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# Using Phylogenetic Diversity Measures to Set Priorities in Conservation: an Example from Southern South America

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**Abstract:** *Phylogenetic diversity measures rank areas for biodiversity conservation priorities based on information encoded in phylogenies (cladograms). The goal of these ranks for conservation is to consider as many factors as possible that provide additional taxic information, such as taxa richness, taxa distributional patterns, area endemism, and complementarity between areas. At present there are many measures that consider phylogenetic information, including node-based, genetic-distance, and feature-based measures. We devised a modified phylogenetic node-based index that we call “taxonomic endemism standardized weight,” which considers not only the taxonomic distinctness of the taxa that inhabit a given area but their endemism as well. Once the standardized weight of the taxonomic endemism identifies the area of highest priority, complementarity can be used to identify the second area and so on. We used this node-based index to rank priority areas for conservation in southern South America, and we compared the results of our rankings to results based on other node-based indexes. Our index identified Santiago district, in Central Chile province, as the highest priority area for conservation, followed by Maule, Malvinas, and districts of Subantarctic province. Malvinas exhibits greater complementarity relative to Santiago than Maule does, however, so Malvinas is ranked second in priority. Indexes based on phylogenetic information measure the evolutionary component of biodiversity and allow one to identify areas that will ensure the preservation of evolutionary potential and phylogenetically rare taxa. The modified index we propose is sensitive to taxic distinctness and endemism as well and allows information from diverse taxa to be combined (i.e., different cladograms). The use of complementarity allows for preservation of the maximum quantity of taxa in a minimal number of protected areas.*

Utilización de Medidas de Diversidad Filogenética para Definir Prioridades en Conservación: un Ejemplo del Sur de América del Sur

**Resumen:** *Las medidas de diversidad filogenética jerarquiza a las áreas para prioridades de conservación de biodiversidad con base en información codificada en filogenias (cladogramas), La meta de estas categorías de conservación requiere tomar en consideración tantos factores que proporcionan información adicional (riqueza de taxones, patrones de distribución de los taxones, endemismo del área y complementariedad entre áreas) como sea posible. Actualmente hay muchas medidas que consideran información filogenética (basadas en nodos, distancia genética y basadas en características). Diseñamos un índice filogenético modificado basado en nodos que denominamos “peso estandarizado de endemismo taxonómico”, el cual considera no solo la peculiaridad genética de los taxa que habitan una región determinada sino también su endemismo. Una vez que el peso estandarizado de endemismo identifica el área de mayor prioridad, la complementariedad se puede usar para identificar la segunda área y así sucesivamente. Utilizamos este índice basado en nodos para jerarquizar áreas prioritarias para conservación en el sur de América del*

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*Sur, y comparamos los resultados de nuestras jerarquizaciones con resultados obtenidos con otros índices basados en nodos. Nuestro índice identificó al distrito de Santiago, en la provincia de Chile Central, como el área de mayor prioridad para conservación, seguido por Maule, Malvinas y distritos de la provincia Subantártica. Sin embargo, Malvinas presenta mayor complementariedad en relación con Santiago que el Maule y, por tanto, Malvinas ocupa la segunda prioridad. Los índices basados en información filogenética miden el componente evolutivo de la biodiversidad y permiten la identificación de áreas que aseguran la preservación de taxones con potencial evolutivo y filogenéticamente peculiares. El índice modificado que proponemos es sensible tanto a la peculiaridad de los taxones como a la endemidad y permite combinar información de diversos taxones (i.e. cladogramas diferentes). El uso de la complementariedad permite la preservación de la mayor cantidad de taxones en un número mínimo de áreas protegidas.*

## Introduction

Conservation planning requires indexes of biodiversity to be distinguished, labeled, and related to specific areas. These tasks are central problems in the conservation of features of biodiversity such as species and communities (Pressey et al. 1993).

Conservation biologists traditionally have measured biodiversity in terms of species richness, such as the total number of species known for a particular place (Schluter & Ricklefs 1993). But not all taxa need be treated equally when priorities for conservation are set. From a systematic point of view, two main aspects must be considered for biodiversity conservation: (1) taxonomic distinctness and (2) geographical distributional patterns of taxa (Vane-Wright et al. 1991). The most appropriate measures of species differences are likely to be made in terms of historical relationships between taxa, as embodied in cladistic classifications (Ackery & Vane-Wright 1984). Taxonomic distinctness is a relative value between species which measures their "uniqueness." It is therefore desirable to apply measures that allow us to estimate both aspects of biodiversity mentioned above. Such measures would give priority to taxonomically distinct taxa (i.e., species not closely related to other living species) and taxa that exhibit restricted areas of distribution (endemism).

