

University of Nebraska - Lincoln

DigitalCommons@University of Nebraska - Lincoln

Nebraska Cooperative Fish & Wildlife Research
Unit -- Staff Publications

Nebraska Cooperative Fish & Wildlife Research
Unit

2007

A test of the cross-scale resilience model: Functional richness in Mediterranean-climate ecosystems

Donald A. Wardwell
University of Nebraska-Lincoln

Craig R. Allen
University of Nebraska - Lincoln

Garry D. Peterson
McGill University, Montreal, Quebec, Canada

Andrew J. Tyre
University of Nebraska-Lincoln

Follow this and additional works at: <http://digitalcommons.unl.edu/ncfwrustaff>



Part of the [Other Environmental Sciences Commons](#)

Wardwell, Donald A.; Allen, Craig R.; Peterson, Garry D.; and Tyre, Andrew J., "A test of the cross-scale resilience model: Functional richness in Mediterranean-climate ecosystems" (2007). *Nebraska Cooperative Fish & Wildlife Research Unit -- Staff Publications*. 22.
<http://digitalcommons.unl.edu/ncfwrustaff/22>

This Article is brought to you for free and open access by the Nebraska Cooperative Fish & Wildlife Research Unit at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Nebraska Cooperative Fish & Wildlife Research Unit -- Staff Publications by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

available at www.sciencedirect.comjournal homepage: <http://www.elsevier.com/locate/ecocom>

A test of the cross-scale resilience model: Functional richness in Mediterranean-climate ecosystems

Donald A. Wardwell^{a,*}, Craig R. Allen^b, Garry D. Peterson^c, Andrew J. Tyre^d

^aNebraska Cooperative Fish and Wildlife Research Unit, 122 Hardin Hall, University of Nebraska-Lincoln, Lincoln, NE 68583, USA

^bUSGS - Nebraska Cooperative Fish and Wildlife Research Unit, 423 Hardin Hall, University of Nebraska-Lincoln, Lincoln, NE 68583, USA

^cDepartment of Geography & McGill School of the Environment, McGill University, Montreal, Quebec, Canada H3A 2K6

^dSchool of Natural Resources, 416 Hardin Hall, University of Nebraska-Lincoln, Lincoln, NE 68583, USA

ARTICLE INFO

Article history:

Received 2 January 2007

Received in revised form

16 November 2007

Accepted 30 November 2007

Keywords:

Diversity

Body mass

Scale

Discontinuity

Gap rarity index

ABSTRACT

Ecological resilience has been proposed to be generated, in part, in the discontinuous structure of complex systems. Environmental discontinuities are reflected in discontinuous, aggregated animal body mass distributions. Diversity of functional groups within body mass aggregations (scales) and redundancy of functional groups across body mass aggregations (scales) has been proposed to increase resilience. We evaluate that proposition by analyzing mammalian and avian communities of Mediterranean-climate ecosystems. We first determined that body mass distributions for each animal community were discontinuous. We then calculated the variance in richness of function across aggregations in each community, and compared observed values with distributions created by 1000 simulations using a null of random distribution of function, with the same n , number of discontinuities and number of functional groups as the observed data. Variance in the richness of functional groups across scales was significantly lower in real communities than in simulations in eight of nine sites. The distribution of function across body mass aggregations in the animal communities we analyzed was non-random, and supports the contentions of the cross-scale resilience model.

© 2007 Elsevier B.V. All rights reserved.

1. Introduction

Ecological processes are scale-specific in their effects, and create heterogeneous landscapes with scale-specific structure and pattern (Turner et al., 2001). Spatial and temporal heterogeneity, in turn, contributes to the structure of animal communities. Spatial patterns affect an organism's ability to disperse, which in turn limits resource availability, gene flow, diversification, and other ecological processes (Turner et al.,

2001; Coulon et al., 2004; Vignieri, 2005). Spatial and temporal patterns within landscapes are also reflected in animal body mass distributions (Allen and Holling, 2002).

The Textural Discontinuity Hypothesis proposed that body mass distributions of animal communities reflect landscape structure (Holling, 1992). Holling proposed that landscapes are structured by a relatively few key processes, each operating at distinct spatial and temporal scales. The actions of those processes and the scales at which they operate are reflected in

* Corresponding author. Tel.: +1 402 472 0449; fax: +1 402 472 2722.

E-mail addresses: wardwell@bigred.unl.edu (D.A. Wardwell), allencr@unl.edu (C.R. Allen), garry.peterson@mcgill.ca (G.D. Peterson), atyre2@unl.edu (A.J. Tyre).

1476-945X/\$ – see front matter © 2007 Elsevier B.V. All rights reserved.

doi:10.1016/j.ecocom.2007.11.001

discontinuous patterns of structure and resource distribution upon landscapes. Discontinuous structure in landscapes may result in discontinuous, aggregated animal body mass patterns, which reflect the scales of structure available to animals within a given landscape. Discontinuous body mass distributions have been observed in numerous ecological systems and among several taxa, including birds, mammals, reptiles and amphibians, fish and bats (Allen and Holling, 2002).

Ecological resilience appears to be generated, in part, in the discontinuous structure of these complex systems (Peterson et al., 1998). Ecological resilience is a measure of the amount of change needed to transform an ecosystem from one set of processes and structures to a different set (Holling, 1973; Gunderson, 2000). An ecosystem with high resilience would require a substantial amount of energy to transform, whereas a low resilience system would transform with a relatively small amount of energy. Peterson et al. (1998) expanded upon Holling's Textural Discontinuity Hypothesis by proposing that functional diversity within body mass aggregations and redundancy of functional groups across body mass aggregations (i.e., scales) increases resilience. Resilience is increased by overlap of function by species of different functional groups operating at similar scales. A diversity of function within a scale provides a system with a wide latitude of response to a variety of different perturbations. Redundancy of functional groups across scales provides reinforcement of function, increasing resilience. Having functions reinforced at different scales provides a system with a robust control of perturbations when they exceed controls at a given scale.

The model Peterson et al. (1998) proposed has not been tested. However, the authors suggest several potential tests of their cross-scale resilience model, including analysis of empirical data, simulations, and field experimentation. They proposed testing the idea that ecological function is distributed across scales by analyzing the distribution of functional groups and determining if species of the same functional groups are dispersed across scales. In this paper, we evaluate this proposition by analyzing the distribution of function across scales in mammal and bird communities of several Mediterranean-climate ecosystems in various regions of the world. Specifically, we determined the variance in the distribution of functional richness across scales. Low variance in functional richness across scales would indirectly indicate both elements of the cross-scale resilience model, functional diversity within scales and redundancy across scales.

2. Methods

Despite being geographically and evolutionarily isolated with flora and fauna differing among regions, Mediterranean-climate ecosystems are ecologically similar in structure and function (Di Castri and Mooney, 1973; Kalin Arroyo et al., 1995). They typically display high species diversity and are present in disparate regions of the world (Lavorel, 1999). Mediterranean-climate ecosystems are characterized by wet winters, dry summers, and mild temperatures. These systems occur in subtropical latitudes on the western coast of continental land masses (California, Chile, southwestern Australia, and the

Cape Town area of South Africa) and the coast of the Mediterranean Sea (Davis and Richardson, 1995).

Species' distributions and body mass estimates were determined for bird and mammal communities in several Mediterranean-climate ecosystems. Avian community species' distributions were determined for Mediterranean ecosystems in San Diego County, California (Unitt, 1984), Spain (Cramp, 1978–1994), South Africa (Winterbottom, 1966) and southwestern Australia (Saunders and Ingram, 1995). All avian body masses were obtained from Dunning (1993), except for Spain which were determined from Cramp (1978–1994). Mammalian community species' distributions and body mass estimates were determined for Mediterranean ecosystems in California (Quinn, 1990; Silva and Downing, 1995), South Africa (Smithers, 1983; Silva and Downing, 1995), Spain (Cheylan, 1991), Chile (Miller, 1980, corroborated with Redford and Eisenberg, 1992), and southwestern Australia (Strahan, 1995). Only species that had established breeding populations in each respective region were included, and non-indigenous species were not included. Pelagic birds and bats were excluded because they interact with their environment differently than terrestrial species (Allen et al., 1999). In all cases, adult male and female body masses were averaged.

Each community was analyzed for discontinuities in their body mass distributions. All species within a community were ranked in order of body mass. The logs of the body masses were calculated, and discontinuities were determined with the gap rarity index (GRI) (Restrepo et al., 1997; Allen and Holling, 2002; Stow et al., 2007). The GRI uses the GRI statistic, which is the probability that the observed discontinuities in the body size spectrum occur by chance alone, to compare observed body mass distributions with a unimodal null distribution that is produced by a kernel density estimator (Silverman, 1981), which smoothes the observed data into a continuous null. This null distribution was then sampled 10 000 times and an absolute discontinuity value:

$$d_i = \log_{10}(M_n + 1) - \log_{10}(M_n)$$

was calculated for each species in each simulation. The ranked distribution of the observed body masses was compared with the distribution of the differences for the n th largest species from the simulations. The GRI for each species in the actual assemblage is the proportion of the simulated discontinuity values that were smaller than the observed discontinuity value. The significance of each GRI value was then determined by testing the null hypothesis that the value was drawn from a continuous distribution with an alpha of <0.05 . Unusually large gap values were considered significant and determined the location of discontinuities that bound body mass aggregations. The results were confirmed by conducting a SAS Cluster analysis using the Ward option based on variance reduction (SAS Institute Inc., 1999).

