Appendix B. Details on the second case study

## **1. Selection of the traits**

We discarded 6 traits, although they were available in Pantheria, because of their high correlation with body mass (see Figures B.1 to B.6): codes for those traits in Pantheria are "X13.1\_AdultHeadBodyLen\_mm", "X9.1\_GestationLen\_d", "X15.1\_LitterSize", "X17.1\_MaxLongevity\_m", "X5.3\_NeonateBodyMass\_g", "X23.1\_SexualMaturityAge\_d".



Adult body mass (log scale)

Fig. B.1 As expected body mass was highly correlated with body length



Fig. B.2 With few exceptions, high gestation length was associated with large body mass and eye opening at birth.



Fig. B.3 Litter size decreased with body mass



Fig. B.4 Maximum longevity increased with body mass



Fig. B.5 Adult and neonate body mass were highly correlated



Fig. B.6 Age at sexual maturity, as maximum longevity, increased with body mass

## 2. Tests for phylogenetic signal

The phylogenetic tree used in this case study is displayed in Figure B.7.



Fig. B.7. Phylogenetic tree for the second case study (extracted from Nyakatura and Bininda-Edmonds, 2012)

We used permutation tests for phylogenetic signal and 1000 permutations of data in each test.

Phylogenetic signal in trophic level was significant: Maddison and Slatkin test, Pvalue = 0.015, 2 levels, observed number of evolutionary transitions = 8, median of this number obtained by randomization = 13 (min. 7, max 16) [Maddison and Slatkin test was applied to all traits with unordered transitions among all levels (even rates)]. Details are given in Fig. B.8.



Transitions.in.Randomizations

Fig. B.8 Details on Maddison and Slatkin (1991) test applied to trophic level providing on the left the histogram of null number of transitions and the observed number of transitions (red arrow), and on the right the phylogenetic tree with each color on the tips showing different trait states [Blue = carnivore; Green = omnivore].

Phylogenetic signal in terrestriality was not tested as all species were classified fossorial and/or ground dwelling only in Pantheria except Procyon\_lotor which was classified as above ground dwelling.

Phylogenetic signal in activity cycle was not significant: Maddison and Slatkin test, Pvalue = 0.379, 3 levels, observed number of evolutionary transitions = 12, median of this number obtained by randomization = 13 (min. 8, max 14). Details are given in Fig. B.9.



Transitions.in.Randomizations

Fig. B.9 Details on Maddison and Slatkin (1991) test applied to activity cycle [on 36 species due to missing data]: on the left the histogram of null number of transitions and the observed number of transitions (red arrow), and on the right the phylogenetic tree with each color on the tips showing different trait states [Green = nocturnal only; Dark blue = nocturnal/crepuscular, cathemeral, crepuscular or diurnal/crepuscular; Light blue = diurnal only].

Phylogenetic signal was significant in body mass ( $K^{*}=0.98$ , P-value=0.001; Kw=0.73, P-value=0.001), age at eye opening ( $K^{*}=1.12$ , P-value=0.001; Kw=0.87, P-value=0.001), interbirth interval ( $K^{*}=0.55$ , P-value=0.002; Kw=0.78, P-value=0.001), weaning age ( $K^{*}=0.62$ , P-value=0.001; Kw=0.92, P-value=0.02).

Diet breadth and habitat breadth are discrete quantitative traits. We tested phylogenetic signal in these traits using Maddison and Slatkin (1991) test but considering different rates of transitions between levels (rates are equal only between similar differences in breadth for example from 1 to 2 and from 2 to 3, but the rate of transitions from 1, 2, or 3 to 6 is assumed to be different from that between 1 and 2). Habitat breadth is the number of habitat layers used by each species from 1 to 3. Diet breadth is the number of dietary categories eaten by each species from 1 to 6. Phylogenetic signal was significant in habitat breadth (P-value = 0.000, 3 levels, observed number of evolutionary transitions = 6, median of this number obtained by randomization = 12 [min. 7, max 13]) and diet breadth (P-value = 0.009, 4 levels, observed number of evolutionary transitions = 28, median of this number obtained by randomization = 40 [min. 27, max 49]); details in Figs B.10 and B.11.