Heard and Mooers (2000) demonstrate that phylogenetic information is one of the most important factors involved in any given level of extinction. This means that loss of evolutionary history depends on the kind of diversification processes that gave rise to the clade under consideration—in particular, on the topology of the phylogenetic tree, which depends in turn on underlying variation in diversification rates across lineages within the clade.

We could use many measures to assess priority areas, from raw species richness to endemism, but those measures do not include phylogenetic information and, consequently, ignore the evolutionary history of the taxa. To tackle that problem, the use of indexes based on phylogenetic information have been proposed. Vane-Wright

et al. (1991) propounds that information encoded in cladistic relationships among taxa can be translated into an index of phylogenetic diversity as a measure of their distinctness. At present, there are many measures that consider the phylogenetic information relevant to conservation evaluation, including node-based methods (Vane-Wright et al. 1991), genetic-distance methods (Crozier 1992, 1997; Faith 1994a), and feature-based methods (Faith 1992a, 1992b, 1993, 1994b, 1994c). We used indexes *I* and *W* of Vane-Wright et al. (1991), a node-based method. These indexes give priority to basal taxa because they are phylogenetically rare. Thus, those areas rich in basal taxa have an increased value for conservation because they contain phylogenetically rare taxa.

Index *I* measures information in a hierarchical classification, that is, the number of monophyletic groups to which each taxon belongs. Index *W* measures information in a phylogenetic classification but was specifically designed to measure the proportion each taxon contributes to the total diversity of the group. Both indexes give higher priority to the basal taxon in the phylogeny. These index values are nonparametrical, and there is no significant test to compare them. Because the indexes are dependant on the system studied, it is not possible to compare values obtained from different studies, but it is possible to compare the relative placement of the areas in different rankings.

Indexes *I* and *W*, along with distributional information (especially endemism) and complementarity between biotas, allow scientists to rank priority areas for conservation. The complementarity index measures the number of species not shared between two areas. Numerically, it is the inverse of the Jaccard index (Collwell & Coddington 1994). A complementarity index allows the number of areas protected to be minimized, while the number of species preserved is maximized.

We focused on the temperate areas of southern South America (Fig. 1). The Andean highlands north of latitude 30° south are in the same biogeographical subregion, called the Andean subregion. Southern South America is temperate to cold-temperate, and its biota exhibits complex relationships with those of the remaining part of the