Functional group classifications were determined for each species. A functional group is essentially the classification of an organism's ecological "role". For this study, we have defined functional groups as the combination of the species' diet and foraging strata. Data on diet and foraging strata were collected from published sources (Cramp, 1978–1994; Brown et al., 1982; Smithers, 1983; Blakers et al., 1984; Urban et al., 1986; Ehrlich et al., 1988; Fry et al., 1988; Jameson and Peeters,

1988; Keith et al., 1992; Redford and Eisenberg, 1992; Strahan, 1995; Urban et al., 1997; Wilson and Ruff, 1999; Fry et al., 2000, 2004; MacDonald and Barrett, 2001). For species where more than one food source or foraging stratum were possible, the first item listed was used. The first listed item was assumed to be the most prominent food source in the species' diet. The diets of each species were then classified as one of seven categories: insectivore, piscivore, carnivore, granivore, nectarivore, herbivore, and omnivore. All invertebrate sources were categorized as insectivore, carrion feeders were classified as carnivorous, and fruits and nuts were considered herbivorous. In each community, a diet classification had to represent 5% of the total community or have an $n=5$, otherwise it was put into another diet classification, in order to maintain minimal numbers within each category for analysis. When necessary, insectivores and piscivores were classified as carnivores and granivores and nectarivores were classified as herbivores. Omnivores were classified according to the food source that was most present in their diets. The foraging stratum for each species was classified as one of the following: terrestrial and aquatic for both avian and mammalian fauna; aerial, bark, and foliage for avian fauna only; arboreal and fossorial for mammalian fauna only. The diets and foraging strata for each species were combined to create functional groups.

Body mass distributions were then analyzed to calculate the richness of function within size classes (i.e., the number of functional groups present within a given body mass aggregation), and the variance in richness of function across size classes. Although the cross-scale resilience model of Peterson et al. (1998) did not directly address the variance in the distribution of functional richness across scales, it follows that variance in richness should be low if diversity within scales and redundancy across scales are high. However, it is possible that even if observed variance in richness was low the identity of functions present could differ. We could not address that issue directly because of phylogenetic constraints on the body size of some functional groups. For example, granivores are more likely to be smaller animals. Thus, in our randomizations, which do not incorporate phylogenetic constraint, random distributions of individual functional groups will invariably be more dispersed than distributions in real communities. Therefore, we used the variance in richness of function across aggregations as an indirect assessment of the predictions of the cross-scale resilience model.

We used computer resampling to generate the distribution of variances that would be observed if there was no relationship between aggregations and functional groups. The basic dataset consists of a list of species, which aggregation they are in, and which functional group they belong to. The observed functional richness for the i th aggregation, R_i , is simply the number of unique functional groups observed in that aggregation. The estimated variance in functional richness across scales is then calculated as the variance of the R_i ,

$$\widehat{\text{var}}(R) = \sum_i \frac{(R_i - \bar{R})^2}{n-1}$$

where n is the number of aggregations present, and \bar{R} is the average functional richness. To determine if this value is low, we generated 1000 permutations of the list of functional

groups; a permutation randomly reorders a list without changing the elements of that list. The permutation preserves both the number of species in each aggregation, and the number of species in each functional group; only the relationship between functional groups and aggregations is randomized. For each permutation j we calculated the variance of functional richness across scales in the same way as for the observed data. The observed variance is then ranked within the randomized distribution. Output from the simulations is the proportion of runs with variance above, equal, and below that of the observed variance of functional richness across aggregations. If the output shows a lower variance in the simulated distributions of functional diversity than in the observed, then the hypothesis proposed by Peterson et al. – that functions tend to be distributed evenly across scales – is not supported. If the variance of functional richness across scales of the observed systems is smaller than the random distributions, the model of Peterson et al. (1998) is supported. The combined above and equal proportions (hereafter, “above”) from the simulated runs were tested for correlation with number of species in the community (N), number of body mass aggregations, and the number of functional groups.

3. Results

The body mass distributions of all the bird and mammal study communities were discontinuous (see Table 1). Distinct aggregations of body mass were detected among all sites with both methods. The number of aggregations ranged from four in the Chilean mammal community to 16 in the southwest Australian bird community. There were typically more aggregations in bird communities (ranging from 9 to 16) than in mammal communities (ranging from 4 to 9). This may be related to the higher number of species in the bird communities (81–141 species) than in mammal communities (27–65 species), and/or to differences in the manner in which terrestrial mammals and flighted birds interact with environmental structure.

The simulation runs produced greater proportions of variances ranked above or equal to the observed variance in all of the study sites, except Spain mammals (Table 1). The proportions of above and equal variances were higher in the bird communities of San Diego County ($p=0.996$), Spain ($p=0.702$), South Africa ($p=0.689$), and southwestern Australia ($p=0.885$), than in the mammal communities of California ($p=0.665$), Spain ($p=0.152$), South Africa ($p=0.582$), Chile ($p=0.509$) and southwestern Australia ($p=0.654$). The ranking of above proportions were positively correlated with N ($r=0.65$, $p=0.059$), number of body mass aggregations ($r=0.60$, $p=0.088$), but not with the number of functional groups ($r=0.48$, $p=0.194$) (Table 1). The results of the correlation tests change dramatically when the data for Spain mammals, which is substantially different from the other eight replicates, is excluded. The ranking of above proportions, excluding Spain mammals, were positively correlated with N ($r=0.78$, $p=0.021$), number of body mass aggregations ($r=0.72$, $p=0.044$), and number of functional groups ($r=0.79$, $p=0.021$). Because the sample sizes were small, the expected power of each individual simulation is not

Table 1 – Provided is the ranking of observed variance in relation to 1000 simulations of a random null model (above + equal), the number of species in the community (N), number of body mass aggregations (No. Aggs), and number of functional groups (No. FnGrps)

	Above + equal	N	No. Aggs	No. FnGrps
Chile mammals	509	27	4	9
California mammals	665	32	6	7
San Diego birds	996	117	12	14
South Africa birds	689	81	9	11
South Africa mammals	582	65	9	6
Spain birds	702	119	14	12
SW Australia birds	885	141	16	13
SW Australia mammals	654	42	6	7
Spain mammals	152	50	7	10
(r) w/Spain mammals		0.6484	0.6000	0.4776
(r) w/o Spain mammals		0.7818	0.7194	0.7863

Also included are the Pearson correlation results between above and equal proportions with N, number of body mass aggregations, and number of functional groups. The results of the correlation tests excluding the Spain mammals data are included as well.

high. However, if there is genuinely no effect across all replicate ecosystems, then the proportion of combined above and equal distributions across all replicates will be drawn randomly from a uniform distribution between 0 and 1. We used Fisher's test of uniform random numbers to determine if the observed results followed a uniform random distribution (e.g. McCarthy et al., 2001). The test statistic

$$L = -2 \sum_{i=1}^n \ln p_i$$

has a Chi-square distribution with $2n$ degrees of freedom for n uniformly distributed random numbers (Fisher, 1954). The ranking of the observed variances in the lower half of the simulated variance distributions was an unlikely random outcome for a uniform distribution ($L = 9.57$, $p = 0.054$). Removing the Spain mammals from the analysis yielded a stronger result ($L = 5.803$, $p = 0.009$).

4. Discussion

Peterson et al.'s (1998) hypothesis which suggests that function should be non-randomly distributed within and across scales is supported by the results of our simulations (Table 1). Random simulations of functional distribution within and across body mass aggregations yielded distributions with higher variance of functional richness across scales than our data from Mediterranean-climate ecosystems. We did not test the relationship with resilience, as an effective method of estimating resilience is not yet known. However, our results do fit the predictions of the cross-scale resilience model proposed by Peterson et al. (1998), without explicitly testing it. The rankings of the observed data in the distribution generated by the null model were higher in avian communities than in mammalian communities. The four avian communities also had more species, more body mass aggregations, and more functional groups than did the mammalian communities. The correlations identify a positive relationship between these three variables and the rankings of the observed data. As the number of species, body mass classes,

or functional groups increases, so does the proportion of above variances in the simulated runs. The relationship is substantially stronger when the Spain mammal data are excluded.

Peterson et al. (1998) suggest that the process of inter-specific competition could be the mechanism driving a non-random distribution of function within and across scales. Species of the same functional group, for example foliage insectivores, are more likely to interact with each other and compete than with members of other functional groups. Similarly, species exploiting their environment at the same range of scale, that is, species with body mass that place them in the same body mass aggregation, are more likely to interact with each other, and potentially compete, than with species that exploit their environment at larger or smaller scales. Thus, coexistence of species within the same functional group will be facilitated if they exploit their environment at different scales, and species operating at the same scale are likely to be member of different functional groups. Compartmentalization of species interactions by scale, driving within-scale diversity and cross-scale redundancy, is likely to be adaptive because it creates resilient and thus persistent species combinations, by maximizing response diversity within scales and by providing a robust check to perturbations that tend to scale up, such as insect outbreaks.

Because of the complex and unpredictable nature of ecosystems, the task of increasing, or even maintaining, ecological resilience is daunting. Estimating or predicting resilience is one of the challenges ecologists face in the management of ecosystems. Recent improvements in estimating ecological resilience have been made with the use of models, however, these methods are still relatively new and their utility has not been effectively tested (Peterson, 2002). Allen et al. (2005) propose that resilience may be operationalized in the discontinuous structure of complex systems. They suggest that numbers of body mass aggregations, richness of function within and across aggregations, and the location of species turnover are measures that can be used to determine the relative resilience of system. Our analysis shows that ecological systems exhibit a non-random distribution of function within and across aggregations. Documenting a non-random distribution of function across aggregations is

key for developing effective, quantifiable methods of operationalizing resilience in the discontinuous structure of ecological systems.

