

## Patterns of commonness and rarity in central European birds: reliability of the core-satellite hypothesis within a large scale

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The frequency distribution of species' area of occupancy is often bimodal, most species being either very rare or very common in terms of number of occupied sites. This pattern has been attributed to the nonlinearity associated with metapopulation dynamics of the species, but there are also other explanations comprising sampling artifact and frequency distribution of suitable habitats. We tested whether the bimodal frequency distribution of occupied squares in central European birds could be derived solely from the frequency distribution of species population sizes (i.e. the sampling artifact hypothesis) or from the spatial distribution of their preferred habitats. Both models predict high proportion of very common species, i.e. the right side of frequency distribution. Bimodality itself is well predicted by models based on random placement of individuals according to their abundances but neither model predicts the observed prevalence of rare species. Even the combined models that assume random placement of individuals within the squares with suitable habitat do not predict such a high proportion of rare species. The observed distribution is more aggregated, rare species occupying a smaller portion of suitable habitat than predicted on the basis of their abundance. The pattern is consistent with metapopulation processes involving local population extinctions. The involvement of these processes is supported by two further observations. First, species rarity is associated with significant population trend and/or location on the edge of their ranges within central Europe, both situations presumably associated with metapopulation processes. Second, suitable habitats seem to be either saturated or almost unoccupied, which is consistent with the predictions of the metapopulation model based on nonlinear dynamics of extinction and colonization. Although the habitat suitability is an important determinant of species distribution, the rarity of many species of birds within this scale of observation seems to be affected by other factors, including local population extinctions associated with fragmentation of species' habitats.

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Although the distribution of species abundances within an area is mostly approximately lognormal (Preston 1960), the frequency distribution of species' area of occupancy is often bimodal, most species being either widely distributed or rare (Hanski 1999). This pattern has been documented already in 1910 (Raunkiaer 1910) and since then it has been observed in many taxa and

many regions (Hanski 1999). Although there are so many exceptions that the pattern can not be considered as a rule, it is so common that it must be treated seriously.

There are three main hypotheses concerning the pattern. The first one proposes that the pattern is only a statistical byproduct of species abundance distribution

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(Nee et al. 1991, Papp and Izsak 1997). Since species abundances have lognormal or log-series distribution, most species are rare, and thus occupy also a small proportion of an area. On the other hand, when species abundances reach some limit (that depends on spatial scale of sampling), they have high probability of occupying most suitable sites. Thus, species occupy either small proportion of sampling units, because most species have low abundances, or high proportion of them, because even slightly more common species easily reach the limit of “saturation” of most of sampling units. The hypothesis has been tested by numerical simulations, assuming random spatial distribution of individuals, but its applicability to the situations where distribution of individuals is somehow constrained by habitat suitability and local populations of a species are independent to each other has been questioned (Hanski 1999). Moreover, even if bimodality is simply by-product of distribution of species abundances, it is not clear to what extent the sampling effect resemble the exact pattern of commonness and rarity expressed in terms of proportion of area occupied.

Hanski (1982) proposed another hypothesis. Bimodal distribution results, according to his hypothesis, from the nonlinearity associated with population-extinction dynamics. The per-population extinction rate decreases with proportion of occupied patches due to rescue effect. Thus, a large proportion of occupied patches leads to increasing colonization rate/extinction rate ratio (and accordingly many species occupy most of suitable patches), whereas a small proportion of occupied patches is not sufficient for colonizing other patches and even can not be sufficient for population persistence. The hypothesis predicts that most species will be either common or rare even if all species are identical, and moreover, that species can shift their status from the “core” to the “satellite” class and vice versa. Further modification of the hypothesis (Hanski and Gyllenberg 1993) assume interspecific and inter-patch differences, such that some patches serve as refuges for the satellite species.

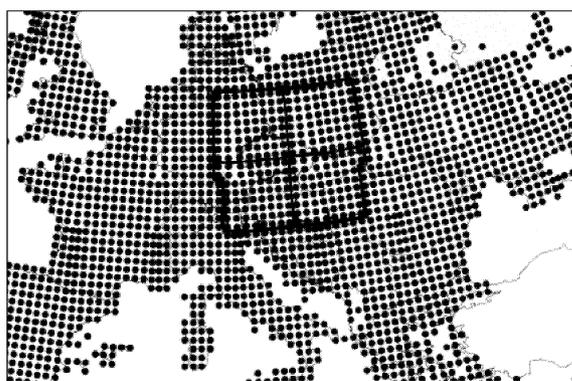


Fig. 1. Location of the central European study area. The dots represent individual mapping squares.

The third hypothesis is based on niche requirements of species. Brown (1984) suggested that habitat specialists occupy low proportion of patches, whereas generalists are widespread. However, it is not clear why the resulting pattern should be bimodal. Gaston (1994) claimed that the bimodal pattern is apparent within smaller and less heterogeneous areas, where the spatial autocorrelation of environment is relatively high and the sampling units are similar to each other. In this environment many species should live in most of patches, whereas some species with narrow requirements are rare, because their habitats are rare within such spatially autocorrelated environment.

