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COMPARING BIOGEOGRAPHIC PATTERNS OF BUTTERFLIES, ORTHOPTERANS AND VASCULAR PLANTS IN THE SWISS WESTERN PREALPS

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par

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Abstract

Aims: In this study, using datasets for butterflies, orthopterans and plants sampled in the Swiss Western Prealps, we aimed at assessing (i) the capacity of macroecological models (MEMs) to predict species richness for these taxonomic groups ("taxa") and the effect of the *rare* species component on the modeling outcome, (ii) the degree of similarity among the predicted richness patterns within and among taxa and (iii) the congruence between their potential hotspots of richness.

Methods: Three richness models were built per taxonomic group, fitted either on (i) the whole dataset (*all* species), (ii) the pool of *common* species (> 30 occurrences), or (iii) the complementary pool of *rare* species. We compared the performance of the models as well as the predicted richness patterns across the study area among and within taxa, and then identified the emerging diversity hotspots.

Results: The performance was greatest for models fitted on *common* species for butterflies and plants, and on *all* species in the case of orthopterans. Most models predicted highest richness at mid-elevation, mainly in slopes facing south. The richness patterns of the three taxonomic groups were generally positively correlated. Finally, while hotspots for each group covered relatively extensive areas, hotspots for multiple groups were scarce.

Main conclusions: (i) The accuracy of MEMs' richness predictions is influenced by the inclusion of *rare* species differentially across taxa and may be related to the closeness of the ecological needs of *common* and *rare* species and to how well these are accounted for by the models. (ii) *Common* and *rare* species contribute in diverging ways to the overall richness patterns in these three taxa. (iii) The scarce overlap of the hotspots of these groups highlights the conservational value of the south-oriented open spaces at low to mid-elevations.

Keywords: Species richness, butterflies, plants, orthopterans, common species, rare species, macroecological models, richness pattern, elevational gradient, Spearman rank correlation test.

Résumé

Objectifs: Dans cette étude, en utilisant des données sur les papillons, les orthoptères et les plantes échantillonnés dans les Préalpes occidentales suisses, nous avons cherché à évaluer (i) la capacité des modèles macroécologiques (MEMs) à prédire la richesse spécifique pour ces différents groupes taxonomiques ("taxons") et l'effet des espèces *rares* sur la prédiction des modèles, (ii) le degré de similitude entre les patrons de richesse prédits au sein et entre taxons et (iii) la congruence entre leurs potentiels "hotspots" de richesse.

Méthodes: Trois modèles de richesse ont été construits par groupe taxonomique à partir des données de (i) *toutes* les espèces, (ii) l'ensemble des espèces *communes* (> 30 occurrences), ou (iii) l'ensemble complémentaire de espèces *rares*. Nous avons comparé la performance des modèles ainsi que les patrons de richesse prédits dans la zone d'étude au sein et entre les groupes taxonomiques, et identifié les "hostpots" de diversité émergents.

Résultats: Les modèles les plus performants étaient ceux pour les espèces *communes* dans le cas des papillons et des plantes, et celui pour *toutes* les espèces dans le cas des orthoptères. Dans la plupart des cas, les modèles ont prédit de plus grandes richesses à moyenne élévation, surtout dans les pentes exposées au sud. Les patrons de richesse des trois groupes taxonomiques étaient généralement positivement corrélés. Enfin, alors que les "hotspots" de chacun des groupes étaient relativement étendus, les "hotspots" pour plusieurs groupes étaient rares.

Conclusions principales: (i) L'exactitude des prédictions de richesse des MEMs est influencée par l'inclusion des espèces *rares* de manière différente entre taxons, ce qui pourrait être lié à la similitude des besoins écologiques des espèces *communes* et *rares* ainsi que à la façon dont ceux-ci sont pris en compte par les modèles. (ii) Les espèces *communes* et *rares* contribuent de façon divergente aux tendances globales de la richesse dans chacun des trois groupes taxonomiques. (iii) Les "hotspots" de ces groupes taxonomiques se chevauchent rarement ce qui souligne l'importance de préserver ces espaces ouverts exposés au sud à basses et moyennes altitudes.

Mots-clés: Richesse spécifique, papillons, plantes, orthoptères, espèces communes, espèces rares, modèles macroécologiques, patron de richesse, gradien d'élévation, test de corrélation de rang de Spearman.

1 Introduction

Studying richness patterns along environmental gradients helps elucidating the rules expected to govern diversity (Rosenzweig 1991). Species richness, the number of species of a defined group and in a defined area (Mcintosh 1967), has been, so far, the most studied macroecological property as it is the most intuitive and directly quantifiable facet of biodiversity.

Although the definition of species richness is quite simple (assuming a simple definition of the concept of *species*), measuring this property of assemblages is a highly effort-demanding task which hardly ever yields exhaustive species lists (Gotelli and Colwell 2011). Predictive spatial modelling is a powerful statistical tool widely used in the case of observed data scarcity to still obtain a broad view of communities' attributes in a defined spatio-temporal context (Ferrier and Guisan 2006). In spatial ecology, such models relate community or species data sampled in the field to a set of relevant environmental variables for which exhaustive spatial data (*i.e.* maps obtained through remote sensing or modelling) are available thus allowing to extrapolate the values of the response variable to the whole study area.

Two main types of models are currently used to predict species richness: macroecological models (MEMs; Fischer 1960; Rahbek and Graves 2001) and stacked-species distribution models (S-SDMs; Guisan and Theurillat 2000; Ferrier and Guisan 2006). As a result of their diverging theoretical basis, the input data, and the statistical procedures, they generate outputs different in scope and in precision. MEMs are associated to the 'assemble first, predict later' theoretical approach (Ferrier and Guisan 2006) according to which communities are stable entities composed of fixed co-occurring species (Baselga and Araújo 2010). Consequently, richness is directly related to predictors which account for macroecological biotic and abiotic constraints of the environment over communities (*e.g.* carrying capacity). However, MEMs do not provide predictions of the identity of the species in the assemblages. Alternatively, S-SDMs

follow the 'predict first, assemble later' theoretical approach (Ferrier and Guisan 2006) for which communities are the result of the combination of single species' responses to abiotic factors. In this view, community properties are expected to be reconstructed by the aggregation of those of its individual constituent species. In S-SDMs, species probability of occurrence are modelled independently by species distribution models (SDMs; Guisan and Theurillat 2000; Guisan and Thuiller 2005; Elith and Graham 2009) converted in binary maps which are then stacked (summed) to obtain a S-SDM that yields predictions of both community species richness and composition (D'Amen et al. 2015a). There are however two main drawbacks associated with this strategy. First, the resulting predictions are totally independent from macroecological forces. Second, because accurate SDMs cannot be generated for species with few occurrences, S-SDMs cannot include rare species (Wisz et al. 2008; Guisan and Rahbek 2011).

These two modelling strategies, as for *models* in general, generate approximations of the highly complex reality of nature, that is, they only account for few particular aspects of a system and always include some residual error. Detecting the causes of inaccuracy and searching for possibilities to improve model performance is a whole axis of research in spatial ecology. The comparison of richness patterns is particularly interesting as it allows to address essential questions concerning the structuring of biological communities (Guisan and Rahbek 2011). Such comparisons may *e.g.* highlight the commonness of some trends and so the major role of some variables (Gaston 2000; Ferrier and Guisan 2006; McCain and Grytnes 2010; Nogués-Bravo et al. 2008; Hawkins et al. 2003), acknowledge the relationship among taxa (Wolters et al. 2006) or support (or question) the use of a taxon as bioindicator (Carroll and Pearson 1998). Beyond the ecological insights, these studies can also be used to support conservation decisions including monitoring strategies and delineation of regions of conservation value (Pearman and Weber 2007; Grytnes 2003; Heino 2002; Guisan et al. 2013).

The studies on richness patterns carried out at different scales and in different regions of the world, across key *landforms* and for multiple taxa, have revealed particular rich-

ness clines, principally along latitudinal and elevation gradients (Gaston 2000; Rahbek 1995). In this work, we focus on the latter. Elevational (or altitudinal) gradients offer suitable conditions to investigate richness patterns (Körner 2000; Becker et al. 2007) as (i) altitude is a surrogate variable for several correlated climatic and topographic factors varying remarkably in relatively short distances and thought to exert a direct influence on community diversity, (ii) they encompass bounded areas (top and bottom of the mountain) and so they allow to work at relatively high resolutions implying more representative measures and estimations of the local richness in particular for low-mobility organisms (Rahbek 2005), (iii) they exist across the globe and so provide a large number of possible replicates. Thus, the study of elevational richness patterns helps bringing to light concrete relationships between well-defined communities and their environment at rather small scales while allowing to step back to larger scales by confronting comparable local results obtained along different altitudinal gradients.

The two richness-elevation relationships most described in literature are a monotonically decreasing and a hump-shaped curves (McCain and Grytnes 2010). It has been argued that the lack of consensus between the patterns found is likely due to an effect of different scale and extent implying an omission of part of the gradient (Nogués-Bravo et al. 2008) or to differences in area and sampling-effort (Rahbek 1995). According to McCain and Grytnes (2010) these differences may also depend on the taxonomic group under focus.

In this project, we modelled and studied the richness patterns of butterflies, orthopterans and plants taxa across the same study area located in the Western Alps of Switzerland and presenting and important altitudinal gradient. The aim of this study was two-fold. First, we focused on the *performance of richness models* for the different taxonomic groups when considering all, only common or only rare species. The subsets of common and rare species were defined according to the number of times a species was observed in the field. More precisely, we asked: which is the difference in terms of performance between MEMs fit on the data for the whole taxon and those fit with

data at the intra-taxonomic level? What is, in particular, the influence of rare species on these differences? As rare species are commonly excluded from S-SDMs because they are poorly modelled by SDMs, the results could reveal a possible source of bias in the estimate of richness by using different approaches. Second, using the predictions of the models obtained in the previous part, we investigated the *degree of similarity between the predicted richness patterns* of our three focal groups in the study area. The comparisons were performed within taxa, in order to evaluate the contribution of rare and of common species to the overall spatial variations of a taxon, and among taxa, to appraise the representativity of these taxa for one another. Finally, we identified the congruence of richness hotspots for each taxa in the study area *e.g.* to subsequently assess the contributions and limitations of the use of richness patterns in the design of conservation programs.

2 Materials & Methods

2.1 Data source and collection

2.1.1 Study area

The study area is located in the Alps of Canton Vaud (Western Alps of Switzerland, 46°10′ to 46°30′N ; 6°50′ to 7°10′E) (Figure 1). It comprises *ca.* 700 km² and presents a strong elevational gradient ranging from 372 to 3210 m a.s.l. The climate in this region is temperate: from the lowlands (600 m) to the summits (3000 m) the annual mean temperatures vary from 8°C to 5°C and the annual mean precipitations, from 1200 mm to 2500 mm (Bouët and Oguey 1985). The vegetation belts follow the typical altitudinal sequence for such calcareous substratum in the Alps: a *colline belt* with deciduous forests; a *montane belt* with mixed forests; a *sub-alpine belt* with coniferous forests; an *alpine belt* with heathlands, meadows and grasslands and a *nival belt* with a cover of sparse vegetation (Randin et al. 2006). Such structure of the vegetation, the landscapes

and the habitats along the elevational gradient, are all influenced both by the climate and by human activities. In particular, this region is affected by agriculture, which includes mowing, pasturage and fertilization, more intensively applied at low elevations yet reaching the low alpine belt.

2.1.2 Sampling strategy & species data

In this study we considered three taxonomic groups (hereafter, "taxa"): vascular plants, orthopterans (grasshoppers [suborder: *Ensifera*] and crickets [suborder: *Caelifera*]) and butterflies (Papilionoidea superfamily, Hesperiidae and Zygaenidae families and one representative of the Sphingidae family, *Macroglossum stellatarum*, active during the day). Community data for the three groups throughout several field surveys conducted on 912 plots between 2002 and 2009 for plants (Dubuis et al. 2011), on 202 plots during 2012 for orthopterans (Pradervand et al. 2013b) and on 211 plots in 2009, 2010 and 2014 for butterflies (Pellissier et al. 2012, present work) (Figure 1). Overall, 199 plots were common to the three groups. Plot selection was limited to non-forested areas – *i.e.* grasslands, meadows, rocks and scree – and followed a random-stratified sampling design (Hirzel and Guisan 2002) with elevation, aspect and slope as stratifying variables. Such sampling strategy aimed to avoid sampling bias by selecting sites which represent equally the different conditions defined by these three gradients. Furthermore, a minimum distance of 200 m between two plots was used as it was previously shown to avoid spatial autocorrelation (Schmid 2015).

Surveys were performed in ways that optimized the sampling effort (costs) and the quality of the data (number of species detected) in order to obtain relevant data for our modelling purposes. The dimensions of the plots were of 50 * 50 m^2 for insects and of 2 * 2 m^2 for plants. This last measure for plant sampling was assumed to be representative of the vegetation of the surrounding 50 * 50 m^2 plot (Chytrý et al. 2003) and had been confirmed for 192 plots (Pellissier et al. 2013). To obtain representative richness numbers, plant sampling consisted in one visit, *orthoptera* sampling required one

to two, and butterfly sampling required three to six surveys during the activity season of species (for further details on plant and *orthoptera* sampling, see Dubuis et al. 2011 and Pradervand et al. 2013b). As part of this Master project, during the summer 2014, I sampled butterflies communities in 23 additional plots located between 410 and 2100 m a.s.l., thus completing the taxon data set for most of the altitudinal gradient. The sampling protocol was consistent with that of the previous surveys (Pellissier et al. 2012). Captures were carried out with a net during a period of 45 minutes per survey followed by on-site identification. Samplings were constrained to the conditions required for the time of highest butterfly activity (between 10:00 and 17:00), sunny weather (enough to project shadows), temperatures (>18°C below 1000 m or >14°C above 1000 m), and no or low wind ($\leq$ 3 beauforts). Problematic identifications (photographies or samples) were later vetted for accuracy by a specialist. Sites located below 1000 m were visited six times from May to August and those above, three times, from mid June to August. This protocol was developed according to (Pollard and Yates 1994) and the document "Z7 – Papillons diurnes" (BDM 2012) which establishes the procedure for butterfly monitoring in Switzerland.

For each taxon we defined three groups including: (1) the totality of sampled species (hereafter called "*all species* subset"), (2) the species recorded in more than 30 plots (hereafter called the "*common* species subset") and (3) the complementary species with 30 or less occurrences (hereafter called the "*rare* species subset". We chose the threshold to define *rare* species subsets on the basis of the minimum number of occurrences fairly modelled by classic SDMs (Wisz et al. 2008).

2.1.3 Environmental predictors

We worked with 50 m-resolution raster layers (or grids) for insects and with 25 m- and 50 m-resolution raster layers for plants.

The raster layers for the *climatic* and *topographic* variables used in our study were derived

from a set of remotely derived grids provided by the Swiss Federal Institute for Forest, Snow and Landscape Research with meteorological data (covering the period from 1961 to 1990) at a 25 m-resolution for the whole Switzerland. First, we computed additional ecologically relevant variables (*e.g.* mean values of precipitation, temperature, moisture or cloudiness during summer or spring, *i.e.* the growing season). Then, we cropped the raster layers of the resulting set of variables to the extent of our study area. Finally, we aggregated the raster layers at 25 m to obtain a resolution of 50 m. We performed all the manipulations of these grids in the R environment (version 3.1.1, R Core Team 2014), using the 'raster' (Hijmans 2014) and 'rgdal' (Bivand et al. 2014) packages.

Furthermore, we used grids of two *landscape* predictors: the Normalized Difference Vegetation Index (NDVI, an index of plant photosynthetic activity) and the distance to the forest. The NDVI had been computed from remotely sensed data from the Spot5 Radcor Mosaic of Switzerland (Swisstopo) at a 10 m-resolution (Rein and Séchaud 2014). The distance to the forest was calculated as the Euclidian distance to the nearest forest. These were obtained using the ArcGIS software (version 10.1, ESRI 2014).

We inspected our initial sets of variables (18 for plants and 17 for insects) and the relations between them through Principal Component Analysis and pairwise Pearson correlations, using the packages 'ade4' (Dray and Dufour 2007) and 'corrgram' (Wright 2014). We selected only environmental predictors correlated to others by less than $<|0.75|$ in order to limit the risk of multicollinearity in the models (Dormann et al. 2013). The selection of predictor variables was also guided by previous studies of species modelling carried out in the same study area for the considered groups (Dubuis et al. 2011; Pellissier et al. 2012; Rein and Séchaud 2014). This process led to the following sets of variables: degree-days, solar radiations, frost days and NDVI for insects, and degree-days, solar radiations and slope for plants (Table 1).