Our simulations determine if richness is spread evenly across body mass aggregations, but does not determine whether a particular functional group is spread across aggregations more than expected. The latter is assumed to follow the former; however we do not explicitly test this. Also, we have not accounted for phylogenetic constraints on body mass. Functional groups may be constrained to species of certain body masses. For example, we can predict a granivorous, foliage-gleaning bird to be of a relatively small body mass, or an aerial carnivore to be amongst the larger birds in a community. On the other hand, these constraints are not hard and fast. Baleen whales are especially large insectivores, feeding on tiny invertebrates. Likewise, fire ants (*Solenopsis invicta*) may feed upon animals much larger than themselves (Allen et al., 2004). Regardless, it is not necessary to have every functional group spread across every aggregation in order to support Peterson et al.'s (1998) hypothesis. Our tests confirm that functional groups are more dispersed than would be expected if they were randomly assembled.

As landscapes globally become increasingly altered by humans, animal communities also will change. Improving our knowledge of the relationship between landscape structure and animal body mass distributions may enhance our understanding of ecological resilience and the role biodiversity plays in maintaining resilience. Many current management strategies fail because they attempt to control disturbances or fluctuations, or manage for only one or a few species (Gunderson, 2000; Folke et al., 2004). These strategies do not account for the unpredictable nature of complex ecosystems. By maintaining or increasing resilience in these systems, the likelihood of transformations to undesired, alternative states of ecological processes and structure may be reduced. We must also adapt to the gradual, and often unexpected, changes that affect resilience using

approaches that operate at multiple scales (Gunderson, 2000; Gunderson and Holling, 2002; Folke et al., 2004).

In order to develop more advanced methods of estimating resilience, it is important to understand how resilience is generated within ecosystems. Peterson et al. (1998) believed that resilience is generated, in part, in the discontinuous structure of these systems through functional diversity of species within scales and the redundancy of function across scales. Our study supports this proposition, and together with future empirical and field tests may help provide a thorough understanding of how ecological resilience is generated. By determining the body mass distributions and functional makeup of animal communities, we may be able to predict which species are at the highest risks and how to best maintain an ecosystem's resilience. Using and improving these tools may be a key element to better management of ecological systems in the future.

Acknowledgements

Support was provided by the James S. McDonnell Foundation 21st Century Research Award/Studying Complex Systems (Allen). The Nebraska Cooperative Fish and Wildlife Research Unit is jointly supported by a cooperative agreement between the United States Geological Survey-Biological Resources Division, the Nebraska Game and Parks Commission, the University of Nebraska-Lincoln and the Wildlife Management Institute.

Appendix A

Bird species distribution for Mediterranean-climate: San Diego County, California, USA; Spain; southwestern Australia; South Africa (Tables A1–A4) and mammal species distribution for Mediterranean-climate: California, USA; South Africa; southwestern Australia; Chile; Spain (Tables A5–A9).

Table A1 – Bird species distribution for Mediterranean-climate San Diego County, California, USA

Latin name	Body mass	Aggregation	Functional group
<i>Archilochus costae</i>	0.491	1	HeAe
<i>Cyananthus latirostris</i>	0.491	1	HeAe
<i>Archilochus alexandri</i>	0.531	1	HeAe
<i>Archilochus anna</i>	0.623	1	HeAe
<i>Polioptila melanura</i>	0.708	1	InFo
<i>Psaltriparius minimus</i>	0.724	1	InFo
<i>Polioptila caerulea</i>	0.778	1	InFo
<i>Wilsonia pusilla</i>	0.839	2	InFo
<i>Dendroica nigrescens</i>	0.922	2	InFo
<i>Vireo bellii pusillus</i>	0.929	2	InFo
<i>Vermivora celata</i>	0.954	2	InFo
<i>Carduelis psaltria</i>	0.978	2	InFo
<i>Dendroica petechia</i>	0.978	2	GrFo
<i>Thryomanes bewickii</i>	0.996	2	InTe
<i>Empidonax difficilis</i>	1.000	2	InAe
<i>Geothlypis trichas</i>	1.004	2	InFo
<i>Parus gambeli baileyae</i>	1.033	2	InFo
<i>Troglodytes aedon</i>	1.037	2	InTe

Table A1 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Carduelis lawrencei</i>	1.039	2	GrFo
<i>Cistothorus palustris</i>	1.051	2	InTe
<i>Vireo huttoni huttoni</i>	1.064	2	InFo
<i>Spizella atrogularis cana</i>	1.076	2	InTe
<i>Spizella passerina</i>	1.090	2	InTe
<i>Salpinctes mexicanus</i>	1.100	2	InTe
<i>Contopus sordidulus</i>	1.107	2	InAe
<i>Vireo vicinior</i>	1.107	2	InFo
<i>Carduelis tristis</i>	1.111	2	GrFo
<i>Empidonax traillii</i>	1.127	2	InAe
<i>Tachycineta thalassina</i>	1.151	2	InAe
<i>Chamaea fasciata</i>	1.166	2	InFo
<i>Vireo gilvus</i>	1.170	2	InFo
<i>Stelgidopteryx ruficollis</i>	1.182	2	InAe
<i>Passerina amoena</i>	1.190	2	InTe
<i>Vireo solitarius</i>	1.220	3	InFo
<i>Ammodramus savannarum</i>	1.230	3	InTe
<i>Parus inornatus</i>	1.243	3	InAe
<i>Sayornis nigricans</i>	1.271	3	InAe
<i>Aimophila ruficeps</i>	1.272	3	InTe
<i>Aimophila belli</i>	1.286	3	InTe
<i>Zonotrichia melodia</i>	1.291	3	InTe
<i>Sitta carolinensis</i>	1.324	4	InBa
<i>Sayornis saya</i>	1.326	4	InAe
<i>Carpodacus mexicanus</i>	1.330	4	GrTe
<i>Hirundo pyrrhonota</i>	1.334	4	InAe
<i>Phainopepla nitens</i>	1.380	5	HeFo
<i>Icterus cucullatus</i>	1.386	5	InFo
<i>Carpodacus purpureus</i>	1.396	5	GrTe
<i>Icteria virens auricollis</i>	1.403	5	InFo
<i>Dendrocopos pubescens</i>	1.431	5	InBa
<i>Myiarchus cinerascens</i>	1.435	5	InAe
<i>Sialia mexicana</i>	1.448	5	InAe
<i>Passerina caerulea</i>	1.453	5	InTe
<i>Chondestes grammacus</i>	1.462	5	GrTe
<i>Pipilo chlorurus</i>	1.468	5	InTe
<i>Catharus ustulatus</i>	1.489	5	InFo
<i>Eremophila alpestris</i>	1.496	5	GrTe
<i>Aeronautes saxatalis</i>	1.507	5	InAe
<i>Passerella iliaca</i>	1.509	5	InTe
<i>Icterus galbula parvus</i>	1.526	5	InFo
<i>Dendrocopos nuttallii</i>	1.583	6	InBa
<i>Campylorhynchus brunneicapillus</i>	1.590	6	InTe
<i>Tyrannus verticalis</i>	1.598	6	InAe
<i>Pipilo erythrophthalmus</i>	1.610	6	InTe
<i>Pheucticus melanocephalus</i>	1.623	6	InFo
<i>Molothrus ater</i>	1.642	6	InTe
<i>Pipilo fuscus senicula</i>	1.647	6	GrTe
<i>Tyrannus vociferans</i>	1.659	6	InAe
<i>Lanius ludovicianus</i>	1.676	6	InAe
<i>Mimus polyglottos</i>	1.686	6	InTe
<i>Progne subis subis</i>	1.694	6	InAe
<i>Chordeiles acutipennis</i>	1.698	6	InAe
<i>Phalaenoptilus nuttallii</i>	1.713	6	InAe
<i>Agelaius phoeniceus</i>	1.721	6	InTe
<i>Agelaius tricolor</i>	1.769	7	InTe
<i>Euphagus cyanocephalus</i>	1.797	7	InTe
<i>Coccyzus americanus</i>	1.806	7	InFo
<i>Xanthocephalus xanthocephalus</i>	1.810	7	InTe
<i>Porzana carolina</i>	1.873	8	GrTe
<i>Aphelocoma coerulescens</i>	1.904	8	OmTe
<i>Melanerpes formicivorus</i>	1.906	8	OmBa
<i>Rallus limicola limicola</i>	1.914	8	InAq
<i>Toxostoma redivivum</i>	1.926	8	InTe
<i>Ixobrychus exilis hesperis</i>	1.936	8	CaAq
<i>Charadrius vociferus</i>	1.985	9	InTe