These three hypotheses have only rarely been tested simultaneously (but see van Rensburg et al. 2000). The testing of “sampling artifact” hypothesis relied almost exclusively on simulation models assuming random placement of individuals within whole area, whereas the “habitat autocorrelation” hypothesis has not been tested at all. We used the data of bird distribution in central Europe within two spatial scales to test the hypotheses, ascertaining that frequency distributions of square occupancy of individual bird species within the Czech Republic, as well as within the whole central Europe are truly bimodal (cf. Novotný and Drozd 2000). Since both the data of population abundances of individual species and real spatial distribution of habitats within the area of the Czech Republic were available, we could compare the observed bird distribution with the models based on spatial distribution of suitable habitat and species population numbers. We also tested whether species “commonness” and “rarity”, respectively, could be attributed to the species characteristics, i.e. habitat suitability, body size, geographic location of species range or population trend, assuming that some of these characteristics associated with commonness and rarity might support particular hypothesis.

## Data material

We analyzed data from two spatial scales: central Europe and the Czech Republic. The detailed data concerning spatial distribution of habitats and population abundances were, however, available only within the smaller spatial scale (the Czech Republic), and therefore all the detailed analyses were performed on this scale of resolution.

Analyses of occupancy patterns within the large scale, i.e. the central Europe, was based on the EBCC Atlas of European Breeding Birds (Hagemeijer and Blair 1997). We defined “central Europe” for the purposes of our analyses as ca 800 × 800-km square containing 256 50 × 50-km mapping squares (16 × 16 squares) (see Fig. 1). It covers the Czech Republic and

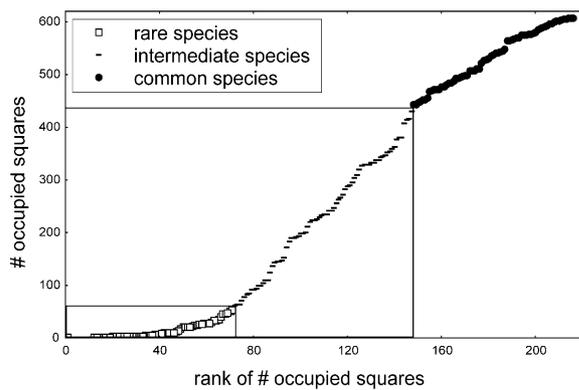


Fig. 2. Classification of species according to their location within frequency distribution of number of occupied squares, here revealed by rank-occupation plot. The three groups were denominated using the breakpoints in the relationship.

the Slovak Republic, most of Poland, Austria and Hungary, eastern part of Germany, and small proportion of northern Italy and Slovenia. The selected area was chosen such that all  $50 \times 50$ -km squares were well covered by species and no square included coastal areas. Data of species distribution within the Czech Republic has been obtained from the Atlas of breeding distribution of birds in the Czech Republic 1985–1989 (Štátný et al. 1996). The birds were mapped on 628  $12 \times 11.1$ -km squares. Because several squares were underrepresented, only 616 squares have been used for further analyses. Only records of probable or confirmed breeding were included in the analyses.

The estimated maximum and minimum population abundances of species living in the Czech Republic were obtained from Hudec et al. (1995). Presence/absence of habitat types on individual squares was taken from CORINE Land Cover Database based on satellite imagery data. Some of the 37 land cover types originally recognized in the database have been joined together in such a way that resulting 17 habitat types represent habitats distinctly occupied by birds (see Appendix). Each square was also characterized by minimum and maximum altitude.

## Methods

The bimodality of square occupancy distribution was tested according to Tokeshi (1992). The significance was calculated as a probability that left and right peak of the distribution, respectively, would reach the observed values by chance. In the first step, we used the multinomial distribution for calculation the probability that the outer peaks of the distribution would contain the number of species that is equal or higher than the observed number by random selection from a set of all possible measurements (with given total number of

species). In the second step, the probability was calculated (using binomial distribution) separately for both left and right peaks of distribution (Tokeshi 1992).

Habitat suitability for each species was estimated using presence/absence of individual habitat types within the squares (determined by Land Cover Database), and the knowledge of breeding habitats of individual birds. There is a risk of circularity since the breeding habitats are dependent on species distribution. We eliminated this risk as much as possible using information that is not based on the atlas data, i.e. from Hudec and Černý (1977) and Hudec (1983, 1994), and by using habitat types whose suitability for the species is easy to determine (see Appendix). The number of squares with suitable habitat was calculated as the sum of squares in which at least one breeding habitat type of respective species was present, and where the altitudinal extent of the square overlapped with the breeding altitudinal extent of the species.