2.2 Richness models

We modelled species richness for *all*, *common* and *rare* species subsets of each taxon using Generalized Linear Models (GLMs; McCullagh and Nelder 1989). This modelling technique is commonly used to predict species richness and yields results easy to interpret, *e.g.* ecologically meaningful parameters and response curves expressing how the explanatory variables influence the predictions of the response variable (Guisan and Zimmermann 2000; Lehmann et al. 2002; Guisan et al. 2002). GLMs were calibrated with the *full* data sets – they will therefore be called *full* models – assuming species richness is a Poisson-distributed variable and using a *log* link function (*i.e.* logarithmic relationship between the dependent and the independent variables). They were allowed up to second order terms of the predictor variables (*i.e.* polynomial regression). For each data set, a stepwise process iteratively testing for variable importance for multiple variable sets retained the model with the smallest AIC (a version of the Akaike Information Criterion; Akaike 1973), *i.e.* the model better supported by the data.

Model performance was assessed through 100 repetitions of a split-sample cross-validation procedure (Guisan and Thuiller 2005). In each iteration, 70% of the data were used to fit the model (*training data*) and the remaining 30% to independently evaluate it (*test data*) (Dubuis et al. 2011). In each repetition, we calculated the index of deviance reduction (D^2) – a measure of the explained variance of the model, following the formula: $D^2 = (Null\ deviance - Residual\ deviance)/Null\ deviance$ (Guisan and Zimmermann 2000) – as well as the Spearman correlation coefficient between the observed and predicted species richness in the evaluation data set (ρ) – a measure of the predictive accuracy of the model. We then averaged each term across the repetitions to obtain the models' mean explanatory (mD^2) and predictive ($m\rho$) powers on which subsequent model performance comparisons were based.

Finally, maps of the potential richness in each pixel of the study area were generated by supplying the corresponding pixel-values of the predictors to the final models.

2.3 Comparative analyses

The analyses in this work consisted of comparisons carried out at two levels, *within* taxa – *i.e.* among the richness patterns of species belonging to *the same taxon but to different subsets* – and *among* taxa – *i.e.* among the richness patterns of species from *different taxa but from the same corresponding subset*.

2.3.1 Comparison of model performance

In order to compare the performance of the models of *all*, *common* and *rare* species, we ran Student t-tests to test for significant differences in the D^2 and in the ρ metrics considering the models scores across the cross-validation process. In addition, we compared the linear regressions between the predicted richness and the observed richness in our sampling plots to $y = x$, the line of slope 1 and intercept 0 corresponding to a perfect model, so as to identify potential differences between the prediction errors of the models (Algar et al. 2009).

2.3.2 Comparison of richness patterns

The comparison of richness patterns *within* and *among* taxa was performed through graphical and statistical approaches. The latter consisted of pairwise Spearman rank correlation tests (ρ). We first assessed the extent to which the richness patterns across the study area (hereafter also called richness patterns "across space") of two groups were similar based on the whole richness projections generated by the models (pixel by pixel correlations). A second approach of richness patterns was that of richness across elevation (hereafter also referred to as "elevational" richness patterns) which allowed us to assess whether the relationship between two dataset was consistent across elevation or changed at different altitudes. This was quantified by correlating the richness predicted in 200 random plots (the same set for the two groups being compared) in each

of ten elevational bands of 282.2 m wide each (Table 2). We finally averaged the correlations per band to obtain a measure of the overall degree of similarity of elevational richness patterns.

2.3.3 Hotspots of species richness

For each taxon, we defined two types of biodiversity hotspots based on richness while recognizing that other criteria, e.g. endemism, rare species *s.l.* or threats, can be used to define them (Reid 1998). The first type, named *85%-thresholded hotspots*, consists of regions with a proportion of species higher than 85% of the maximum predicted richness. The second type, named *top 10% hotspots*, corresponds to the 10% surface of the study area holding the highest numbers of species. We considered *all* species data only, for the quality of the corresponding models would allow to make biologically meaningful analyses. The thresholds at 85% and 10% were *ad-hoc* and determined empirically, in order to capture a large proportion of species and a rather small proportion of area, respectively.

The resulting maps for single taxon hotspots were used to make qualitative cross-taxa and cross-hotspot-definitions comparisons. Finally, they were combined to examine the extent of the overlap, that is, the extent of hotspots for multiple taxonomic groups.

3 Results

3.1 Field data

Overall, we had data for 795 plant, 41 *orthoptera* and 139 butterfly species forming the *all* species data sets (Table 3, and Table S1 to Table S3). The sampling of 2014 added twelve supplementary butterfly species to the existing database. The ratio of *rare* to *all* species number reached 63%, 74% and 76% of the total species of butterflies, plants and

orthopterans, respectively, meaning that in all taxa, the *rare* species subset included *ca.* three times more species than the subset of *common* species.

In addition, most species classified as nearly threatened, vulnerable, endangered and critically endangered in the national red lists belonged to the *rare* species subsets of our study. Only three nearly threatened butterfly (*Aporia crataegi*, *Maculinea arion*, *Melitaea diamina*) and orthopteran (*Polysarcus denticauda*) species and one endangered butterfly species (*Euphydryas aurinia*) at the national level were classified as *common* according to our criteria in the study area.

In the next sections, we will not present the results obtained for the plant richness modelled at a 25 m resolution as they were entirely consistent with those obtained at a resolution of 50 m, yet they can be found in the supplementary material (Table S4, and Figure S4 to Figure S7).

3.2 Comparison of model performance

The final models retained all the predictors set from our previous selection process (Table 4). The same predictors were used in the richness models of the three subsets of a taxon. All models explain more than 20% of the variance and richness predictions had correlation values (ρ) between 0.517 and 0.788 and, except for *rare* butterflies and plants ($D^2 \leq 0.89$ and $\rho \leq 0.352$) (Table 5). All the models overpredict in plots with few observed species (*false positives* or *type I error*) and underpredict in plots with the highest numbers of observations (*false negatives* or *type II error*) (Figure 2). For further detail concerning the distribution of prediction errors, see the supplementary material (Figure S1).

Within taxa comparisons

According to both evaluation metrics (mD^2 and $m\rho$), the model quality within taxa, for butterflies and plants follows the sequence: $common > all > rare$, whereas for or-

thopterans this is: $all > common > rare$ (Table 5). Furthermore, the models fit with the data of *rare* butterflies or *rare* plants have low explanatory and predictive powers (mD^2 and $m\rho < 0.2$), while those of the model of *rare* orthopterans are fairly higher (mD^2 and $m\rho > 0.6$). All the above differences of performance were significant ($p < 0.01$, Student t-tests), except between the predictive powers of the models of *common* and of *rare* species in the case of orthopterans ($p = 0.23$, Student t-test).

Among taxa comparisons

According to both evaluation metrics, the model performance among taxa follows the order: $orthopterans > butterflies > plants$ (Table 5). The differences of performance are all significant ($p < 0.01$, Student t-tests), except between the predictive power of the models of *common* species of butterflies and of *common* species of orthopterans ($p = 0.36$, Student t-test). Moreover, the observed-predicted richness regression lines for orthopterans are closer to the perfect fit line than those of butterflies and plants (Figure 2).

3.3 Comparison of richness patterns

Richness patterns across space

The highest richness predictions in the study area are located at mid-elevations whereas the regions with the lowest richness correspond to the highest south-eastern mountain peaks and to the lowest agricultural lands in the western Rhône Valley (Figure 3). Furthermore, for *all* and *common* species, rich areas are predicted both in south- and north-facing slopes, with a predominance in the former in the case of insects. For *rare* species, richness above the mean is predicted only in few south-oriented slopes. The map of *rare* plants is less marked by this pattern and presents only few and isolated pixels with important numbers of species. Additionally, the maps of orthopterans feature a marbled pattern in the western lowland fringe. Although less noticeable, such arrangement also

appears in the maps of *all* and *common* butterflies.

The *intra*-taxon pairwise correlations of predicted richness across the whole study area are all positive and moderate to strong ($0.62 \leq \rho \leq 0.98$) except between the richness patterns of *common* and *rare* orthopterans ($\rho = 0.32$) (*wProj* in Table 6). The richness of the *all* species subset is highly correlated to the richness of the *common* species subset for butterflies and plants, and to the richness of the *rare* species subset for orthopterans. The *inter*-taxa pairwise comparisons of richness patterns across the whole study area, are also positive and moderate to strong ($0.57 \leq \rho \leq 0.96$) except between the richness of the subsets of *rare* butterflies and orthopterans ($\rho = 0.39$) (*wProj* in Table 7). The relative strength of inter-taxa correlations depends on whether the *all*, *common* or *rare* data sets are considered.

Richness patterns across elevation

The richness predictions in our sampling plots delineate elevational trends very similar to those described by the observed data (Figure 4 and Figure 5) for all taxa and subsets. Consistent results were obtained when considering predicted richness in 2000 random plots equally distributed across ten bands of elevation instead of richness in our sampling plots only (Figure 6 and Figure 7).

In all cases, richness presents an overall decrease with increasing elevation. However, we observe three different situations: (i) for all taxa, the richness patterns of the subsets of *all* and *common* species are net hump-shaped curves with maxima between between 650 and 2000 m, (ii) the subset of *rare* orthopterans present a slight initial increase of richness up to band 2, followed by a monotonic decrease and (iii) the subsets of *rare* butterflies and plants barely show an increase in richness.

For the three taxa, the relative strength of the pairwise correlations across bands of elevation follows the sequence *all vs. common* > *all vs. rare* > *common vs. rare* (Figure 6 and *mB* in Table 6). This relationship is valid for butterflies and plants when considering each band separately, but it is not always the case for orthopterans as the richness of the

all species subset is more strongly correlated to the richness of the *rare* species subset up to band 6 and then to the richness of the *common* species subset (Figure 6 and *b1* to *b10* in Table 6).

When considering the similarities among taxa, we found that the richness patterns of insects are more correlated together than with those of plants (Figure 7 and *mB* in Table 7). More precisely, the strength of the correlation between insects' richness patterns is higher in the montane and lower sub-alpine belts (bands 3 to 7) ; *all* and *common* butterflies and plants are less correlated in the montane belt (bands 3 to 5): and *all* and *common* orthopterans and plants are the least correlated groups, if at all (Figure 7 and *b1* to *b10* in Table 7). Finally, the richness of the subsets of *rare* species among taxa also appear to be moderate- to strongly correlated at intermediate elevations (bands 3 to 6) but weakly in the extreme bands .

For a visual representation of correlation values, see the supplementary material (Figure S2 and Figure S3)

3.4 Hotspots of species richness

According to both definitions of hotspots –*H85* including all the plots with a richness of at least 85% of the maximum predicted richness and *H10* including the 10% richest regions– these are mainly located at mid-elevations, in slopes facing south (Figure 8 and Figure 9). The *H85* of butterflies include 31 to 36 species in 40.1 km² spread across the study area (Figure 8 and Table 8.*1a*). For orthopterans, the H85 are smaller patches reaching a total extent of 11 km², mainly distributed towards the Rhône Valley and including 12 to 14 species. Finally, the H85 of plants include 39 to 45 species and, although they are also chiefly located nearby the Rhône Valley, they substantially spread to the east of the study area, resulting in 116.2 km² of more interconnected sites than for insects. In comparison, the *H10*, extending over *ca.* 68 km², represent total areas of approximately 1.7, 6.2 and 0.6 times the surfaces of the *H85* of butterflies, orthopterans

and plants, respectively (Figure 9 and Table 8.2*a*). These span one additional species of each group of insects, and one less species of plants.

The union of the hostpots for the three taxa cover a similar extent of ca. 148 km² for both *H85* and *H10* criteria. (Figure 10 *top maps* and Table 8.3*a*) from which, 65.9% are common to both (Figure 10 *bottom map* and Table 8.3*b*).

Furthermore, the overlap of hotspots of different taxa is rather rare (Table 8.1*b* and .2*b*) for either definition. For *H85*, the maximum overlap occurs between butterflies and plants with 7.5% of the total extent of *H85*, and all the hotspots for other taxa combinations do not exceed 2% (Figure 11 and Table 8.1*b*). For *H10*, the maximum overlap among insects rises to 22.5% of the total extent of *H10* (Table 8.2*b*), while the hotspots for other taxa combinations do not exceed 4%. Finally, hotspots for the three taxa are remarkably scarce extending over 2.8 km² and 5.9 km² according to *H85* and *H10*, respectivelly.

4 Discussion

In this work we assessed the capacity of macroecological models to predict species richness for different components of biodiversity namely, plants, butterflies and orthopterans, considering their respective subsets of *all*, *common* and *rare* species. A second objective was to measure the degree of similarity of the spatial richness patterns among the subsets of each taxon and among taxa. Finally, using two different criteria to define diversity hotspots we assessed the extent to which these were congruent among taxa.

We found that the accuracy of MEMs' richness predictions is influenced by the inclusion of *rare* species differentially across taxa and that it is possibly related to how well *rare* species are modelled using the same predictors as those used to model the richness of the most frequently observed species. Furthermore, our analyses showed that *common*

and *rare* species contribute in diverging ways to the overall richness patterns in these three taxa. Finally, we found that the species richness patterns are generally positively correlated among the three taxonomic groups but that their hotspots of diversity barely overlap.

We discuss these results in more detail in the following sections.

4.1 Comparison of model performance

4.1.1 *Are some taxa better modelled than others?*

Overall, we obtained richness models of better quality for orthopterans than for butterflies and for the two insect taxa than for plants. Given the comparable quality of the data used to fit the models among taxa (in terms of sampling strategy -including the scale- and their ratios of *rare* and *common* species) this parameter is, a priori, not the main source of differences of model performance among taxa. Rather, we attribute the differences to the relevance of the predictors used as well as to the number of species in each group. That is, we can suppose that the explanatory variables we used were more relevant to predict orthopterans' richness than butterflies' and plants'. Other studies carried out in the same study area had used partially different predictor sets, *e.g.* to model plant richness Dubuis et al. (2011) additionally used a moisture index over the growing season, the potential evapotranspiration and the topographic position, and to model butterflies D'Amen et al. (2015b) additionally used the summer temperature and the distance to the forest.

4.1.2 *How do MEMs deal with rare species?*

Our results showed that for butterflies and plants, the richness of the *rare* species subset was much less well modelled than that of *common* species but this difference was not significant in orthopterans (*i.e.* the richness model of the *rare* species subsets was as

good as that of the *common* species subset).

Such response of MEMs to rarity in the case of butterflies and plants could be explained by *rare* species having different ecological needs than *common* species, in these taxa (Lennon et al. 2011). If so, and because our variable selection was guided by the predictor sets used in studies which focused on the richness of the commoner species, we likely missed relevant factors explaining part of the variation of these *rare* species' richness. In contrast, *rare* and *common* orthopterans' richness might covary with the same environmental factors.

These considerations would in turn explain why the inclusion of *rare* species led to more performant richness models for the *all* species subset than those for the *common* species subset for orthopterans ($all > common$) but not for butterflies, nor for plants ($common > all$): if *rare* and *common* orthopterans respond to the same predictors, merging the observed data of both groups (to build the *all* species set) means that potentially more records of the *response* variable are provided and so the models can be fit more efficiently. In contrast, if *rare* species of butterflies (or plants) were not sensitive to the explanatory variables used in the model, the fact of adding their observed data to that of *common* species would amount to adding unexplained noise resulting in an increase of the error in the model fit.

Finally, these results advocate that even though richness models are not sensitive to the number of occurrences of single species (contrarily to S-SDMs) and can thus be fitted with data of *rare* species, meaningful predictor variables of the latter should also be included so as to compensate for the traditional bias of using determinants accounting for wide-ranging species only (Rahbek and Graves 2001) and achieving higher predictive performance. In most taxa, the majority of species are *rare* in that they show small range sizes (Gaston 2000) and (for this and other reasons) are often among the most threatened species (Table S1 to Table S3): it is then essential to enlighten their properties and get to model them properly if we are to understand the causes of overall richness variations and develop adapted conservation measures to preserve them.

4.2 Comparison of richness patterns

4.2.1 *How are the richness patterns of these taxa and of their subgroups?*

In most cases, species richness showed a clear spatial structuring with the richest areas located at mid elevations, mainly in slopes facing south. More precisely, the *all* and *common* species subsets of the three taxa presented *actual* mid-elevation peaks defined as an increase in richness of at least 25% of the richness found at the bottom and top sites (McCain and Grytnes 2010). These results are in accordance with the elevational unimodal trend identified by multiple previous studies for these and other taxa, in the same and other study areas (Dubuis et al. 2011; Pradervand et al. 2013b; Pellissier et al. 2012; Plattner and Nobis 2008; McCain and Grytnes 2010 and references therein). In the particular case of the *rare* species subset of orthopterans, it is likely that the "incomplete" peak of the elevational pattern derives from a truncated field sampling, *i.e.* by not sampling the lowest part of the elevational gradient (lowest plot at 420 m.a.s.l.) the whole cline of diversity might not have been encompassed, thus concealing a decrease of richness towards lower elevations. Furthermore, the variability of the predicted richness across elevation (in particular for insects) likely reflects the variability of the predictors less correlated to this gradient, namely solar radiations (lower in the northern slopes) and the NDVI (varying with the structure of ground cover which is strongly influenced by humans).