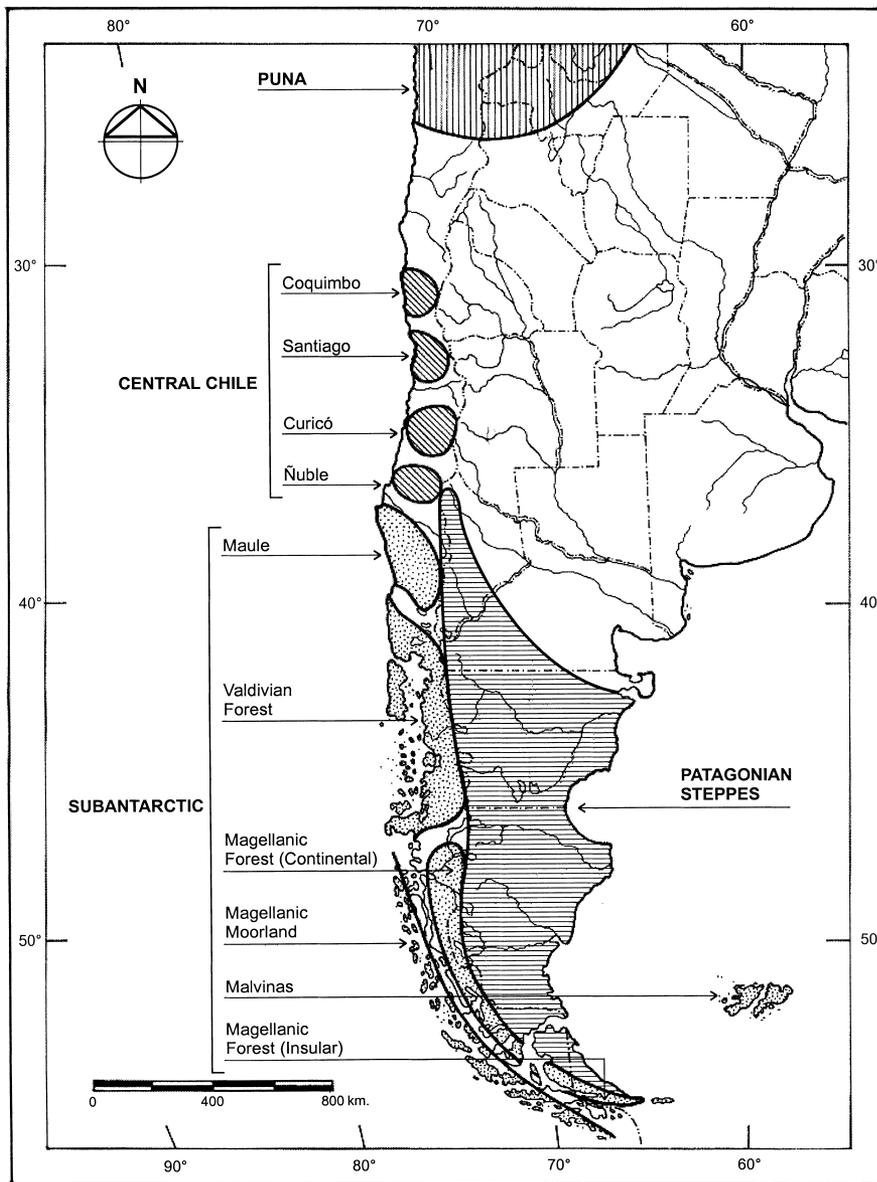


Figure 1. Analyzed areas of southern South America according to the biogeographic schemes proposed by Morrone (1994a) and Morrone et al. (1997).

subcontinent (Neotropical subregion) and with other temperate areas of the southern hemisphere such as Australia, New Zealand, New Caledonia, Tasmania, and New Guinea (Crisci et al. 1991).

Such areas are relevant to biodiversity conservation because "they are rich in phylogenetically valuable species and are environmentally threatened" (Morrone et al. 1996). Dinerstein et al. (1995) consider most of southern South America to be a "high regional priority area" for conservation on the basis of biological distinctness, defined by these authors as species richness, endemism, and the distinctness of ecological processes, and state of conservation. The most important threats to the biodiversity of this region are deforestation, overgrazing, and exotic species (Dinerstein et al. 1995).

Using the standard protocol of Vane-Wright et al. (1991), Freire et al. (1998) applied phylogenetic diversity mea-

asures (indexes *I* and *W*) to eight areas of South America based on the information encoded on seven cladograms from angiosperms (Asteraceae) and weevils (Curculionidae). They considered several biogeographical provinces from both the Andean and the Neotropical subregions (Páramo, Puna, Chaco, Pampa, Central Chile, Patagonia, Subantarctic, and Islas Malvinas) as geographical units. They concluded that the Subantarctic province should have the highest priority (23% of total biodiversity), followed by Central Chile (19%).

We used the Central Chile and the Subantarctic provinces as units to achieve a more detailed evaluation of the high-priority areas identified by Freire et al. (1998). Most taxa included in our study belong to the same families considered by Freire et al. (1998), and the remaining taxa belong to Arthropoda, including three genera of Araneae and one genus of Carabidae (Coleoptera).

Our objectives were (1) to apply old (Vane-Wright et al. 1991) and new (standardized weight of taxonomic endemicity) phylogenetic indexes to southern South America and (2) to evaluate their sensitivity to factors such as richness or endemicity.

We proposed a modified protocol based on Vane-Wright et al. (1991) for data analysis which accounts for both endemicity and phylogenetic information. Using these two parameters, along with complementarity, we produced a sequence of priority areas for conservation. The protocol requires a previous definition of the areas (e.g., a biogeographical scheme) and phylogenetic information for some taxa inhabiting them, and it includes endemicity and standardization of the indexes.

## Methods

### Study Area

We considered 12 areas in southern South America and used data from previous historical biogeographic studies (Morrone 1994a; Morrone et al. 1997) (Fig. 1).

Puna province is a high mountain semidesert area that covers central and southern Peru, western Bolivia, northwestern Argentina, and northern Chile. Much of it is over 3000 m in elevation. The Puna province belongs to the Andean subregion (Morrone 1994a, 1996; Posadas et al. 1997), and the vegetation of this area is defined as montane grassland (Dinerstein et al. 1995).

Central Chile province belongs to the Andean subregion (Morrone 1994a; Posadas et al. 1997). We used the districts of Central Chile as defined by Morrone et al. (1997) as units. In this province the vegetation is xeric, defined as mediterranean scrub (Dinerstein et al. 1995). We examined the following areas: the Coquimbo district, which extends along the Andes from latitude 30° to 31° south; Santiago district, which extends along the Andes from latitude 32° to 34°30' south; Curicó district, which extends along the Andes from latitude 35° to 36° south; and Ñuble district, which extends along the Andes from latitude 36° to 37° south.

