# **CHAPTER 5**

Taxonomic and phylogenetic distinctiveness in regional conservation assessments: A case study based on extant South African Chiroptera and Carnivora

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#### Abstract

The current study investigates whether a simple measure of taxonomic diversity (Taxonomic Distinctiveness - TD) can be used as a proxy for different measures of phylogenetic diversity (Phylogenetic Distinctiveness - PD) in determining species of regional conservation priority, and uses extant South African Chiroptera and Carnivora as a case study. Published phylogenies for the two mammalian Orders allowed the quantification of a node-based measure that was considered to represent phylogenetic diversity (PD<sub>NODE</sub>), as well as a branch length-based measure that was considered to represent the amount of evolutionary change over time (PD<sub>BRANCH</sub>). Both the PD<sub>NODE</sub> and PD<sub>BRANCH</sub>, together with TD were included in our regional conservation priority assessment. Although no statistically significant differences were detected between the PD<sub>NODE</sub>, PD<sub>BRANCH</sub> and the TD for both the Chiroptera and Carnivora, these measures were also shown to be correlated with each other. More importantly, inclusion of either the PD<sub>NODE</sub>, PD<sub>BRANCH</sub>, or TD in our analysis did not significantly alter the species that were identified to be of regional conservation priority. Both regional priority scores for the South African Chiroptera and Carnivora and their respective rankings were broadly consistent across the three potential indicators of conservation status utilised. These results suggest that the inclusion of either the PD<sub>NODE</sub> and/or PD<sub>BRANCH</sub> in conservation prioritisation exercises may not add value to that currently provided by the TD. Consequently, this implies that in the absence of relevant PD data, the utilisation of the TD in regional conservation priority settings may provide the appropriate information on evolutionary diversity.

**Key words:** Phylogenetic/Taxonomic diversity/distinctiveness, regional conservation assessments, Chiroptera, Carnivora, South Africa.

## Introduction

Setting conservation priorities for species is a crucial first step in developing conservation strategies, particularly in the context of increasing financial and logistical constraints (Master 1991; Dunn, Hussel & Welsh 1999). In general, species conservation prioritisation focuses on taxa that are rare and threatened with extinction (Master 1991; Freitag & van Jaarsveld 1997; Dunn et al. 1999). Using rarity as the sole indicator of a species' potential conservation status (or risk of extinction) is considered insufficient, as various secondary components, such as body mass, population variability and dispersal ability may also be important in determining the vulnerability to extinction (Terborgh 1974; Burke & Humphrey 1987; Lande 1993; Dobson, Yu & Smith 1995; Cardillo & Bromham 2001). Consequently, additional variables have been proposed for use in species priority setting exercises, such as ecological specialization, systematic significance, and a series of threat variables (Millsap et al. 1990; Master 1991; IUCN 1994; Freitag & van Jaarsveld 1997; Dunn et al. 1999; Harcourt & Parks 2003).

In addition to the risk of extinction, determining the conservation value of a species is also important in conservation priority setting exercises. While there are a variety of approaches for determining conservation values for species (Vane-Wright, Humphries, & Williams 1991; Crozier 1992; Faith 1992; Heard & Mooers 2000), phylogenetically distinct species are generally considered to be of a higher conservation value than species with close genetic relatives (Vane-Wright et al. 1991; Freitag & van Jaarsveld 1997; Gittleman & Purvis 1998; Heard & Mooers 2000; Polasky et al. 2001; Rodriguez & Gaston 2002). Phylogenetic analyses have allowed the ranking of species according to their degrees of phylogenetic diversity, therefore, highlighting the evolutionary history and genetic diversity of unique species (Freitag & van Jaarsveld 1997; Virolainen et al. 1999; Rodrigues & Gaston 2002). Nevertheless, the paucity of comprehensive and inclusive phylogenies has led to a search for alternative measures for identifying distinct species (Polasky et al. 2001; Rodrigues & Gaston 2002). In some studies, simple measures of generic species richness (e.g., see Rodrigues & Gaston 2002) served as a surrogate for more complex measures of phylogenetic diversity (Whiting et al. 2000; Polasky et al. 2001; Rodrigues & Gaston 2002).

During the past few years, a variety of comprehensive published ordinal phylogenies for some South African mammals have become available, such as that for the extant Primata (Purvis 1995), Chiroptera (Jones et al. 2002), Carnivora (Bininda-Emonds, Gittleman & Purvis 1999), Insectivora (Greyner & Purvis 2003), and the Lagomorpha (Stoner et al. 2003). In order to explore the relationship

between an assortment of surrogate measures of phylogenetic diversity for conservation prioritisation purposes, the phylogenies of members of two extant orders, the Chiroptera and Carnivora, were used as a case study in the present investigation. Apart from the availability of published phylogenies, members of these two Orders also represent a large proportion of South African species.