While this study did not focus on identifying the determinants of species richness, the hump-shaped richness curves obtained may be related to the area available as in this study area the surface of the bands of elevation increases from the second up to the fourth band then decreases at higher elevations (Table 2).In the first band, where a large surface is available but the richness in the three taxa is the lowest, it is likely that factors deriving from human activities override the role of surface on richness as suggested by the checkered pattern in the projection maps of insects which is clearly linked to urban or agricultural lands.

4.2.2 *How similar are the richness patterns among taxa?*

Our results showed that the richness patterns of our focal taxa were always positively correlated (when the correlation was significant) and that the strength of this relationship varied according to the altitudinal band and the subset under consideration.

According to Gaston (1996), the reasons underlying strong positive correlations between species richness of different groups can derive from the sharing of common environmental determinants, from the correlation between the (unshared) determinants of each group, from the biotic interactions between the latter, or finally, from random mechanisms. Thus, because of the similar ecological requirements of insects (Baur et al. 2006; LSPN 1987), we could expect that their richness would be strongly correlated. The fact that the correlations where lower in the extreme bands and higher in the central ones suggest then a differentiation of their ecological needs or of their response to environmental conditions (including human pressures). Otherwise, the moderate to strong relationship between insect and plant richness described by our results could be attributed to the trophic relationship between plants and herbivores (only during the larval stage in the case of butterflies), as well as to the structuring role of vegetation (also suggested by the influence of the NDVI –assumed to account for vegetation types– in our projection maps) (Pradervand et al. 2013b). However, we also found weak or non-significant correlations at some elevational bands evidencing that biotic interactions between insects and plants are not the only determinant shaping their richness patterns. As reported by Pellissier et al. (2013), such varying results were obtained also in previous studies and "might arise from the fact that measures of plant species richness do not always accurately reflect the functional space available to herbivores" (*i.e.* the potential room for herbivore species diversity).

4.2.3 *How similar are the richness patterns within taxa?*

Our results suggest that the contribution of (*i.e.* the correlation strength between) *rare* and *common* species to (and) the overall richness patterns varies according to the taxon. Thus, for butterflies and plants, the richness patterns of the subset of *all* species was shown to be more correlated to the richness pattern of *common* species than to that of *rare* species. This is consistent with what Pearman and Weber (2007) found for birds and plants in Switzerland and what Lennon et al. (2004) found for birds in South Africa and in Great Britain. Contrastingly, we found that for orthopterans, the contribution of *rare* species to the overall richness pattern was nearly as important as (across elevation) or more important than (across space) *common* species' contribution.

Moreover, for butterflies and plants, the richness of *common* and *rare* species across the whole projections and in most altitudinal bands were moderate- to strongly correlated. These results suggest that, for these taxa, the variations in richness of *common* species represent well the variations in rare species' richness. In the case of orthopterans, the opposite was suggested by a very low correlation between the whole projections of the *rare* and *common* subsets, in accordance with the shifted peaks of the elevational patterns of these two subsets (Figure 6).

4.3 Hotspots of species richness

The identification of biodiversity hotspots constitutes one possible concrete application of richness predictive models. Our study case is particular in that we defined hotspots based on data at a very high resolution. Consequently, while conservation planning for large geographical areas could not be derived from it (contrarily to what is usually done, *e.g.* Reid 1998; Myers et al. 2000), the signalled hotspots in this study can be precisely delineated and the predictions of richness easily validated, which constitute clear advantages in actual conservation programs.

In this study we used two definitions of hotspots, called *85%-thresholded hotspots* (*H85*) and *top 10% hotspots* (*H10*), based on the number of species predicted by the models for *all* species. By construction, the areas returned by these two definitions for a given taxon are such that the smallest is a subset of the largest (and so, in the case of equal surface, the two types of hotspots signalled would be identical). The advantage is that while these definitions provide different adjustable thresholds that generate different results, these results will be coherent making that the only criteria for choosing one or the other is the conservation purpose they are to which they are aimed to respond.

More into detail, the first definition, *H85*, was based on a proportion of species richness on the maximum predicted richness. This definition can lead to variable hotspot surfaces according to the threshold selected. For some data, a given threshold on species richness could result in extreme cases, such as severely small hotspots, or contrariwise, a large majority of the study area as hotspot. With the 85% threshold we chose, we can be certain that, independently of their size, the hotspots defined for our three taxa included high numbers of species. The second definition, *H10*, was based on a proportion of the total surface of the study area. Although simplistic, it is suitable, *e.g.* in a "real-world" conservation situation where only a limited surface can be protected (Cabeza et al. 2004). However, these hotspots might include regions with few species diversity, or, contrariwise, exclude very rich regions. These two situations illustrate the limitations of this definition, which does not take into account the absolute richness of regions, but only the richness of one region, relatively to another's.

Our results showed that, in the "efficiency" perspective of including most species in the smallest area (Reid 1998), the results lead by *H85* were better for insects while *H10* yielded better results for plants. For all taxa and for both definitions, all hotspots were located in southern slopes from low to intermediate elevations. These results hence evidence the importance of preserving the open spaces of such regions which are currently decreasing as a result of intensive farming and recolonization by forests (Pradervand et al. 2013a).

Furthermore, we found that the overlap of the diversity hotspots of these three taxa was scarce, thus partially questioning their role as indicator groups. This result is congruent with Plattner and Nobis (2008) and Prendergast et al. (1993) whose conclusions regarding the conservation implications can be applied to our study system: richness patterns of one single taxon are not sufficient to define conservation areas targeting multiple and diverse taxa.

In addition, given that *rare species* patterns do not always follow that of *common* species, further studies assessing hotspots overlap between these two subsets of each taxon as well as the overlap of *rare* species hotspots among taxa could reveal valuable for conservation-related decision making.

Finally, we are aware that species richness alone cannot account for the entire complexity that characterizes biodiversity, for the reasons cited above concerning the representativity between groups but also because this diversity measure does not provide much (if any) information on biodiversity's dynamism (Cabeza et al. 2004) or on the functional complementarity of species needed to preserve the ecosystem services (Prendergast et al. 1993). However, it remains an indicator of biodiversity providing practical advantages for it is relatively easy to measure, and modelling richness can provide a first, prospective broad insight of the organization of communities across space.

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5 Figures

Butterflies
211 plots; 50 x 50 m^2
2009, 2010 & 2014

Orthopterans
202 plots; 50 x 50 m^2
2012

Plants
912 plots; 2 x 2 m^2
2002 to 2009

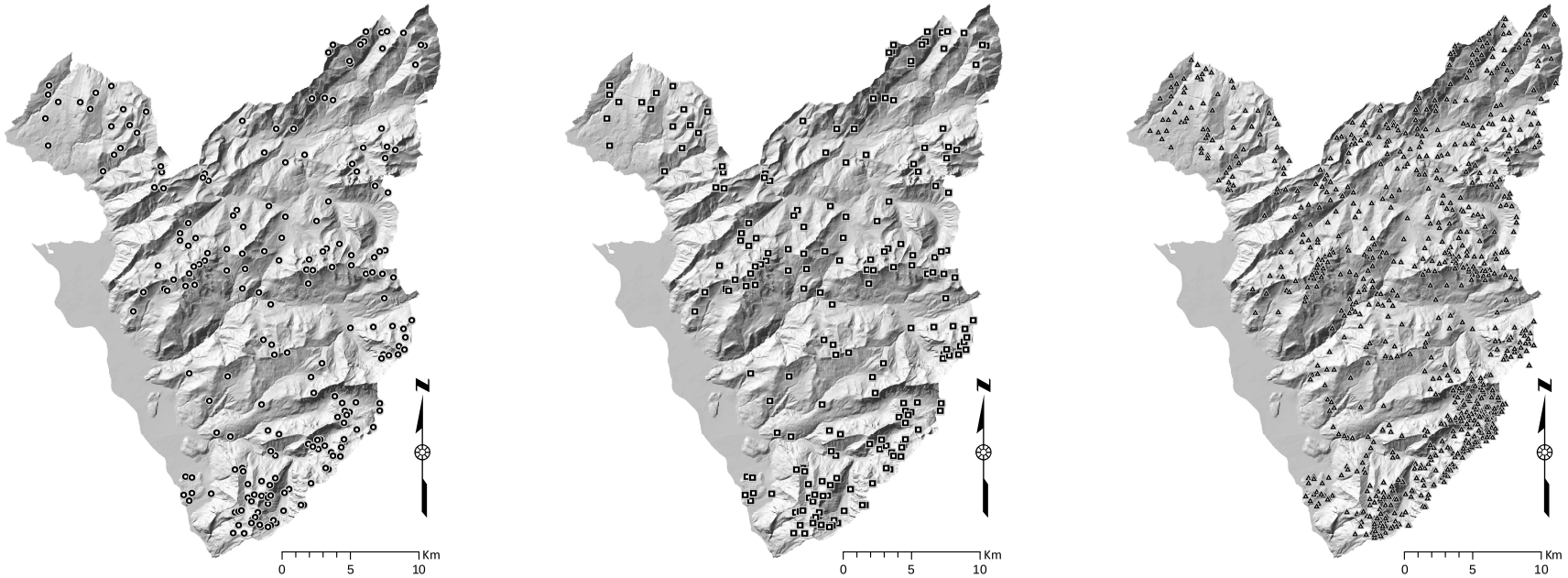

Figure 1: *Top*: Location of the study area in the Western Alps of Switzerland. *Bottom*: Number, size, years of sampling and distribution of the sites where community data of each taxonomic group were collected.

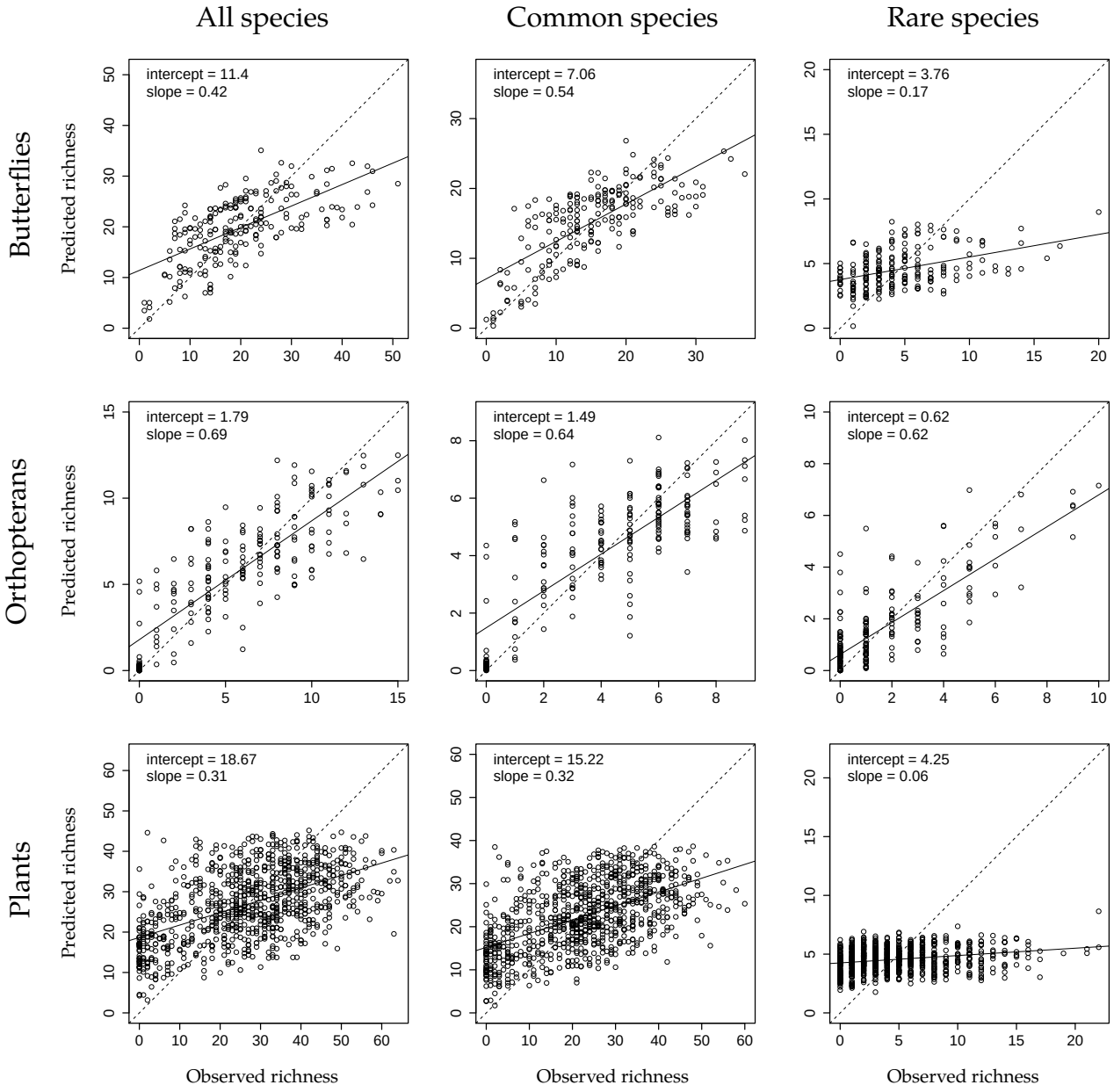

Figure 2: Predicted against observed species richness of each taxon in their respective sampling sites. The linear regression (—) and the perfect correspondence line (- - -) are also represented allowing to visually assess over- and underprediction.

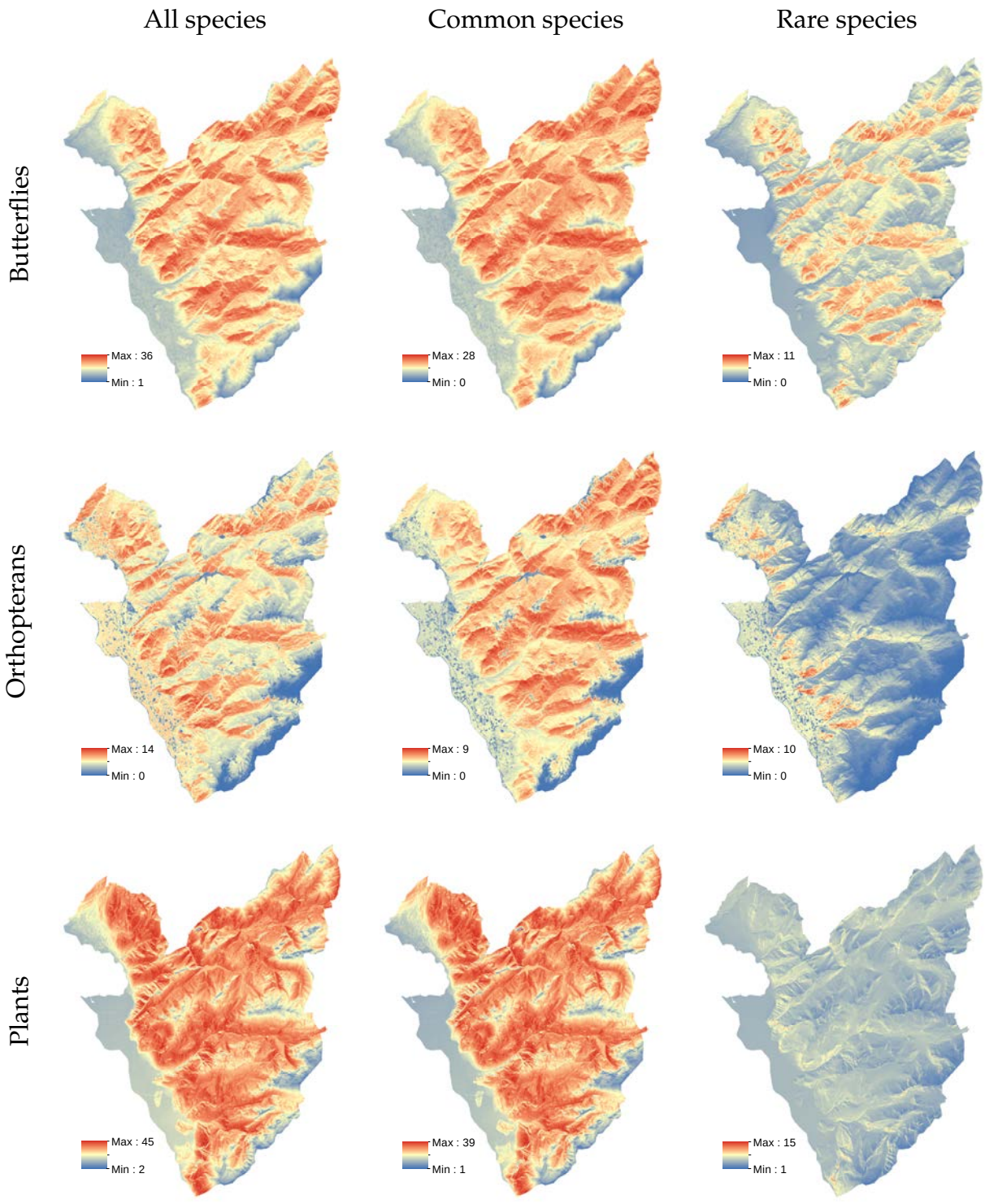

Figure 3: Spatial distribution of the potential richness of each subset of butterflies, orthopterans and plants across the study area as predicted by the macroecological models. The scales give the minima (*blue*) and maxima (*red*) number of species predicted, with average richness in yellow.