Table A1 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Sturnella neglecta</i>	2.003	9	InTe
<i>Falco sparverius</i>	2.063	9	InAe
<i>Zenaidra macroura</i>	2.076	9	GrTe
<i>Colaptes auratus</i>	2.102	9	InTe
<i>Cyanocitta stelleri</i>	2.107	9	OmTe
<i>Otus kennicottii</i>	2.155	9	CaAe
<i>Athene cucularia</i>	2.190	9	InAe
<i>Callipepla gambelii</i>	2.220	9	GrTe
<i>Callipepla californica</i>	2.238	9	GrTe
<i>Ardeola striata anthonyi</i>	2.326	10	CaAq
<i>Callipepla picta</i>	2.367	10	GrTe
<i>Asio otus wilsonianus</i>	2.418	10	CaAe
<i>Elanus leucurus</i>	2.522	11	CaAe
<i>Egretta ibis ibis</i>	2.529	11	InTe
<i>Geococcyx californianus</i>	2.575	11	InTe
<i>Columba fasciata</i>	2.593	11	HeFo
<i>Circus cyaneus hudsonius</i>	2.639	11	CaAe
<i>Accipiter cooperii</i>	2.642	11	CaAe
<i>Corvus brachyrhynchos</i>	2.651	11	OmTe
<i>Tyto alba pratincola</i>	2.719	11	CaAe
<i>Buteo lineatus</i>	2.747	11	CaAe
<i>Strix occidentalis</i>	2.785	11	CaAe
<i>Falco mexicanus</i>	2.850	11	CaAe
<i>Dendrocygna bicolor</i>	2.851	11	HeAq
<i>Falco peregrinus</i>	2.893	11	CaAe
<i>Nycticorax nycticorax</i>	2.946	11	CaAq
<i>Buteo swainsoni</i>	2.995	11	CaAe
<i>Buteo jamaicensis</i>	3.052	11	CaAe
<i>Corvus corax clarionensis</i>	3.079	11	OmTe
<i>Bubo virginianus</i>	3.117	11	CaAe
<i>Cathartes aura</i>	3.166	11	CaAe
<i>Aquila chrysaetos</i>	3.623	12	CaAe
<i>Gymnogyps californicus</i>	4.004	12	CaAe

Each distribution includes Latin names, log₁₀-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A2 – Bird species distribution for Mediterranean-climate Spain

Latin name	Body mass	Aggregation	Functional group
<i>Aegithalos caudatus</i>	0.895	1	InFo
<i>Phylloscopus bonelli</i>	0.913	1	InFo
<i>Certhia brachydactyla</i>	0.914	1	InBa
<i>Cisticola juncidis</i>	0.940	1	InTe
<i>Sylvia cantillans</i>	0.964	1	InFo
<i>Troglodytes troglodytes</i>	0.973	1	InFo
<i>Sylvia undata</i>	0.973	1	InTe
<i>Parus ater</i>	0.987	1	InFo
<i>Sylvia conspicillata</i>	1.004	1	InFo
<i>Parus caeruleus</i>	1.029	1	InFo
<i>Hippolais pallida</i>	1.039	1	InFo
<i>Hippolais polyglotta</i>	1.041	1	InFo
<i>Serinus serinus</i>	1.077	1	GrTe
<i>Parus cristatus</i>	1.099	1	InFo
<i>Riparia riparia</i>	1.119	1	InAe
<i>Cettia cetti</i>	1.125	1	InTe
<i>Sylvia melanocephala</i>	1.129	1	InTe
<i>Saxicola torquata</i>	1.161	1	InAe
<i>Muscicapa striata</i>	1.197	2	InAe
<i>Carduelis carduelis</i>	1.210	2	GrTe
<i>Phoenicurus ochruros</i>	1.211	2	InTe

Please cite this article in press as: Wardwell, D.A. et al., A test of the cross-scale resilience model: Functional richness in Mediterranean-climate ecosystems, *Ecol. Complex.* (2008), doi:10.1016/j.ecocom.2007.11.001

Table A2 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Oenanthe hispanica</i>	1.217	2	InTe
<i>Erithacus rubecula</i>	1.223	2	InTe
<i>Motacilla cinerea</i>	1.261	3	InTe
<i>Motacilla flava</i>	1.268	3	InTe
<i>Parus major</i>	1.272	3	InFo
<i>Hirundo rustica</i>	1.281	3	InAe
<i>Carduelis cannabina</i>	1.290	3	GrTe
<i>Delichon urbica</i>	1.291	3	InAe
<i>Sylvia atricapilla</i>	1.291	3	InFo
<i>Luscinia megarhynchos</i>	1.312	3	InTe
<i>Motacilla alba</i>	1.322	3	InTe
<i>Sylvia hortensis</i>	1.324	3	InFo
<i>Fringilla coelebs</i>	1.331	3	GrTe
<i>Calandrella brachydactyla</i>	1.347	3	InTe
<i>Hirundo daurica</i>	1.347	3	InAe
<i>Ptyonprogne rupestris</i>	1.364	3	InAe
<i>Emberiza cia</i>	1.366	3	GrTe
<i>Calandrella rufescens</i>	1.377	3	InTe
<i>Cercotrichas galactotes</i>	1.387	3	InTe
<i>Oenanthe oenanthe</i>	1.389	3	InTe
<i>Emberiza cirius</i>	1.408	3	GrTe
<i>Lullula arborea</i>	1.417	3	InTe
<i>Carduelis chloris</i>	1.418	3	GrTe
<i>Anthus campestris</i>	1.459	4	InTe
<i>Passer domesticus</i>	1.478	4	GrTe
<i>Acrocephalus arundinaceus</i>	1.479	4	InFo
<i>Lanius senator</i>	1.512	4	InAe
<i>Alcedo atthis</i>	1.550	5	CaAe
<i>Galerida theklae</i>	1.566	5	InTe
<i>Alauda arvensis</i>	1.585	5	InTe
<i>Oenanthe leucura</i>	1.600	5	InTe
<i>Apus apus</i>	1.630	5	InAe
<i>Galerida cristata</i>	1.650	5	GrTe
<i>Milaria calandra</i>	1.694	6	GrTe
<i>Merops apiaster</i>	1.741	6	InAe
<i>Monticola solitarius</i>	1.756	6	InAe
<i>Coccothraustes coccothraustes</i>	1.763	6	GrFo
<i>Cinclus cinclus</i>	1.778	6	InAq
<i>Melanocorypha calandra</i>	1.783	6	InTe
<i>Larius excubitor</i>	1.802	6	InAe
<i>Turnix sylvatica</i>	1.813	6	GrTe
<i>Upupa epops</i>	1.830	6	InTe
<i>Caprimulgus ruficollis</i>	1.836	6	InAe
<i>Oriolus oriolus</i>	1.847	6	InFo
<i>Glareola pratincola</i>	1.904	7	InAe
<i>Dendrocopos major</i>	1.906	7	InBa
<i>Caprimulgus europaeus</i>	1.929	7	InAe
<i>Otus scops</i>	1.930	7	InAe
<i>Sturnus unicolor</i>	1.938	7	InTe
<i>Turdus merula</i>	1.967	7	InTe
<i>Coturnix coturnix</i>	2.007	7	GrTe
<i>Apus (Tachymarptis) melba</i>	2.017	7	InAe
<i>Rallus aquaticus</i>	2.063	8	InAq
<i>Cuculus canorus</i>	2.065	8	InFo
<i>Turdus viscivorus</i>	2.071	8	InTe
<i>Tachybaptus ruficollis</i>	2.130	9	InAq
<i>Streptopelia turtur</i>	2.135	9	GrTe
<i>Coracias garrulus</i>	2.167	9	InAe
<i>Ixobrychus minutus</i>	2.169	9	CaAq
<i>Falco naumanni</i>	2.182	9	InAe
<i>Clamator glandarius</i>	2.186	9	InFo
<i>Athene noctua</i>	2.196	9	CaAe
<i>Garrulus glandarius</i>	2.214	9	InFo
<i>Picus viridis</i>	2.244	9	InTe
<i>Accipiter nisus</i>	2.310	10	CaAe
<i>Falco subbuteo</i>	2.324	10	CaAe

Table A2 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Falco tinnunculus</i>	2.366	10	CaAe
<i>Corvus monedula</i>	2.376	10	InTe
<i>Pterocles alchata</i>	2.376	10	GrTe
<i>Asio Otus</i>	2.423	10	CaAe
<i>Tyto alba</i>	2.454	10	CaAe
<i>Columba livia</i>	2.469	10	GrTe
<i>Gallinula chloropus</i>	2.477	10	HeAq
<i>Circus pygargus</i>	2.499	10	CaAe
<i>Pterocles orientalis</i>	2.608	11	GrTe
<i>Strix aluco</i>	2.663	11	CaAe
<i>Burhinus oedicnemus</i>	2.665	11	InAq
<i>Alectoris rufa</i>	2.679	11	GrTe
<i>Columba palumbus</i>	2.689	11	HeTe
<i>Corvus corone</i>	2.691	11	InTe
<i>Podiceps cristatus</i>	2.889	12	CaAq
<i>Milvus migrans</i>	2.918	12	CaAe
<i>Hieraetus pennatus</i>	2.925	12	CaAe
<i>Buteo buteo</i>	2.929	12	CaAe
<i>Ardea purpurea</i>	2.941	12	CaAq
<i>Falco peregrinus</i>	2.949	12	CaAe
<i>Accipiter gentilis</i>	2.967	12	CaAe
<i>Milvus milvus</i>	3.020	12	CaAe
<i>Corvus corax</i>	3.054	12	CaTe
<i>Circaetus gallicus</i>	3.230	13	CaAe
<i>Hieraetus fasciatus</i>	3.312	13	CaAe
<i>Neophron percnopterus</i>	3.320	13	CaAe
<i>Bubo bubo</i>	3.347	13	CaAe
<i>Aquila heliaca</i>	3.514	14	CaAe
<i>Ciconia ciconia</i>	3.538	14	CaTe
<i>Aquila chrysaetos</i>	3.642	14	CaAe
<i>Otis tarda</i>	3.862	14	InTe
<i>Gyps fulvus</i>	3.870	14	CaAe

Each distribution includes Latin names, log10-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A3 – Bird species distribution for Mediterranean-climate southwestern Australia

