

# Hot spots, indicator taxa, complementarity and optimal networks of taiga

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If hot spots for different taxa coincide, priority-setting surveys in a region could be carried out more cheaply by focusing on indicator taxa. Several previous studies show that hot spots of different taxa rarely coincide. However, in tropical areas indicator taxa may be used in selecting complementary networks to represent biodiversity as a whole. We studied beetles (Coleoptera), Heteroptera, polypores or bracket fungi (Polyporaceae) and vascular plants of old growth boreal taiga forests. Optimal networks for Heteroptera maximized the high overall species richness of beetles and vascular plants, but these networks were least favourable options for polypores. Polypores are an important group indicating the conservation value of old growth taiga forests. Random selection provided a better option. Thus, certain groups may function as good indicators for maximizing the overall species richness of some taxonomic groups, but all taxa should be examined separately.

**Keywords:** biodiversity; hot spots; indicator taxa; nature conservation; reserve selection; taiga forests

## 1. INTRODUCTION

Hot spots are centres of exceptional biological wealth and have high conservation value (e.g. Myers 1988; Prendergast *et al.* 1993; Lombard 1995). High congruence in species richness is also interesting from an evolutionary perspective (Howard *et al.* 1998; Williams 1999). Detailed biodiversity inventories have been shown to represent a very good conservation investment (Freitag & Van Jaarsveld 1998; Balmford & Gaston 1999). However, if hot spots for different taxa coincide, priority-setting surveys in a region could be carried out more cheaply by focusing on one or two indicator taxa (Lombard 1995; Dobson *et al.* 1997). Several studies demonstrate that (i) hot spots do not usually represent all species; (ii) hot spots of different taxa infrequently coincide; and (iii) hot spots for some taxa often coincide with cold spots for others (Prendergast *et al.* 1993; Curnutt *et al.* 1994; Lombard 1995; Mugo *et al.* 1995; Dobson *et al.* 1997; Howard *et al.* 1998; Van Jaarsveld *et al.* 1998). Lack of the high congruence in hot spots is insufficient justification for rejecting the use of indicator taxa for reserve selection because a network of sites may complement one another biologically (Ryti 1992; Balmford 1998; Howard *et al.* 1998). When hot spots and complementary networks have been compared, conservation areas based on hot spots have rarely coincided with complementary reserves (Williams *et al.* 1996; Reid 1998). For instance, this has been noted for several taxa in the tropics (Lombard 1995; Mugo *et al.* 1995; Lawton *et al.* 1998; Van Jaarsveld *et al.* 1998). In addition, complementary sets across taxa have rarely overlapped (Sætersdal *et al.* 1993; Van Jaarsveld *et al.* 1998). The results indicate that complementary selection may favour areas that are at the edge of species distribution ranges (e.g. Lombard 1995), and that ecological requirements of different taxa may not show similar

responses to major changes in habitat (Lawton *et al.* 1998). Complementary networks of different taxa may not overlap, but the species composition of the taxa may show a nested subset pattern. The species composition can be said to show a nested subset pattern if the species present in small biotas are also present in richer ones (e.g. Worthen 1996). Nested subset analysis can provide information about community structure. For instance, rare species might be indicators of total species richness because they would typically occur only in species-rich communities (Worthen 1996).

Balmford (1998) noted that priority sites for individual taxa may not overlap, but it is essential that priority sites for an indicator group contain high total biodiversity. Indicator taxa should be selected carefully so that they are taxonomically well characterized and easy to measure or observe (e.g. Noss 1990; Kremen 1994). A recent study from Uganda showed that some groups could indicate the overall conservation importance of forests (Howard *et al.* 1998). Complementary networks based on one group captured species richness in other groups as well as networks selected using information on all taxa at once. The extent to which data on a single taxon can be used to establish an efficient network for conserving all groups may depend on the extent to which hot spots overlap among taxa, but also on the extent to which complementary networks for different taxa overlap (Williams *et al.* 1996). This point has only recently been recognized, and remains almost completely untested (Howard *et al.* 1998).

A hierarchy of hot spots can be defined from global, regional, national and local to specific priority sites (Myers 1988; Mittermeier & Myers 1988). The selection of conservation areas in Fennoscandia covers a small number of sites at fine geographical scale. We used data on four taxa (beetles, Heteroptera, polypores and vascular plants) to examine hot spots, complementary conservation areas and optimal networks of boreal taiga forests (Csuti *et al.* 1997). We tested how well priority

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Table 1. *Number of species (average  $\pm$  s.d.) in each taxonomic group in individual study areas and the total number of species*

taxon	no. of species in study sites	total no. of species
beetles	122 ( $\pm$ 34.0 s.d.)	382
Heteroptera	10 ( $\pm$ 1.5 s.d.)	63
polypores	7 ( $\pm$ 0.5 s.d.)	29
vascular plants	44 ( $\pm$ 3.4 s.d.)	172
total no. of species		646

networks based on a single indicator taxon and on all groups represent biodiversity as a whole. In addition, we explored the extent to which these networks capture individual taxa. Our analysis should not be taken as a measurement of how much land must be protected to conserve each taxon but rather as an approximate indication of the success of a reserve network to capture different taxa.