The Subantarctic province belongs to the Andean subregion (Morrone 1994a). Again, we used the districts of this province as defined by Morrone et al. (1994) as units. The Maule district is a narrow band along the Andes from latitude 37° to 40° south. The Valdivian Forest district extends along Chile and beyond the Argentina border in some places from latitude 40° to 48° south. The Magellanic Forest continental area is restricted to the western flanks of the southern Andes at latitude 48° south, and the Magellanic Forest insular area is the portion of the Magellanic Forest that corresponds to Tierra del Fuego archipelago. Although the Magellanic Forest (continental and insular areas) constitutes just one biogeographical district, we divided it to obtain better resolution.

The Magellanic Moorland district extends from the Golfo de Peñas at latitude 46° south to Cape Horn and is bounded by the Pacific Ocean on the west and the Magellanic Forest on the east. The Malvinas district consists of two main islands and several small ones and is located on the Atlantic Ocean between latitude 51°–52° south and longitude 58°–62° west.

The vegetation of the districts of the Subantarctic province is mainly that of a temperate broadleaf forest: from Ñuble to Valdivia districts the forest is temperate *Nothofagus* (southern beeches), it becomes a subpolar *Nothofagus* forest from the Magellanic Forest district to the Magellanic Moorland district (Dinerstein et al. 1995). Malvinas exhibits Patagonian grassland vegetation (Dinerstein et al. 1995).

The Patagonian Steppe extends from the southern Andes to the Atlantic coast in Argentina and in some places to Chile (Morrone 1994a; Posadas et al. 1997). The vegetation of most of this area is steppes and grasslands (Dinerstein et al. 1995).

### Analyzed Taxa and Calculations

The phylogenetic indexes and comparisons between them were calculated on the basis of 115 species of arthropods and vascular plants grouped as 13 supraspecific taxa for which phylogenetic analyses were available (Table 1). Distributional information on the taxa was obtained from the literature.

Six of the species included in the cladograms we analyzed are not present in southern South America. These species were used to calculate the indexes in the corresponding cladogram, and their values were assigned to a hypothetical area called "out."

Vane-Wright et al. (1991) suggest methods to measure the amount of information contained in cladograms based on a value of taxonomic distinctness between taxa. One measure, index  $I$ , assigns equal values to sister taxa. To calculate  $I$ , a value of 1 is assigned to each terminal taxon that belongs to a pair of terminal sister taxa. The taxon that constitutes the sister group of this pair receives a value of 2 (equal to the sum of its sister group), and so on for each taxon in the cladogram (Fig. 2).

A second measure, index  $W$ , assigns an information value ( $i$ ) to each terminal taxon. This value is calculated as the number of phylogenetically informative statements that can be made for each taxon. It is equivalent to the number of groups (nodes) to which each taxon belongs. The basic phylogenetic weight ( $Q$ ) is calculated for each terminal taxon as  $Q_j = \sum i/i_j$ , where  $j$  is each specified taxon. Individual  $Q$  values reflect the proportion of the total diversity of the group contributed by each taxon (Vane-Wright et al. 1991). Then, the value of index  $W$  is obtained for each  $Q$  value as  $W = Q/Q_{\min}$  (Fig. 2).

The calculated  $I$  and  $W$  values for each species inhabiting a particular area (be they part of the same or differ-

**Table 1.** List of supraspecific taxa used to calculate the phylogenetic indexes *I* and *W*, with the studies containing the cladistic analyses for each taxon.

<i>Arthropoda</i>	<i>Family</i>	<i>Genus</i>	<i>Study</i>
Araneae	Nemessidae	<i>Acanthogonatus</i>	Goloboff (1995)
	Gnaphosidae	<i>Ecbemoides</i>	Platnick (1983)
Coleoptera	Anyphaenidae	<i>Acanthoceto</i>	Ramírez (1997)
	Carabidae	<i>Creobina</i>	Roig-Juñent (1995)
	Curculionidae	<i>Acrostomus</i>	Morrone (1994b)
		<i>Antarctobius</i>	Morrone (1992a)
		<i>Falklandius</i>	Morrone (1992b)
		Generic group	Morrone & Anderson (1995)
			Morrone (1997)
		Morrone (1993)	
		Morrone (1994c)	
		Morrone (1996)	
Asteraceae	Mutisieae	<i>Leucheria</i>	Morrone et al. (1997)
		<i>Triptilion</i>	Katinas et al. (1992)

ent higher taxa) are used to produce scores, and the sum of the scores is the value assigned to that area (Morrone et al. 1996).