Latin name	Body mass	Aggregation	Functional group
<i>Smicromis brevirostris</i>	0.708	1	GrFo
<i>Gerygone fusca</i>	0.783	1	InFo
<i>Malurus leucopterus</i>	0.785	1	InFo
<i>Acanthiza inornata</i>	0.845	2	InTe
<i>Poephila guttata</i>	0.845	2	GrTe
<i>Acanthiza uropygialis</i>	0.874	2	InFo
<i>Stipiturus malachurus</i>	0.879	2	InTe
<i>Acanthiza apicalis</i>	0.881	2	InFo
<i>Certhionyx niger</i>	0.892	2	NeFo
<i>Petroica goodenovii</i>	0.903	2	InAe
<i>Rhipidura fuliginosa</i>	0.903	2	InAe
<i>Malurus lamberti</i>	0.903	2	InFo
<i>Dicaeum hirundinaceum</i>	0.903	2	HeTe
<i>Acanthiza chrysorrhoa</i>	0.944	3	InFo
<i>Pardalotus punctatus</i>	0.964	3	InFo
<i>Malurus pulcherrimus</i>	0.978	3	InFo
<i>Petroica multicolor</i>	0.982	3	InTe
<i>Malurus splendens</i>	1.000	3	InFo
<i>Malurus elegans</i>	1.000	3	InFo
<i>Ephthianura tricolor</i>	1.024	3	InTe
<i>Acanthorhynchus superciliosus</i>	1.033	3	NeFo

Table A3 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Sericornis brunneus</i>	1.052	3	InTe
<i>Cecropis ariel</i>	1.053	3	InAe
<i>Emblema oculata</i>	1.070	3	GrFo
<i>Daphoenositta chrysoptera</i>	1.076	3	InBa
<i>Ephthianura albifrons</i>	1.079	3	InTe
<i>Pardalotus striatus</i>	1.086	3	InFo
<i>Aphelocephala leucopsis</i>	1.101	3	InTe
<i>Sericornis frontalis</i>	1.107	3	InTe
<i>Lichmera indistincta</i>	1.114	3	NeFo
<i>Sericornis cautus</i>	1.153	4	InTe
<i>Melithreptus brevirostris</i>	1.164	4	NeFo
<i>Hirundo neoxena</i>	1.167	4	InAe
<i>Melithreptus lunatus</i>	1.167	4	NeFo
<i>Cheramoeca leucosternum</i>	1.170	4	InAe
<i>Cecropis nigricans</i>	1.175	4	InAe
<i>Microeca leucophaea</i>	1.196	4	InAe
<i>Lichenostomus ornatus</i>	1.250	5	NeFo
<i>Phylidonyris albifrons</i>	1.255	5	NeFo
<i>Pachycephala rufiventris</i>	1.258	5	InTe
<i>Phylidonyris nigra</i>	1.262	5	NeFo
<i>Phylidonyris melanops</i>	1.267	5	NeFo
<i>Lichenostomus cracticus</i>	1.292	5	InFo
<i>Lichenostomus penicillatus</i>	1.297	5	HeFo
<i>Phylidonyris novaehollandiae</i>	1.301	5	NeFo
<i>Sericornis fuliginosus</i>	1.319	5	InFo
<i>Melanodryas cucullata</i>	1.326	5	InAe
<i>Eopsaltria griseogularis</i>	1.336	5	InTe
<i>Amytornis textilis</i>	1.356	5	GrTe
<i>Chrysococcyx basalis</i>	1.358	5	InFo
<i>Lichenostomus leucotis</i>	1.364	5	HeFo
<i>Myiagra inquieta</i>	1.380	5	InAe
<i>Anthus novaeseelandiae</i>	1.384	5	InTe
<i>Lichenostomus virescens</i>	1.391	5	NeFo
<i>Chrysococcyx lucidus</i>	1.394	5	InFo
<i>Cinclorhamphus mathewsi</i>	1.398	5	GrTe
<i>Certhionyx variegatus</i>	1.414	5	NeFo
<i>Lalage sueurii</i>	1.415	5	InTe
<i>Rhipidura leucophrys</i>	1.442	5	InAe
<i>Cinclorhamphus cruralis</i>	1.447	5	InTe
<i>Falcunculus frontatus</i>	1.456	5	InBa
<i>Chrysococcyx osculans</i>	1.458	5	InFo
<i>Merops ornatus</i>	1.459	5	InAe
<i>Melopsittacus undulatus</i>	1.462	5	GrTe
<i>Pachycephala inornata</i>	1.515	6	InTe
<i>Pachycephala pectoralis</i>	1.515	6	InTe
<i>Climacteris rufa</i>	1.526	6	InBa
<i>Pomatostomus superciliosus</i>	1.544	6	InTe
<i>Artamus cinereus</i>	1.544	6	InAe
<i>Artamus personatus</i>	1.549	6	InAe
<i>Geopelia cuneata</i>	1.550	6	GrTe
<i>Drymodes brunneopygia</i>	1.568	6	InTe
<i>Artamus cyanopterus</i>	1.602	7	InAe
<i>Turnix velox</i>	1.613	7	GrTe
<i>Halcyon sancta</i>	1.620	7	InTe
<i>Neophema elegans</i>	1.633	7	GrTe
<i>Glossopsitta porphyrocephala</i>	1.641	7	HeFo
<i>Acanthagenys rufogularis</i>	1.643	7	InAe
<i>Cuculus pyrrhophanus</i>	1.679	8	InTe
<i>Aegotheles cristatus</i>	1.699	8	InTe
<i>Halcyon pyrrhopygia</i>	1.719	8	InTe
<i>Psephotus varius</i>	1.778	9	GrTe
<i>Oreoica gutturalis</i>	1.792	9	InTe
<i>Platycercus icterotis</i>	1.801	9	GrFo
<i>Manorina flavigula</i>	1.829	9	NeFo
<i>Cinlosoma castanotum</i>	1.865	9	GrTe
<i>Anthochaera chrysoptera</i>	1.871	9	NeFo

Table A3 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Colluricincla harmonica</i>	1.879	9	InFo
<i>Cuculus pallidus</i>	1.934	10	HeTe
<i>Turnix varia</i>	1.944	10	GrTe
<i>Caprimulgus guttatus</i>	1.945	10	InAe
<i>Grallina cyanoleuca</i>	1.949	10	InTe
<i>Nymphicus hollandicus</i>	1.954	10	GrTe
<i>Cracticus torquatus</i>	1.966	10	InFo
<i>Peltohyas australis</i>	1.966	10	InTe
<i>Coracina novaehollandiae</i>	1.970	10	InTe
<i>Coturnix australis</i>	1.974	10	GrTe
<i>Polytelis anthopeplus</i>	2.057	11	GrTe
<i>Anthochaera carunculata</i>	2.097	11	NeFo
<i>Purpurecephalus spurius</i>	2.107	11	GrFo
<i>Barnardius zonarius</i>	2.125	11	NeFo
<i>Coracina maxima</i>	2.126	11	InTe
<i>Falco cenchroides</i>	2.193	12	InAe
<i>Cracticus nigrogularis</i>	2.193	12	InTe
<i>Ninox novaeseelandiae</i>	2.241	12	InAe
<i>Accipiter cirrhocephalus</i>	2.255	12	CaAe
<i>Ocyphaps lophotes</i>	2.264	12	GrTe
<i>Vanellus tricolor</i>	2.265	12	InTe
<i>Phaps elegans</i>	2.301	12	GrTe
<i>Elanus notatus</i>	2.398	13	CaAe
<i>Falco longipennis</i>	2.403	13	CaAe
<i>Phaps chalcoptera</i>	2.491	13	GrFo
<i>Cacatua leadbeateri</i>	2.491	13	HeFo
<i>Gymnorhina tibicen</i>	2.497	13	InTe
<i>Cacatua roseicapilla</i>	2.505	13	GrTe
<i>Podargus strigoides</i>	2.544	13	InTe
<i>Circus assimilis</i>	2.623	14	InAe
<i>Ninox connivens</i>	2.665	14	CaAe
<i>Lophoictinia isura</i>	2.700	14	CaAe
<i>Accipiter fasciatus</i>	2.708	14	CaAe
<i>Tyto alba</i>	2.719	14	CaAe
<i>Cacatua sanguinea</i>	2.720	14	GrTe
<i>Falco berigora</i>	2.740	14	CaTe
<i>Ardea novaehollandiae</i>	2.742	14	CaAq
<i>Tyto novaehollandiae</i>	2.785	14	CaAe
<i>Calyptorhynchus magnificus</i>	2.796	14	HeFo
<i>Ardea pacifica</i>	2.813	14	CaAq
<i>Corvus coronoides</i>	2.829	14	CaTe
<i>Burhinus magnirostris</i>	2.836	14	InTe
<i>Cacatua tenuirostris</i>	2.869	14	HeTe
<i>Falco peregrinus</i>	2.893	14	CaAe
<i>Haliastur sphenurus</i>	2.903	14	CaAe
<i>Calyptorhynchus funereus</i>	2.904	14	GrFo
<i>Hieraetus morphnoides</i>	2.924	14	CaAe
<i>Chenonetta jubata</i>	2.940	14	HeTe
<i>Tadorna tadornoides</i>	3.111	15	HeAq
<i>Threskiornis spinicollis</i>	3.255	15	InTe
<i>Leipoa ocellata</i>	3.273	15	HeTe
<i>Aquila audax</i>	3.544	16	CaAe
<i>Ardeotis australis</i>	3.799	16	InTe
<i>Dromaius novaehollandiae</i>	4.494	16	HeTe

Each distribution includes Latin names, log₁₀-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A4 – Bird species distribution for Mediterranean-climate South Africa