From the large number of potential measures of phylogenetic diversity, including those proposed by Vane-Wright et al. (1991), Faith (1992, 1994), Williams & Humphries (1996), Hacker, Colishaw & Williams (1998); Posadas, Miranda Esquivel & Crisci (2001), Polasky et al. (2001), and Alexandre & Diniz-Fihlo (2004), we opted to use the following two measures of Phylogenetic Diversity (PD):

- 1.) The node-based phylogenetic diversity (PD<sub>NODE</sub>) score following Vane-Wright et al. (1991) and Posadas et al. (2001). The PD measure was selected due to its simplicity and sensitivity. It reflects the number of phylogenetically informative statements derived from the number of nodes on a phylogenetic tree to which each species belongs (Vane Wright et al. 1991; Crozier 1992; Posadas et al. 2001).
- 2.) Branch lengths ( $PD_{BRANCH}$ ) extracted from a recent complete carnivore phylogeny (Bininda-Emonds et al. 1999).  $PD_{BRANCH}$  represents the amount of evolutionary change over time (in millions of years) for each species with reference to its terminal branch. Such an approach allows for a comparative analysis of the average ages of species in a phylogeny (Sechrest et al. 2002).

For comparison with both the  $PD_{NODE}$  and  $PD_{BRANCH}$  as PD measures, a "simple" measure of taxonomic distinctiveness (TD) was also used in this study. The TD has previously been applied to terrestrial African mammals across various geographic scales in Southern Africa in particular and Africa as a continent in general (Freitag & van Jaarsveld 1997; Mills, Freitag & van Jaarsveld 2001). The TD measure is based on the number of regionally represented species relative to the number of genera within the Family and the number of Families within the Order under consideration (Freitag & van Jaarsveld 1997). This approach assumes that taxonomically more distinct taxa contribute more to regional biodiversity than more speciose species (Freitag & van Jaarsveld 1997).

In an attempt to explore the impact of using either the PD measures or the TD approach when conducting conservation priority setting, we employ a multi-criteria conservation setting technique, the Regional Priority Score (RPS - Freitag & van Jaarsveld 1997). The present investigation uses

phylogenetic data of extant members of the Chiroptera and Carnivora from South Africa as a case study to assess if a "simple" measure of taxonomic distinctiveness can be a substitute for PD measures in the absence of complete phylogenies.

## **Materials and Methods**

The recently available comprehensive ordinal phylogenies for bats (Jones et al. 2002) and carnivores (Bininda-Emonds et al. 1999) were used to extract data for 51 and 34 extant South African bat and carnivore species, respectively.

In order to calculate  $PD_{NODE}$ , the technique described by Vane-Wright et al. (1991) and Posadas et al. (2001) was applied (see Figure 1).  $PD_{NODE}$  essentially attempts to reflect phylogenetic information for each species based on the number of nodes on a phylogenetic tree to which each species belongs. This basic measure of phylogenetic information (I) for each terminal species is in turn allocated a phylogenetic weight (Q) that reflects each species' contribution to the total diversity of the group (Vane-Wright et al. 1991), and is calculated as:

$$Q_{j} = \frac{\sum I}{I_{j}}$$

where, *j* represents a specific species.

The resulting phylogenetic weight is then standardized (W) by dividing a terminal species' Q value with the lowest derived Q value among all terminal taxa under consideration, i.e.:

$$W_j = \frac{Q_j}{Q_{min}}$$

Such an adjustment allows for the lowest ranking species to be equal to one. To obtain the required  $PD_{NODE}$  value, the standardised weight value (W) is further adjusted as:

$$PD_{NODE j} = \frac{W_j}{\sum W}$$

The associated "best estimate" branch lengths obtained from the terminal node (Beninda-Emonds et al 1999) of each of the 34 extant South African carnivores were used to compile  $PD_{BRANCH}$  in order to assess the relative evolutionary age for each species in a phylogeny over time (in millions of years). The Chiroptera were not considered in the current  $PD_{BRANCH}$  analysis because Chiropteran branch length data are currently not available in the literature (K. Jones, pers comm.).

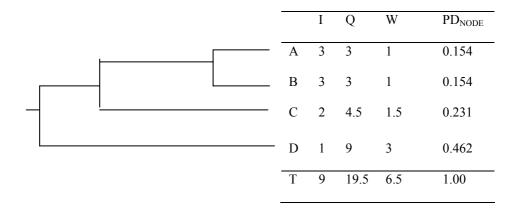


Figure 1. An example of the calculation of Phylogenetic Distinctiveness ( $PD_{NODE}$ ). Column I indicates the number of groups to which each terminal species belongs, I being the basic measure of taxonomic information. Q gives the quotient of the total information for each species. W is standardised weight of each species. PD gives the contribution of each terminal species to the total diversity in terms of the aggregated values for Q and W (Modified from Vane-Wright et al. 1991)

In order to assess the taxonomic distinctiveness, the TD was calculated following the procedure outlined by Freitag & van Jaarsveld (1997) as:

$$TD = \frac{1}{\sqrt{\text{# of regionally represente d Families x # of Genera x # of Species}}}$$

TD reflects the taxonomic rarity of a species where species with fewer rather than many extant relatives are considered to be of a higher conservation value.

Regional Priority Scores (RPS) components

The RPS technique used in the current study has the advantage of systematically evaluating indigenous species in terms of various components that could also accommodate for the inclusion and subsequent assessment of the effect of any specific measure of phylogenetic rarity. Two bat species, the flatheaded free-tail bat, *Sauromys petrophilus* (Family Molossidae) and the butterfly bat, *Glauconycteris variegates* (Family Vespertilionidae) were omitted from all RPS analyses because they are not represented in the Chiropteran super tree (Jones et al. 2002).