Transitions.in.Randomizations

Fig. B.10 Details on Maddison and Slatkin (1991) test applied to habitat breadth: on the left the histogram of null number of transitions and the observed number of transitions (red arrow), and on the right the phylogenetic tree with each color on the tips showing different trait states [Green = 1 habitat layer is used by the species; Dark blue = 2; Light blue = 3].



Transitions.in.Randomizations

Fig. B.11 Details on Maddison and Slatkin (1991) test applied to diet breadth: on the left the histogram of null number of transitions and the observed number of transitions (red arrow), and on the right the phylogenetic tree with each color on the tips showing different trait states [Green = 1 diet category is used by the species; Dark blue = 2; Light blue = 3; Grey = 6].

## 3. Dealing with identical sets of species.

Translating the problem of measuring originality from phylogeny to a small set of traits raises a critical new question because, according to a limited set of discrete traits (such as nominal or binary traits), two or more species might be identical (i.e, these species form an apparently *identical set* of species). Two species thus belong to the same identical set if they have identical values for all traits considered. This raises the question of whether these apparently identical species are considered as not distinctive at all (originality measure = 0). According to PE and NN these species will be indeed non distinctive. However, with the other indices they can be attributes positive originalities. First, a species within a speciose identical set can be considered as less original than a species within an identical set of a few species. Second, sets of identical species are not equally distinct; some might be very different from others in trait space. In this case, species within a relatively distinct set will be considered more functionally distinct than species within less distinct identical sets, all else being equal. Overall, we can state that the originality of a species increases with the originality of the identical set.

With the QE-based index (QEb), our solution is to partition the originality of an identical set equally among the species within it. An identical set of S species and originality I will contain species each with a originality value of I/S. As the quadratic entropy is unchanged by splitting a set of identical species (Shimatani 2001), the vector of originality defined by this process also maximizes the quadratic entropy (which is the criterion used by Pavoine *et al.* 2005 to define QEb; Pavoine and Bonsall 2009).

With the Fair-proportion (FP) and Equal-Split (ES) indices, the tree is modified by adding artificial branches of length 0 at the tips. Each tip represents an identical set and there are as many artificial branches at that tip as there are species within the identical set. Note that with this rule, ES shares the following property with QEb: if an identical set contains S species and has originality equal to I, then the originality of each species in the set is I/S.

With AV, the formula is unaltered as the relative originality of a species decreases with the presence of several zero distances with other species. Consider that a species is the sole member of its identical set and that its originality value is D/n, where D is the sum of all distances between this focal species and the other n species. Now we add s species identical to the focal species. The total distance D remains unchanged, but the number of distances increases by s: the originality of the species is reduced to D/(n+s).

With Rb, as with AV, the formula was unaltered (although for a given *i*, the  $d_{ij}$  were allowed to be zero for one or several *j* but not all) and the observed correlations between AV and Rb were maintained with sets of identical species in our Carnivora case study as shown below.

## 4. Analyses per trait or group of traits

Correlations between phylogenetic and functional originalities were low for all traits except those related to the reproduction (Table B.1). They were even negative for some traits like those related to the habitat and for example for body size when indices Rb and AV are used to

measure originality. The effect of the use of a clustering approach before applying Rb and AV depends on the traits used. For example using a clustering approach increased correlations between functional and phylogenetic originalities as measured by Rb and AV with all combined traits and with body mass. However those correlations were decreased with reproduction and the Ward clustering approach.

In general, the choice of the clustering approach (Ward versus UPGMA) had low effect on the vectors of functional originalities but this also depended on the traits considered and on the originality index selected (Table B.2). For example, the lowest correlations between the originality vectors obtained after the Ward versus the UPGMA approach were observed with body size, particularly when using tb-AV and tb-Rb (Table B.2).

Regarding the link between our new originality index Rb and the other originality indices, this also depended on the traits used, except for AV (Table B.3). Correlations between Rb and AV were close to unity whatever the traits used. Correlations between Rb and uniqueness (NN and PE) varied from 0 with body mass to 0.6 with all combined traits. Correlations between Rb and tb-Rb were higher with the UPGMA approach implying that, at least in this example, the UPGMA may less distort the functional distances among species than the Ward approach.