Latin name	Body mass	Aggregation	Functional group
<i>Estrilda astrild</i>	0.875	1	GrFo
<i>Nectarinia chalybea</i>	0.937	1	NeAe
<i>Cisticola fulvicapilla</i>	0.954	1	InTe
<i>Nectarinia violacea</i>	0.964	1	NeFo
<i>Prinia maculosa</i>	1.000	1	InFo
<i>Cisticola subruficapilla</i>	1.021	1	InFo
<i>Sylvietta rufescens</i>	1.053	1	InFo
<i>Apalis thoracica</i>	1.083	1	InFo
<i>Batis capensis</i>	1.107	1	InFo
<i>Cisticola timmiens</i>	1.111	1	InTe
<i>Riparia paludicola</i>	1.127	1	InAe
<i>Zosterops virens</i>	1.127	1	NeFo
<i>Serinus canicollis</i>	1.140	1	GrTe
<i>Saxicola torquata</i>	1.185	2	InAe
<i>Parisoma subcaeruleum</i>	1.193	2	InFo
<i>Hirundo rustica</i>	1.204	2	InAe
<i>Euplectes orix</i>	1.211	2	GrTe
<i>Serinus flaviventris</i>	1.212	2	GrTe
<i>Nectarinia famosa</i>	1.233	2	NeFo
<i>Euplectes capensis</i>	1.260	2	GrTe
<i>Cercomela sinuata</i>	1.270	2	InAe
<i>Hirundo rupestris</i>	1.279	2	InAe
<i>Serinus sulphuratus</i>	1.283	2	GrTe
<i>Parus afer</i>	1.297	2	InBa
<i>Calandrella cinerea</i>	1.316	2	InTe
<i>Motacilla capensis</i>	1.318	2	InTe
<i>Hirundo albigularis</i>	1.328	2	InAe
<i>Passer melanurus</i>	1.340	2	GrTe
<i>Cercomela familiaris</i>	1.342	2	InTe
<i>Emberiza capensis</i>	1.350	2	GrTe
<i>Anthus novaeseelandiae</i>	1.384	3	InTe
<i>Sigelus silens</i>	1.408	3	InAe
<i>Serinus albogularis</i>	1.413	3	GrTe
<i>Hirundo cucullata</i>	1.431	3	InAe
<i>Anthus leucophrys</i>	1.431	3	InTe
<i>Cossypha caffra</i>	1.455	3	InTe
<i>Mirafrapa apiata</i>	1.487	3	InTe
<i>Sphenoecus afer</i>	1.497	3	InTe
<i>Lybius leucomelas</i>	1.508	3	HeFo
<i>Pycnonotus capensis</i>	1.597	4	HeFo
<i>Promerops cafer</i>	1.606	4	NeFo
<i>Oena capensis</i>	1.608	4	GrTe
<i>Colius colius</i>	1.617	4	HeFo
<i>Lanius collaris</i>	1.618	4	InTe
<i>Ploceus capensis</i>	1.627	4	InTe
<i>Apus barbatus</i>	1.631	4	InAe
<i>Caprimulgus pectoralis</i>	1.674	5	InAe
<i>Macronyx capensis</i>	1.677	5	InTe
<i>Lanius ferrugineus</i>	1.688	5	InTe
<i>Colius striatus</i>	1.708	5	HeFo
<i>Colius indicus</i>	1.751	6	HeFo
<i>Monticola rupestris</i>	1.778	6	InTe
<i>Upupa epops</i>	1.788	6	InTe
<i>Malacconotus zeylonus</i>	1.797	6	InTe
<i>Creatophora cinerea</i>	1.826	6	InTe
<i>Turdus olivaceus</i>	1.868	6	InTe
<i>Apus melba</i>	1.881	6	InAe
<i>Streptopelia senegalensis</i>	2.004	7	GrTe
<i>Spreo bicolor</i>	2.021	7	InTe
<i>Geocolaptes olivaceus</i>	2.079	7	InTe
<i>Onychognathus morio</i>	2.124	7	InTe
<i>Streptopelia capicola</i>	2.152	7	GrTe
<i>Vanellus coronatus</i>	2.223	7	InTe
<i>Falco tinnunculus</i>	2.304	7	CaAe
<i>Elanus caeruleus</i>	2.522	8	CaAe

Table A4 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Bubulcus (=Ardeola) ibis</i>	2.529	8	InTe
<i>Columba guinea</i>	2.547	8	GrTe
<i>Francolinus africanus</i>	2.592	8	HeTe
<i>Burhinus capensis</i>	2.626	8	InTe
<i>Circus ranivorus</i>	2.705	8	CaAe
<i>Corvus albus</i>	2.723	8	HeTe
<i>Francolinus capensis</i>	2.814	8	HeTe
<i>Afrotis afra</i>	2.840	8	InTe
<i>Corvus capensis</i>	2.843	8	InTe
<i>Buteo buteo</i>	2.942	8	CaAe
<i>Corvus albicollis</i>	2.954	8	InTe
<i>Ardea melanocephala</i>	3.025	8	InTe
<i>Buteo rufofuscus</i>	3.066	8	CaAe
<i>Sagittarius serpentarius</i>	3.557	9	InTe
<i>Aquila verreauxi</i>	3.613	9	CaAe
<i>Otis denhami</i>	3.615	9	InTe

Each distribution includes Latin names, log10-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A5 – Mammal species distribution for Mediterranean-climate California, USA

Latin name	Body mass	Aggregation	Functional group
<i>Sorex ornatus</i>	0.698	1	InTe
<i>Sorex vagrans</i>	0.707	1	InTe
<i>Reithrodontomys megalotis</i>	1.049	1	GrTe
<i>Peromyscus maniculatus</i>	1.299	2	GrTe
<i>Peromyscus boylii</i>	1.329	2	HeAr
<i>Peromyscus truei</i>	1.427	2	GrTe
<i>Peromyscus californicus</i>	1.656	3	GrTe
<i>Tamias obscurus</i>	1.748	3	HeAr
<i>Dipodomys heermanni</i>	1.857	3	GrTe
<i>Tamias merriami</i>	1.875	3	GrTe
<i>Dipodomys venustus</i>	1.929	3	GrTe
<i>Dipodomys elephantinus</i>	1.930	3	GrTe
<i>Thomomys bottae</i>	2.049	3	HeFs
<i>Neotoma lepida</i>	2.164	3	HeTe
<i>Mustela frenata</i>	2.167	3	CaTe
<i>Peromyscus eremicus</i>	2.276	3	GrTe
<i>Neotoma fuscipes</i>	2.281	3	HeAr
<i>Spermophilus beecheyi</i>	2.781	4	HeTe
<i>Sylvilagus bachmani</i>	2.785	4	HeTe
<i>Sylvilagus auduboni</i>	2.879	4	HeTe
<i>Spilogale gracilis</i>	2.888	4	CaTe
<i>Bassaricus astutus</i>	3.053	4	CaTe
<i>Mephitis mephitis</i>	3.253	4	InTe
<i>Urocyon cinereoargenteus</i>	3.548	5	CaTe
<i>Procyon lotor psora</i>	3.557	5	OmTe
<i>Taxidea taxus</i>	3.857	5	CaTe
<i>Lynx rufus</i>	3.889	5	CaTe
<i>Canis latrans</i>	4.102	5	CaTe
<i>Odocoileus hemionus</i>	4.635	6	HeTe
<i>Felis concolor</i>	4.754	6	CaTe
<i>Felis onca</i>	5.061	6	CaTe
<i>Ursos arctos</i>	5.190	6	OmTe

Each distribution includes Latin names, log10-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A6 – Mammal species distribution for Mediterranean-climate South Africa

Latin name	Body mass	Aggregation	Functional group
<i>Mus minutoides</i>	0.767	1	HeTe
<i>Suncus varilla</i>	0.813	1	InTe
<i>Dendromus melanotis</i>	0.826	1	InTe
<i>Crocidura cyanea</i>	0.934	1	InTe
<i>Dendromus mesomelas</i>	1.053	1	InTe
<i>Malacothrix typica</i>	1.127	1	HeTe
<i>Myosorex varius</i>	1.130	1	InTe
<i>Acomys subspinosus</i>	1.325	2	HeTe
<i>Steatomys krebsi</i>	1.380	2	HeTe
<i>Graphiurus murinus</i>	1.450	2	InTe
<i>Gerbillurus paeba</i>	1.511	2	HeTe
<i>Rhabdomys pumilo</i>	1.559	2	HeTe
<i>Macroscelides proboscideus</i>	1.582	2	InTe
<i>Myomyscus verroxii</i>	1.613	2	InTe
<i>Desmodillus auricularis</i>	1.664	2	HeTe
<i>Aethomys namequensis</i>	1.688	2	HeTe
<i>Chrysochloris asiatica</i>	1.690	2	InFs
<i>Amblysomus hottentotus</i>	1.832	3	InFs
<i>Graphiurus ocularis</i>	1.838	3	InTe
<i>Cryptomys hottentotus</i>	1.897	3	HeFs
<i>Mystromys albicaudatus</i>	1.939	3	HeTe
<i>Dasymys incomtus</i>	1.972	3	HeTe
<i>Tatera afra</i>	1.987	3	HeTe
<i>Otomys saundersiae</i>	2.013	3	HeTe
<i>Otomys irroratus</i>	2.072	3	HeTe
<i>Crocidura flavescens</i>	2.088	3	InTe
<i>Otomys unisulcatus</i>	2.095	3	HeTe
<i>Otomys laminatus</i>	2.176	3	HeTe
<i>Georchus capensis</i>	2.338	4	HeTe
<i>Poecilogale albinucha</i>	2.338	4	CaTe
<i>Bathyergus suillus</i>	2.796	4	HeFs
<i>Ictonyx striatus</i>	2.866	4	InTe
<i>Herpestes pulverulenta</i>	2.901	4	InTe
<i>Cynictis penicillata</i>	2.919	4	InTe
<i>Pronolagus rupestris</i>	3.210	5	HeTe
<i>Genetta tigrina</i>	3.270	5	CaTe
<i>Genetta genetta</i>	3.279	5	CaTe
<i>Lepus capensis</i>	3.310	5	HeTe
<i>Vulpes chama</i>	3.423	5	CaTe
<i>Procavia capensis</i>	3.480	5	HeTe
<i>Atilax paludinosus</i>	3.531	5	CaTe
<i>Lepus saxatilis</i>	3.556	5	HeTe
<i>Felis libyca</i>	3.633	5	CaTe
<i>Proteles cristatus</i>	3.840	6	InTe
<i>Canis mesomelas</i>	3.898	6	CaTe
<i>Mellivora capensis</i>	3.899	6	CaTe
<i>Oreotragus oreotragus</i>	4.009	6	HeTe
<i>Raphicerus melanotis</i>	4.011	6	HeTe
<i>Felis caracal</i>	4.029	6	CaTe
<i>Felis serval</i>	4.047	6	CaTe
<i>Raphicerus campestris</i>	4.053	6	HeTe
<i>Aonyx capensis</i>	4.061	6	CaAq
<i>Hystrix africaeaustralis</i>	4.097	6	HeTe
<i>Sylvicapra grimmia</i>	4.207	6	HeTe
<i>Pelea capreolus</i>	4.352	7	HeTe
<i>Papio ursinus</i>	4.365	7	HeTe
<i>Panthera pardus</i>	4.416	7	CaTe
<i>Hyaena brunnea</i>	4.583	8	CaTe
<i>Orycteropus afer</i>	4.719	8	InTe
<i>Damaliscus dorcas dorcas</i>	4.826	8	HeTe
<i>Alcelaphus buselaphus</i>	5.134	9	HeTe
<i>Panthera leo</i>	5.193	9	CaTe
<i>Equus zebra</i>	5.388	9	HeTe