In order to evaluate the effect of incorporating  $PD_{NODE}$  and  $PD_{BRANCH}$  in regional priority assessments, the RPS technique proposed by Freitag & van Jaarsveld (1997) was used. To include the  $PD_{NODE}$  and  $PD_{BRANCH}$  values in the respective RPS technique, an adjustment to the score was required. The PD values for each species were expressed as a value less than one (Vane-Wright et al. 1991; Posadas et al. 2001). Consequently, to allow for carnivore  $PD_{BRANCH}$  to be expressed as a value less than 1.0,  $PD_{BRANCH}$  was adjusted as:

$$PD_{BRANCH} = \frac{Millions of years}{100}$$

In addition to the use of measures of either a taxonomic distinctiveness or a phylogenetic diversity, the conventional rarity and threat components used by the RPS technique include Regional Occupancy (RO), Relative Endemism (RE) and Relative Vulnerability (RV) (Freitag & van Jaarsveld 1997), as well as components of Body Mass (BM) (M. Keith unpubl. data) and Human Population Density (HD) (Central Statistical Services 1998; M. Keith unpubl. data).

The calculation of the employed rarity and threat components were undertaken as follows:

(a) Relative Occupancy (RO): Based on species distributional data derived from museum records at quarter degree grid squares (QDS; Freitag & van Jaarsveld 1995; Freitag & van Jaarsveld 1997) and computed as:

$$RO = \frac{1}{\text{number of quarter degree squares (QDS) occupied in South Africa}}$$

- (b) Relative Endemism (RE): Denotes the extent to which a species' total African distribution is limited to South Africa and was scored as:
  - 1.0: Endemic to South Africa only (excluding Swaziland and Lesotho);
  - 0.8: 75-99% distribution in South Africa;
  - 0.6: 50-74% distribution in South Africa;
  - 0.4: 25-49% distribution in South Africa; and
  - 0.2: 0-24% distribution in South Africa.
- (c) Relative Vulnerability (RV): Based on Mills et al. (2001). The regional IUCN Red Data List assessment of the regional Conservation Assessment and Management Plan (CAMP) for South African mammals (Friedmann and Daly 2004) were used in scoring the vulnerability categories as:
  - 1.0: Critically Endangered (CR);
  - 0.80: Endangered (EN);
  - 0.70: Vulnerable (VU);
  - 0.56: Near Threatened (NT);
  - 0.42: Data Deficient (DD);
  - 0.00: Least Concern (LC) or Not evaluated (NE) or not listed.
  - (d) Relative Human Density (RHD): Initially computed for each species as:

$$HumanDensity(HD) = \frac{\sum (Averaged human density across a species' distribution (QDS))}{Number of QDS in which he species occurs in}$$

In order to obtain a relative human density (Central Statistical Service 1998) value for each species across its known distributional range (in QDS), HD was standardised by dividing it by the species that scored the highest human density value (HD<sub>max</sub>) within each of the two Orders, i.e.:

$$RHD = \frac{HD}{HD_{max}}$$

By so doing, the large eared free tailed bat, *Otomops martiensseni* scored the highest HD value for bats, with most of its QDS distribution falling within the Durban metropolitan area, with 256 people/km<sup>2</sup>. This HD value was not used as HD<sub>max</sub> for bats and was treated as an outlier value, and converted to 1. Consequently, the second ranking bat species, the peak-saddle horseshoe bat, *Rhinolophus blassii* with an HD value of 207.88 people/km<sup>2</sup> was instead used as the HD<sub>max</sub> value for bats. The carnivore HD<sub>max</sub> value was based on the human density value obtained for the white-tailed mongoose, *Ichneumia albicauda* that had an HD value of 87.84 people/km<sup>2</sup>.

(e) Relative Body Mass (RBM): Based on average body weights (in grams) for each species as obtained from Dorst & Dandelot (1972), Haltenorth & Diller (1980), and Skinner & Smithers (1990), and was computed as:

$$RBM = \frac{\log (body mass (g) (BM))}{\log (BM_{max})}$$

RBM was incorporated in this current assessment as a potential estimator for human conflict following Mills et al (2001). The rationale behind this was that larger-bodied species are more likely to be negatively influenced by human populations (Mills *et al.*, 2001, Harcourt and Parks, 2003). However, despite numerous documented relationships between body size and ecological and taxonomic variables (see Kunin & Gaston, 1997; Gittleman 1985; Jones, Purvis and Gittleman. 2003), the effects of body size and characteristics of threat remain unclear (Dobson and Yu, 1993; Arita *et al.*, 1997; Dobson, Smith & Yu, 1997).

Regional Priority Score (RPS)

To ascertain standard regional priority without any influence of either  $PD_{NODE}$ ,  $PD_{BRANCH}$  or TD,  $RPS_S$  was calculated, using five rarity and threat criteria:

$$RPS_{S} = \frac{RO + RE + RV + RHD + RBM}{5}$$

The  $PD_{NODE}$  measure was included within the priority setting exercise in addition to the components used to calculate  $RPS_s$ , for both carnivore and chiropteran species, as:

$$RPS_{NODE} = \frac{RO + RE + RV + RHD + RBM + PD_{NODE}}{6}$$

Carnivore branch length data were incorporated into the RPS technique as follows:

$$RPS_{BRANCH} = \frac{RO + RE + RV + RHD + RBM + PD_{BRANCH}}{6}$$

RPS<sub>TD</sub> was subsequently calculated in similar fashion to PD RPS as:

$$RPS_{TD} = \frac{RO + RE + RV + RHD + RBM + TD}{6}$$

Statistical analysis

The PD<sub>NODE</sub>, PD<sub>BRANCH</sub>, and TD values for the extant South African chiroptera and carnivora species were tested for statistically significant differences using a Mann-Whitney U test (Zar 1996). Statistical correlations were explored using Spearman's R (Zar 1996). Jackknife randomisation tests (re-sampling without replacement) (Manly 1991; MathSoft 1999) for correlations between PD<sub>NODE</sub>, PD<sub>BRANCH</sub> and TD were also undertaken. Statistical analyses to assess differences and correlations (Zar 1996) between the derived RPS scores for RPS<sub>S</sub>, RPS<sub>NODE</sub>, RPS<sub>BRANCH</sub> and RPS<sub>TD</sub> included Kruskal-Wallis Analysis of Variance (ANOVA) by Ranks as well as Wilcoxon Matched Pair tests (Zar 1996). Spearman's R correlation was also used to test for statistical correlations between the various different RPS scores. The derived RPS scores and associated rankings were used to calculate a corrected coefficient of variation ( $CV^*$  for small sample sizes; n = 3 in this case; Sokal & Rohlf 1981) to assess the nature and extent of variation in RPS scores associated with each of the three techniques for both the Carnivore and Chiropteran species. All statistical analyses were executed using STATISTICA, version 5.5 (StatSoft Inc. 1995).

#### Results

Chiroptera

A Mann-Whitney U test shows that the PD<sub>NODE</sub> and TD values for the 51 bat species were not significantly different from each other (U = 1442, n = 51; P = 0.40), and were weakly negatively correlated with each other (R = -0.29; n = 51; P < 0.05). The jackknife randomisation tests indicated that the Spearman R value between PD<sub>NODE</sub> and TD were not significantly different from random (R = -0.29; n = 50; P = 0.66). Only the Family Vespertilionidae (R = 0.051; n = 23; P < 0.05) indicated towards a very weak positive correlation between taxa.

The Mann-Whitney U test revealed statistically significant differences between RPS<sub>S</sub> and RPS<sub>NODE</sub> values (U = 927.0, n = 51; P < 0.05) and between RPS<sub>S</sub> and RPS<sub>TD</sub> values (U = 1660.00, n = 100.00).

51; P < 0.05) (Table 1). RPS<sub>NODE</sub> and RPS<sub>TD</sub> values did not differ significantly from each other. Although the RPS<sub>S</sub> values for bats were considerably larger than the values of RPS<sub>NODE</sub> and RPS<sub>TD</sub>, the chiropteran RPS<sub>S</sub>, RPS<sub>NODE</sub> and RPS<sub>TD</sub> values and their associated rankings yielded broadly similar priority scores (Wilcoxon Matched Pair test:  $T \ge 10.5$ , n = 51, P > 0.058). Generally, the corrected coefficients of variation (CV\*) were low for all South African chiropteran species (Table 2). However, Spearman's R correlation analysis of the Chiroptera showed all three RPS techniques to be highly and significantly correlated with each other (Table 1). The large-eared free-tailed bat, Otomops martiensseni with an IUCN threat categorization of VU D2 (Friedmann & Daly 2004) scored the highest value in all three priority-scoring techniques and was consequently ranked highest with regard to bat conservation importance in South Africa. The additional four top priority bat species were the short-eared trident bat, Cloeotis percivali, Welwitsch's hairy bat, Myotis welwitschii, hairy slit-faced bat, Nycteris hispida, and Cape horseshoe bat, Rhinolophus capensis which retained a reasonably steady RPS score by both RPS<sub>NODE</sub>, RPS<sub>TD</sub>, and RPS<sub>S</sub>, although some shifts in rank occurred between these species. Only two of the top five bats were regarded as Threatened by the regional IUCN Red List (C. percivali: CR A2a, and O. martiensseni: VU D2), while the remaining three species were assessed as Near Threatened (NT).

## Carnivora

PD<sub>NODE</sub> and PD<sub>BRANCH</sub> were not significant different (U = 486; n = 34; P = 0.19), and were strongly positively correlated (R = 0.58; n = 34; P < 0.05). For carnivores, PD<sub>NODE</sub> and TD values were significantly different from each other (U = 152, n = 34; P < 0.001), and were weakly correlated with each other (R = 0.31; n = 34; P < 0.05). PD<sub>BRANCH</sub> and TD values were not significantly different (U = 592, n = 34; P = 0.54), and were weakly negatively correlated (R = 0.10; n = 34; P < 0.05). Correlation analysis for various Families within in the Carnivora was not possible due to relatively small sample sizes, but with regard to the negative correlation between PD<sub>BRANCH</sub> and TD, all but the Felidae were very weakly negatively correlated. The jackknife randomisation test between PD<sub>BRANCH</sub> and TD indicated that the Spearman R regression value obtained was not significantly different from random data (R = -0.10; n = 34; P = 0.56).