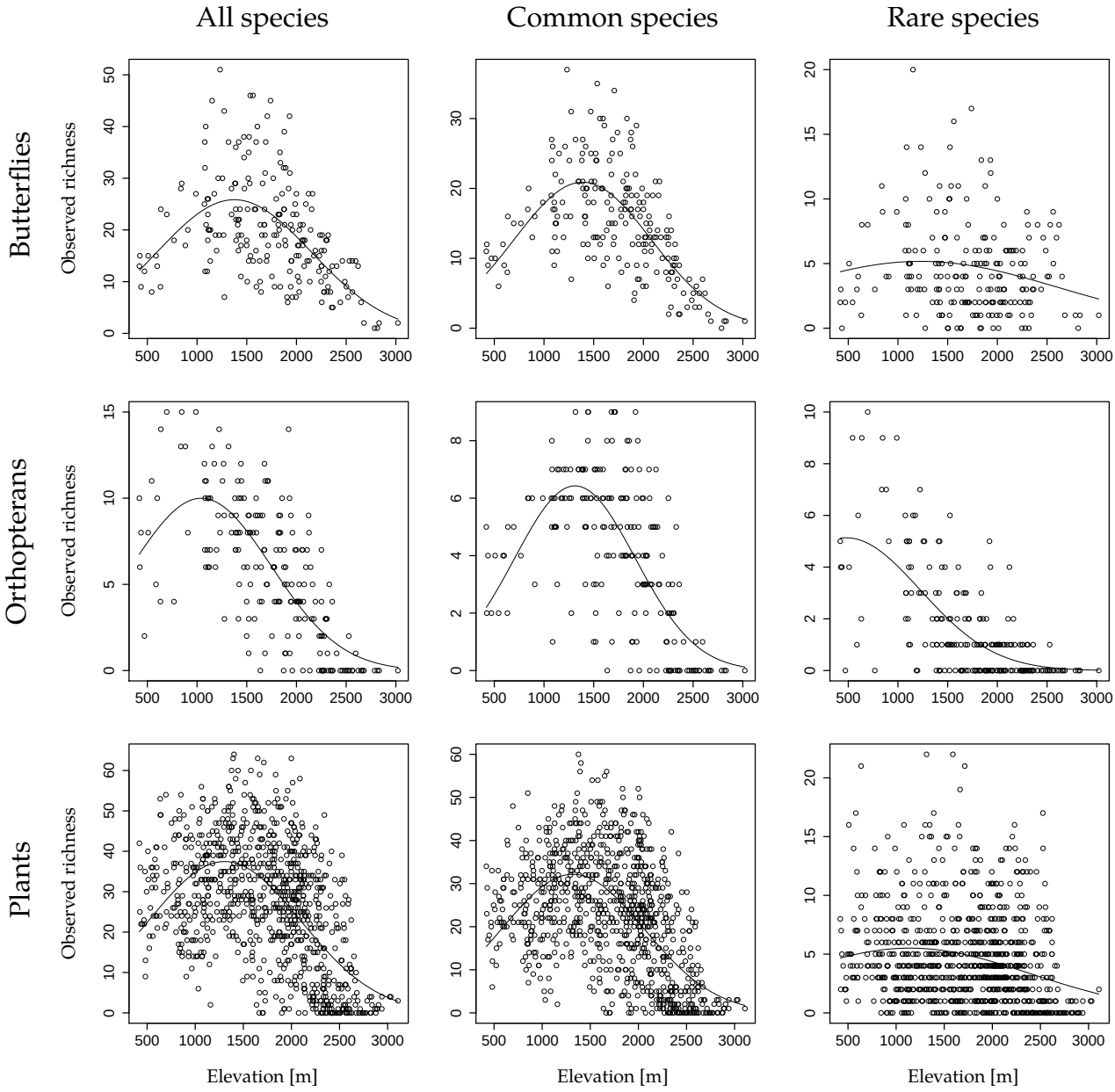

Figure 4: Observed species richness of butterflies, orthopterans and plants for *all*, *common* and *rare* species subsets across elevation. *Circles* represent the richness recorded in the sampling plots and the *curve* the corresponding trendline.

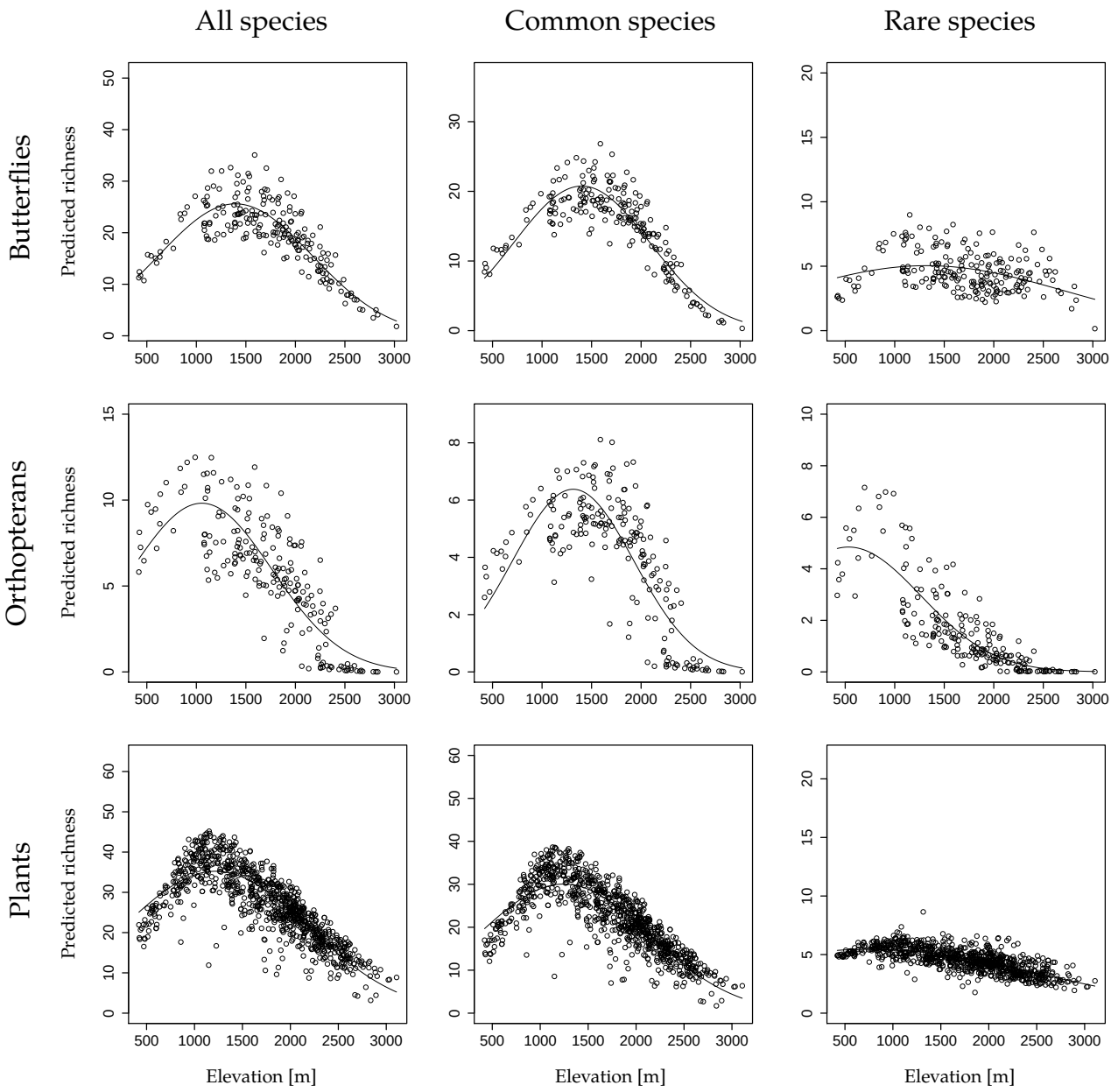

Figure 5: Predicted species richness of butterflies, orthopterans and plants for *all*, *common* and *rare* species subsets across elevation. *Circles* represent richness predicted in the sampling plots and the *curve* the corresponding trendline.

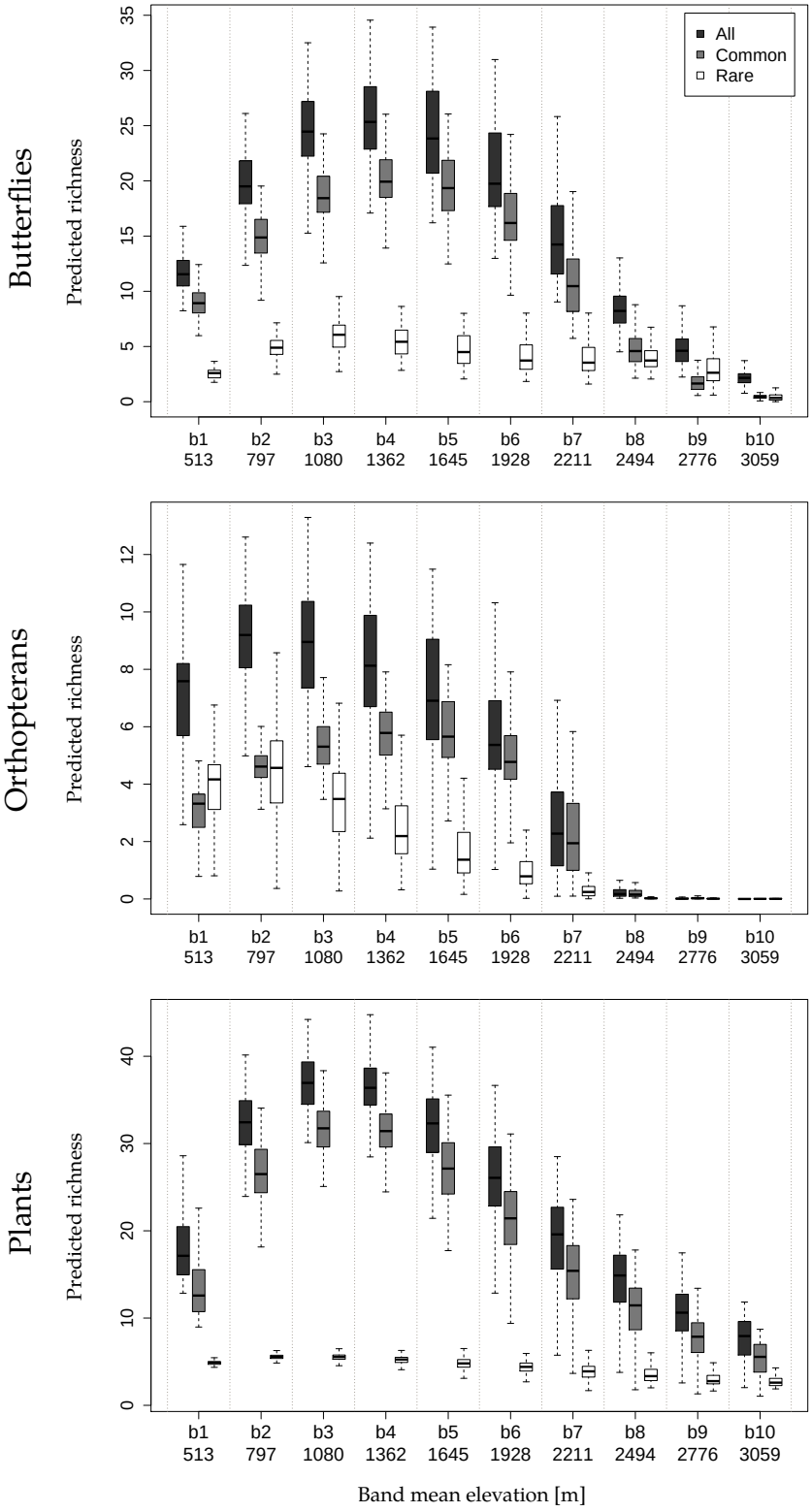

Figure 6: Predicted richness of butterflies, orthopterans and plants for *all*, *common* and *rare* species per band of elevation (*b1* to *b10*). In each graph, the richness values of a band derive from the same set of 200 random points extracted from the projections of the compared groups.

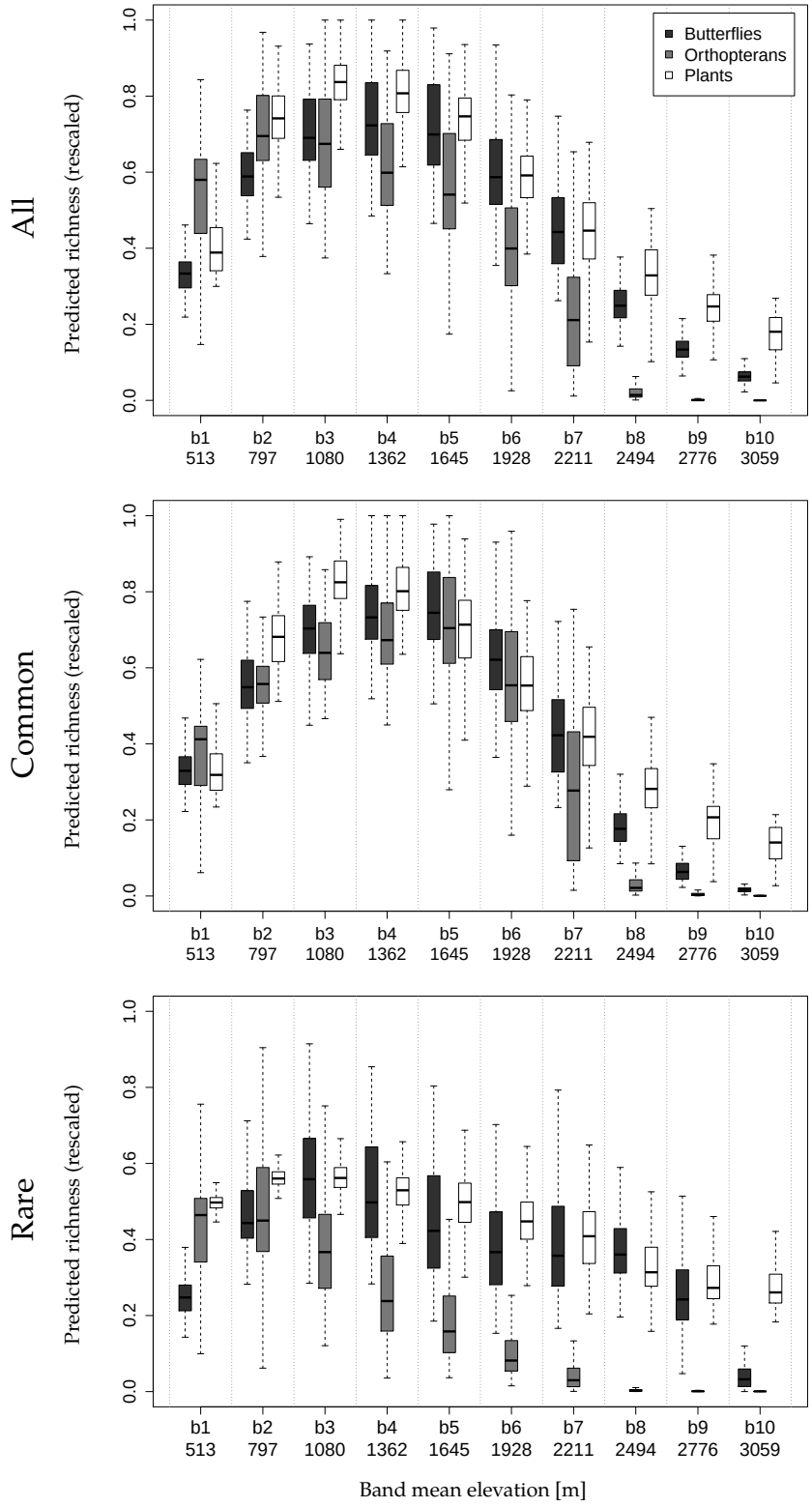

Figure 7: Predicted richness -rescaled between 0 and 1- for *all*, *common* and *rare* species of butterflies, orthopterans and plants per band of elevation (*b1* to *b10*). In each graph, the richness values of a band derive from the same set of 200 random points extracted from the projections of the groups compared.