Introduced species had higher originality according to the phylogeny, all traits together, and behaviour traits (Table B.4). Results for other traits were more mitigated and depended on the originality index chosen. For body size, introduced species were (in terms of median value) more original than other species according to PE, whereas the most original species were the marginal ones according to the other indices. For diet traits, the most original species were either introduced species alone (with M and ES) or both marginal and introduced species (according to the other indices, except uniqueness, i.e. PE and NN). For habitat traits, the most original species were the introduced ones (with M and PE) or the marginal ones (with FP, tb-AV, tb-Rb, AV and Rb). For reproduction traits, the most original species were the introduced ones (with tree-based indices and NN) or the marginal ones (with AV and Rb, with five out of seven marginal species being more original than the most original introduced species with AV and Rb and only one with tb-AV and tb-Rb). The native species were thus the least phylogenetically and functionally original. However, whether the introduced or the marginal species were the most original depended on the index and traits used. Although both used to measure uniqueness, PE and NN disagreed on which of the introduced or marginal species were the most original according to body mass (consensus was obtained with the other traits).

No correlation was observed between the phylogenetic originality of native species and their extinction risk (IUCN Red List status, Table B.5). But there was a weak evidence for a positive relation between the extinction risk and the functional originality, more precisely the strict functional uniqueness, measured by PE for all traits except behaviour traits and body size and according to most originality indices for habitat and reproduction traits. The highest correlations were obtained with PE and NN, both characterizing the strict uniqueness, in habitat traits and all combined traits (correlations between 0.36 and 0.40, Table B.5).

	М	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
All traits - Ward	0.06	0.14	0.30	0.26	0.20	0.21	0.21	0.11	0.06	0.19
All traits - UPGMA	-0.19	0.15	0.30	0.24	0.20	0.19	0.19			
Behaviour - Ward	-0.08	0.26	-0.02	0.16	0.16	0.02	0.03	0.04	0.07	0.26
Behaviour - UPGMA	-0.08	0.26	-0.02	0.16	0.16	0.03	-0.03			
Body Mass - Ward	0.09	0.11	0.10	0.16	0.11	0.02	0.01	-0.38	-0.40	0.06
Body Mass - UPGMA	-0.05	0.09	0.08	0.09	0.02	-0.22	-0.21			
diet - Ward	-0.31	-0.21	-0.23	0.30	0.27	0.34	0.33	0.34	0.34	-0.21
diet - UPGMA	-0.31	-0.21	-0.26	0.30	0.27	0.34	0.37			
Habitat - Ward	-0.37	-0.18	-0.30	-0.11	-0.20	-0.22	-0.22	-0.22	-0.22	-0.18
Habitat - UPGMA	-0.37	-0.18	-0.29	-0.11	-0.20	-0.22	-0.22			
Reproduction - Ward	0.32	0.44	0.49	0.45	0.43	0.04	0.03	0.13	0.12	0.34
Reproduction - UPGMA	0.24	0.45	0.47	0.51	0.36	0.11	0.11			

Table B.1 Spearman correlations between functional and phylogenetic originalities in the Carnivora case study

\* These indices are independent on the clustering approach; for phylogenetic originalities only, AV=tb-AV, Rb=tb-Rb, NN=PE

Table B.2 Correlations between functional originalities obtained with Ward versus UPGMA clustering in the Carnivora case study

	М	PE	ES	FP	Qb	tb-AV	tb-Rb
All traits	0.72	1.00	0.92	0.99	0.94	0.96	0.96
Behaviour	1.00	1.00	1.00	1.00	1.00	0.97	1.00
Body Mass	0.77	1.00	0.97	0.86	0.88	0.58	0.62
Diet	1.00	1.00	1.00	1.00	1.00	1.00	0.97
Habitat	1.00	1.00	1.00	1.00	1.00	1.00	0.99
Reproduction	0.96	1.00	0.99	0.98	0.97	0.92	0.91