Simulation models based on data of estimated population sizes (see Appendix) randomly distributed corresponding number of individuals among the mapping squares according to the probability of square occupancy. We tested three models: 1) random model, where individuals were distributed randomly within all the squares (the probability of square occupancy by an individual was  $1/N$ , where  $N$  is total number of squares), 2) habitat-constrained model, where respective number of individuals was randomly distributed only within the subset of squares with suitable habitat (the probability of square occupancy by an individual was zero for squares with no preferred habitat type, and  $1/N_{SH}$  for all other squares, where  $N_{SH}$  is number of squares with suitable habitat), and 3) habitat area model, where the probability of square occupancy was proportional to the total area of suitable habitat within a square (the probability of square occupancy by an individual is  $P_i/\Sigma P_i$ , where  $P_i$  is the area of suitable habitats within a square and  $\Sigma P_i$  is total area of suitable habitats within the Czech Republic).

All models were compared with real data in terms of frequency distribution of square occupancy and the correlation between predicted and observed number of occupied squares. One hundred runs of all models were performed for both maximum and minimum estimates of species population sizes. Significance of model prediction therefore could be estimated simply as a proportion of simulation runs that reach the observed values of number of species within individual frequency classes.

For relating species rarity or commonness, respectively, to species characteristics, we choose multivariate canonical correspondence analysis (ter Braak 1993). We classified all species to three groups according to their number of occupied squares (see Fig. 2) and tested whether the differences in species composition between the three groups was significantly affected by following

species characteristics: 1) Body weight (BW) – data from Hudec and Černý (1977) and Hudec (1983, 1994). 2) Number of squares with suitable habitats (SUIT) – see above. 3) Geographical bias, indicating whether the Czech Republic is located on the edge of species range. It was calculated from the central European data set, as a correlation between latitude and longitude, respectively, and number of occupied patches within a row or column in the square representing central Europe (longitudinal or latitudinal band). Two indices were derived: SOUTHBIAS (negative value of correlation of latitude and number of occupied squares within longitudinal bands, indicating increasing occupancy toward the south), and MAXBIAS (maximum of absolute values of both correlation coefficients, indicating maximum strength of the bias). 4) Population trend (TREND) Each species was assigned by a qualitative index of population trend, using information from Št'astný et al. (1996) (0 = no apparent trend; 1 = increasing or decreasing population size, 2 = rapidly expanding or vanishing species range).

All interspecific comparisons can be in principle biased because individual species do not represent statistically independent units due to their phylogeny (Harvey and Pagel 1991). No statistical tests directly filtering out the effect of phylogeny in canonical multivariate analyses were available, however, we partially filter out such effects by setting individual bird taxa (orders) as covariables and performing the Monte Carlo tests within blocks determined by these covariables. We also tested the effect of individual variables by the Forward Selection procedure (ter Braak 1993).

## Results

### Patterns of species square occupancy

The frequency distribution of number of occupied squares is apparently bimodal in both spatial scales (Fig. 3). The bimodal pattern is statistically significant in both cases ( $p < 0.0001$  except the right peak in the Czech Republic where  $p < 0.05$ ) and is even more pronounced in the scale of whole central Europe. The bimodality was apparent even if frequency distribution within each quarter of the central European study area was analyzed separately, indicating that the pattern is not attributable to some specific geographic location of the study plot.

Number of occupied squares within the smaller scale correlates well with the number in the other scale (Spearman rank order correlation  $r_s = 0.922$ ,  $p < 0.001$ ): rare species (in terms of number of occupied squares) in the Czech Republic are generally also rare in the central Europe as a whole. It allowed us to perform all the detailed analyses only within the smaller scale, assuming that similar processes are responsible for the patterns in both scales.

### Patterns in habitat spatial distribution – the habitat suitability model

The frequency distribution of habitat suitability for individual bird species is multimodal rather than bimodal (Fig. 4). Moreover, although the number of squares with suitable habitat correlates significantly with num-