Because the index values are dependant on the cladogram on which they are calculated (e.g., number of terminal taxa, number of nodes, number of branches), it is necessary to standardize the index values to avoid bias

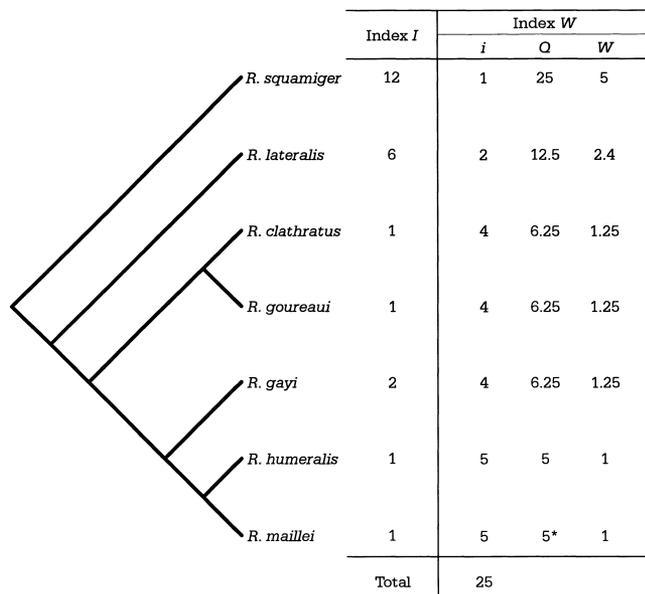
due to different numbers of terminal taxa when summing the index values obtained from different cladograms. This standardization was made because there is no a biological reason to assign a highest value for conservation to a taxon based on the fact that a taxon belongs to a group that is larger than another taxon's group. The standardization was made by dividing each taxon value in each cladogram by the sum of all index values in the corresponding cladogram (the indexes standardized were called  $I_s$  and  $W_s$ ).

We calculated the index values for those taxa involved in polytomies as the arithmetic average of the values calculated for all possible resolved trees. An example of the calculation of phylogenetic diversity indexes involving polytomies is shown in Fig. 3 on the cladogram of the *Leucheria rosea* species group.

**Widespread Taxa (Endemicity)**

It is possible to include a measure of the degree of endemicity of each taxon. When one taxon was widespread (present in two or more areas) we used the following two rules: (1) the index value was assigned to all areas where it was present, and (2) the index value was divided equally among the number of areas where the taxon was present. Application of the second rule implies the inclusion of endemicity as a factor in resulting index values. The first rule was applied here to test the consideration of endemicity if the inclusion of endemicity modified the rankings of conservation priority areas.

We calculated eight phylogenetic diversity measures for each area: raw indexes (*I* and *W*), raw endemicity weight ( $I_e$  and  $W_e$ ), total standardized weight ( $I_s$  and  $W_s$ ), and endemicity standardized weight ( $I_{es}$  and  $W_{es}$ ). The last measure avoids over-weighting of an area because of widespread taxa (meaning this measure considers ende-



**Figure 2.** Calculation of indexes *I* and *W* on the cladogram of *Rhyephenes*. Index *I* assigns the same value to sister groups. Index *W* assigns to each terminal taxon a value equal to the number of phylogenetic statements for it (*i*). Then the score of each terminal taxon is divided into the sum of *i* values (*Q*); each *Q* value is standardized by dividing it by the lowest *Q* value of the group (indicated by an asterisk).

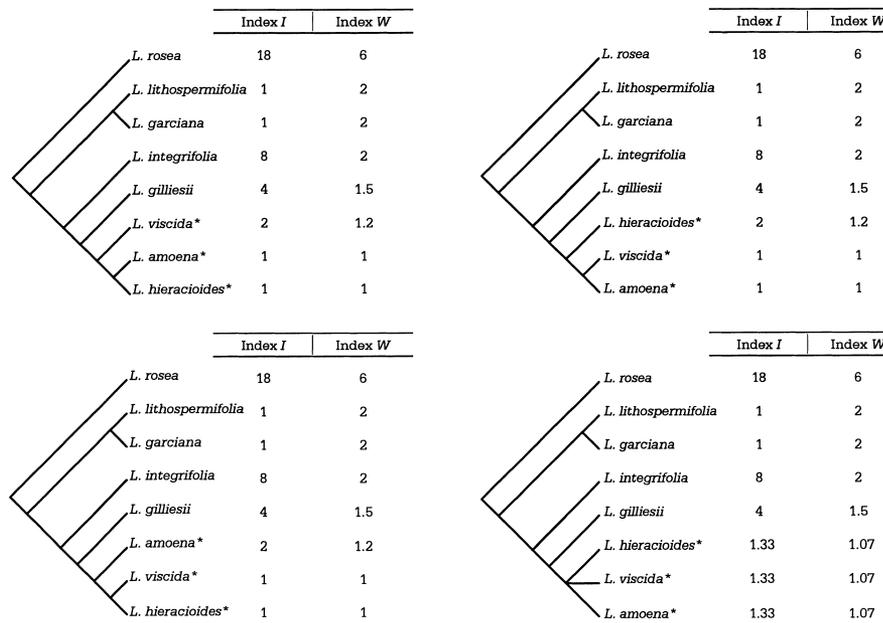


Figure 3. Index values I and W for the *Leucheria rosea* species group, including a polytomy as an example for the calculation. The values in the polytomy are calculated as the average for all possible resolved trees. Taxa involved in the polytomy are indicated by an asterisk.

micity) or because of cladograms with a large number of terminal taxa.