## 2. MATERIAL AND METHODS

### (a) Study sites

Old-growth taiga forests in Fennoscandia support many rare and threatened species and comprise one of the most valuable land types in the area (Anonymous 1996). We used data from 16 old-growth forests, most of which are nature reserves (Suomi *et al.* 1997). In each forest we had study plots of equal size and applied exactly the same techniques in data collection. Eight study sites were located in Finland; five were on islands and three on the mainland. Eight study sites were identified in Sweden; four on islands and four on the mainland. The unique nature of this region has come about due to the exceptionally rapid post-glacial uplift of land and thus, forest habitats have developed heterogeneous biotas. Study areas were surveyed twice in the summer. The forests in Finland were surveyed during 1995 and in Sweden during 1996. Study plots were randomly selected. In each forest the data were collected from four study plots (100 m  $\times$  100 m). Consequently, the total study area in each site was 4 ha. We used pooled data from the four plots to determine species richness for each taxon: beetles (Coleoptera), Heteroptera, polypores or bracket fungi (Polyporaceae) and vascular plants (table 1). Insects were collected using four methods: one window trap per study square (Rutanan 1994), eight pitfall traps per study square (Southwood 1978), sweep nets from trees, bushes and wands, and visual searching for Coleoptera and *Ardus* (Heteroptera) from polypores, dead tree trunks and animal dung (total of 16 h in

each forest). The total number of species in all groups was 646.

### (b) Selection of priority sites

The selection of priority sites was based on species richness defined as the number of species per study site. A computer program selected networks ranging from one to 16 old-growth forests using an optimizing algorithm (Sætersdal *et al.* 1993; Csuti *et al.* 1997), a heuristic procedure (Pressey & Nicholls 1989; Pressey *et al.* 1993; Williams 1999) and random selection. The computer program calculated cumulative species richness for each taxon and for all groups combined. The selection methods proceeded as follows.

The optimizing algorithm selected all the possible forest networks with maximum number of species for each indicator taxon. In some cases several networks with the maximum number of species were found (table 2). For each network, the program calculated mean, maximum and minimum values for species richness of the target taxa.

Heuristic algorithm used data on species richness of all four taxa combined and proceeded iteratively: (i) the first step selected a forest with the highest species richness; (ii) all selected species were removed from further selections; (iii) species richness was recalculated for each remaining forest; and (iv) the program selected the forest with the highest recalculated species richness, etc. In the case of ties, the program used the total number of species initially recorded from each study site. In the case of further ties, it used random selection. The selection continued until all species (or all sites) were selected.

The null hypothesis might be that results of reserve selection may have occurred by chance. We tested the success of reserve selection by comparing each selected network to the results of random selections. We used 19 random selections to calculate a 95% empirical confidence interval. Random selection was calculated for each network separately. Hot spots were ranked in the order of highest overall species richness.

## 3. RESULTS

We compared conservation areas identified by means of richness hot spots based on all groups to complementary conservation networks (Williams *et al.* 1996). The success of each network in encompassing different taxa was examined. Due to economical or political constraints only some of the candidate sites can often be purchased for protection. For instance, we selected priority sets of four (25%) forests by a hot spot analysis and a complementary algorithm. The network of four hot spots covered 389 species (60%) in total, whereas the total number of species in the complementary network was 414 (64%).

Table 2. *The number of all the possible optimal solutions for each indicator taxon. The number of sites in networks vary from one to 16 taiga forests*

indicator taxon	number of sites in an optimal network															
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
beetles	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1
Heteroptera	1	1	1	1	1	5	4	12	13	6	1	4	6	4	1	1
polypores	1	3	2	3	4	27	52	48	22	4	18	34	35	21	7	1
vascular plants	1	1	1	1	2	1	1	2	1	3	2	5	4	1	2	1

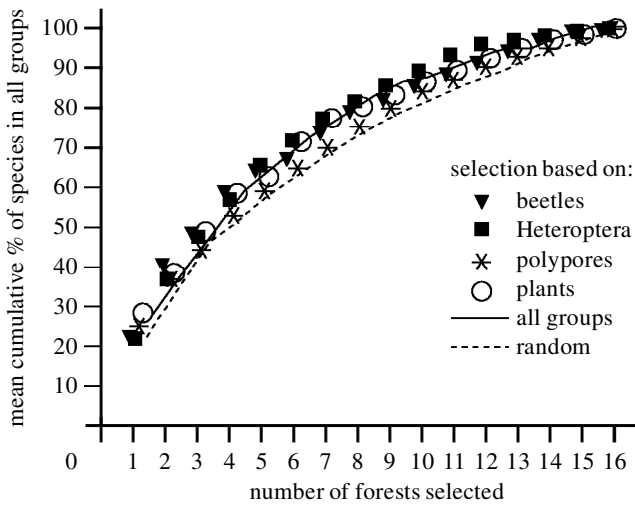


Figure 1. Mean cumulative number of species in all four groups (beetles, Heteroptera, polypores and plants) as a function of cumulative number of sites in network. Networks were selected using optimizing algorithm for a single taxa, heuristic iterative algorithm for all groups together and random selection.

