Misleading results from conventional gap analysis – Messages from the warming north

Heini Kujala [a,*], Miguel B. Araújo [b,c], Wilfried Thuiller [d], Mar Cabeza [a,b]

[a] Metapopulation Research Group, Department of Biosciences, P.O. Box 65, 00014 University of Helsinki, Finland
[b] Biodiversity and Global Change Lab, Museo Nacional de Ciencias Naturales, CSIC, C/ José Gutiérrez Abascal 2, Madrid 28006, Spain
[c] Rui Nabeiro Biodiversity Chair, CIBIO, Universidade de Évora, Largo dos Colegiais, 7000 Évora, Portugal
[d] Laboratoire d'Ecologie Alpine, UMR-CNRS 5553, Université Joseph Fourier, BP 53, 38041 Grenoble Cedex 9, France

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ABSTRACT

Gap analysis is a widely used method for assessing the representation of species in protected area (PA) networks. However, representation does not imply persistence. Here, we investigated whether gap analysis may result in misleading conservation guidelines by comparing the representation to two indicators of persistence. We ran a gap analysis with Finnish breeding birds and identified conservation priorities based on current distribution patterns. We tested the sensitivity of these results by using two target setting schemes and several thresholds defining the amount of protected area, and found the levels of representation identified by gap analysis to be robust. We then compared the gap analysis results with recent population trends and projected changes in potential suitable climate under different climate change scenarios for the year 2050. We show that although high latitude species are well represented in PAs, they are currently declining and are projected to lose climatic suitability in the near future. In contrast, low latitude species with poor representation in PAs have increasing population trends and are generally expected to expand their ranges into protected areas in the near future. This study demonstrates with empirical data a mismatch between representation in PAs and population trends, resulting in misleading understanding of current PA effectiveness. The mismatch is linked to the latitude of species distributions and corresponds to expected future changes, indicating that the patterns are potentially driven by climate change. We therefore urge practitioners and researchers to include better indicators of persistence in gap-analysis frameworks even for short term assessments.

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1. Introduction

Gap analysis is a conservation tool designed to assess the representativeness of existing protected area networks and to identify conservation priorities (Jennings, 2000; Margules and Pressey, 2000; Scott et al., 1993). It has been used at a variety of scales (e.g. Rodrigues et al., 2004a; Sowa et al., 2007), gaining popularity in scientific studies (e.g. 220 publications since 1992), as well as in practical assessments (GAP, 2010; Langhammer et al., 2007). Gap analysis is essentially a comparison of the distributions of species (or any other feature of conservation interest) with that of protected areas, used to define the degree to which species are represented in the protected areas, and to compare the representations to prescribed targets (Margules and Pressey, 2000; Scott et al., 1993). Species can then be classified as *true gap species* – species not represented in any of the protected areas; *partial gap species* – species underrepresented in protected areas, thus not achieving

the targets set for them; and *covered species* – species that are represented in the protected areas and that achieve their targets (e.g. Rodrigues et al., 2004a,b). The main outcome of gap analysis is to identify the true or partial gap species which need further protection. Species identified as covered are assumed to be well protected. Although this information can be used to guide the selection of new protected areas, gap analysis per se does not prescribe methods for protected area design and is not a primary tool for selecting new areas for conservation. One fundamental assumption behind gap analysis is proactive conservation, i.e. not to focus only on rare species but also on common species. This is believed to be more cost-efficient (Scott et al., 1987) and exhibit a higher probability of success (Tear et al., 1993) than trying to save species when they are on the brink of extinction.

Gap analysis has known shortcomings. Like any other conservation planning analysis, the coarseness and/or correctness of data can influence the results (Hulbert and Jetz, 2007; Rondinini et al., 2006). A further source of uncertainty can arise from mismatching resolutions of species and protected areas data (Araújo, 2004). Thus, the true representation of biodiversity features in protected

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* Corresponding author. Tel.: +358 9 191 57922; fax: +358 9 191 57694.
  E-mail address: heini.kujala@helsinki.fi (H. Kujala).

areas often cannot be guaranteed (Jennings, 2000) and more de-tailed surveys are needed for fine-tuning the results before priori-tization can be made (Jennings, 2000; Scott et al., 1993). This is closely followed by the question of what is an adequate represen-tation level and whether it is even possible to determine one (Jennings, 2000; Rodrigues et al., 2004b). By focusing exclusively on species presence or absence in protected areas, gap analysis does not explicitly account for future threats nor does it assess the long-term persistence of biodiversity in protected areas (Cabeza and Moilanen, 2001). However there is no reason why gap analysis cannot incorporate assessments of the long-term changes in species distributions and studies have already been undertaken by looking at expected species distribution shifts un-der climate change (e.g. Dockerty et al., 2003; Hannah et al., 2007). Despite these shortcomings, gap analysis is widely used be-cause it offers a simple, quantitative, and standardized method for evaluating the representativeness of protected area networks. But in a rapidly changing world, what conclusions could be drawn from gap analysis based on observed species distribution data and how should it be used when evaluating priorities for conservation?