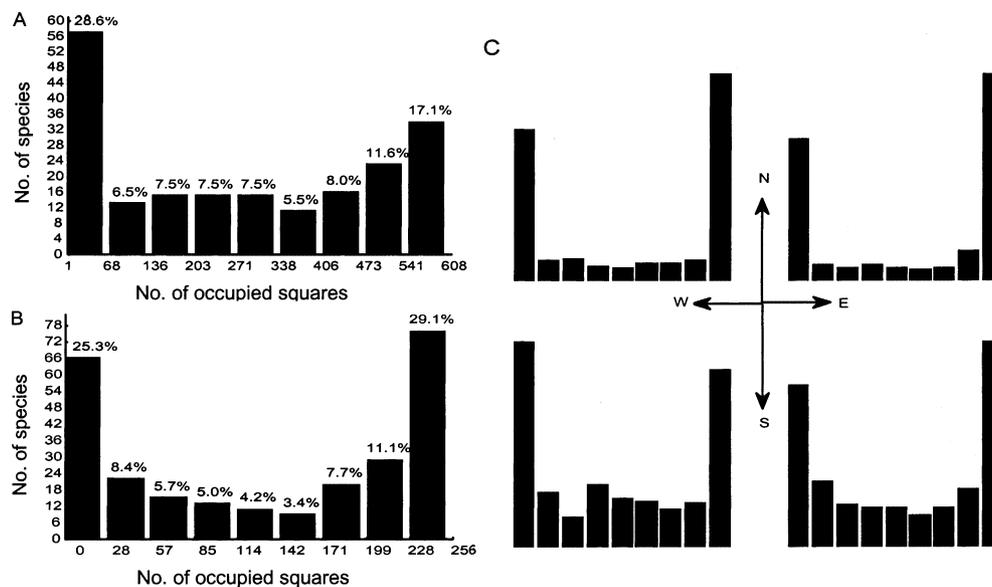
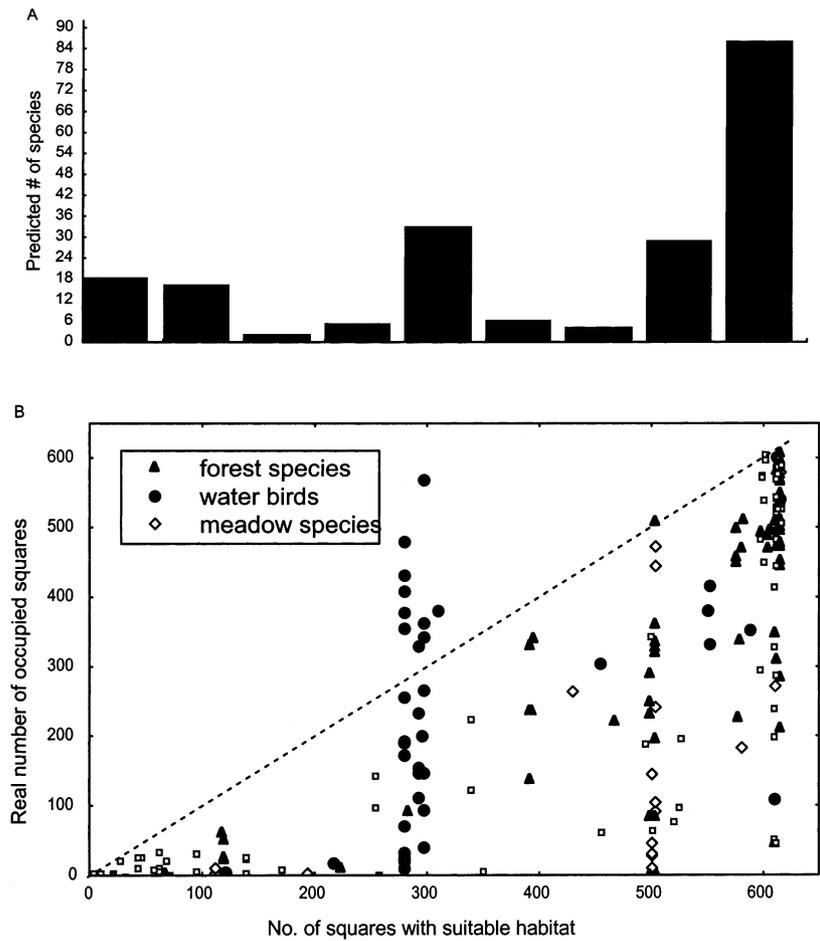


Fig. 3. Frequency distribution of the number of occupied squares in the Czech Republic (A), central Europe (B), and four quarters of the central European study plot (C), ordered according to their location within the central European plot (see Fig. 1).

Fig. 4. Frequency distribution of number of squares with suitable habitat for each species (A) and the relationship between the number of squares with suitable habitat and observed number of occupied squares (B). Three groups of species generally differing in habitat preferences are marked. The diagonal line represents a theoretical upper boundary, where no. of squares with suitable habitat = no. of occupied habitat. Note that many water bird species occupy more squares than those with suitable habitat, probably because small water bodies were not detected using satellite data.



ber of occupied squares ( $r_s = 0.807$ ,  $p < 0.001$ ), it is apparent that habitat is a poor predictor of square occupancy in many cases. The prediction for species inhabiting water bodies seems to be especially wrong. The number of squares occupied by water birds ranged from very few to almost all squares, and observed number of occupied squares was in this case often even larger than the habitat-based prediction, probably due to the inability to record the small water bodies within many squares by satellite data. Also species inhabiting meadows were generally rarer than predicted by the relative commonness of meadows within the Czech Republic. On the other hand, species whose habitats were present within most of the squares were almost as widespread as predicted. Perhaps the most important point is that all the species whose habitats were present on less than one-third of all squares were very rare regardless on their habitat requirements and exact predicted number of squares. Generally, the prediction based on habitat suitability differed from the observed number of occupied squares more strongly in rare species (Fig. 5): the standardized deviation between the habitat model and real data correlates negatively with number

of squares with suitable habitat ( $r_s = -0.647$ ,  $p < 0.001$ ). Moreover, the deviation itself has bimodal distribution ( $p < 0.0025$  for the peak of the smallest deviation and  $p < 0.015$  for the other extreme), indicating that habitats were either saturated or almost unoccupied.