Richness is a common measure of diversity (Schluter & Ricklefs 1993). We calculated rough richness values for each area as the total number of species present in it. We also calculated an endemism index for each area as the quotient between the number of endemic species and the total species (richness) in that area.

We calculated a complementarity index between each pair of areas (Collwell & Coddington 1994) to estimate the shared species between areas. The index has a maximum value of 1, meaning there are no species in common between the areas considered, and a minimum value of 0, meaning both areas considered contain exactly the same species. All calculations including indexes, endemism, richness, and complementarity were performed

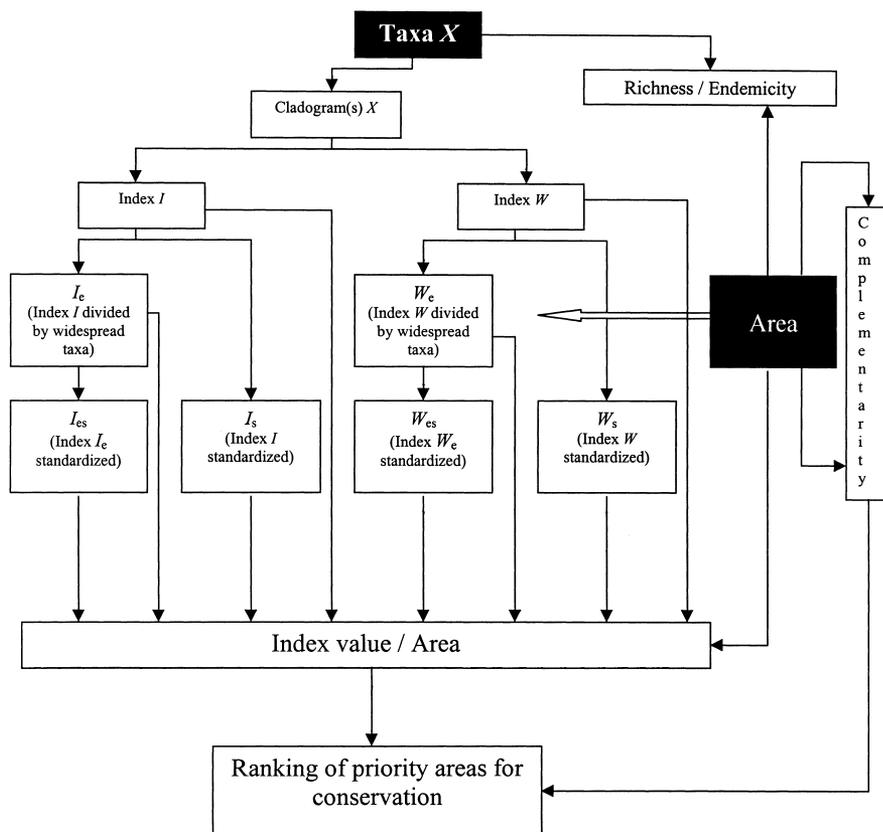


Figure 4. Flowchart indicating the steps for the protocol proposed in the methods section.

**Table 2. Raw and standardized index (*I* and *W*)<sup>a</sup> values including or not including endemism, number of species per area (richness), and endemism for each area.<sup>b</sup>**