Table B.3 Spearman correlations between Rb and the other originality indices in the Carnivora case study using groups of traits

	Μ	PE	ES	FP	Qb	tb-AV	tb-Rb*	AV*	NN*
Ward									
All traits	0.62	0.62	0.69	0.85	0.77	0.89	0.89	0.99	0.62
Behaviour	0.56	0.30	0.59	0.95	0.95	0.92	0.95	0.99	0.30
Body mass	0.16	0.06	0.17	0.46	0.22	0.49	0.53	0.99	0.04
Diet	0.29	0.31	0.33	0.93	0.93	1.00	0.99	1.00	0.31
Habitat	0.45	0.34	0.48	1.00	1.00	1.00	1.00	1.00	0.34
Reproduction	0.66	0.56	0.63	0.77	0.65	0.72	0.71	1.00	0.48
UPGMA									
All traits	0.34	0.62	0.80	0.83	0.77	0.90	0.90		
Behaviour	0.59	0.30	0.58	0.95	0.95	0.95	0.95		
Body mass	0.63	0.06	0.30	0.60	0.55	0.85	0.85		

Diet	0.29	0.31	0.33	0.93	0.93	1.00	0.98	
Habitat	0.51	0.34	0.51	1.00	1.00	1.00	0.99	
Reproduction	0.65	0.59	0.62	0.73	0.71	0.83	0.83	

\* AV and NN are independent of the clustering method (Ward versus UPGMA); with phylogenetic data, tb-AV=AV, tb-Rb=Rb and PE=NN.

Table B.4 Median of species relative originalities (expressed as %) per group of species: Introduced species (Int), Marginal species (Mar), Native species (Nat) (Carnivora Case Study) Phylogeny

i nyiogeny										
	Μ	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Int	3.60	4.72	4.39	4.22	6.05	2.80	2.88			
Mar	2.00	2.00	2.05	2.11	1.27	2.49	2.36			
Nat	2.67	0.90	2.42	2.57	2.49	2.48	2.33			
All traits - Ward										
	М	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Int	3.25	5.12	4.18	3.43	4.34	2.92	3.01	2.92	3.04	5.39
Mar	2.41	1.47	1.79	2.43	1.70	2.89	2.95	2.81	2.83	1.11
Nat	2.41	1.57	2.21	2.52	2.22	2.58	2.60	2.50	2.43	1.25
All traits - UPGMA										
	М	PE	ES	FP	Qb	tb-AV	tb-Rb			
Int	2.69	5.04	3.82	3.73	3.63	2.94	3.08			
Mar	2.24	1.38	1.61	2.04	1.11	2.85	2.89			
Nat	2.24	1.66	2.28	2.15	1.49	2.51	2.45			
Behaviour - Ward										
	М	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Int	4.16	0	5.09	4.58	4.75	3.59	3.60	3.89	4.18	0
Mar	2.05	0	0.18	1.38	0.99	1.93	1.83	1.99	1.79	0
Nat	1.68	C	0.05	1.38	0.99	1.93	1.83	1.99	1.79	0
Behaviour - UPGMA								•	•	•
	М	PE	ES	FP	Qb	tb-AV	tb-Rb			
Int	3.69	0	4.49	3.99	3.66	3.81	4.02			
Mar	1.85	0	0.18	1.12	0.90	1.87	1.69			
Nat	1.68	0	0.05	1.12	0.90	1.87	1.69			
Body mass - Ward										
	М	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Int	2.39	1.15	1.75	2.33	1.85	2.53	2.52	2.19	1.95	1.43
Mar	2.87	0.98	2.66	2.51	2.70	2.80	2.85	3.11	3.03	1.47
Nat	2.39	0.82	1.85	2.29	1.95	2.61	2.67	2.16	1.89	1.06
Body mass - UPGMA										
	М	PE	ES	FP	Qb	tb-AV	tb-Rb			
Int	2.07	1.03	1.72	1.83	1.10	2.25	2.09			
Mar	2.21	0.94	1.91	2.19	1.32	3.45	3.65			
Nat	2.21	0.78	1.60	1.84	1.31	2.28	2.12			
Diet - Ward										