Whitney U test revealed statistically significant differences between the scores of the

Table 1. Mann Whitney U test and Spearman Rank order correlation (R - values included in parenthesis) for extant South African Chiroptera RPS scores using three different RPS techniques (RPS<sub>S</sub>, RPS<sub>PD</sub> and RPS<sub>TD</sub>; see text) (Statistical significance: \* = P < 0.05; ns = not statistically significant)

	RPS <sub>NODE</sub>	RPS <sub>TD</sub>
RPS <sub>S</sub>	927.0*(0.99*)	1660.0* (0.99*)
$RPS_{NODE}$	-	$1318.0^{\text{ns}} (0.99^*)$

Table 2. Regional Priority Scores and ranking of extant South African Chiroptera species based on the three RPS techniques (RPS<sub>S</sub>, RPS<sub>TD</sub>, and RPS<sub>PD</sub>; see text). Regional IUCN assessments of risk of extinction from the recent regional IUCN Red List (Friedmann & Daly 2004).  $CV^*$  = corrected coefficient of variation values calculated for the RPS scores. Taxa highlighted in bold form the top five ranking taxa as identified by the three priority techniques.

Species name	IUCN	$RPS_S$	RPS	$RPS_{TD}$	Rank	Rank	Rank	CV*
	Red List		NODE		$RPS_{S}$	$RPS_{NODE}$	$RPS_{TD}$	
Chaerephon ansorgei	LC	0.27	0.23	0.23	42	42	42	10.6
C. pumila	LC	0.26	0.22	0.22	46	46	46	9.28
Cloeotis percivali	CR A2 a	0.5	0.42	0.43	5	5	2	10.3
Epomorphorus gambianus	DD	0.37	0.31	0.32	26	26	23	10.3
E. wahlbergi	LC	0.39	0.33	0.33	20	20	19	10.6
Eptesicus hottentotus	LC	0.37	0.31	0.32	24	25	24	10.9
Glauconycteris variegatus	NT	0.37	0.31	0.32	25	24	25	10.5
Hipposideros caffer	DD	0.31	0.26	0.27	35	35	34	9.92
H. commersoni	NA	0.38	0.32	0.33	22	22	21	10.6
Kerivoula argentata	EN B1ab (iii) &	0.46	0.39	0.39	10	10	10	10.9
	2ab (iii)							
K. lanosa	NT	0.34	0.28	0.28	31	31	31	10.7
Laephotis botswanae	VU D2	0.4	0.34	0.34	17	17	17	10.9
L. wintoni	VU D2	0.44	0.37	0.37	11	11	11	11
Miniopterus fraterculus	NT	0.48	0.4	0.4	8	8	8	11.1
M. schreibersi	NT	0.35	0.3	0.3	29	29	29	10.8
Mops condylurus	LC	0.27	0.23	0.23	43	43	43	10.6
M. midas	LC	0.29	0.25	0.25	38	38	38	10.7
Myotis bocagei	DD	0.43	0.37	0.36	12	12	12	11
M. lesueuri	NT	0.49	0.41	0.41	7	6	7	11.3
M. seabrai	VU D2	0.41	0.35	0.35	15	15	16	11.1
M. tricolour	NT	0.47	0.4	0.39	9	9	9	11.1
M. welwitschii	NT	0.5	0.42	0.42	4	3	5	11.2
Neoromicia capensis	LC	0.21	0.18	0.18	51	51	51	10.6
N. melckorum	NA	0.23	0.2	0.2	49	49	49	10.7
N. somalicus	NA	0.18	0.15	0.15	52	52	52	10.4
Nycteris hispida	NT	0.5	0.42	0.43	2	2	3	10.7
N. thebaica	LC	0.22	0.18	0.19	50	50	50	9.91
N. woodi	EN B2 ab(v)	0.41	0.35	0.35	14	14	14	10.5
Nycticeius schlieffenii	LC	0.16	0.14	0.14	53	53	53	9.74
Otomops martiensseni	VU D2	0.64	0.54	0.54	1	1	1	11.1
Pipistrellus anchietai	NT	0.39	0.33	0.33	18	18	20	10.9
P. kuhlii	LC	0.25	0.21	0.21	47	47	47	10.9

5. Taxonomic and phylogenetic distinctiveness

Species name	IUCN	$RPS_S$	RPS NODE	$RPS_{TD}$	Rank RPS <sub>S</sub>	Rank RPS <sub>NODE</sub>	Rank RPS <sub>TD</sub>	CV*
P. nanus	LC	0.25	0.21	0.21	48	48	48	10.9
P. rueppellii	NA	0.27	0.23	0.23	45	45	45	10.9
P. rusticus	NT	0.3	0.25	0.25	37	36	37	10.6
Rhinolophus blasii	VU D2	0.49	0.41	0.41	6	7	6	11.3
R. capensis	NT	0.5	0.42	0.42	3	4	4	11.4
R. clivosus	NT	0.38	0.32	0.32	21	21	22	11.1
R. darlingi	NT	0.35	0.29	0.29	30	30	30	11
R. denti	NT	0.37	0.31	0.31	23	23	26	11.1
R. fumigatus	NT	0.36	0.3	0.3	28	28	28	11
R. hildebrandtii	NT	0.36	0.31	0.31	27	27	27	11
R. landeri	NT	0.33	0.27	0.27	33	33	33	10.9
R. simulator	LC	0.32	0.27	0.27	34	34	36	11.2
R. swinnyi	EN C2a (i)	0.42	0.35	0.35	13	13	13	11
Rousettus aegyptiacus	LC	0.4	0.34	0.35	16	16	15	10.3
Sauromys petrophilus	LC	0.28	0.24	0.24	39	39	39	10.4
Scotophilus dinganii	LC	0.28	0.23	0.23	40	40	41	11
S. viridis	LC	0.27	0.23	0.23	41	41	44	10.9
Tadarida aegyptiaca	LC	0.27	0.23	0.24	44	44	40	10.6
T. fulminans	NA	0.33	0.28	0.28	32	32	32	11
Taphozous mauritianus	LC	0.3	0.25	0.27	36	37	35	10
T. perforatus	NA	0.39	0.33	0.34	19	19	18	10.4