In this paper, we evaluate existing protected areas in Finland and demonstrate how conventional gap analysis using distribution data for breeding birds results in potentially misleading conserva-tion guidelines. We do a gap analysis to evaluate representation of Finnish breeding birds, and compare the results to two indicators of persistence: recent population trends from the past ca. 25 years and projections of distributional shifts under climate change sce-narios. Population trends are a dynamic measure of the status of species, which correlate strongly with extinction risk (O'Grady et al., 2004) and can act as an indicator of conservation success (Donald et al., 2007). Future changes are more difficult to antici-pate, but out of all processes that can negatively affect biodiversity, climate change will very likely take place regardless of our current actions (IPCC, 2007). Several techniques are available to project some of the impacts of climate change, especially for projecting species potential distributional shifts (e.g. Guisan and Thuiller, 2005; Heikkinen et al., 2006). We thus evaluate the potential fu-ture impacts of climate change on bird distributions, using projec-tions from bioclimatic envelope models for 2050.

These analyses allow us to evaluate (i) what are the representa-tion gaps in the current protected area network; and (ii) how does the representation in current protected areas correspond to short term persistence (i.e. population trends) or to (iii) long term persis-tence (i.e. projections).

2. Material and methods

2.1. Gap analysis

The bird data are based on the combined information of the first and second Finnish Bird Atlases (Hyytiä et al., 1983; Väisänen et al., 1998), which have been compiled from bird surveys done during 1974–1979 and 1986–1989. The combined atlas contains an index of breeding probability (ranging from 0 = not found; to 4 = con-firmed breeding) of 248 bird species on a 10 km × 10 km uniform grid that covers nearly the entire area of Finland (totaling 3813 grid cells). The species fall into 10 groups according to their pre-ferred habitat (Väisänen et al., 1998, and Table 1). We excluded all species pertaining to agricultural and built-up areas (n = 38), as protected areas are not expected to be the means to protect them. We also excluded *Anser caerulescens* (snow goose) because of its unclear status as a wild bird species in Europe (R.A. Väisänen, personal communication). The breeding probabilities of the remaining 209 species were then converted into presence/absence data by defining a species to be absent in cells where probability of

Table 1

Proportions of true gap, partial gap and covered species in each habitat group based on the 20% threshold for protected cells and using two target setting schemes (see Section 2.1). Classification and numbering of groups follow Väisänen et al. (1998) except for the group lakes and seas, which includes both species of Baltic archipelago and coasts, and species of oligotrophic lakes from Väisänen et al. (1998).

Habitat				
Target scheme	Gap	Partial gap	Covered	n
0. Lakes and seas				46
$T_{(a)}$	4.3	58.7	37.0	
$T_{(t)}$	4.3	60.9	34.8	
1. Forest generalists				15
$T_{(a)}$	0.0	60.0	40.0	
$T_{(t)}$	0.0	66.7	33.3	
2. Coniferous forests				28
$T_{(a)}$	3.6	71.4	25.0	
$T_{(t)}$	3.6	78.6	17.9	
3. Old-growth forests				15
$T_{(a)}$	0.0	66.7	33.3	
$T_{(t)}$	0.0	86.7	13.3	
4. Deciduous forests				19
$T_{(a)}$	15.8	78.9	5.3	
$T_{(t)}$	15.8	78.9	5.3	
5. Bushes and saplings				13
$T_{(a)}$	23.1	76.9	0.0	
$T_{(t)}$	23.1	76.9	0.0	
7. Open peatlands				19
$T_{(a)}$	0.0	10.5	89.5	
$T_{(t)}$	0.0	36.8	63.2	
8. Arctic mountains				21
$T_{(a)}$	0.0	9.5	90.5	
$T_{(t)}$	0.0	23.8	76.2	
9. Wetlands				33
$T_{(a)}$	18.2	66.7	15.2	
$T_{(t)}$	18.2	66.7	15.2	

Target setting schemes: $T_{(a)}$ = Distribution area, $T_{(t)}$ = Threat categories.

breeding was unlikely or the species was not observed (classes 0 and 1), and present if the probability was possible or higher (clas-ses 2–4).

The protected area network data include coordinates and spa-tial configuration of 3148 protected areas, national parks and wil-derness areas representing 94.3% of the total area of the Finnish protected area network (36,942 km^2) (Fig. 1a). The data were com-piled in an earlier project and are a combination of polygons ex-tracted from the WDPA 2005 (World Database on Protected Areas, IUCN and UNEP, 2005) and from the archives of the Finnish Environmental Institute (see details in Appendix A). Although more recent versions of WDPA are available, we have found that there are still considerable errors in the records for Finland such as missing areas (especially in North-Finland), wrongly shaped sites and duplicated records even in the newest version of 2011. After careful comparisons we have concluded that the protected area network data used in this study is more accurate than the one provided by WDPA alone and therefore provides a more com-prehensive representation of the existing network.

All records that included discontinuous sites were divided into individual protected areas and adjacent protected areas were joined and considered as single protected areas, increasing the number of sites to 6613. Following the steps of Rodrigues et al. (2004b), we excluded from the analyses all sites smaller than 1 km^2 (100 ha) as they are likely to have a negligible role in con-serving intact communities of vertebrate species (although they may play other important roles within a protected area network, for discussion see Rodrigues et al., 2004b; Gurd et al., 2001). Areas designated as gray seal reserves (n = 5) were also excluded because they are mostly open water. Exclusion of gray seal reserves and