#### Patterns of square occupancy predicted by abundance

Abundance-based models of square occupancy generally predicted bimodality (Fig. 6). Random models that did not assume unequal amount of suitable habitat failed to predict several small peaks apparent within real data, but those peaks arose when the unequal suitability of squares was included in the model. Only the habitat area model that assumed that probability of square occupancy was proportional to the total area of suitable habitat, predicted the right peak of occupancy distribution quite realistically (although it was still significantly higher than observed) – the other models strongly overestimated the right peak. The proportion of very rare species remained significantly lower than observed in all the models: even maximum values

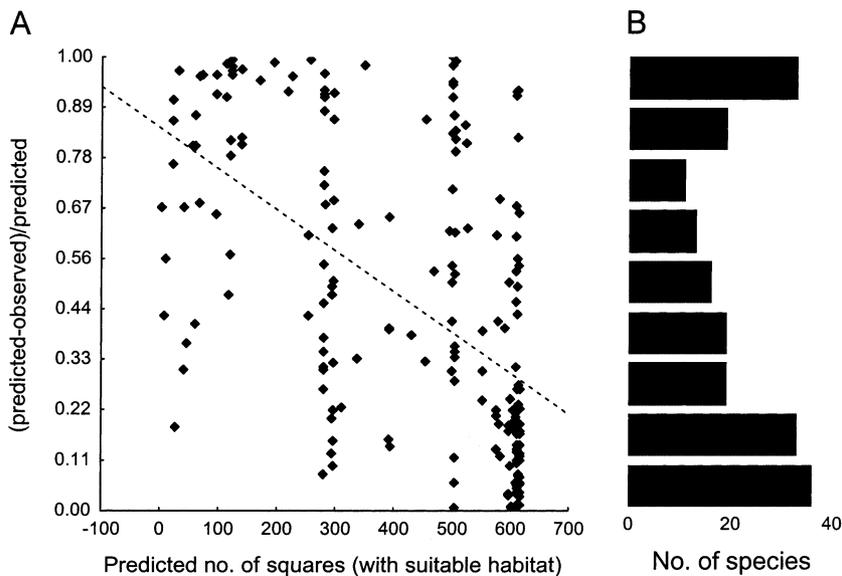


Fig. 5. Relationship between number of squares with suitable habitat and the standardized deviation between this number and the observed number of occupied squares, calculated as an absolute value of  $(\text{predicted-observed})/\text{predicted}$  (A), and frequency distribution of the deviation (B).

from the 100 runs of the simulations did not reach the observed values in this frequency class. On the other hand, adding habitat suitability improved the reliability of the model. The distribution of square occupancy was more similar to the real distribution, and the correlation between observed and predicted number of squares for each species was higher when habitat suitability was included in the model and the highest when the habitat area was considered (Fig. 7).

### Correlates of commonness and rarity

The differences between common, rare, and intermediate species were attributable mainly to the suitability of

habitats (Fig. 8) – not surprisingly, the first axis correlating with habitat suitability ordinate species groups from the rare to the common (73.9% of explained variance). However, the second axis that correlated mainly with indices of geographic bias and population trend, separated the moderately common species from both the common and rare groups (26.1% of explained variance). The Forward Selection Analysis (Table 1) showed that the effect of indices of geographic bias and population trend remained significant even if the effect of habitat suitability had been factored out and after other indices had been factored out by a step-by-step manner. Therefore, although habitat suitability appeared as a main factor determining the number of occupied sites, both geographic location of species