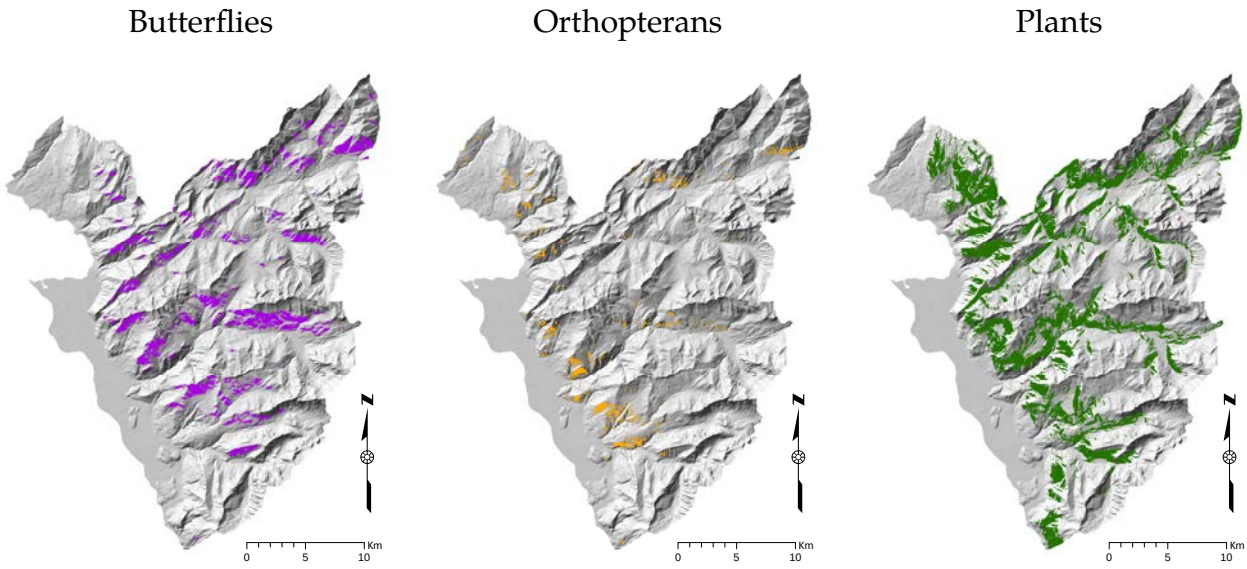

Figure 8: Maps of the sites with at least 85% of the maximal predicted richness for *all* species of butterflies (*violet*), orthopterans (*orange*) or plants (*green*).

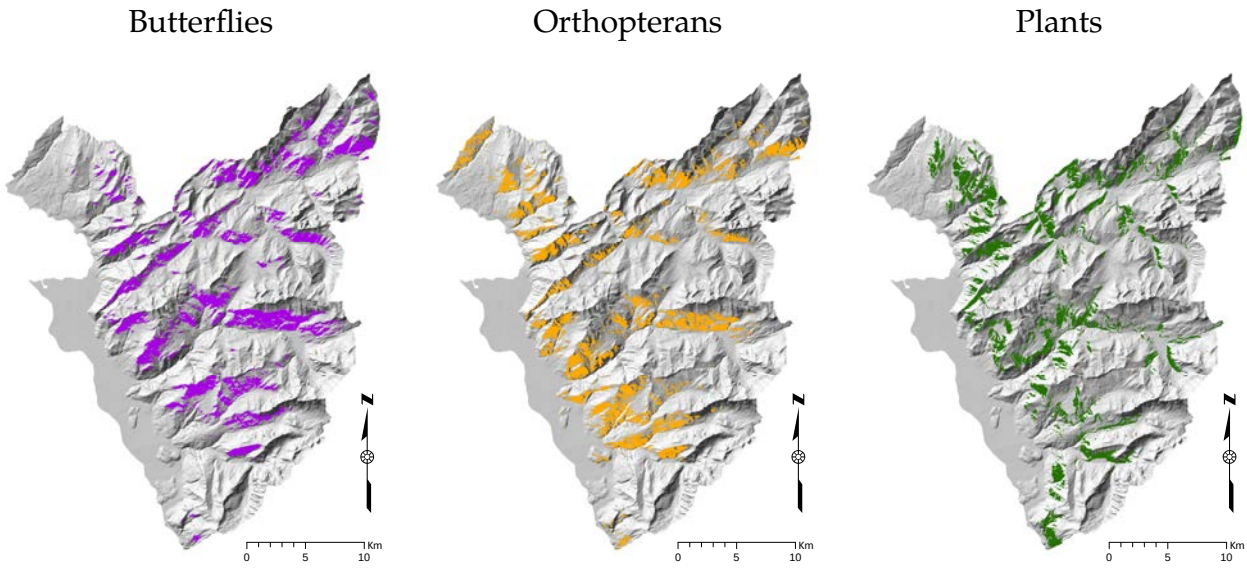

Figure 9: Maps of the predicted 10% richest sites for *all* species of butterflies (*violet*), orthopterans (*orange*) or plants (*green*).

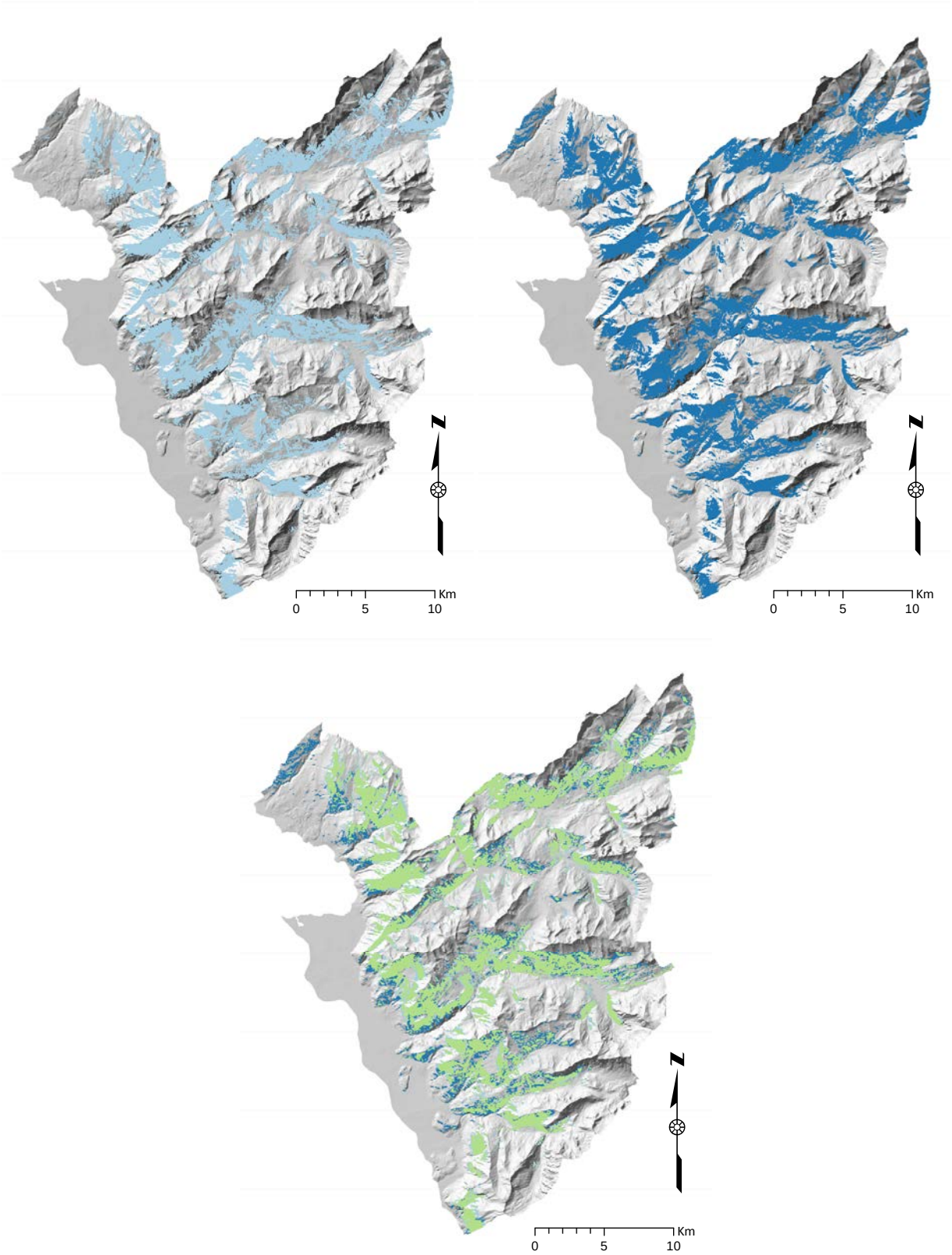

Figure 10: *Top*: Maps of the spatial distribution of the sites with at least 85% of the max. predicted richness (*light blue*) and of the 10% richest sites (*dark blue*) for all species from at least one of the three taxa. *Bottom*: Location of the overlap (*green*) areas of the two "hotspot" types defined above.

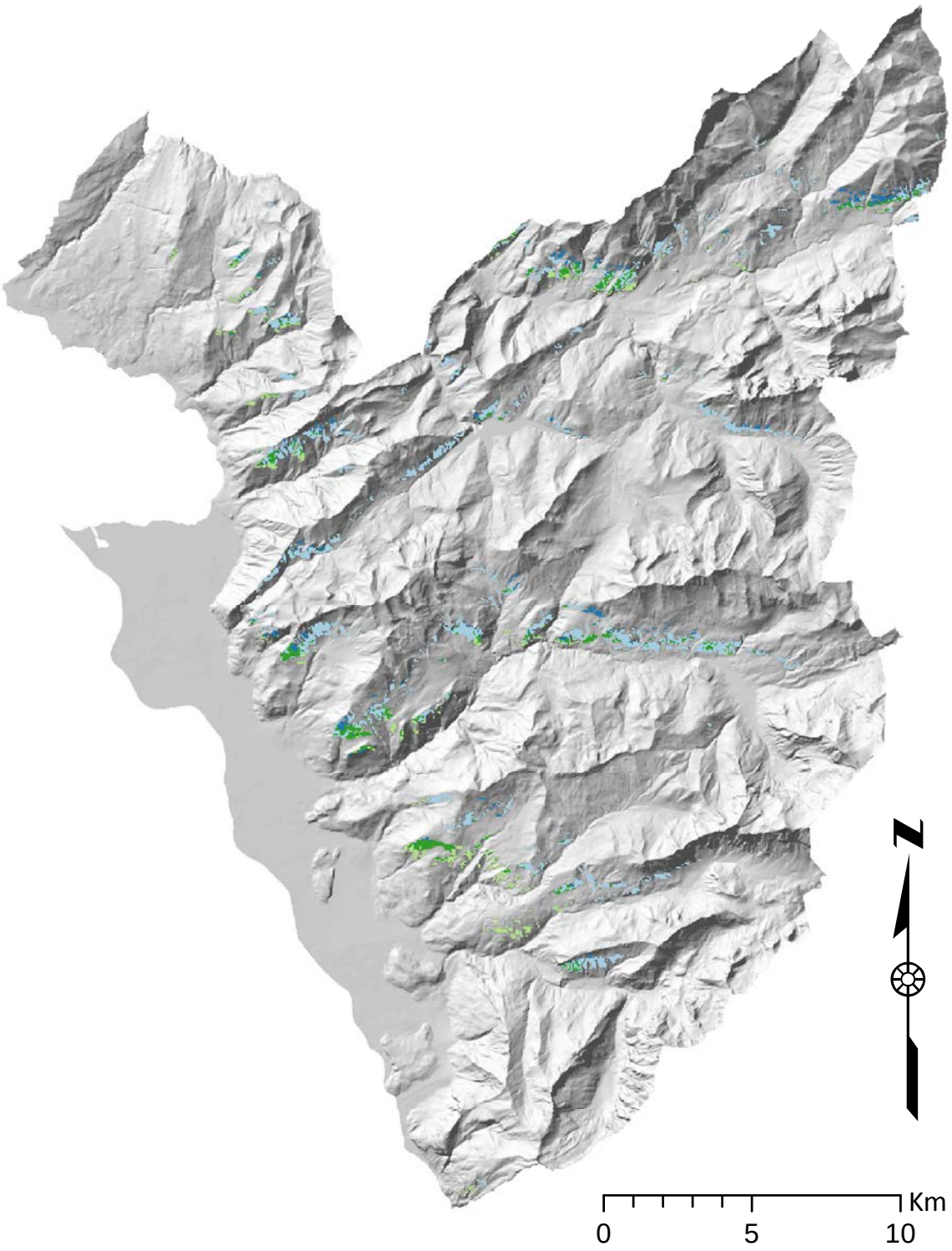

Figure 11: Location of the sites with at least 85% of the maximal predicted richness for two or three of the taxa (B, O or P) considering all species (ie. where taxa "hotspots" overlap). Legend: *dark blue*: B and O; *light blue*: B and P; *light green*: O and P ; *dark green*: B, O and P.

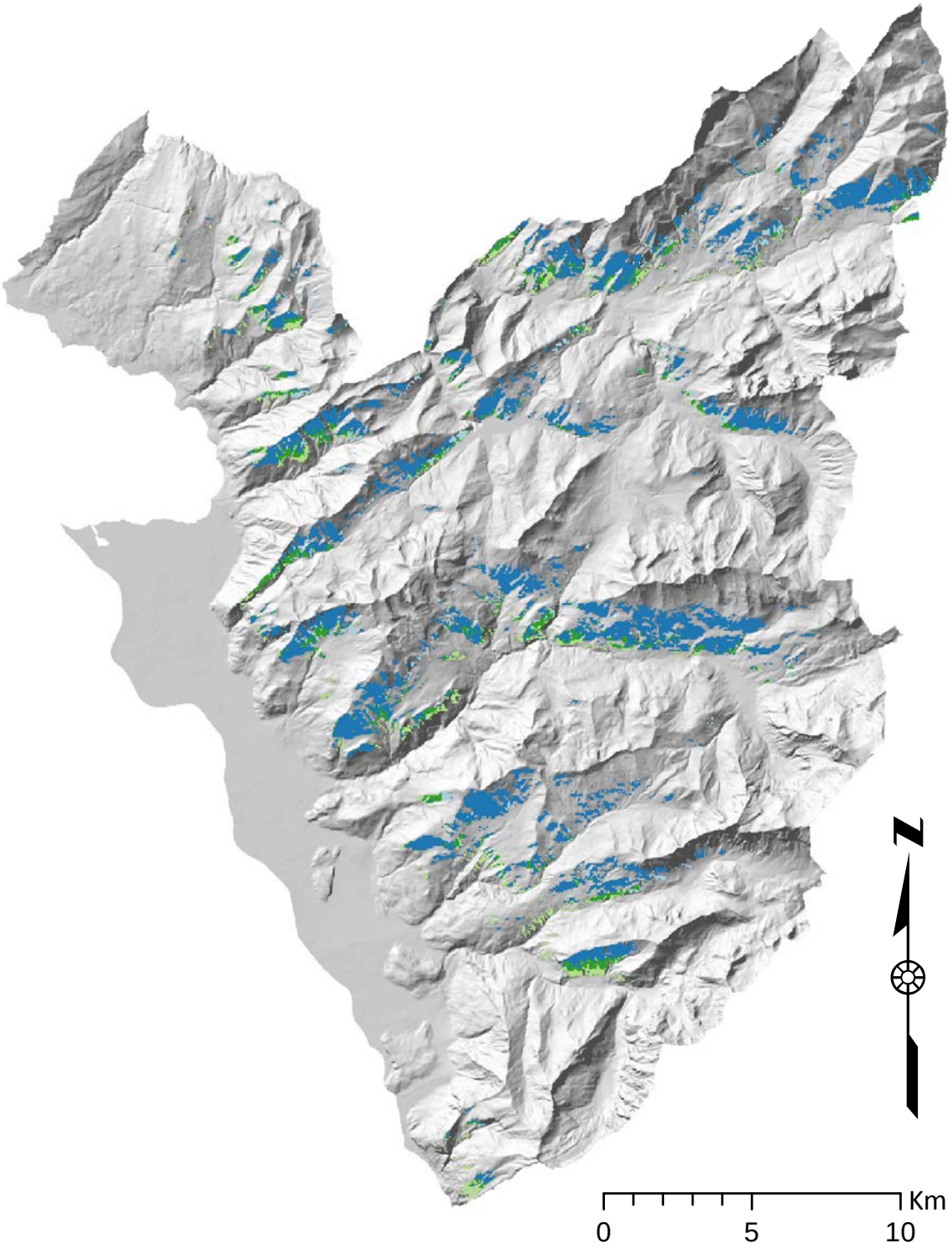

Figure 12: Maps of the predicted 10% richest sites for two or three of the taxa (B, O and P) considering all species (ie. where taxa "hotspots" overlap). Legend: *dark blue*: B and O; *light blue*: B and P; *light green*: O and P; *dark green*: B, O and P.

6 Tables

Table 1: Description of the predictors used to fit the macroecological models.