Table A6 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Taurotragus oryx</i>	5.587	9	HeTe
<i>Diceros bicornis</i>	5.939	9	HeTe

Each distribution includes Latin names, log10-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A7 – Mammal species distribution for Mediterranean-climate southwestern Australia

Latin name	Body mass	Aggregation	Functional group
<i>Tarsipes rostratus</i>	0.954	1	HeAr
<i>Cercartetus concinnus</i>	1.114	1	InAr
<i>Sminthopsis dolichura</i>	1.134	1	InTe
<i>Sminthopsis crassicaudata</i>	1.176	1	InTe
<i>Sminthopsis griseoventer</i>	1.243	1	InTe
<i>Sminthopsis gilberti</i>	1.290	1	InTe
<i>Sminthopsis granulipes</i>	1.398	1	InTe
<i>Pseudomys albocinereus</i>	1.484	1	HeTe
<i>Pseudomys nanus</i>	1.531	1	HeTe
<i>Pseudomys occidentalis</i>	1.531	1	HeTe
<i>Notomys alexis</i>	1.544	1	GrTe
<i>Antichinus flavipes</i>	1.653	1	InTe
<i>Pseudomys fieldi</i>	1.653	1	HeTe
<i>Phascogale calura</i>	1.712	1	InAr
<i>Notomys mitchelli</i>	1.716	1	GrTe
<i>Parantechinus apicalis</i>	1.837	2	InTe
<i>Pseudomys shortridgei</i>	1.845	2	HeTe
<i>Notomys longicaudatus</i>	2.000	2	GrTe
<i>Rattus tunneyi</i>	2.093	2	HeTe
<i>Rattus fuscipes</i>	2.122	2	InTe
<i>Phascogale tapoatafa</i>	2.287	3	InAr
<i>Perameles bougainville</i>	2.354	3	HeTe
<i>Myrmecobius fasciatus</i>	2.673	3	InTe
<i>Hydromys chrysogaster</i>	2.833	4	InAq
<i>Isoodon obesulus</i>	2.889	4	InTe
<i>Pseudocheirus occidentalis</i>	3.000	4	HeAr
<i>Dasyurus geoffroyi</i>	3.041	4	CaTe
<i>Potorus tridactylus</i>	3.041	4	HeTe
<i>Lagorchestes hirsutus</i>	3.102	4	HeTe
<i>Bettongia penicillata</i>	3.114	4	HeTe
<i>Bettongia leseur</i>	3.176	4	HeTe
<i>Lagostrophus fasciatus</i>	3.230	4	HeTe
<i>Trichosurus vulpecula</i>	3.419	5	HeAr
<i>Setonix brachyurus</i>	3.512	5	HeTe
<i>Onychogalea lunata</i>	3.544	5	HeTe
<i>Petrogale lateralis</i>	3.602	5	HeTe
<i>Tachyglossus aculeatus</i>	3.653	5	InTe
<i>Macropus eugenii</i>	3.813	5	HeTe
<i>Macropus irma</i>	3.903	5	HeTe
<i>Canis lupus</i>	4.225	6	CaTe
<i>Macropus robustus</i>	4.327	6	HeTe
<i>Macropus fuliginosus</i>	4.345	6	HeTe

Each distribution includes Latin names, log10-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A8 – Mammal species distribution for Mediterranean-climate Chile

Latin name	Body mass	Aggregation	Functional group
<i>Marmosa elegans</i>	1.481	1	InTe
<i>Oryzomys longicaudatus</i>	1.560	1	GrTe
<i>Akodon olivaceus</i>	1.639	1	GrTe
<i>Phyllotis darwini</i>	1.789	2	HeTe
<i>Akodon longipilis</i>	1.796	2	InTe
<i>Chelemys macronyx</i>	1.865	2	GrTe
<i>Euneomys mordax</i>	1.914	2	HeTe
<i>Octodon bridgesi</i>	1.966	2	HeTe
<i>Spalacopus cyanus</i>	2.011	2	HeFs
<i>Aconaemys fuscus</i>	2.090	2	HeTe
<i>Ctenomys maulinus</i>	2.215	2	HeTe
<i>Octodon degus</i>	2.264	2	HeAr
<i>Abrocoma bennetti</i>	2.363	2	HeAr
<i>Octodon lunatus</i>	2.367	2	HeTe
<i>Lagidium viscacia</i>	3.188	3	HeTe
<i>Galictis guia</i>	3.199	3	CaTe
<i>Conepatus chinga</i>	3.275	3	InTe
<i>Felis Guigna</i>	3.348	3	CaTe
<i>Felis Colocolo</i>	3.470	3	CaAr
<i>Myocaster coypus</i>	3.579	3	HeAq
<i>Dusicyon griseus</i>	3.601	3	CaTe
<i>Lutra felina</i>	3.653	3	InAq
<i>Dusicyon culpaeus</i>	3.867	3	CaTe
<i>Pudu puda</i>	3.989	3	HeTe
<i>Felis concolor</i>	4.549	4	CaTe
<i>Hippocamelus bisulcus</i>	4.845	4	HeTe
<i>Lama guanicoe</i>	5.079	4	HeTe

Each distribution includes Latin names, log10-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

Table A9 – Mammal species distribution for Mediterranean-climate Spain

Latin name	Body mass	Aggregation	Functional group
<i>Suncus etruscus</i>	0.352	1	InTe
<i>Sorex minutus</i>	0.477	1	InTe
<i>Micromys minutus</i>	0.756	1	GrTe
<i>Sorex granarius</i>	0.796	1	GrTe
<i>Crocidura russula</i>	0.806	1	InTe
<i>Crocidura suaveolens</i>	0.825	1	InTe
<i>Mus spretus</i>	1.090	2	GrTe
<i>Neomys fodiens</i>	1.114	2	InAq
<i>Neomys anomalus</i>	1.134	2	InTe
<i>Pitymys lusitanicus</i>	1.212	2	HeTe
<i>Microtus arvalis</i>	1.262	2	HeFs
<i>Mus domesticus</i>	1.283	2	GrTe
<i>Clethrionomys glareolus</i>	1.288	2	HeTe
<i>Apodemus sylvaticus</i>	1.344	2	InTe
<i>Microtis agrestis</i>	1.344	2	HeTe
<i>Pitymys duodecimcostatus</i>	1.345	2	HeTe
<i>Talpa caeca</i>	1.505	3	InFs
<i>Microtus nivalis</i>	1.591	3	HeTe
<i>Galemys pyrenaicus</i>	1.760	3	InAq
<i>Talpa europaea</i>	1.881	3	InFs
<i>Talpa romana</i>	1.966	3	InFs
<i>Eliomys quercinus</i>	1.980	3	HeTe
<i>Rattus rattus</i>	2.092	3	HeTe
<i>Mustela nivalis</i>	2.150	3	CaTe

Table A9 (Continued)

Latin name	Body mass	Aggregation	Functional group
<i>Arvicola sapidus</i>	2.230	3	HeAq
<i>Myoxis glis</i>	2.284	3	HeAr
<i>Sciurus vulgaris</i>	2.398	3	HeAr
<i>Rattus norvegicus</i>	2.455	3	HeTe
<i>Erinaceus europaeus</i>	2.805	4	InTe
<i>Erinaceus algirus</i>	2.845	4	InTe
<i>Mustela putorius</i>	3.000	4	CaTe
<i>Martes foina</i>	3.000	4	CaTe
<i>Oryctolagus cuniculus</i>	3.196	5	HeTe
<i>Genetta genetta</i>	3.236	5	CaTe
<i>Lepus capensis</i>	3.310	5	HeTe
<i>Lepus granatensis</i>	3.334	5	HeTe
<i>Felis silvestris</i>	3.385	5	CaTe
<i>Herspestes ichneumon</i>	3.474	5	CaTe
<i>Vulpes vulpes</i>	3.678	6	CaTe
<i>Lutra lutra</i>	3.796	6	CaAq
<i>Meles meles</i>	3.964	6	InTe
<i>Lynx pardinus</i>	4.043	6	CaTe
<i>Macaca sylvanus</i>	4.049	6	HeTe
<i>Capreolus capreolus</i>	4.079	6	HeTe
<i>Castor fiber</i>	4.145	6	HeTe
<i>Canis lupus</i>	4.632	7	CaTe
<i>Sus scrofa</i>	4.740	7	HeTe
<i>Capra pyrenaica</i>	4.760	7	HeTe
<i>Cervus elaphus</i>	5.176	7	HeTe
<i>Ursus arctos</i>	5.247	7	HeTe

Each distribution includes Latin names, log10-transformed body masses, body mass aggregation membership, and functional group code used in richness simulations. The first two letters (prefix) of the functional group code represent the diet component and the latter two letters (suffix) represent foraging strata. Key to prefixes: Ca = carnivore; Gr = granivore; He = herbivore; In = insectivore; Ne = nectarivore; Om = omnivore. Key to suffixes: Ae = aerial; Aq = aquatic; Ar = arboreal; Ba = bark; Fo = foliage; Fs = fossorial; Te = terrestrial.