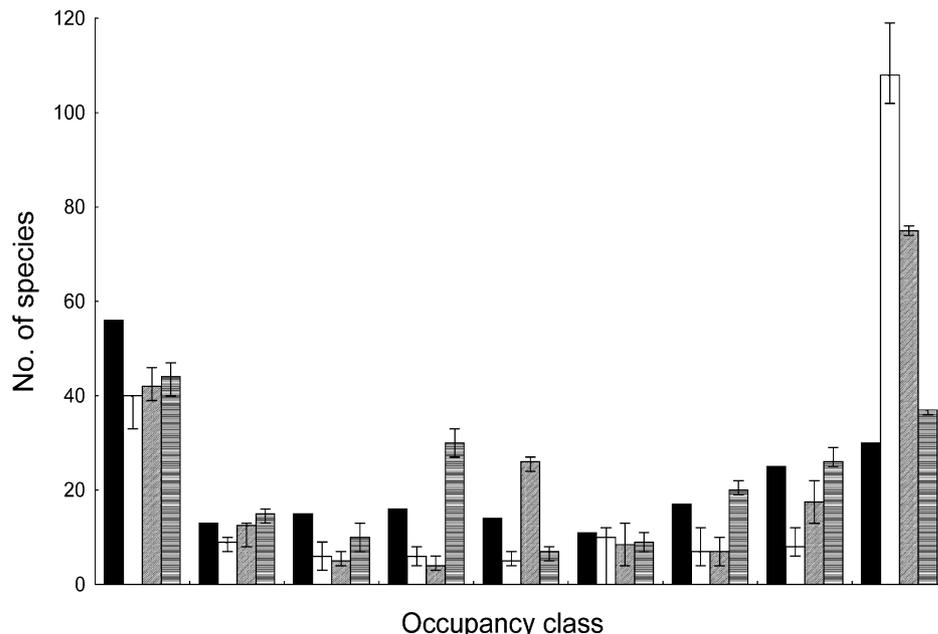


Fig. 6. Comparison between real frequency distribution of number of occupied squares and the number predicted by the models based on random or constrained location of individuals according to their abundance. Legend: filled bars – real data; open bars – random model; dashed bars – habitat constrained model; stripped bars – habitat area model. The error bars show the maximum and minimum values from all simulation runs for each frequency class.

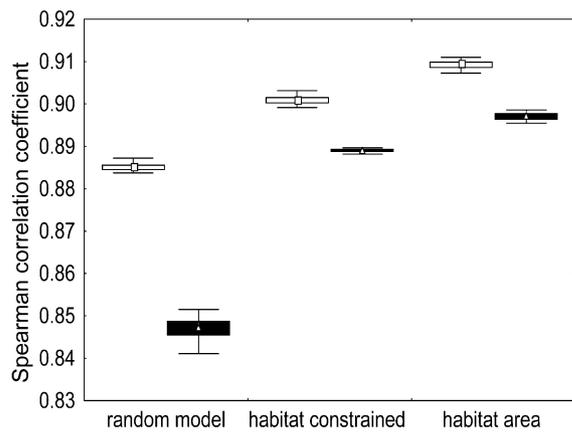


Fig. 7. Ranges of correlation coefficients between observed species square occupancy and those predicted by the three classes of simulation models for models based on minimum (open boxes) and maximum (filled boxes) estimated population sizes, respectively.

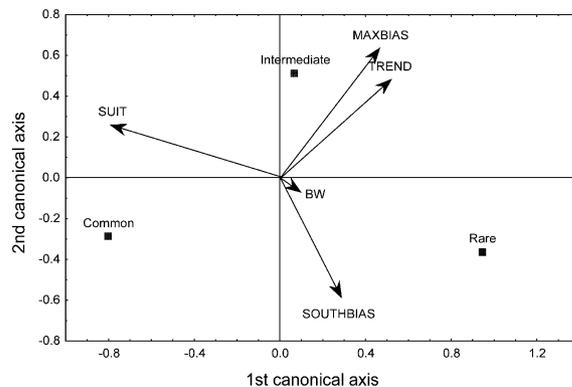


Fig. 8. The ordination plot showing results of canonical correspondence analysis. The first ordination axis represents the gradient from common species, whose habitats are widespread, to rare species that reveal some geographic bias and population trend. The second axis discriminates the intermediate species with stronger population trend and higher strength of geographic bias. Interestingly, these species are negatively associated with SOUTHBIAS, indicating that most of them are, on the contrary to rare species, more common in the northern part of Europe (see also Fig. 9).

range and population trend affected resulting distribution of occupied patches. Rare species could be generally characterized by lower habitat suitability, significant population trend and/or increasing number of occupied patches toward the south of Europe. On the other hand, the intermediate species also revealed population trend and geographic bias in number of occupied squares, but the negative association with SOUTHBIAS indicated that they were more common in the northern part of Europe. It was confirmed by plotting species number of each group in differently located squares within central Europe (Fig. 9).

## Discussion

We have documented the bimodal site occupancy distribution on a large spatial scale, probably the largest ever considered in the studies concerning the core-satellite hypothesis. Many potentially possible explanations of the pattern (Gaston 1994, van Rensburg et al. 2000) therefore do not seem relevant. For instance, the pattern can not be attributed to pure sampling bias and/or small number of sample sites (Williams 1964), since data comprising both rare and common species have been collected repeatedly by many observers within very large scale of observation. Similarly, the “satellite” mode cannot represent a “tourist” species only incidentally occurring within study area (Nee et al. 1991), because the data comprise only records of breeding bird species. On the other hand, some sensitivity of scale of observation was detected. Within the central Europe study area, the number of species in “satellite” mode was roughly equal to the number of “core” species, whereas within the smaller scale of observation the satellite species prevailed, according to observation of Williams (1964). We did not confirm, however, the observation that the incidence of bimodality decrease with an increase in the spatial extent covered (Gaston 1994, Gaston and Blackburn 2000, van Rensburg et al. 2000).