Variable	Unit	Description
degree-days	$[°C * day]$	annual sum of °C for days with a mean temperature above 3°C; a measure of heating or cooling related to the amount of heat required by an organism to develop.
frost days	$[day]$	annual average number of frost days during the growing season
normalized difference vegetation index	unitless	$[NDVI = (NIR - R)/(NIR + R)]$ where, NIR is the reflectance of the canopy in the near-infrared bands of the spectrum and R its reflectance in the red bands
slope	[°]	slope inclination
solar radiations	$[kJ * m^{-2} * day^{-1}]$	annual sum of the monthly average of the potential global solar radiation accounting for both direct and diffuse shortwave radiations

Table 2: Information on the elevational bands

Band #	1	2	3	4	5	6	7	8	9	10
Mean elev. [m]	513	797	1080	1362	1645	1928	2211	2494	2776	3059
Area [km^2]	111.1	53.5	101.8	160.6	150.3	81.2	27.8	12.2	5.0	0.6
Area [%]	15.8	7.6	14.4	22.8	21.3	11.5	3.9	1.7	0.7	0.1

Table 3: Numbers of *all* (A), *common* (C) and *rare* (R) species collected per taxon.

Taxon	A	C	R	C/A	R/A
Butterflies	139	52	87	37%	63%
Orthopterans	41	10	31	24%	76%
Plants	795	204	591	26%	74%

Table 4: Lists of the predictors retained in the final full models. Each of these was the best GLM obtained through a stepwise model selection process and was fit on the whole corresponding data set (with A for *all*, C for *common* and R for *rare* species). The stars represent the level of significance of the coefficient computed for each predictor. A hyphen appears when the variable was not used in a model.

Predictors		Butterflies			Orthopterans			Plants		
		A	C	R	A	C	R	A	C	R
linear	degree-days	***	**	***	*	-	***	***	***	***
	frost days	***	***	***	-	***	-	-	-	-
	NDVI	*	***	-	***	***	*	-	-	-
	slope	-	-	-	-	-	-	***	***	-
	solar radiations	-	-	-	-	-	-	***	***	***
quadratic	degree-days^2	***	***	***	*	***	**	***	***	***
	frost days^2	-	-	***	*	-	-	-	-	-
	NDVI^2	-	-	-	***	***	*	-	-	-
	slope^2	-	-	-	-	-	-	***	***	***
	solar radiations^2	***	***	***	***	***	***	***	***	***

Significance code: *** when $p < 0.001$; ** when $p < 0.01$; * when $p < 0.05$

Table 5: Evaluation metrics of the models built for the subsets of the three taxa with variables at a 50 m resolution: the *mean* index of deviance reduction (mD^2) and the *mean* Spearman correlation coefficient ($m\rho$) derived from the 100 models generated in the cross-validation process.

a) Explanatory power of the models

mD^2	Butterflies	Orthopterans	Plants
All species	0.470	0.722	0.278
Common species	0.592	0.683	0.297
Rare species	0.189	0.602	0.066

b) Predictive power of the models

$m\rho$ *	Butterflies	Orthopterans	Plants
All species	0.639	0.788	0.517
Common species	0.699	0.707	0.546
Rare species	0.352	0.696	0.236

* All significant, with $p < 0.05$

Table 6: Spearman correlation values (ρ) between the predicted richness of the subgroups of each taxon. For each band of elevation (*b1* to *b10*), the correlation coefficients were computed using the richness values from the same set of 200 random points extracted from the projections of the groups compared (same data sets used for boxplots). The mean across bands is also given (*mB*). The overall correlation between predictions (*wProj*) was computed using the whole projections.

Range	b1	b2	b3	b4	b5	b6	b7	b8	b9	b10	mB	wProj
Taxon: Butterflies												
A vs. C	**0.97**	**0.97**	**0.96**	**0.97**	**0.98**	**0.96**	**0.95**	**0.94**	**0.94**	**0.94**	**0.96**	**0.98**
A vs. R	**0.89**	**0.88**	**0.91**	**0.93**	**0.95**	**0.91**	**0.7**	**0.62**	**0.97**	**0.95**	**0.87**	**0.88**
C vs. R	**0.77**	**0.76**	**0.78**	**0.83**	**0.89**	**0.78**	0.47	0.36	**0.87**	**0.99**	**0.75**	**0.8**
Taxon: Orthopterans												
A vs. C	**0.98**	**0.85**	**0.92**	**0.93**	**0.95**	**0.94**	**0.99**	**0.99**	**0.96**	**0.87**	**0.94**	**0.72**
A vs. R	**0.94**	**0.95**	**0.96**	**0.97**	**0.98**	**0.97**	**0.97**	**0.89**	**0.77**	0.45	**0.89**	**0.87**
C vs. R	**0.87**	**0.67**	**0.79**	**0.83**	**0.89**	**0.86**	**0.94**	**0.87**	**0.87**	**0.74**	**0.83**	0.32
Taxon: Plants												
A vs. C	**1**	**0.98**	**0.99**	**0.99**	**0.99**	**0.99**	**0.99**	**0.98**	**0.98**	**0.99**	**0.99**	**0.99**
A vs. R	**0.94**	**0.58**	**0.75**	**0.8**	**0.78**	**0.63**	**0.59**	**0.67**	**0.69**	**0.58**	**0.70**	**0.69**
C vs. R	**0.93**	0.47	**0.66**	**0.71**	**0.68**	**0.52**	0.48	**0.55**	**0.58**	0.48	**0.61**	**0.62**

Bold: Moderate to strong correlations (*i.e.* $\rho > 0.5$) ; "n.s.": non-significant (*i.e.* $p > 0.05/30$).

Table 7: Spearman correlation values (ρ) between the predicted richness of a given subgroup of a taxon and that of it's counterpart in another taxon. For each band of elevation (*b1* to *b10*), the correlation coefficients were computed using the richness values from the same set of 200 random points extracted from the projections of the groups compared (same data sets used for boxplots). The mean across bands is also given (*mB*). The overall correlation between predictions (*wProj*) was computed using the whole projections.

Range	b1	b2	b3	b4	b5	b6	b7	b8	b9	b10	mB	wProj
Subset: All species												
B vs. O	**0.7**	0.47	**0.85**	**0.95**	**0.97**	**0.85**	**0.77**	**0.54**	**0.75**	**0.7**	**0.76**	**0.67**
B vs. P	**0.84**	**0.53**	**0.51**	0.41	**0.51**	**0.62**	**0.68**	**0.69**	**0.64**	**0.7**	**0.61**	**0.76**
O vs. P	0.38	n.s.	0.46	0.47	**0.52**	**0.55**	0.45	n.s.	n.s.	n.s.	**0.47**	**0.57**
Subset: Commons species												
B vs. O	**0.85**	**0.78**	**0.9**	**0.97**	**0.97**	**0.92**	**0.86**	**0.6**	**0.72**	**0.6**	**0.82**	**0.96**
B vs. P	**0.76**	**0.56**	0.34	0.4	0.33	**0.55**	**0.64**	0.48	**0.5**	**0.53**	**0.51**	**0.73**
O vs. P	0.44	0.3	0.35	0.4	0.25	0.46	0.42	n.s.	n.s.	n.s.	0.37	**0.68**
Subset: Rare species												
B vs. O	0.39	**0.51**	**0.91**	**0.95**	**0.98**	**0.81**	0.48	0.23	0.38	n.s.	**0.63**	0.39
B vs. P	**0.95**	**0.56**	**0.74**	**0.84**	**0.74**	**0.71**	**0.66**	**0.74**	**0.59**	0.29	**0.68**	**0.65**
O vs. P	0.41	**0.56**	**0.77**	**0.8**	**0.7**	**0.51**	**0.53**	0.42	**0.5**	n.s.	**0.58**	**0.67**

Bold: Moderate to strong correlations (*i.e.* $\rho > 0.5$) ; "n.s.": non-significant (*i.e.* $p > 0.05/30$).

Table 8: Total extent (*1a*) of the *85%-thresholded hotspots* per taxon (*H85*), (*2a*) of *top 10% hotspots* per taxon (*H10*) and (*1b* and *2b*) of their overlap, considering *all* species. The cumulative area of the three taxa hotspots for each type (*3a*) and their overlap (*3b*) are also presented.

1a) *H85* of :	B	O	P
Extent [km^2]	40.1	11.0	116.2
% on total study area	5.7	1.6	16.5
# of species	31-36	12-14	39-45

1b) *H85* of :	onlyB	onlyO	onlyP	B&O	B&P	O&P	B&O&P
Extent [km^2]	24.6	4.2	99.8	1.5	11.0	2.4	2.8
% on *H85* total extent	16.8	2.9	68.1	1.0	7.5	1.7	1.9
% on total study area	3.5	0.6	14.2	0.2	1.6	0.3	0.4

2a) *H10* of :	B	O	P
Extent [km^2]	67.9	68.5	67.1
% on total study area	9.6	9.7	9. 5
# of species	30-36	11-14	40-45

2b) *H10* of :	onlyB	onlyO	onlyP	B&O	B&P	O&P	B&O&P
Extent [km^2]	25.0	23.7	52.4	33.5	3.5	5.3	5.9
% on *H10* total extent	16.7	15.9	35.1	22.5	2.3	3.6	3.9
% on total study area	3.5	3.4	7.4	4.8	0.5	0.8	0.8

3a) Hotspots type	*H85*	*H10*
Extent [km^2]	146.5	149.3
% on total study area	20.8	21.2

3b) Hotspot type	only*H85*	only*H10*	*H85*&*H10*
Extent [km^2]	29.0	31.8	117.5
% on total extent of *H85* and *H10*	16.3	17.8	65.9
% on total study area	4.1	4.5	16.7

7 Supplementary material

Table S1: List of the butterfly species in the subsets of *common* species [>30 occurrences] and of *rare* species, number of occurrences in the study area (*Occ.*) and status in the Red List of Switzerland (*CH-RLs*; with LC: Least Concernern, NT: Nearly Threatened, VU: Vulnerable, EN: Endangered; Wermeille et al. 2014).

#	Butterflies	Occ.	CH-RLs
***Common* species subset**			
1	*Aglais urticae*	178	LC
2	*Anthocharis cardamines*	50	LC
3	*Aphantopus hyperantus*	46	LC
4	*Argynnis aglaja*	76	LC
5	*Aricia artaxerxes*	46	LC
6	*Aricia eumedon*	46	LC
7	*Boloria euphrosyne*	52	LC
8	*Boloria napaea*	34	LC
9	*Boloria pales*	72	LC
10	*Boloria titania*	76	LC
11	*Callophrys rubi*	31	LC
12	*Coenonympha gardetta*	80	LC
13	*Coenonympha pamphilus*	63	LC
14	*Colias phicomone*	70	LC
15	*Cupido minimus*	137	LC
16	*Erebia aethiops*	86	LC
17	*Erebia euryale*	38	LC
18	*Erebia ligea*	48	LC
19	*Erebia manto*	87	LC
20	*Erebia melampus*	94	LC
21	*Erebia oeme*	78	LC
22	*Erebia pandrose*	39	LC
23	*Erebia pharte*	57	LC
24	*Erynnis tages*	56	LC
25	*Euphydryas aurinia*	64	LC
26	*Hesperia comma*	37	LC

#	Butterflies	Occ.	CH-RLs
27	*Lasiommata maera*	64	LC
28	*Lasiommata petropolitana*	34	LC
29	*Leptidea reali/sinapis*	62	LC
30	*Lycaena hippothoe*	36	LC
31	*Lycaena tityrus*	42	LC
32	*Maniola jurtina*	61	LC
33	*Melanargia galathea*	49	LC
34	*Melitaea athalia*	42	LC
35	*Ochlodes venata*	39	LC
36	*Papilio machaon*	92	LC
37	*Pieris brassicae*	47	LC
38	*Pieris bryoniae*	76	LC
39	*Pieris napi*	74	LC
40	*Pieris rapae*	78	LC
41	*Polyommatus coridon*	40	LC
42	*Polyommatus icarus*	66	LC
43	*Polyommatus semiargus*	113	LC
44	*Pyrgus alveus*	33	LC
45	*Pyrgus serratulae*	37	LC
46	*Thymelicus lineola*	80	LC
47	*Thymelicus sylvestris*	37	LC
48	*Vanessa cardui*	56	LC
49	*Zygaena filipendulae*	58	LC
50	*Aporia crataegi*	64	NT
51	*Maculinea arion*	49	NT
52	*Melitaea diamina*	64	NT
53	*Euphydryas aurinia*	64	EN
***Rare* species subset**			
54	*Argynnis adippe*	19	LC
55	*Argynnis niobe*	26	LC
56	*Argynnis paphia*	10	LC
57	*Aricia agestis*	3	LC

#	Butterflies	Occ.	CH-RLs
58	*Brenthis daphne*	9	LC
59	*Carterocephalus palaemon*	18	LC
60	*Celastrina argiolus*	2	LC
61	*Colias alfacariensis*	21	LC
62	*Colias croceus*	21	LC
63	*Colias hyale*	10	LC
64	*Erebia alberganus*	6	LC
65	*Erebia cassioides*	12	LC
66	*Erebia epiphron*	28	LC
67	*Erebia eriphyle*	6	LC
68	*Erebia gorge*	22	LC
69	*Erebia meolans*	9	LC
70	*Erebia mnestra*	1	LC
71	*Erebia montana*	6	LC
72	*Erebia pluto*	18	LC
73	*Erebia pronoe*	23	LC
74	*Erebia tyndarus*	29	LC
75	*Gonepteryx rhamni*	1	LC
76	*Inachis io*	10	LC
77	*Issoria lathonia*	11	LC
78	*Lasiommata megera*	9	LC
79	*Limenitis camilla*	1	LC
80	*Lycaena phlaeas*	3	LC
81	*Oeneis glacialis*	5	LC
82	*Pararge aegeria*	9	LC
83	*Parnassius phoebus*	6	LC
84	*Plebeius glandon*	18	LC
85	*Plebeius orbitulus*	10	LC
86	*Polygonia c-album*	8	LC
87	*Polyommatus bellargus*	23	LC
88	*Polyommatus eros*	27	LC
89	*Pyrgus andromedae*	9	LC
90	*Pyrgus cacaliae*	10	LC

#	Butterflies	Occ.	CH-RLs
91	*Pyrgus malvae*	25	LC
92	*Pyrgus malvoides*	4	LC
93	*Vanessa atalanta*	29	LC
94	*Zygaena exulans*	24	LC
95	*Zygaena lonicerae*	23	LC
96	*Zygaena loti*	15	LC
97	*Zygaena transalpina*	28	LC
98	*Adscita geryon*	22	NT
99	*Adscita statices*	4	NT
100	*Apatura iris*	1	NT
101	*Boloria dia*	11	NT
102	*Boloria selene*	2	NT
103	*Brenthis ino*	17	NT
104	*Brintesia circe*	8	NT
105	*Colias palaeno*	6	NT
106	*Cupido alcetas*	6	NT
107	*Cupido argiades*	8	NT
108	*Erebia medusa*	6	NT
109	*Euphydryas cynthia*	3	NT
110	*Hamearis lucina*	12	NT
111	*Minois dryas*	3	NT
112	*Parnassius apollo*	21	NT
113	*Pieris mannii*	1	NT
114	*Plebeius argus*	19	NT
115	*Plebeius idas*	7	NT
116	*Polyommatus dorylas*	9	NT
117	*Pontia callidice*	12	NT
118	*Spialia sertorius*	16	NT
119	*Zygaena purpuralis*	5	NT
120	*Euchloe simplonia*	6	VU
121	*Glaucopsyche alexis*	1	VU
122	*Lycaena alciphron*	1	VU
123	*Lycaena helle*	5	VU

#	Butterflies	Occ.	CH-RLs
124	*Maculinea rebeli*	1	VU
125	*Melitaea cinxia*	5	VU
126	*Melitaea parthenoides*	12	VU
127	*Nymphalis antiopa*	1	VU
128	*Parnassius mnemosyne*	8	VU
129	*Polyommatus damon*	27	VU
130	*Polyommatus thersites*	15	VU
131	*Pyrgus carlinae*	3	VU
132	*Zygaena fausta*	4	VU
133	*Boloria aquilonaris*	2	EN
134	*Carcharodus floccifera*	1	EN
135	*Cupido osiris*	2	EN
136	*Maculinea alcon*	1	EN
137	*Maculinea nausithous*	2	EN
138	*Melitaea aurelia*	1	EN
139	*Macroglossum stellatarum*	26	NA

Table S2: List of the orthopteran species in the subsets of *common* species [>30 occurrences] and of *rare* species, number of occurrences in the study area (*Occ.*) and status in the Red List of Switzerland (*CH-RLs*; with LC: Least Concernern, NT: Nearly Threatened, VU: Vulnerable; Monnerat et al. 2007).