	М	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Int	2.39	(	0.48	2.86	1.67	3.10	3.09	3.12	3.12	0
Mar	1.89	(	0.10	2.86	1.67	3.10	3.09	3.12	3.12	0
Nat	1.71	(	0.05	2.08	1.25	2.26	2.25	2.25	2.24	0
Diet - UPGMA						•				
	М	PE	ES	FP	Qb	tb-AV	tb-Rb			
Int	2.39	(	00.46	2.49	1.74	3.08	3.03			
Mar	1.89	(	0.11	2.49	1.74	3.08	3.03			
Nat	1.71	(	0.04	1.79	1.19	2.24	2.19			
Habitat - Ward										
	Μ	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Int	2.46	(	0.39	2.69	2.10	3.04	3.00	2.87	2.54	0
Mar	1.64	(	0.03	3.71	2.33	4.17	4.12	3.87	3.31	0
Nat	1.79	(	0.04	1.67	1.88	1.90	1.89	1.86	1.77	0
Habitat - UPGMA										
	Μ	PE	ES	FP	Qb	tb-AV	tb-Rb			
Int	2.31	(	0.36	1.90	1.77	2.89	2.59			
Mar	1.63	(	0.03	2.49	2.49	3.97	3.53			
Nat	1.63	(	0.03	1.30	1.05	1.82	1.66			
Reproduction - Ward										
	Μ	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Int	2.71	4.06	3.05	2.44	2.82	2.59	2.50	2.06	1.66	1.61
Mar	2.11	1.10	1.33	1.75	1.27	2.59	2.50	2.75	2.64	0.30
Nat	2.46	0.63	1.81	1.80	1.48	2.59	2.50	2.36	2.11	0.55
Reproduction - UPGMA										
	Μ	PE	ES	FP	Qb	tb-AV	tb-Rb			
Int	2.25	3.01	2.91	2.36	1.42	2.30	2.00			
Mar	1.87	0.76	1.27	1.36	0.59	2.28	1.97			
Nat	1.87	0.60	1.27	1.47	0.52	2.28	1.96			

\* These indices are independent on the clustering approach; for phylogenetic originalities only, AV=tb-AV, Rb=tb-Rb, NN=PE

Table B.5 Spearman correlation between originality and extinction risks (Carnivora case study)

	М	PE	ES	FP	Qb	tb-AV	tb-Rb	AV*	Rb*	NN*
Phylogeny	0.01	0.14	0.14	0.08	0.05	-0.12	-0.13			
All traits - Ward	0.24	0.36	0.32	0.26	0.27	0.12	0.13	0.26	0.29	0.40
All traits - UPGMA	0.18	0.36	0.24	0.27	0.22	0.14	0.14			
Behaviour - Ward	0.05	0.00	0.05	0.09	0.09	0.09	0.09	0.11	0.09	0.00
Behaviour - UPGMA	0.04	0.00	0.04	0.09	0.09	0.09	0.09			
Body Size - Ward	-0.38	-0.12	-0.31	-0.02	-0.34	0.24	0.21	0.15	0.13	-0.15
Body Size - UPGMA	-0.23	-0.10	-0.27	-0.19	-0.23	-0.19	-0.19			
Diet - Ward	0.06	0.29	0.05	0.18	0.18	0.11	0.11	0.11	0.11	0.29
Diet - UPGMA	0.06	0.29	0.05	0.18	0.18	0.11	0.07			

Habitat - Ward	0.19	0.39	0.20	0.33	0.33	0.33	0.33	0.33	0.33	0.39
Habitat - UPGMA	0.19	0.39	0.20	0.33	0.33	0.33	0.33			
Reproduction - Ward	0.19	0.35	0.26	0.32	0.25	0.25	0.26	0.23	0.23	0.15
Reproduction - UPGMA	0.20	0.38	0.25	0.34	0.27	0.22	0.22			

\* These indices are independent on the clustering approach; for phylogenetic originalities only, AV=tb-AV, Rb=tb-Rb, NN=PE