It is evident that the bimodal distribution of square occupancy is not explainable by habitat suitability and specialist-generalist gradient, because habitat suitability has multimodal frequency distribution rather than bimodal (see Fig. 4). Habitat autocorrelation within smaller scales has been regarded as a major reason why the occupied area has the bimodal distribution only within smaller scales. Gaston and Blackburn (2000), for instance, documented that whereas the distribution was bimodal within the scale of, e.g., Berkshire, it was strongly right-skewed for whole Great Britain. Our data indicate, however, that habitat autocorrelation is

Table 1. Results of the Forward Selection procedure. The variables are ordered according to the additional variance the variable explained, given the variables already included in the model (conditional effect). Lambda-A refers to the increase in sum of all canonical eigenvalues (expressing explained variance) when the variable is added to the model and p-value refers to the significance of the variable at that time (Monte Carlo permutation test). The effect of all variables except the body weight remained significant even if the other variables had been added to the model.

Variable	Lambda-A	p	F
SUIT	0.41	0.005	59.72
MAXBIAS	0.12	0.005	19.87
TREND	0.08	0.005	13.9
SOUTHBIAS	0.02	0.030	3.23
Body weight (BW)	0.00	0.460	0.90

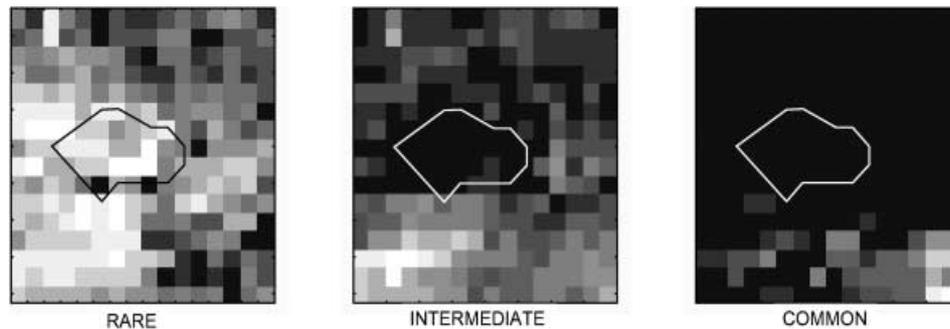


Fig. 9. Number of bird species within individual central European mapping squares according to their classification to the three classes of commonness/rarity within the Czech Republic (white = minimum species number; black = maximum species number). The polygon represents approximate location of the Czech Republic. The species that are rare within the Czech Republic are more frequent in the southeastern and northeastern part of central Europe, whereas the intermediate species are mainly those occupying the northern part of central Europe. Common species occur in most mapping squares except the southernmost part of the area.

not sufficient to explain the pattern, and moreover, that the pattern can occur within much larger scales (the central European study area is larger than the U.K.).

All our models based on random or habitat constrained placement of individuals within squares according to their estimated abundance predicted bimodality. Therefore, the sampling effect itself is sufficient for producing the core-satellite pattern. However, it does not seem that the exact form of the pattern is attributable only to the pure sampling effect. First, the predictive power of most models is low. The model based on solely random placement of individuals did not predict the moderate multimodality that is pronounced in real data, and all models repeatedly underestimated observed proportion of “satellite” species and overestimated proportion of “core” species. Second, it is probable that estimated abundance itself is not a variable independent on biological processes that generate patterns of square occupancy. In fact, Hanski (1982) in his metapopulation model predicted tight interdependency between occupancy and abundance. Therefore, the models based on population sizes do not rule out the role of metapopulation dynamics, because the total population size itself might be a product of the dynamics (Hanski 1992, Hubbell 2001). Moreover, the habitat area model that best fitted to the real data assumed a relationship between habitat area and probability of occupancy, which is inherent in many metapopulation models (Hanski 1999).

Since both habitat suitability and pure sampling effects are not sufficient for the explanation of prevalence of satellite species, and all models overestimate the proportion of core species and underestimate the proportion of satellite species, the species apparently occur on less patches than possible. It could be attributed to the dynamics associated with local population extinction, and the pattern is consistent with metapopulation processes proposed by Hanski (1982). Although the metapopulation processes cannot be directly assessed

from the pattern, this view is supported by the fact that species belonging to the satellite category, and even more those intermediate, are either living on the edge of their range within the Czech Republic, and/or their populations are expanding or vanishing there. Metapopulation structure, i.e. fragmented local populations revealing extinction and recolonization has been supposed to occur both in the range edge and in the time when a species expands its range or is vanishing from the former area of occupancy (Harrison and Taylor 1997).

