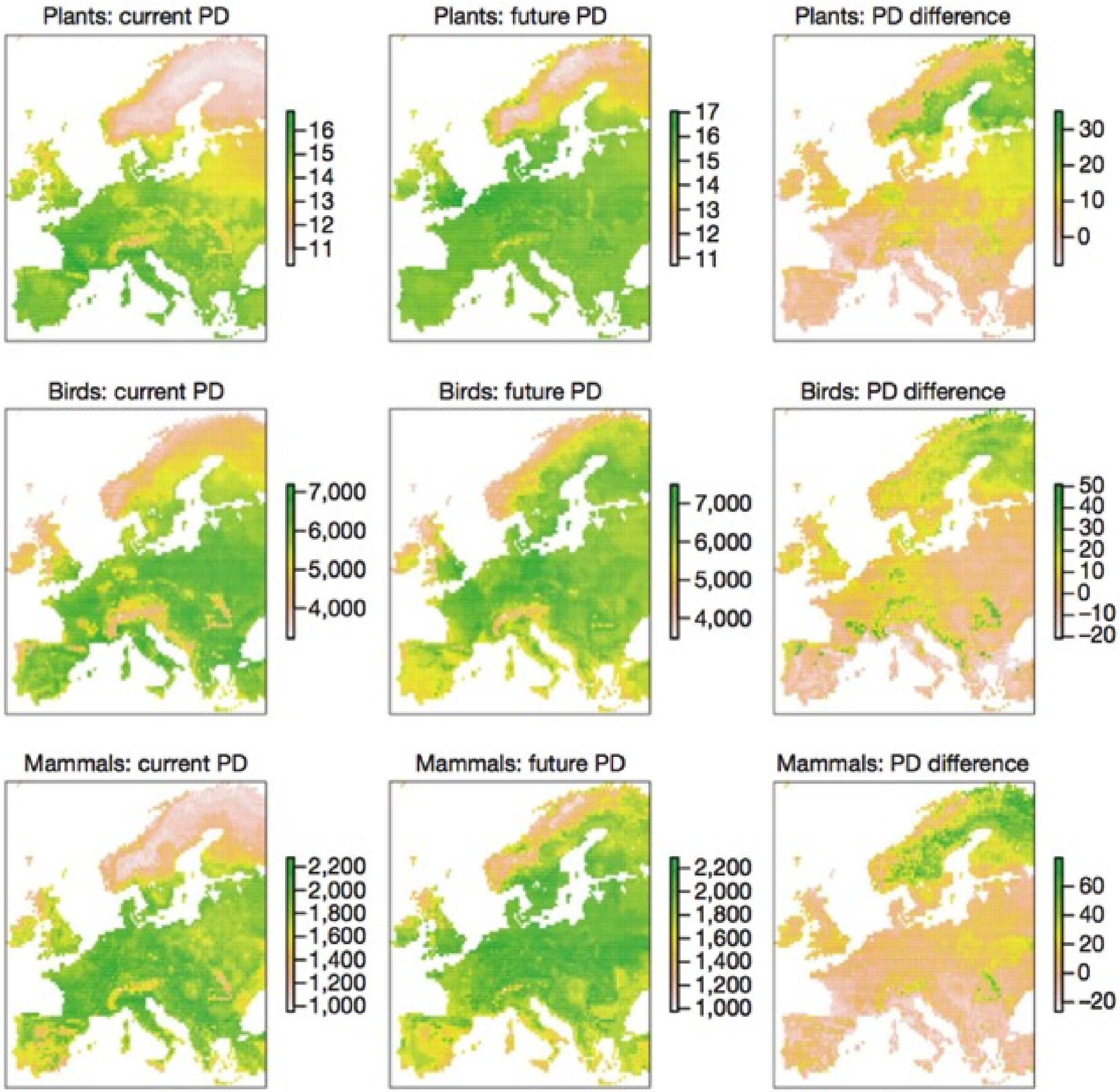