Closer analysis of the networks revealed that the hot spot areas encompassed 58% of beetles, 56% of Heteroptera, 48% of polypores and 70% plants, and complementary networks represented 63%, 62%, 41% and 71%, respectively. Priority sets of eight (50%) taiga forests selected by the hot spot analysis covered 514 (80%) of the total 646 species, and those selected by heuristic algorithm contained 553 (86%) species.

We also studied the optimal networks for maximizing species richness for each taxon. Overlapping sites were identified between Heteroptera and vascular plants, and beetles and vascular plants. Only one site coincided in the optimal networks for beetles and Heteroptera, and for Heteroptera and polypores. Hot spots of species richness may be insufficient for testing the ability of one taxon to indicate the overall value of different sites (Howard *et al.* 1998). When we examined how well optimal sets based on one taxon capture the diversity of all groups combined, we found that most sets of priority forests based on one group captured species richness of all groups with the same efficiency as using information on all taxa simultaneously (figure 1). All four taxa performed better than random selection regardless of the number of selected sites. Beetles, Heteroptera, plants and all groups produced

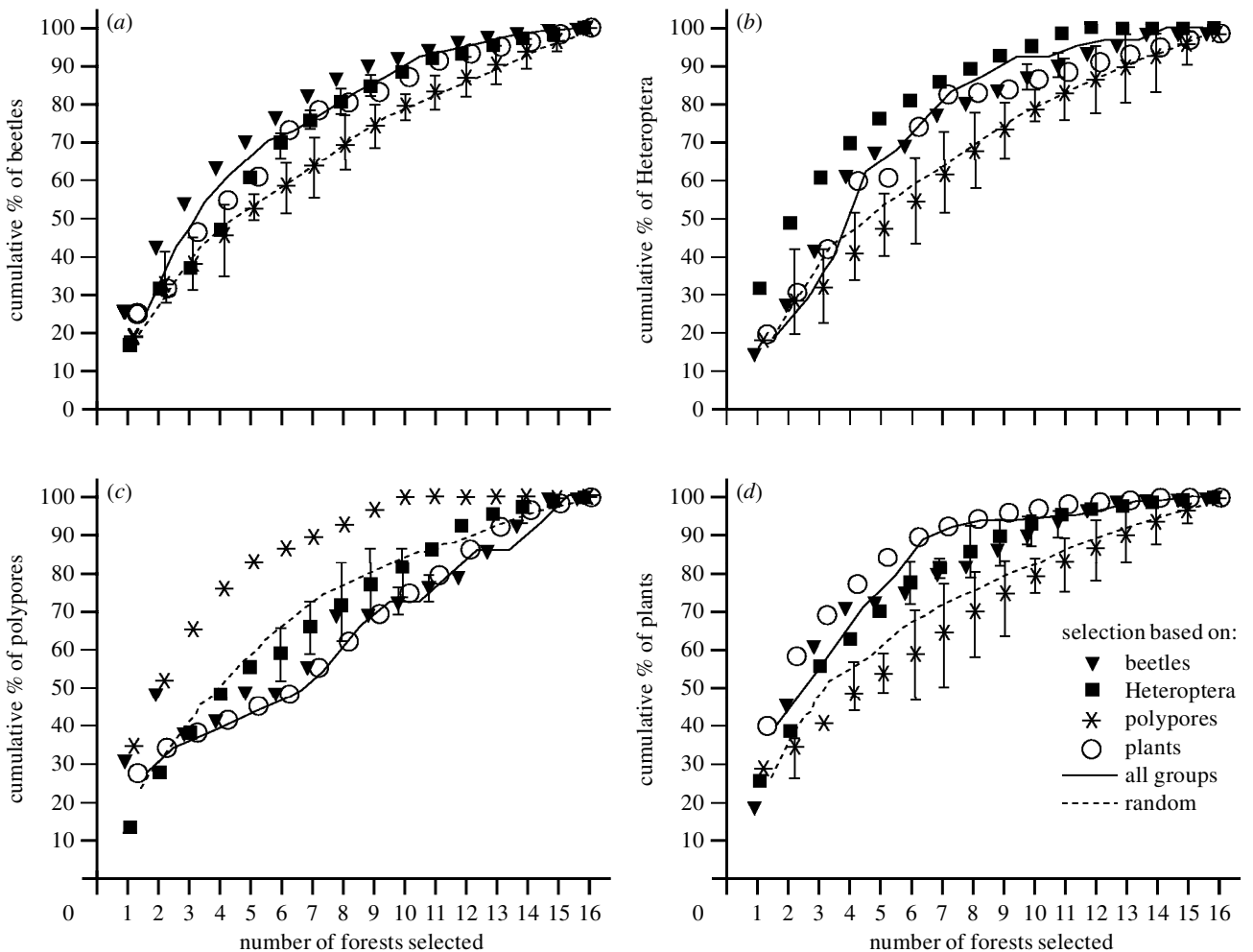


Figure 2. Cumulative percentage of species as a function of cumulative number of sites in network (a) beetles, (b) Heteroptera, (c) polypores and (d) vascular plants. Networks were selected using optimizing algorithm for a single taxa, heuristic iterative algorithm for all groups together and random selection. All possible options for optimal solutions are shown. Bars indicate minimum, maximum and average species richness of a target taxon captured by optimal network of the indicator taxon.

almost similar results. Selection based on polypores was the least favourable option. For instance, the best option for an optimal network of eight (50%) forests was selected using data on Heteroptera and it covered 82% all 646 species. The least favourable option was randomly selected network that encompassed 74% of all species (figure 1). The difference between the best and the least favourable options was 51 (8%) species.

Optimal networks for individual taxa were efficient in covering the total species richness, but these networks did not represent all taxa equally. The priority networks for beetles, Heteroptera and vascular plants supported one another relatively efficiently (figure 2*a,b,d*). The network based on all groups was more efficient than networks based on beetles or Heteroptera in containing high plant species richness. All these networks performed better than random selection, but they were poor in capturing high species richness of polypores (figure 2*c*). Only the optimal network of two forests for beetles represented polypores well, but when the number of sites increased, random selection provided a better option. In addition, selection based on all groups was among the least favourable options.