REFERENCES

- Allen, C.R., Holling, C.S., 2002. Cross-scale structure and scale breaks in ecosystems and other complex systems. *Ecosystems* 5, 315–318.
- Allen, C.R., Forys, E.A., Holling, C.S., 1999. Body mass patterns predict invasions and extinctions in transforming landscapes. *Ecosystems* 2, 114–121.
- Allen, C.R., Epperson, D., Garmestani, A., 2004. The impacts of fire ants on wildlife: a decade of research. *Am. Midl. Nat.* 152, 88–103.
- Allen, C.R., Gunderson, L., Johnson, A.R., 2005. The use of discontinuities and functional groups to assess relative resilience in complex systems. *Ecosystems* 8, 958–966.
- Blakers, M., Davies, S.J.J.F., Reilly, P.N. (Eds.), 1984. *The Atlas of Australian Birds*. Melbourne University Press, Carlton, Victoria.
- Brown, L.H., Urban, E.K., Newman, K. (Eds.), 1982. *The Birds of Africa*, vol. 1. Academic Press London Inc., London.
- Cheyilan, G., 1991. Patterns of Pleistocene turnover, current distribution and speciation among Mediterranean mammals. In: Groves, R.H., Di Castri, (Eds.), *Biogeography of Mediterranean Invasions*. Cambridge University Press, Cambridge, pp. 227–262.
- Coulon, A., Cosson, J.F., Angibault, J.M., Cargnelutti, B., Galan, M., Morellet, N., Petit, E., Aulagnier, S., Hewison, A.J.M., 2004. Landscape connectivity influences gene flow in a roe deer population inhabiting a fragmented landscape: an individual-based approach. *Mol. Ecol.* 13, 2841–2850.
- Cramp, S. (Ed.), 1978–1994. *Handbook of the Birds of Europe the Middle East and North Africa*, 9 volumes. Oxford University Press, New York.
- Davis, G.W., Richardson, D.M. (Eds.), 1995. *Mediterranean-Type Ecosystems: the Function of Biodiversity*. Springer-Verlag, New York.
- Di Castri, F., Mooney, H.A., 1973. *Mediterranean Type Ecosystems: Origins and Structure*. Springer-Verlag, New York.
- Dunning Jr., J.B., 1993. *CRC Handbook of Avian Body Masses*. CRC Press, Ann Arbor, MI.
- Ehrlich, P.R., Dobkin, D.S., Wheye, D., 1988. *The Birder's Handbook: a Field Guide to the Natural History of North American Birds*. Simon and Schuster Inc., New York.
- Fisher, R.A., 1954. *Statistical Methods for Research Workers*, 12th ed. Oliver and Boyd, Edinburgh, UK.
- Folke, C., Carpenter, S., Walker, B., Scheffer, M., Elmqvist, T., Gunderson, L., Holling, C.S., 2004. Regime shifts, resilience, and biodiversity in ecosystem management. *Ann. Rev. Ecol. Syst.* 35, 557–581.
- Fry, C.H., Keith, S., Urban, E.K., 1988. *The Birds of Africa*, vol. 3. Academic Press London Inc., London.
- Fry, C.H., Keith, S., Urban, E.K., 2000. *The Birds of Africa*, vol. 6. Academic Press London Inc., London.
- Fry, C.H., Keith, S., Urban, E.K., 2004. *The Birds of Africa*, vol. 7. Academic Press London Inc., London.
- Gunderson, L.H., 2000. Ecological resilience-in theory and application. *Ann. Rev. Ecol. Syst.* 31, 425–439.
- Gunderson, L.H., Holling, C.S., 2002. *Panarchy: Understanding Transformations in Human and Natural Systems*. Island Press, Washington, DC.
- Holling, C.S., 1973. Resilience and the stability of ecological systems. *Ann. Rev. Ecol. Syst.* 4, 1–23.
- Holling, C.S., 1992. Cross-scale morphology, geometry, and dynamics of ecosystems. *Ecol. Mon.* 62, 447–502.
- Jameson, E.W., Peeters, H.J., 1988. *California Mammals*. University of California Press, Berkeley, CA.

- Kalin Arroyo, M.T., Zedler, P.H., Fox, M.D., 1995. Ecology and Biogeography of Mediterranean Ecosystems in Chile, California, and Australia. Springer-Verlag, New York.
- Keith, S., Urban, E.K., Fry, C.H., 1992. The Birds of Africa, vol. 4. Academic Press London Inc., London.
- Lavorel, S., 1999. Ecological diversity and resilience of Mediterranean vegetation to disturbance. *Div. Dist.* 5, 3–13.
- MacDonald, D.W., Barrett, P., 2001. Mammals of Europe. Princeton University Press, Princeton, NJ.
- McCarthy, M.A., Possingham, H.P., Day, J.P., Tyre, A.J., 2001. Testing the accuracy of population viability analysis. *Con. Bio.* 15, 1030–1038.
- Miller, S., 1980. Human influences on the distribution and abundance of wild Chilean mammals: prehistoric—present. Ph.D. Dissertation, University of Washington.
- Peterson, G.D., 2002. Estimating resilience across landscapes. *Con. Ecol.* 6 (1), 17.
- Peterson, G., Allen, C.R., Holling, C.S., 1998. Ecological resilience, biodiversity, and scale. *Ecosystems* 1, 6–18.
- Quinn, R.D., 1990. Habitat preferences and distribution of mammals in California chaparral. Research Paper PSW-202. Pacific Southwest Research Station, U.S.D.A. Forest Service, Berkeley, CA.
- Redford, K.H., Eisenberg, J.F., 1992. Mammals of the Neotropics. vol. 2. The Southern Cone. University of Chicago Press, Chicago, IL.
- Restrepo, C., Renjifo, L.M., Marples, P., 1997. Frugivorous birds in fragmented neotropical montane forests: landscape pattern and body mass distribution. In: Laurance, W.F., Bierregaard, R.O., Moritz, C. (Eds.), *Tropical Forest Remnants: Ecology, Management and Conservation of Fragmented Communities*. University of Chicago Press, Chicago, IL, pp. 171–189.
- SAS Institute Inc., 1999. SAS/STAT user's guide, Version 8, vol. 2. SAS Institute Inc., Cary, NC.
- Saunders, D.A., Ingram, J.A., 1995. Birds of Southwestern Australia. Surrey Beatty and Sons Pty Limited, New South Wales.
- Silva, M., Downing, J.A., 1995. CRC Handbook of Mammalian Body Masses. CRC Press, Ann Arbor, MI.
- Silverman, B.W., 1981. Using kernel density estimates to investigate multimodality. *J. Roy. Stat. Soc.* 43, 97–99.
- Smithers, R.H.N., 1983. The Mammals of the Southern African Subregion. University of Pretoria, South Africa.
- Strahan, R. (Ed.), 1995. Mammals of Australia. Smithsonian Inst. Press, Washington, DC.
- Stow, C., Allen, C.R., Garmestani, A.S., 2007. Evaluating discontinuities in complex systems: toward quantitative measures of resilience. *Ecology and Society* 12 (1), 26 [online]. URL: <http://www.ecologyandsociety.org/vol12/iss1/art26/>.
- Turner, T.G., Gardner, R.H., O'Neill, R.V., 2001. Landscape Ecology in Theory and Practice. Springer-Verlag, New York.
- Unitt, P., 1984. The birds of San Diego county. Memoir 13, San Diego Society of Natural History. United States Fish and Wildlife Service. (1991). Endangered and threatened wildlife and plants (50 CFR 17.11 and 17.12). United States Department of the Interior, Washington, DC.
- Urban, E.K., Fry, C.H., Keith, S., 1986. The Birds of Africa, vol. 2. Academic Press London Inc., London.
- Urban, E.K., Fry, C.H., Keith, S., 1997. The Birds of Africa, vol. 5. Academic Press London Inc., London.
- Vignieri, S.N., 2005. Streams over mountains: influence of riparian connectivity on gene flow in the Pacific jumping mouse (*Zapus trinotatus*). *Mol. Ecol.* 14, 1925–1937.
- Wilson, D.E., Ruff, S. (Eds.), 1999. The Smithsonian Book of North American Mammals. Smithsonian Institution Press, Washington, DC.
- Winterbottom, J.M., 1966. Ecological distribution of the birds in the indigenous vegetation of the southwestern cape. *Ostrich* 37, 76–91.