#	Orthopterans	Occ.	CH-RLs
***Common* species subset**			
1	*Chorthippus biguttulus*	71	LC
2	*Chorthippus parallelus*	137	LC
3	*Euthystira brachyptera*	79	LC
4	*Metrioptera roeselii*	63	LC
5	*Metrioptera saussuriana*	105	LC
6	*Miramella alpina*	110	LC
7	*Omocestus viridulus*	99	LC
8	*Stauroderus scalaris*	89	LC

#	Orthopterans	Occ.	CH-RLs
9	*Stenobothrus lineatus*	42	LC
10	*Polysarcus denticauda*	32	NT
***Rare* species subset**			
11	*Barbitistes serricauda*	1	LC
12	*Chorthippus apricarius*	10	LC
13	*Chorthippus brunneus*	21	LC
14	*Chorthippus dorsatus*	17	LC
15	*Gomphocerippus rufus*	19	LC
16	*Gomphocerus sibiricus*	15	LC
17	*Gryllus campestris*	16	LC
18	*Leptophyes punctatissima*	2	LC
19	*Meconema meridionale*	2	LC
20	*Mecostethus parapleurus*	17	LC
21	*Nemobius sylvestris*	9	LC
22	*Pholidoptera griseoaptera*	25	LC
23	*Podisma pedestris*	21	LC
24	*Tetrix subulata*	1	LC
25	*Tetrix tenuicornis*	3	LC
26	*Tettigonia cantans*	29	LC
27	*Tettigonia viridissima*	12	LC
28	*Chrysochraon dispar*	10	NT
29	*Decticus verrucivorus*	26	NT
30	*Oedipoda caerulescens*	3	NT
31	*Omocestus rufipes*	3	NT
32	*Platycleis albopunctata albopunctata*	13	NT
33	*Ruspolia nitidula*	3	NT
34	*Tetrix bipunctata*	9	NT
35	*Anonconotus alpinus*	5	VU
36	*Arcyptera fusca*	10	VU
37	*Chorthippus montanus*	6	VU
38	*Oedipoda germanica*	1	VU
39	*Phaneroptera falcata*	3	VU

#	Orthopterans	Occ.	CH-RLs
40	*Psophus stridulus*	10	VU
41	*Stethophyma grossum*	6	VU

Table S3: List of the vascular plant species in the subsets of *common* species [>30 occurrences] and of *rare* species, number of occurrences in the study area (*Occ.*) and status in the Red List of Switzerland (*CH-RLs*; with LC: Least Concernern, NT: Nearly Threatened, VU: Vulnerable, EN: Endangered, CR: Critically endangered; Regionally Extinct and NA: Non-Assessed; Moser et al. 2002).

#	Plants	Occ.	CH-RLs
	***Common* species subset**		
1	*Acer pseudoplatanus*	45	LC
2	*Achillea millefolium*	125	LC
3	*Acinos alpinus*	31	LC
4	*Adenostyles glabra*	38	LC
5	*Agrostis capillaris*	284	LC
6	*Agrostis rupestris*	38	LC
7	*Agrostis stolonifera*	36	LC
8	*Ajuga reptans*	140	LC
9	*Alchemilla conjuncta* aggr.	139	LC
10	*Alchemilla coriacea* aggr.	56	LC
11	*Alchemilla glabra* aggr.	57	LC
12	*Alchemilla vulgaris* aggr.	165	LC
13	*Androsace chamaejasme*	37	LC
14	*Aposeris foetida*	96	LC
15	*Arnica montana*	45	LC
16	*Arrhenatherum elatius*	87	LC
17	*Aster bellidiastrum*	120	LC
18	*Astrantia major*	127	LC
19	*Bartsia alpina*	97	LC
20	*Bellis perennis*	52	LC
21	*Brachypodium pinnatum*	79	LC

#	Plants	Occ.	CH-RLs
22	*Briza media*	165	LC
23	*Bromus erectus* s.str.	89	LC
24	*Calamagrostis varia*	56	LC
25	*Campanula barbata*	35	LC
26	*Campanula cochleariifolia*	82	LC
27	*Campanula rhomboidalis*	82	LC
28	*Campanula rotundifolia*	60	LC
29	*Campanula scheuchzeri*	234	LC
30	*Cardamine pratensis*	36	LC
31	*Carex caryophyllea*	36	LC
32	*Carex ferruginea*	81	LC
33	*Carex flacca*	131	LC
34	*Carex montana*	70	LC
35	*Carex nigra*	36	LC
36	*Carex pallescens*	96	LC
37	*Carex sempervirens*	232	LC
38	*Carex sylvatica*	32	LC
39	*Carlina acaulis* subsp. *caulescens*	79	LC
40	*Carum carvi*	109	LC
41	*Centaurea jacea* s.str.	58	LC
42	*Centaurea montana*	34	LC
43	*Cerastium latifolium*	54	LC
44	*Cirsium acaule*	44	LC
45	*Cirsium palustre*	33	LC
46	*Cirsium spinosissimum*	43	LC
47	*Crepis aurea*	95	LC
48	*Crepis biennis*	41	LC
49	*Crepis pyrenaica*	78	LC
50	*Crocus albiflorus*	95	LC
51	*Cruciata laevipes*	33	LC
52	*Cynosurus cristatus*	218	LC
53	*Dactylis glomerata*	344	LC
54	*Dactylorhiza fuchsii*	65	LC

#	Plants	Occ.	CH-RLs
55	*Daucus carota*	64	LC
56	*Deschampsia cespitosa*	122	LC
57	*Dryas octopetala*	61	LC
58	*Euphorbia cyparissias*	83	LC
59	*Euphrasia minima*	127	LC
60	*Euphrasia salisburgensis*	33	LC
61	*Festuca quadriflora*	87	LC
62	*Fraxinus excelsior*	43	LC
63	*Galium album*	87	LC
64	*Galium anisophyllon*	203	LC
65	*Galium megalospermum*	37	LC
66	*Galium pumilum*	56	LC
67	*Gentiana acaulis*	32	LC
68	*Gentiana campestris* s.str.	76	LC
69	*Gentiana lutea*	68	LC
70	*Gentiana purpurea*	65	LC
71	*Gentiana verna*	48	LC
72	*Geranium sylvaticum*	251	LC
73	*Geum montanum*	61	LC
74	*Geum rivale*	38	LC
75	*Glechoma hederacea* s.str.	37	LC
76	*Gypsophila repens*	31	LC
77	*Hedysarum hedysaroides*	34	LC
78	*Helictotrichon pubescens*	66	LC
79	*Helictotrichon versicolor*	54	LC
80	*Hieracium bifidum* aggr.	51	LC
81	*Hieracium lactucella*	100	LC
82	*Hieracium murorum* aggr.	71	LC
83	*Hippocrepis comosa*	61	LC
84	*Holcus lanatus*	122	LC
85	*Homogyne alpina*	188	LC
86	*Hypochaeris radicata*	55	LC
87	*Knautia arvensis*	47	LC

#	Plants	Occ.	CH-RLs
88	*Knautia dipsacifolia* s.str.	88	LC
89	*Laserpitium latifolium*	38	LC
90	*Lathyrus pratensis*	169	LC
91	*Leontodon autumnalis*	54	LC
92	*Leontodon helveticus*	55	LC
93	*Ligusticum mutellina*	150	LC
94	*Linaria alpina* s.str.	32	LC
95	*Linum catharticum*	83	LC
96	*Lolium perenne*	113	LC
97	*Luzula campestris*	54	LC
98	*Luzula multiflora*	68	LC
99	*Luzula sylvatica*	54	LC
100	*Medicago lupulina*	60	LC
101	*Myosotis alpestris*	54	LC
102	*Nardus stricta*	117	LC
103	*Parnassia palustris*	45	LC
104	*Phleum hirsutum*	54	LC
105	*Phleum pratense*	63	LC
106	*Phleum rhaeticum*	134	LC
107	*Phyteuma orbiculare*	110	LC
108	*Phyteuma spicatum*	74	LC
109	*Picea abies*	47	LC
110	*Pimpinella major*	116	LC
111	*Plantago alpina*	138	LC
112	*Plantago atrata* s.str.	109	LC
113	*Plantago lanceolata*	270	LC
114	*Plantago media*	107	LC
115	*Poa alpina*	195	LC
116	*Poa minor*	39	LC
117	*Poa pratensis*	75	LC
118	*Polygala alpestris*	48	LC
119	*Polygala chamaebuxus*	35	LC
120	*Polygonum bistorta*	60	LC

#	Plants	Occ.	CH-RLs
121	*Polygonum viviparum*	210	LC
122	*Potentilla aurea*	174	LC
123	*Potentilla crantzii*	56	LC
124	*Potentilla erecta*	192	LC
125	*Primula elatior* s.str.	86	LC
126	*Pritzelago alpina* s.str.	60	LC
127	*Prunella grandiflora*	65	LC
128	*Prunella vulgaris*	233	LC
129	*Ranunculus aconitifolius*	42	LC
130	*Ranunculus alpestris*	65	LC
131	*Ranunculus bulbosus*	65	LC
132	*Ranunculus repens*	42	LC
133	*Rhinanthus alectorolophus*	83	LC
134	*Rumex acetosa*	192	LC
135	*Rumex alpestris*	45	LC
136	*Salix herbacea*	31	LC
137	*Salix retusa*	85	LC
138	*Saxifraga aizoides*	79	LC
139	*Saxifraga oppositifolia*	64	LC
140	*Saxifraga paniculata*	65	LC
141	*Scabiosa lucida*	141	LC
142	*Sedum atratum*	33	LC
143	*Selaginella selaginoides*	100	LC
144	*Senecio doronicum*	38	LC
145	*Sesleria caerulea*	179	LC
146	*Silene acaulis*	47	LC
147	*Soldanella alpina*	185	LC
148	*Stellaria graminea*	58	LC
149	*Taraxacum officinale* aggr.	269	LC
150	*Thesium alpinum*	37	LC
151	*Thlaspi rotundifolium* s.str.	55	LC
152	*Thymus praecox* subsp. *polytrichus*	72	LC
153	*Thymus pulegioides* s.str.	103	LC

#	Plants	Occ.	CH-RLs
154	*Trifolium badium*	61	LC
155	*Trifolium medium*	67	LC
156	*Trifolium repens* s.str.	334	LC
157	*Trifolium thalii*	59	LC
158	*Trisetum flavescens*	166	LC
159	*Trollius europaeus*	134	LC
160	*Vaccinium gaultherioides*	43	LC
161	*Vaccinium myrtillus*	71	LC
162	*Vaccinium vitis idaea*	35	LC
163	*Valeriana montana*	39	LC
164	*Veratrum album* subsp. *lobelianum*	68	LC
165	*Veronica alpina*	38	LC
166	*Veronica aphylla*	42	LC
167	*Veronica arvensis*	39	LC
168	*Veronica chamaedrys*	245	LC
169	*Vicia cracca* s.str.	64	LC
170	*Vicia sepium*	77	LC
171	*Viola biflora*	48	LC
172	*Alchemilla xanthochlora* aggr.	243	NA
173	*Hieracium villosum* aggr.	35	NA
174	*Leucanthemum vulgare* aggr.	256	NA
175	*Anthoxanthum odoratum* aggr.	384	NA
176	*Anthyllis vulneraria* s.l.	161	NA
177	*Arabis alpina* s.l.	35	NA
178	*Carduus defloratus* s.l.	96	NA
179	*Cerastium fontanum* s.l.	197	NA
180	*Chaerophyllum hirsutum* aggr.	104	NA
181	*Festuca ovina* aggr.	37	NA
182	*Festuca pratensis* s.l.	224	NA
183	*Festuca rubra* aggr.	434	NA
184	*Festuca violacea* aggr.	105	NA
185	*Helianthemum nummularium* s.l.	120	NA
186	*Heracleum sphondylium* s.l.	93	NA

#	Plants	Occ.	CH-RLs
187	*Hypericum maculatum* s.l.	75	NA
188	*Leontodon hispidus* s.l.	355	NA
189	*Lotus corniculatus* aggr.	381	NA
190	*Pimpinella saxifraga* aggr.	36	NA
191	*Plantago major* s.l.	54	NA
192	*Poa trivialis* s.l.	145	NA
193	*Polygala vulgaris* s.l.	66	NA
194	*Primula veris* s.l.	66	NA
195	*Pulsatilla alpina* s.l.	73	NA
196	*Ranunculus acris* s.l.	285	NA
197	*Ranunculus montanus* aggr.	207	NA
198	*Ranunculus nemorosus* aggr.	144	NA
199	*Sanguisorba minor* s.l.	92	NA
200	*Silene vulgaris* s.l.	87	NA
201	*Solidago virgaurea* s.l.	42	NA
202	*Tragopogon pratensis* s.l.	52	NA
203	*Trifolium pratense* s.l.	421	NA
204	*Veronica serpyllifolia* s.l.	68	NA
	***Rare* species subset**		
205	*Abies alba*	10	LC
206	*Acer campestre*	4	LC
207	*Acer platanoides*	1	LC
208	*Achillea atrata*	27	LC
209	*Achillea macrophylla*	1	LC
210	*Achnatherum calamagrostis*	4	LC
211	*Acinos arvensis*	3	LC
212	*Aconitum neomontanum*	3	LC
213	*Adenostyles alliariae*	19	LC
214	*Aegopodium podagraria*	6	LC
215	*Agrimonia eupatoria*	9	LC
216	*Agropyron repens*	7	LC
217	*Agrostis alpina*	27	LC

#	Plants	Occ.	CH-RLs
218	*Agrostis gigantea*	1	LC
219	*Agrostis schleicheri*	1	LC
220	*Agrostis schraderiana*	23	LC
221	*Ajuga pyramidalis*	4	LC
222	*Alchemilla alpina* aggr.	5	LC
223	*Alchemilla decumbens* aggr.	12	LC
224	*Alchemilla firma* aggr.	1	LC
225	*Alchemilla fissa*	9	LC
226	*Alchemilla hybrida* aggr.	6	LC
227	*Alchemilla pentaphyllea*	12	LC
228	*Allium lusitanicum*	5	LC
229	*Allium oleraceum*	4	LC
230	*Allium schoenoprasum*	17	LC
231	*Allium sphaerocephalon*	1	LC
232	*Allium victorialis*	1	LC
233	*Allium vineale*	2	LC
234	*Alnus glutinosa*	1	LC
235	*Alnus viridis*	8	LC
236	*Alopecurus pratensis*	9	LC
237	*Androsace helvetica*	12	LC
238	*Androsace puberula*	1	LC
239	*Androsace vandellii*	1	LC
240	*Anemone narcissiflora*	24	LC
241	*Anemone nemorosa*	16	LC
242	*Angelica sylvestris*	4	LC
243	*Antennaria carpatica*	8	LC
244	*Antennaria dioica*	14	LC
245	*Anthericum liliago*	2	LC
246	*Anthericum ramosum*	2	LC
247	*Anthriscus sylvestris*	25	LC
248	*Aquilegia atrata*	1	LC
249	*Aquilegia vulgaris*	1	LC
250	*Arabis bellidifolia* s.str.	11	LC

#	Plants	Occ.	CH-RLs
251	*Arabis caerulea*	17	LC
252	*Arabis ciliata*	12	LC
253	*Arabis hirsuta*	8	LC
254	*Arctostaphylos alpina*	6	LC
255	*Arctostaphylos uva ursi*	6	LC
256	*Arenaria ciliata*	8	LC
257	*Arenaria multicaulis*	7	LC
258	*Arenaria serpyllifolia*	5	LC
259	*Artemisia genipi*	2	LC
260	*Artemisia umbelliformis*	1	LC
261	*Asperula cynanchica*	1	LC
262	*Asplenium ruta muraria*	2	LC
263	*Asplenium trichomanes*	3	LC
264	*Asplenium viride*	18	LC
265	*Aster alpinus*	8	LC
266	*Astragalus alpinus*	8	LC
267	*Astragalus frigidus*	9	LC
268	*Astragalus glycyphyllos*	1	LC
269	*Astrantia minor*	13	LC
270	*Athamanta cretensis*	20	LC
271	*Athyrium distentifolium*	1	LC
272	*Athyrium filix femina*	2	LC
273	*Avenella flexuosa*	18	LC
274	*Barbarea vulgaris*	5	LC
275	*Betula pubescens*	2	LC
276	*Biscutella laevigata*	14	LC
277	*Blysmus compressus*	5	LC
278	*Botrychium lunaria*	26	LC
279	*Bromus benekenii*	1	LC
280	*Bromus hordeaceus*	27	LC
281	*Bromus inermis*	1	LC
282	*Bromus squarrosus*	1	LC
283	*Bromus sterilis*	1	LC

#	Plants	Occ.	CH-RLs
284	*Buphthalmum salicifolium*	9	LC
285	*Calamagrostis epigejos*	1	LC
286	*Calamagrostis villosa*	1	LC
287	*Caltha palustris*	24	LC
288	*Calystegia sepium*	1	LC
289	*Campanula cenisia*	4	LC
290	*Campanula rapunculoides*	1	LC
291	*Campanula thyrsoides*	3	LC
292	*Campanula trachelium*	1	LC
293	*Capsella bursa pastoris*	7	LC
294	*Cardamine hirsuta*	8	LC
295	*Cardamine rivularis*	1	LC
296	*Carduus crispus*	1	LC
297	*Carduus personata*	2	LC
298	*Carex canescens*	2	LC
299	*Carex capillaris*	9	LC
300	*Carex curvula* subsp. *rosae*	1	LC
301	*Carex davalliana*	7	LC
302	*Carex echinata*	11	LC
303	*Carex firma*	12	LC
304	*Carex flava*	16	LC
305	*Carex foetida*	5	LC
306	*Carex halleriana*	1	LC
307	*Carex hirta*	8	LC
308	*Carex hostiana*	5	LC
309	*Carex leporina*	13	LC
310	*Carex ornithopoda*	28	LC
311	*Carex ornithopodioides*	6	LC
312	*Carex panicea*	24	LC
313	*Carex paniculata*	7	LC
314	*Carex parviflora*	7	LC
315	*Carex pilulifera*	2	LC
316	*Carex rostrata*	2	LC