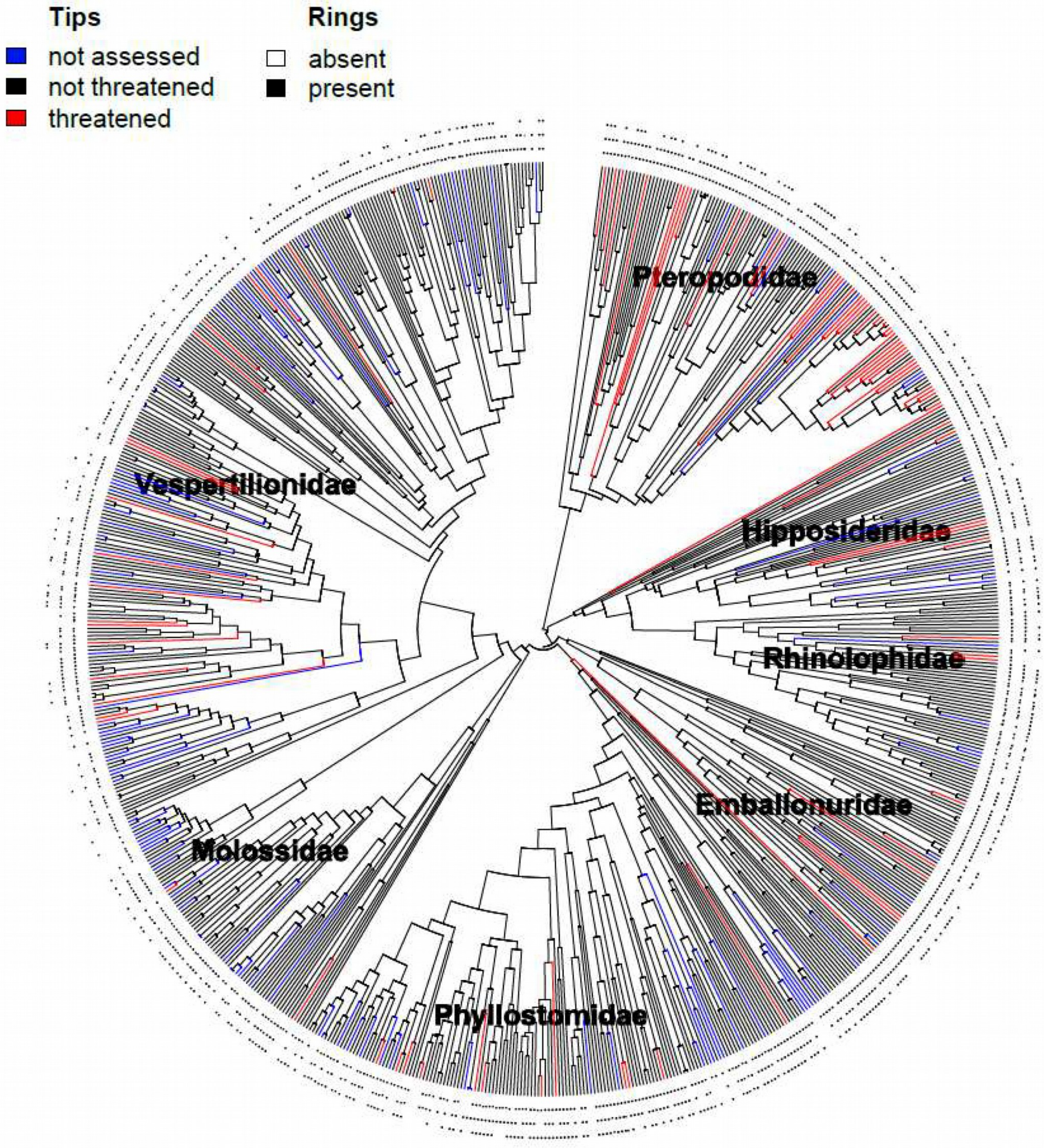