It does not mean that the species behave exactly as predicted by metapopulation model of Hanski and Gyllenberg (1993). The model assumes strong rescue effect to sustain populations of core species, but it is not necessary to produce the “core” mode in our study – the core species may represent rather a continuous population than any type of metapopulation. On the other hand, the other feature of the Hanski and Gyllenberg model, i.e. the tendency of species occupying only a part of suitable patches to become extinct on many of them, may play a role, as suggested by the fact that habitats are either saturated or very unsaturated, and the habitats that are relatively rare are mostly unsaturated (Fig. 5). Large part of the “intermediate” species, that reveal a population trend, perhaps might represent a transient phase in population dynamics directed either toward occupying all the suitable patches or occupying several refuges or eventually becoming extinct. These intermediate species can ultimately behave as a “core” species in some areas, and “satellite” species in other, according to local conditions, proportion of suitable habitat and total population abundances.

Metapopulation dynamics, although considered relatively unimportant in such a mobile group (Gaston and Blackburn 2000, van Rensburg et al. 2000), may play a considerable role in the occupancy patterns of bird species, because many of them may have a transient dynamics associated with metapopulation processes.







Species	No. of squares		Trend	Estim. no. pairs		Rarity class	Habitat types																Elev.								
	CR	C		Europe	min		max																								
Loc.fluv	333	206	1	10 000	20 000	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	1	0
Loc.lusc	71	172	1	400	750	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
Acr.scho	233	206	0	40 000	80 000	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	0
Acr.palu	444	250	0	80 000	160 000	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Acr.scir	381	233	0	50 000	100 000	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	0	
Acr.arun	191	223	1	1500	3000	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	
Hip.ict	484	220	0	50 000	100 000	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	
Syl.niso	145	190	0	1500	3000	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
Syl.curr	527	249	0	50 000	100 000	3	0	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	
Syl.comm	531	244	0	90 000	180 000	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Syl.bori	478	243	0	200 000	400 000	3	1	0	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	
Syl.atri	569	256	0	600 000	1 200 000	3	1	1	1	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	
Phy.troc	1	6	0	1	5	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Phy.sibi	469	237	0	80 000	160 000	3	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Phy.coll	548	255	0	800 000	1 600 000	3	1	1	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	
Phy.troc	508	218	0	500 000	1 000 000	3	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	
Reg.regu	456	227	0	200 000	400 000	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Reg.igni	248	161	0	50 000	100 000	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	
Mus.stri	494	253	0	30 000	60 000	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	
Fic.parv	92	147	1	800	1400	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Fic.albi	236	136	1	25 000	50 000	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	
Fic.hypo	221	189	1	10 000	20 000	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Pan.biar	22	53	1	100	300	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	
Aeg.caud	507	253	0	55 000	110 000	3	1	0	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Par.palu	488	250	0	60 000	120 000	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	
Par.mont	321	211	1	40 000	80 000	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Par.cris	449	218	0	80 000	160 000	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Par.ater	497	238	0	450 000	900 000	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Par.caer	593	254	0	800 000	1 600 000	3	1	0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	
Par.majo	605	255	0	3 000 000	6 000 000	3	1	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	
Sit.euro	581	254	0	600 000	1 200 000	3	1	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Cer.fami	472	231	0	300 000	600 000	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Cer.brac	330	230	0	75 000	150 000	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Rem.pend	267	219	1	2500	5000	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Ori.orio	338	242	0	8000	16 000	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	0	0	0	
Lan.coll	586	256	0	250 000	500 000	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	
Lan.excu	345	166	0	1000	2000	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
Gar.glan	565	252	0	150 000	300 000	3	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Pic.pica	546	254	1	40 000	80 000	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Nuc.cary	230	109	1	2500	5000	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Cor.mone	339	242	1	10 000	20 000	2	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1	1	0	0	
Cor.frug	48	165	1	2600	3600	1	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Cor.coro	201	256	0	9000	18 000	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Cor.cora	212	207	2	250	400	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	1	1	1	
Stu.vulg	604	256	0	800 000	1 600 000	3	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	
Pas.dome	607	255	0	3 000 000	6 000 000	3	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Pas.mont	571	254	0	500 000	1 000 000	3	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Fri.coel	608	256	0	4 000 000	8 000 000	3	1	1	1	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	0	1	1	1	1	1	
Ser.seri	575	252	0	450 000	900 000	3	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Car.chlo	589	256	0	500 000	1 000 000	3	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	
Car.card	578	255	0	200 000	400 000	3	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	
Car.spin	360	206	0	90 000	180 000	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Car.cann	529	241	0	60 000	120 000	3	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	
Car.flam	190	88	2	6000	12 000	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1	1	1	1	
Lox.curv	290	143	0	30 000	100 000	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Car.eryt	65	109	2	350	450	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	
Pyr.pyrr	493	218	0	100 000	200 000	3	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	
Coc.cocc	471	240	0	150 000	300 000	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	
Emb.citr	591	252	0	2 000 000	4 000 000	3	0	0	0	0	0	0	1	0	0	0															