conventional RPS<sub>S</sub> and RPS<sub>NODE</sub> (U = 817.0; n = 34; P < 0.001), between RPS<sub>S</sub> and RPS<sub>BRANCH</sub> (U = 830.0; n = 34; P < 0.001), and between the RPS<sub>S</sub> and RPS<sub>TD</sub> (U = 844.0; n = 34; P < 0.001), but RPS<sub>NODE</sub>, RPS<sub>BRANCH</sub> and RPS<sub>TD</sub> values did not differ significantly from each other (Table 3). The RPS associated rankings yielded broadly similar priority scores (Wilcoxon Matched Pair test:  $T \ge 57.7$ ; n = 34 P = 0.54) and rankings, with relatively low  $CV^*$  (Table 4).

The three RPS techniques yielded highly significantly correlated RPS scores for the carnivore species (Table 4). The wild dog, *Lycaon pictus* (EN D) scored the highest value in all three priority scoring techniques applied and is consequently ranked highest with regard to carnivore conservation importance in South Africa. In turn, the other four carnivore taxa contributing to the top five ranking taxa were the cheetah *Acinonyx jubatus*, brown hyaena, *Parahyaena brunnea*, lion, *Panthera leo*, and the spotted hyaena, *Crocuta crocuta*. These five species were evidently stable in priority scores and ranking. Three of the top five carnivore species were regarded as being threatened (*A. jubatus*: VU D1, *L. pictus*: EN D and *P. leo*: VU D1).

#### **Discussion**

Phylogenetic (PD<sub>NODE</sub> and PD<sub>BRANCH</sub>) and taxonomic (TD) diversity measures used in the current study, revealed statistically varying results between PD and TD values for both South African bats and carnivores. The PD<sub>NODE</sub> and TD values for the Chiroptera, as well as PD<sub>BRANCH</sub> and TD for carnivores were weakly negatively correlated with each other. The reason(s) for the observed negative correlations between the Chiroptera PD<sub>NODE</sub> and TD values, as well as the carnivore PD<sub>BRANCH</sub> and TD remains unclear. The relationship between PD and TD should be generated by both the phylogeny (Crozier 1992) and the relative number of species per Genus and number of genera per Family (Freitag & van Jaarsveld 1997). These would most likely to be influenced by disproportionately large families (e.g., the Vespertilionidae and the Herpestidae), and yet the correlation between the Vespertilionidae species' PD<sub>NODE</sub> and TD were for example, yielded positive values suggesting a significant contribution by one of the smaller Families. The jackknife randomisation tests (resampling without replacement) for both PD and TD correlations between bats and carnivores indicated that the Spearman *R* correlations were not significantly different from random, demonstrating that none of the species are having a disproportionate effect on the correlations found.

Table 3. Mann Whitney U test and Spearman Rank order correlation (R – values included in parenthesis) for extant South African Carnivora RPS scores using four different RPS techniques (RPS<sub>s</sub>, RPS<sub>NODE</sub> RPS<sub>BRANCH</sub> and RPS<sub>TD</sub>; see text) (Statistical significance: \* = P < 0.05; \*\* = P < 0.01; \*\*\* = P < 0.001; ns = not statistically significant)

	RPS <sub>NODE</sub>	RPS <sub>BRANCH</sub>	RPS <sub>TD</sub>
$\overline{RPS_S}$	817.0**** (0.98*)	830.0**** (0.88*)	844.0*** (0.98*)
$RPS_{NODE}$	-	$486.0^{\text{ns}} (0.89^*)$	$656.0^{\text{ns}} (0.98^*)$
$RPS_{BRANCH}$		-	544.0 <sup>ns</sup> (0.89*)

Table 4. Regional Priority Scores and ranking of the extant South African Carnivora species based on the four RPS techniques (RPS<sub>S</sub>, RPS<sub>NODE</sub>, RPS<sub>BRANCH</sub> and RPS<sub>TD</sub>). Regional IUCN assessments of risk of extinction from the recent regional IUCN Red List (Friedmann & Daly 2004) are also included.  $CV^*$  = corrected coefficient of variation values calculated for the RPS scores. Taxa highlighted in bold form the top five ranking taxa as identified by the four priority techniques.