Figure 3 | Map of current and future phylogenetic diversities (A1FI scenario for 2080) and their relative differences for the three species groups. Maps represent average phylogenetic diversity (PD; colour scale) across the sample of 100 phylogenetic trees used for each study group.

Thuiller et al. 2011



Welch & Beaulieu, 2018

Table 2. Results of phylogenetic logistic regressions on single predictors and interactions to identify important correlates of extinction risk in bats. Results for the categorical variable trophic level is reported in the main text. The variable "geo range abbr." excludes bats listed at threaten owing to Criteria B alone. The parameter α represents the phylogenetic correlation parameter, where values near 0 indicate strong phylogenetic signal and values approaching 0.98 indicates very weak phylogenetic signal based on the root age of our tree. Regression coefficients (*b*) are bolded for variables significant at $p \leq 0.05$ according to a Wald test. P(1) represents the probability of odds of increasing threat with a unit increase in the variable. R^2 values are estimated by the Cox & Snell equation with the Nagelkerke correction.

Variables	All Bats				Yinpterochiroptera				Yangochiroptera			
	α	*b*	P(1)	R^2	α	*b*	P(1)	R^2	α	*b*	P(1)	R^2
aspect ratio	0.084	−8.089	0.000	0.058	0.281	−7.379	0.001	0.017	0.148	−7.793	0.000	0.051
diet breadth	0.547	**0.600**	0.646	0.037	0.509	**0.881**	0.707	0.104	0.557	0.401	0.599	0.010
endemism	0.099	**1.643**	0.838	0.139	0.133	**1.035**	0.738	0.067	0.243	**1.942**	0.875	0.138
forearm length	0.160	**3.902**	0.980	0.054	0.246	**4.695**	0.991	0.095	0.678	−2.353	0.087	0.005
litter size	0.082	−23.657	0.000	0.050	0.592	−10.664	0.000	0.010	0.404	−4.755	0.009	0.052
litters per year	0.240	−9.702	0.000	0.062	0.502	−10.511	0.000	0.141	0.448	−2.591	0.070	0.050
mass	0.266	**1.574**	0.828	0.074	0.517	**1.461**	0.812	0.153	0.345	−0.011	0.497	0.000
range	0.020	**−1.462**	0.188	0.468	0.138	−1.284	0.217	0.405	0.028	**−1.774**	0.145	0.527
range abbr.	0.021	**−1.109**	0.248	0.264	0.032	−0.903	0.288	0.221	0.039	**−1.270**	0.219	0.261
wing loading	0.336	−0.584	0.358	0.001	0.293	−0.394	0.403	−0.003	0.413	−0.881	0.293	0.002
range × endemism	0.019	**0.964**	0.724	0.493	0.052	1.017	0.734	0.469	0.029	0.550	0.634	0.537
range × mass	0.020	0.129	0.532	0.373	0.031	0.085	0.521	0.396	0.033	−0.759	0.319	0.340
mass × endemism	0.056	−0.066	0.484	0.123	0.539	0.902	0.711	0.188	0.354	1.319	0.789	0.120

Welch & Beaulieu, 2018

Rank	Family	Species	IUCN Status	Lower Estimate	Median Estimate	Upper Estimate
1	Vespertilionidae	*Eptesicus dimissus*	DD	0.996	***1.000***	1.000
2	Molossidae	*Otomops wroughtoni*	DD	0.992	***1.000***	1.000
3	Vespertilionidae	*Myotis annamiticus*	DD	0.990	***0.998***	1.000
4	Phyllostomidae	*Artibeus incomitatus*	CR	0.963	***0.996***	1.000
5	Vespertilionidae	*Myotis anjouanensis*	DD	0.969	***0.994***	1.000
6	Pteropodidae	*Latidens salimalii*	EN	0.949	***0.986***	1.000
7	Phyllostomidae	*Micronycteris matses*	DD	0.946	***0.986***	1.000
8	Vespertilionidae	*Arielulus cuprosus*	DD	0.914	***0.981***	0.998
9	Craseonycteridae	*Craseonycteris thonglongyai*	VU	0.932	***0.977***	0.998
10	Pteropodidae	*Pteropus voeltzkowi*	VU	0.932	***0.977***	0.998

Welch & Beaulieu, 2018

Breaking news: Bobrovskiy et al., 2018 (Sept 21) Precambrian Ediacaran fossil (*Dickinsonia)* was an animal!