Area	Raw <i>I</i>	<i>I</i> <sub>e</sub>	<i>I</i> <sub>s</sub>	<i>I</i> <sub>es</sub>	Raw <i>W</i>	<i>W</i> <sub>e</sub>	<i>W</i> <sub>s</sub>	<i>W</i> <sub>es</sub>	Richness <sup>c</sup> (%)	Endemism <sup>c</sup>
Puna	10.33	7.83	1.36	0.83	6.22	4.75	1.78	1.24	5 (4.24)	3 (60.00)
Coquimbo	47.33	28.78	3.67	1.81	25.51	15.99	3.79	1.97	17 (14.41)	5 (29.41)
Santiago	161.33	72.59	9.47	5.97	52.58	29.01	8.77	5.42	33 (27.97)	11 (33.33)
Curico	100.33	41.79	6.17	2.96	36.95	17.8	5.8	2.95	20 (16.95)	4 (20.00)
Ñuble	95.33	33.43	4.18	1.53	31.65	12.56	3.8	1.49	18 (15.25)	2 (11.11)
Maule	203.33	84.43	3.78	1.75	52.05	22.84	4.19	1.98	29 (24.58)	6 (20.69)
Valdivia	279	191.73	2.87	1.3	52.62	26.75	3.04	1.34	25 (21.19)	4 (16.00)
Magellanic	86	53.37	1.18	0.7	33.56	16.37	1.77	0.85	20 (16.95)	3 (15.00)
forest continental area	80	35.28	0.98	0.43	29.56	13.41	1.39	0.62	16 (13.56)	2 (12.50)
forest insular area	291	266	1.69	1.41	35.48	30.48	1.42	1.22	14 (11.86)	12 (85.71)
moorland	57	27.25	1.05	0.55	25.73	11.49	1.34	0.61	14 (11.86)	2 (14.29)
Patagonian Steppes	53	41.25	0.86	0.65	11.33	8.08	0.72	0.51	4 (3.390)	1 (25.00)
OUT <sup>d</sup>	283	282.25	1.14	1.09	19.70	18.95	0.88	0.81	8 (6.780)	7 (87.50)

<sup>a</sup> Index *I* assigns equal values to sister taxa, and index *W* assigns an information value (*i*) to each terminal taxon (see Methods).

<sup>b</sup> With index values, letters denote the following: e, including endemism; s, standardized; es, including endemism and standardized.

<sup>c</sup> Richness and endemism values in absolute numbers and percentage.

<sup>d</sup> Species analyzed that are not present in southern South America. These species were used to calculate the indexes in the corresponding cladogram and their values were assigned to this hypothetical OUT area.

with a program in Pascal available from the D.R.M.E. A flow chart for the above protocol is summarized in Fig. 4.

nas had the highest endemism value (85% of the species considered), followed by Puna province (60%), Santiago district (33.33%), and Maule district (20%) (Table 2).

**Results**

**INDEX *I***

**Richness and Endemism**

The total weight index before standardization (*I*) ranked the districts from highest to lowest conservation priority: Malvinas, Valdivia, Maule, and Santiago (Table 2). The inclusion of endemism (*I*<sub>e</sub>) did not modify this ranking, although it did alter the fifth rank (Curico District for *I* and Magellanic Forest continental area for *I*<sub>e</sub>).

Santiago was the richest area, with 33 of the 115 species included in the analysis. Maule (29 species) and Valdivia (25 species) ranked just below Santiago (Table 2). Malvi-

**Table 3. Complementarity of species between areas calculated as an index.<sup>a</sup>**

	Coquimbo	Santiago	Curico	Ñuble	Maule	Valdivia	Magellanic forest continental area	Magellanic forest insular area	Magellanic moorland	Patagonian Steppes
Santiago	0.679									
Curico	0.893	0.757								
Ñuble	0.923	0.868	0.52							
Maule	0.971	0.841	0.75	0.688						
Valdivia	0.968	0.907	0.892	0.813	0.606					
Magellanic Forest continental area	1.000	0.977	0.974	0.971	0.900	0.889				
Magellanic Forest insular area	1.000	1.000	0.971	0.968	0.947	0.941	0.455			
Magellanic Moorland	1.000	1.000	1.000	1.000	0.974	0.906	0.565	0.550		
Malvinas	1.000	1.000	1.000	1.000	1.000	1.000	0.966	0.917	1.000	
Patagonian Steppes	1.000	1.000	1.000	0.950	1.000	0.958	0.905	0.944	1.000	
Puna	0.929	0.929	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
OUT <sup>b</sup>	1.000	1.000	1.000	0.955	1.000	0.962	1.000	1.000	1.000	0.889

<sup>a</sup> Index values: 1, no shared species between the two areas; 0, both areas contain exactly the same species.

<sup>b</sup> Species analyzed that are not present in southern South America. These species were used to calculate the indexes in the corresponding cladogram and their values were assigned to this hypothetical OUT area.

After the values of  $I$  and  $I_e$  were standardized, the ranking changed radically. Santiago and Curicó were ranked first and second, respectively, followed by Ñuble for  $I_s$  and Coquimbo for  $I_{es}$ . Maule was fourth before and after standardization. Malvinas (ranked first prior to standardization) ranked fifth and sixth, respectively. The shift of Malvinas from a high rank before standardization to a low rank after was due to cladograms that included many taxa. For example, *Puranius* has 20 species, and the basal species *P. scaber*, which is endemic to Malvinas, alone adds 132 to the index (total  $I$  value for Malvinas, 291).