#### 4. DISCUSSION

Our survey supported previous findings that hot spots for some taxa coincide with cold spots for others, and that hot spots and complementary networks rarely coincide (Howard *et al.* 1998; Lawton *et al.* 1998; Van Jaarsveld *et al.* 1998). The success of hot spots analyses might depend on the fragmentation of the landscape and the geographical scale under consideration (Curnutt *et al.* 1994; Dobson *et al.* 1997). A study on British birds compared the total coverage of birds in various reserve systems. It showed that complementary networks give the best results, followed by rarity hot spots, followed by species richness hot spots (Williams *et al.* 1996). The reasons for preferring one measure to another depend upon the goals one is trying to fulfil. The use of different measures in area selection is bound to give different answers.

Certain groups may function as good indicators for reserve selection in areas like Uganda, which are characterized by high biogeographical heterogeneity (Howard *et al.* 1998). Howard *et al.* (1998) state that temperate regions are less heterogeneous and relatively species poor, and therefore, complementary areas for indicator taxon may capture diversity in other groups less well. However, our study on boreal taiga forests showed that most sets of priority forests based on one group captured the species richness of all groups with the same efficiency as using information on all taxa at once. In particular, Heteroptera performed well, and high richness of vascular plants indicated high insect species richness in taiga forests. We also found that optimal networks for beetles, Heteroptera and plants supported high species richness of all other groups than polypores. An especially inefficient option for covering polypores was an optimal network based on data on all groups. One explanation may be that the habitat requirements of polypores differ from those of other taxa. In addition, polypores represented only 4% of the total number of species in the old-growth forests. The result indicates that when complementary

networks are selected, taxa with a proportionally small number of species should be analysed separately. Our results were obtained using data on boreal taiga forests and may not be applied to other habitat types or geographical locations. It should not be assumed that richness in one taxon always indicates high richness in another, and therefore, identification of indicator taxa requires careful analysis of the distributions of each target taxa.

Efficient conservation systems incorporate hot spots, sites that efficiently complement the network (Williams *et al.* 1996; Howard *et al.* 1998) and sites that maintain biodiversity in the long term (Virolainen *et al.* 1999). We agree with a previous study (Howard *et al.* 1998) that when possible indicators for reserve selection are evaluated, both cross-taxon congruence in complementarity and species richness should be considered. Indicator taxa may be sufficient in selecting conservation areas with high overall diversity, and we emphasize the need to ensure that these areas also capture the high species richness of different taxa separately.

We thank R. Alatalo, A. S. van Jaarsveld and an anonymous referee for the valuable comments. The Finnish Biodiversity Research Programme, the Academy of Finland and the Green Bridge of the Quark Project funded the study.

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