Species names	IUCN Re	ed RPS <sub>S</sub>	RPS	RPS	RPS	Rank	Rank	Rank	Rank	CV*
	List	st		BRANCH	TD	$RPS_{S}$	$PD_{NODE}$	$PD_{BRANCH} \\$	$RPS_{TD}$	
Acinonyx jubatus	VU D1	0.39	0.34	0.35	0.34	3	3	1	3	7.84
Aonyx capensis	LC	0.23	0.19	0.2	0.2	23	24	26	20	8.41
Atilax palundinosus	LC	0.22	0.19	0.21	0.19	30	29	18	30	8.18
Canis adustus	NT	0.23	0.2	0.2	0.2	20	20	25	22	8.49
C. mesomelas	LC	0.26	0.22	0.22	0.22	11	11	12	11	8.56
Caracal caracal	LC	0.22	0.19	0.2	0.19	29	30	27	28	7.41
Civetticis civetta	LC	0.23	0.2	0.21	0.2	22	21	19	24	7.74
Crocuta crocuta	NT	0.36	0.31	0.32	0.32	6	5	5	5	7.6
Cynictis penicillata	LC	0.24	0.2	0.2	0.21	16	16	23	19	8.61
Felis nigripes	LC	0.27	0.23	0.23	0.23	8	8	10	9	9.08
F. silvestris	LC	0.2	0.17	0.17	0.17	32	32	32	32	8.54
Galerella pulverulenta	LC	0.32	0.27	0.29	0.27	7	7	7	7	8.38
G. sanguinea	LC	0.2	0.17	0.19	0.17	31	31	31	31	7.85
Genetta genetta	LC	0.22	0.19	0.19	0.19	28	28	29	29	8.91
G. tigrina	LC	0.26	0.22	0.22	0.22	12	12	13	12	9.07
Helogale parvula	LC	0.19	0.16	0.16	0.17	33	33	33	34	8.78
Herpestes ichneumon	LC	0.23	0.19	0.19	0.2	26	25	28	26	8.29
Ichneumia albicauda	LC	0.24	0.2	0.22	0.2	18	19	11	21	8.21
Ictonyx striatus	LC	0.19	0.16	0.16	0.17	34	34	34	33	8.78
Leptailurus serval	NT	0.23	0.2	0.22	0.2	24	23	14	23	7.61
Lutra maculicollis	NT	0.36	0.31	0.3	0.31	5	6	6	6	9.22
Lycaon pictus	EN D	0.4	0.34	0.34	0.35	2	1	3	1	9.05
Mellivora capensis	NT	0.23	0.2	0.21	0.21	21	22	17	18	7.3
Mungos mungo	LC	0.22	0.19	0.19	0.19	27	27	30	27	8.96
Otocyon megalotis	LC	0.23	0.2	0.21	0.21	19	13	20	15	6.83
Panthera leo	VU D1	0.4	0.34	0.34	0.34	1	2	2	2	9.39
P. pardus	LC	0.24	0.2	0.2	0.21	13	18	22	16	8.93
Paracynictis selousi	DD	0.24	0.2	0.2	0.21	15	15	21	17	8.61
Parahyaena brunnea	NT	0.37	0.32	0.33	0.33	4	4	4	4	7.68
Poecilogale albinucha	LC	0.24	0.2	0.22	0.21	17	17	15	14	7.43
Proteles cristatus	LC	0.26	0.22	0.24	0.24	10	10	9	8	6.12

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5. Taxonomic and phylogenetic distinctiveness

Species names	IUCN Red	l RPS <sub>s</sub>	RPS	RPS	RPS	Rank	Rank	Rank	Rank	CV*
	List		NODE	BRANCH	TD	$RPS_{S} \\$	$PD_{NODE}$	$PD_{BRANCH}$	$RPS_{TD} \\$	
Rhynchogale melleri	DD	0.26	0.23	0.25	0.23	9	9	8	10	8.04
Suricata suricatta	LC	0.23	0.19	0.21	0.2	25	26	16	25	8.15
Vulpes chama	LC	0.24	0.2	0.2	0.21	14	14	24	13	8.47

Interestingly, Whiting et al. (2000) found a clear correlation between measures of phylogenetic diversity, although these correlations decreased with an increasing number of species. A similar trend is evident in the current study, where small number of species per Family seems to influence an analysis. Consequently, although in some cases the TD seems a reasonable surrogate measure for the more data intensive PD measures, it does not perform statistically well and should be therefore used with caution when substituting it for any measure of PD. It is evident that the implementation of a direct measure of evolutionary history such as PD<sub>BRANCH</sub> into regional conservation setting exercises rather than a diversity derivative such as PD<sub>NODE</sub> is advantageous. Various arguments against the use of PD<sub>NODE</sub> have been raised in the literature such as Crozier (1992) who argued that PD<sub>NODE</sub> is dependent on the topology of the inferred phylogeny as well as the subsequent taxonomic decisions that can be made from the phylogeny. It is also argued that this technique does not take branch lengths into account and may result in some anomalies during analysis (Crozier 1992). In the current study, however, the carnivore PD<sub>NODE</sub> and PD<sub>BRANCH</sub> values were not statistically significantly different and were also strongly positively correlated with each other. This suggests that both PD<sub>NODE</sub> and PD<sub>BRANCH</sub> values may reflect the evolutionary history of species under consideration, at least for the groups investigated here.

More importantly, the  $PD_{NODE}$  can be utilized with limited detailed phylogeny and distance information. It is therefore possible that the  $PD_{NODE}$  technique as proposed by Vane-Wright et al. (1991) and Posadas et al. (2001) can act as a suitable proxy for the more complex  $PD_{BRANCH}$  measure. The  $PD_{NODE}$  as defined here also allows all species to contribute equally to the weighting procedure, and is regarded to be sensitive to phylogenetic diversity (Faith 1994; Posadas et al. 2001). Consequently, this allows information from diverse taxa to be combined and gives priority to phylogenetically rare basal taxa (Vane-Wright et al.1991; Faith 1994; Posadas et al. 2001). Phylogenetically more distinct species receive higher scores than more speciose taxa because of the consideration that such unique species contribute proportionally more to regional biodiversity (Vane-Wright et al. 1991; Freitag & van Jaarsveld 1997).