#### INDEX $W$

The total weight index ( $W$ ) gave Valdivia, Santiago, Maule, and Curicó top priority for conservation. Although  $I$  ranked Malvinas as first,  $W$  ranked it fifth. Both indices give priority to basal taxa, but index  $W$  avoided the over-weighting problem of index  $I$  (Table 2).

When endemicity was considered ( $W_e$ ), Malvinas attained the highest score again, followed by Santiago, Valdivia, and Maule. The positions of Malvinas and Santiago are due to the high degree of endemicity in both areas.

When we standardized values, the positions changed similarly to those of the  $I$  series. In both cases Santiago was ranked first, followed by Curicó and Maule. The fourth and fifth rankings changed to Ñuble and Coquimbo with  $W_s$  and to Coquimbo and Ñuble with  $W_{es}$ .

#### Discussion

Santiago was the area of highest priority for conservation. It had the highest values with both  $I$  and  $W$  indexes after standardization. This ranking agrees with the fact that Santiago is the highest in richness and the second highest in endemicity. Thus, the indexes reflect not only phylogenetic information but also richness and endemicity. Furthermore, Santiago has a mediterranean climate with long, dry summers and winter rainfall, and the Santiago valley has a large number of native flora (species and genera) (Arroyo et al. 1995). Also, Wilson (1992) considers Central Chile to be a "hotspot" because it has more than 3000 plant species (approximately 50% of the known species for Chile) and represents 6% of the total area of the country. Nonetheless, the high richness value for Santiago might be due to the Santiago area being sampled more intensely than the other areas considered here.

Freire et al. (1998) ranked the Subantarctic province as the area of highest priority for conservation, followed by Central Chile. Our highest-priority area was Santiago, a district of Central Chile. This difference in ranking can be attributed to several factors: Freire et al. (1998) used different biogeographic units, basing their study on

provinces rather than districts, used a different data set; did not include endemicity in their evaluation; and did not standardize indexes between cladograms.

The choice of the second-priority area should maximize complementarity to optimize the number of species protected and minimize economic investment. If only index values were considered, the second priority would be Curico. But Curico had low complementarity relative to Santiago (Table 3), meaning they share many species. Because of these complementarity values, we suggest one of the following areas: Magellanic Forest insular area, Magellanic Moorland, Malvinas, or Patagonian Steppes, all of which exhibited the highest possible complementarity value (1) with Santiago. Index values discriminated among these areas and identified Malvinas as the second choice. We then calculated the complementarity between Santiago + Malvinas and the remaining areas. In this case, Magellanic Moorland, Magellanic Forest continental and insular areas, Puna, and Patagonian Steppes yielded the maximum complementarity values. Once again, index values discriminated among them, and the Magellanic Forest continental area was ranked third.

Index  $I$ , including or not including endemicity, shows the influence of the over-weighting of basal taxa in the cladogram. In our work, Malvinas was first ranked in both cases (including endemicity or not) because of the influence of basal taxa in those cladograms that have too many terminal taxa (e.g., *Puranius*). This influence conceals the effects of endemicity. Standardization eliminates this problem.

In spite of the fact that index  $W$  gave the highest values to basal taxa, it did not over-weight these taxa. Inclusion of endemicity modifies the rankings. In our case, first position was Santiago with raw index  $W$  and Malvinas (the area with highest endemicity) for  $W_e$ . After standardization, both indexes showed the same ranking, and the influence of endemicity was not apparent.

Conservation of biodiversity requires knowledge of its history. Barring major advances in molecular genetics, each time a species goes extinct the independent evolutionary features of that lineage are lost forever (Heard & Mooers 2000). Unfortunately, most conservation efforts do not take history into account. Cladograms are a powerful tool with which to summarize the evolutionary history of life. Use of a combination of cladograms and geographical information would represent a step toward including historical information in the conservation of biodiversity.

Indexes based on phylogenetic information (such as  $I$  and  $W$ ) help inform decisions concerning conservation priorities because these indexes consider the evolutionary component of biodiversity and allow identification of those areas that will ensure the preservation of evolutionary potential and phylogenetically rare species (Brooks et al. 1992). The use of endemicity-standardized weight

to rank priority areas for conservation shows that this index is sensitive to taxic distinctness and endemism and reduces weighting differences due to species-rich cladograms. The method allows better use of available information, including surveys, monographs, and collections.

In our present "age of extinction" we have the potential, through choice of conservation strategies, to decide which species are saved and which are sacrificed (Heard & Mooers 2000). The methodology employed here considers not only species richness but also the evolutionary history of the taxa, area endemism, and complementarity between biotas. No single measure is adequate for complete evaluation of biodiversity; it is necessary to integrate different approaches to yield a broad perspective on conservation priorities.

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