With data and time constraints being a major factor when choosing components to include in conservation priority techniques, it is essential that components used for evaluation should be those that are easily obtainable and analysed (Whiting et al. 2000; Harcourt & Parks 2003). Currently, there are limited comprehensive phylogenies for most taxonomic groups, lack of appropriate data such as branch

lengths for large groups of taxa, unresolved phylogenies, as well as conflicting phylogenies arising from the use of independent data sets and techniques (Miyamoto 1981; Whiting et al. 2000; Wiens & Hollingsworth, 2000; Carstens, Lundringan & Myers 2002). Consequently, the application of either complex phylogenetic or character diversity measures on various South African mammals would not be considered a feasible option. For the current analysis, the TD as proposed by Freitag & van Jaarsveld (1997) and Mills et al. (2001), like other RPS components is logistically simple and more feasible for incorporating an evolutionary diversity measure when setting regional conservation priorities.

With limited resources available for conservation, the identification of species that demand special conservation measures or which need to be regionally prioritised provides invaluable information for the execution of conservation plans (Freitag & van Jaarsveld 1997; Whiting et al. 2000; Andelman & Willig 2002). With the recent emphasis on priority setting techniques to incorporate some gauge of evolutionary history and/or genetic diversity/distinctiveness, the use of either PD and/or TD may be the most appropriate procedure. Apart from regions being prioritised with reference to evolutionary and phylogenetic data, these approaches also contribute towards a better understanding of the regional conservation status of species. However, all these analyses ought to take cognisant that the geographic scale under consideration will always have influence arising from components such as rarity, endemism, rates of decline and IUCN Red List assessments (IUCN 1994; Freitag & van Jaarsveld 1995; Mills et al. 2001; Hartley & Kunin 2003).

After including phylogenetic/taxonomic criteria (PD<sub>NODE</sub>, PD<sub>BRANCH</sub> and TD) in the RPS<sub>NODE</sub>, RPS<sub>BRANCH</sub>, and RPS<sub>TD</sub> assessments, there was a significant difference in RPS values obtained for the chiropteran and carnivore species as compared to the use of the conventional RPS<sub>S</sub>. However, the RPS<sub>NODE</sub>, RPS<sub>BRANCH</sub> and RPS<sub>TD</sub> scores and their associated rankings did not differ significantly from each other. However, despite the TD, PD<sub>NODE</sub> and PD<sub>BRANCH</sub> measures not significantly changing the ranking of a species' conservation status, the incorporation of phylogenetic or taxonomic measures had an influence in the final priority scores. Therefore, the assignment of conservation priority scores appears to be insensitive to the specifics of the phylogenetic/taxonomic information included. It is possible that this may be a result of the expected lack of independence and some influence by other criteria included in the RPS assessment, such as endemism and/or vulnerability (Gittleman 1985; Beissinger 2000; Carter et al. 2000; Danell & Aava-Olsson 2002). It is noteworthy that scores for some components are correlated with each other (Purvis et al. 2000) such that it may not necessarily be due

to the lack of biological independence and visa versa. It is possible that some species are exhibiting correlations between components suggesting a pattern of the need for conservation rather than a lack of independence (Carter et al. 2000).

The nature of PD and TD as well as the variation within the two taxonomic groups included in this study may not have been sufficiently large to detect their affect in the scoring and ranking in the RPS technique used. The real impact of introducing any phylogenetic or taxonomic measure in regional priority scoring would most likely emerge when assessing a phylogenetic distinctiveness value across a much broader range of taxa. In the absence of phylogenies spanning various taxonomic Orders, either PD measures would not be a feasible conservation assessment tool (Rodrigues & Gaston 2002). The TD component, however, seems to have performed reasonably well in the past as an across-Order taxonomic measure (Freitag & van Jaarsveld 1997; Mills et al. 2002).

# Conclusion

In the absence of complete phylogenies, phylogenies lacking branch lengths, and especially for conservation priority assessment for species that span various Orders and Families, the inclusion of the Taxonomic Distinctiveness still appears a viable alternative, although it should be implemented with caution. The varying statistically significant findings between PD<sub>NODE</sub>, PD<sub>BRANCH</sub> and TD require further investigation. As more phylogenies become available for South African mammal taxa, it may be advisable to further investigate the application of a more comprehensive phylogenetic diversity measure (e.g., Faith 1994; Rodrigues & Gaston 2002; Faith 2002; Knapp, Russel, & Swihart 2003; Mace et al. 2003), in regional conservation setting techniques.

Carter et al. (2000) cautioned that relying solely on total scores and rankings to set conservation goals may be misleading and may probably be the most common misuse of the prioritisation process. In addition, no scoring system will give the "right" answer for every species or user of the system, no matter how many different components are included or how they are weighted (Millsap et al. 1990, Knapp et al. 2003). The differences among priority ranking systems may be less important than the need for a priority setting process to be undertaken. A much better understanding of the factors driving species warranting conservation action will encourage conservationists to consider

their goals carefully and to develop strategies that will focus activities and resources more effectively (Dunn et al. 1999).

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