#	Plants	Occ.	CH-RLs
317	*Carex rupestris*	2	LC
318	*Carex spicata*	4	LC
319	*Carex tomentosa*	1	LC
320	*Carex umbrosa*	2	LC
321	*Carlina vulgaris*	5	LC
322	*Carpinus betulus*	1	LC
323	*Centaurea nervosa*	1	LC
324	*Cephalanthera rubra*	1	LC
325	*Cerastium cerastoides*	5	LC
326	*Cerastium glomeratum*	1	LC
327	*Cerastium semidecandrum*	1	LC
328	*Cerinthe glabra*	2	LC
329	*Chaerophyllum aureum*	17	LC
330	*Chamorchis alpina*	2	LC
331	*Chenopodium album*	1	LC
332	*Chenopodium bonus henricus*	3	LC
333	*Cicerbita alpina*	1	LC
334	*Cirsium arvense*	11	LC
335	*Cirsium eriophorum* s.str.	16	LC
336	*Cirsium erisithales*	1	LC
337	*Cirsium oleraceum*	21	LC
338	*Cirsium rivulare*	7	LC
339	*Cirsium vulgare*	9	LC
340	*Clinopodium vulgare*	30	LC
341	*Coeloglossum viride*	19	LC
342	*Colchicum autumnale*	27	LC
343	*Convallaria majalis*	1	LC
344	*Convolvulus arvensis*	11	LC
345	*Coronilla vaginalis*	3	LC
346	*Cotoneaster integerrimus*	5	LC
347	*Crataegus monogyna*	1	LC
348	*Crepis alpestris*	1	LC
349	*Crepis bocconei*	5	LC

#	Plants	Occ.	CH-RLs
350	*Crepis conyzifolia*	4	LC
351	*Crepis paludosa*	12	LC
352	*Crepis vesicaria* subsp. *taraxacifolia*	0	LC
353	*Cuscuta epithymum*	5	LC
354	*Cystopteris alpina*	5	LC
355	*Cystopteris fragilis*	15	LC
356	*Dactylorhiza fistulosa*	4	LC
357	*Danthonia decumbens*	7	LC
358	*Daphne mezereum*	8	LC
359	*Dianthus sylvestris*	3	LC
360	*Digitalis grandiflora*	5	LC
361	*Digitalis lutea*	1	LC
362	*Doronicum grandiflorum*	27	LC
363	*Draba aizoides*	14	LC
364	*Draba dubia*	1	LC
365	*Draba tomentosa*	1	LC
366	*Dryopteris filix mas*	2	LC
367	*Dryopteris villarii*	8	LC
368	*Echium vulgare*	2	LC
369	*Elyna myosuroides*	18	LC
370	*Empetrum nigrum* subsp. *hermaphroditum*	2	LC
371	*Epilobium alpestre*	5	LC
372	*Epilobium alsinifolium*	3	LC
373	*Epilobium anagallidifolium*	14	LC
374	*Epilobium angustifolium*	5	LC
375	*Epilobium fleischeri*	4	LC
376	*Epilobium hirsutum*	1	LC
377	*Epilobium montanum*	8	LC
378	*Epilobium nutans*	1	LC
379	*Epilobium palustre*	5	LC
380	*Epilobium parviflorum*	2	LC
381	*Epilobium tetragonum* s.str.	1	LC
382	*Epipactis atrorubens*	3	LC

#	Plants	Occ.	CH-RLs
383	*Equisetum arvense*	9	LC
384	*Equisetum fluviatile*	1	LC
385	*Equisetum palustre*	28	LC
386	*Equisetum sylvaticum*	13	LC
387	*Equisetum telmateia*	1	LC
388	*Erica carnea*	4	LC
389	*Erigeron alpinus*	6	LC
390	*Erigeron glabratus*	6	LC
391	*Erigeron neglectus*	1	LC
392	*Erigeron uniflorus*	21	LC
393	*Erinus alpinus*	3	LC
394	*Eriophorum angustifolium*	1	LC
395	*Eriophorum latifolium*	3	LC
396	*Eriophorum scheuchzeri*	2	LC
397	*Eriophorum vaginatum*	1	LC
398	*Eupatorium cannabinum*	1	LC
399	*Euphorbia amygdaloides*	1	LC
400	*Euphorbia dulcis*	1	LC
401	*Euphrasia alpina*	1	LC
402	*Euphrasia hirtella*	26	LC
403	*Euphrasia picta* s.str.	2	LC
404	*Euphrasia rostkoviana* s.str.	3	LC
405	*Euphrasia stricta*	4	LC
406	*Fagus sylvatica*	2	LC
407	*Festuca acuminata*	1	LC
408	*Festuca alpina*	8	LC
409	*Festuca gigantea*	1	LC
410	*Festuca heterophylla*	1	LC
411	*Festuca nigrescens*	0	LC
412	*Festuca pulchella* s.str.	1	LC
413	*Festuca rupicaprina*	1	LC
414	*Filipendula ulmaria*	19	LC
415	*Fragaria vesca*	29	LC

#	Plants	Occ.	CH-RLs
416	*Galeopsis tetrahit*	15	LC
417	*Galium aparine*	4	LC
418	*Galium boreale*	5	LC
419	*Galium lucidum*	2	LC
420	*Galium mollugo*	20	LC
421	*Galium palustre*	1	LC
422	*Galium rotundifolium*	1	LC
423	*Genista sagittalis*	5	LC
424	*Gentiana asclepiadea*	4	LC
425	*Gentiana bavarica*	21	LC
426	*Gentiana brachyphylla*	13	LC
427	*Gentiana ciliata*	7	LC
428	*Gentiana clusii*	24	LC
429	*Gentiana nivalis*	20	LC
430	*Gentiana orbicularis*	1	LC
431	*Gentiana punctata*	3	LC
432	*Gentiana tenella*	4	LC
433	*Geranium columbinum*	2	LC
434	*Geranium dissectum*	3	LC
435	*Geranium molle*	2	LC
436	*Geranium pusillum*	1	LC
437	*Geranium pyrenaicum*	6	LC
438	*Geranium sanguineum*	7	LC
439	*Geum reptans*	4	LC
440	*Geum urbanum*	16	LC
441	*Globularia bisnagarica*	1	LC
442	*Globularia cordifolia*	28	LC
443	*Globularia nudicaulis*	25	LC
444	*Glyceria notata*	1	LC
445	*Gnaphalium hoppeanum*	3	LC
446	*Gnaphalium norvegicum*	11	LC
447	*Gnaphalium supinum*	13	LC
448	*Gnaphalium sylvaticum*	16	LC

#	Plants	Occ.	CH-RLs
449	*Gymnadenia conopsea*	27	LC
450	*Gymnocarpium robertianum*	2	LC
451	*Hedera helix*	1	LC
452	*Helianthemum alpestre*	11	LC
453	*Helictotrichon pratense*	6	LC
454	*Helleborus foetidus*	2	LC
455	*Hieracium alpinum*	5	LC
456	*Hieracium angustifolium*	3	LC
457	*Hieracium bupleuroides*	2	LC
458	*Hieracium lachenalii*	7	LC
459	*Hieracium laevigatum* aggr.	1	LC
460	*Hieracium piliferum* aggr.	5	LC
461	*Hieracium pilosella*	17	LC
462	*Hieracium piloselloides*	2	LC
463	*Hieracium pilosum*	9	LC
464	*Hieracium prenanthoides* aggr.	4	LC
465	*Hieracium sabaudum* aggr.	1	LC
466	*Hieracium staticifolium*	1	LC
467	*Hieracium umbellatum*	1	LC
468	*Holcus mollis*	1	LC
469	*Huperzia selago*	2	LC
470	*Hypericum montanum*	6	LC
471	*Hypericum perforatum* s.str.	17	LC
472	*Hypericum x desetangsii*	1	LC
473	*Inula conyzae*	1	LC
474	*Juncus articulatus*	16	LC
475	*Juncus effusus*	25	LC
476	*Juncus filiformis*	11	LC
477	*Kernera saxatilis*	1	LC
478	*Laburnum alpinum*	2	LC
479	*Lamium galeobdolon* subsp. *montanum*	1	LC
480	*Lamium maculatum*	3	LC
481	*Larix decidua*	5	LC

#	Plants	Occ.	CH-RLs
482	*Laserpitium halleri*	1	LC
483	*Laserpitium siler*	17	LC
484	*Lathyrus heterophyllus*	3	LC
485	*Lathyrus occidentalis*	7	LC
486	*Lathyrus sylvestris*	1	LC
487	*Lathyrus vernus* s.str.	2	LC
488	*Leontodon montanus*	13	LC
489	*Leontopodium alpinum*	2	LC
490	*Leucanthemopsis alpina*	6	LC
491	*Ligusticum mutellinoides*	26	LC
492	*Lilium martagon*	3	LC
493	*Listera ovata*	6	LC
494	*Loiseleuria procumbens*	13	LC
495	*Lolium multiflorum*	17	LC
496	*Lonicera alpigena*	1	LC
497	*Lonicera caerulea*	2	LC
498	*Lotus maritimus*	2	LC
499	*Luzula alpina*	1	LC
500	*Luzula alpinopilosa*	28	LC
501	*Luzula luzulina*	3	LC
502	*Luzula pilosa*	3	LC
503	*Luzula sieberi*	13	LC
504	*Luzula sudetica*	8	LC
505	*Lysimachia nemorum*	11	LC
506	*Lysimachia nummularia*	14	LC
507	*Maianthemum bifolium*	1	LC
508	*Medicago sativa*	1	LC
509	*Melampyrum pratense*	1	LC
510	*Melampyrum sylvaticum*	5	LC
511	*Melica nutans*	5	LC
512	*Melilotus officinalis*	1	LC
513	*Mentha arvensis*	2	LC
514	*Mentha longifolia*	5	LC

#	Plants	Occ.	CH-RLs
515	*Mercurialis perennis*	9	LC
516	*Minuartia sedoides*	5	LC
517	*Minuartia verna*	14	LC
518	*Moehringia ciliata*	11	LC
519	*Moehringia muscosa*	2	LC
520	*Moehringia trinervia*	1	LC
521	*Molinia arundinacea*	2	LC
522	*Molinia caerulea*	15	LC
523	*Myosotis arvensis*	25	LC
524	*Myosotis decumbens*	8	LC
525	*Myosotis nemorosa*	2	LC
526	*Myosotis scorpioides*	8	LC
527	*Myosotis sylvatica*	4	LC
528	*Nigritella rhellicani*	16	LC
529	*Onobrychis montana*	18	LC
530	*Onobrychis viciifolia*	18	LC
531	*Ononis repens*	12	LC
532	*Orchis mascula*	1	LC
533	*Oreopteris limbosperma*	1	LC
534	*Origanum vulgare*	14	LC
535	*Orobanche caryophyllacea*	6	LC
536	*Orobanche minor*	2	LC
537	*Orobanche teucrii*	1	LC
538	*Oxalis acetosella*	3	LC
539	*Oxyria digyna*	1	LC
540	*Oxytropis jacquinii*	12	LC
541	*Paradisea liliastrum*	5	LC
542	*Pedicularis ascendens*	6	LC
543	*Pedicularis foliosa*	30	LC
544	*Pedicularis verticillata*	29	LC
545	*Petasites albus*	3	LC
546	*Petasites hybridus*	4	LC
547	*Petasites paradoxus*	27	LC

#	Plants	Occ.	CH-RLs
548	*Peucedanum ostruthium*	11	LC
549	*Phragmites australis*	2	LC
550	*Phyteuma betonicifolium*	16	LC
551	*Phyteuma hemisphaericum*	8	LC
552	*Phyteuma ovatum*	1	LC
553	*Pinguicula alpina*	7	LC
554	*Pinguicula vulgaris*	8	LC
555	*Pinus cembra*	1	LC
556	*Pinus mugo* subsp. *uncinata*	2	LC
557	*Platanthera bifolia*	1	LC
558	*Poa annua*	14	LC
559	*Poa cenisia*	23	LC
560	*Poa chaixii*	5	LC
561	*Poa nemoralis*	4	LC
562	*Poa supina*	24	LC
563	*Polygala alpina*	1	LC
564	*Polygala amarella*	4	LC
565	*Polygala comosa*	1	LC
566	*Polygala serpyllifolia*	2	LC
567	*Polygonatum odoratum*	7	LC
568	*Polygonatum verticillatum*	1	LC
569	*Polygonum arenastrum*	1	LC
570	*Polygonum aviculare*	1	LC
571	*Polygonum persicaria*	1	LC
572	*Polystichum lonchitis*	10	LC
573	*Populus tremula*	3	LC
574	*Potentilla brauneana*	3	LC
575	*Potentilla neumanniana*	3	LC
576	*Potentilla palustris*	1	LC
577	*Potentilla reptans*	14	LC
578	*Potentilla sterilis*	23	LC
579	*Prenanthes purpurea*	1	LC
580	*Primula acaulis*	7	LC

#	Plants	Occ.	CH-RLs
581	*Primula auricula*	24	LC
582	*Primula farinosa*	16	LC
583	*Prunus avium*	4	LC
584	*Prunus spinosa*	1	LC
585	*Pseudorchis albida*	13	LC
586	*Pteridium aquilinum*	4	LC
587	*Pulsatilla vernalis*	9	LC
588	*Pyrola minor*	1	LC
589	*Quercus petraea*	1	LC
590	*Quercus pubescens*	3	LC
591	*Quercus robur*	1	LC
592	*Ranunculus ficaria*	8	LC
593	*Ranunculus glacialis*	8	LC
594	*Ranunculus lanuginosus*	1	LC
595	*Ranunculus platanifolius*	1	LC
596	*Rhamnus pumila*	2	LC
597	*Rhinanthus glacialis*	11	LC
598	*Rhinanthus minor*	26	LC
599	*Rhododendron ferrugineum*	17	LC
600	*Rhododendron hirsutum*	5	LC
601	*Rosa arvensis*	1	LC
602	*Rosa canina*	1	LC
603	*Rosa pendulina*	8	LC
604	*Rosa vosagiaca* aggr.	2	LC
605	*Rubus caesius*	2	LC
606	*Rubus idaeus*	10	LC
607	*Rubus saxatilis*	4	LC
608	*Rumex alpinus*	17	LC
609	*Rumex crispus*	27	LC
610	*Rumex obtusifolius*	14	LC
611	*Rumex scutatus*	11	LC
612	*Sagina saginoides*	27	LC
613	*Salix appendiculata*	3	LC

#	Plants	Occ.	CH-RLs
614	*Salix caprea*	8	LC
615	*Salix cinerea*	1	LC
616	*Salix hastata*	7	LC
617	*Salix helvetica*	2	LC
618	*Salix myrsinifolia*	1	LC
619	*Salix reticulata*	25	LC
620	*Salix serpillifolia*	6	LC
621	*Salvia pratensis*	19	LC
622	*Sanguisorba officinalis*	13	LC
623	*Sanicula europaea*	1	LC
624	*Saponaria ocymoides*	1	LC
625	*Saxifraga androsacea*	14	LC
626	*Saxifraga bryoides*	1	LC
627	*Saxifraga caesia*	7	LC
628	*Saxifraga rotundifolia*	7	LC
629	*Saxifraga stellaris*	5	LC
630	*Scirpus sylvaticus*	12	LC
631	*Securigera varia*	2	LC
632	*Sedum album*	5	LC
633	*Sedum montanum*	1	LC
634	*Sedum sexangulare*	3	LC
635	*Sedum telephium* subsp. *maximum*	1	LC
636	*Sempervivum montanum*	5	LC
637	*Senecio alpinus*	2	LC
638	*Senecio erucifolius*	1	LC
639	*Senecio hercynicus*	1	LC
640	*Senecio jacobaea*	5	LC
641	*Sibbaldia procumbens*	7	LC
642	*Silene dioica*	13	LC
643	*Silene flos cuculi*	8	LC
644	*Silene nutans* s.str.	11	LC
645	*Silene pratensis*	5	LC
646	*Sonchus asper*	5	LC

#	Plants	Occ.	CH-RLs
647	*Sorbus aria*	3	LC
648	*Sorbus aucuparia*	4	LC
649	*Sorbus chamaemespilus*	4	LC
650	*Stachys alpina*	4	LC
651	*Stachys sylvatica*	7	LC
652	*Succisa pratensis*	10	LC
653	*Taraxacum alpinum* aggr.	23	LC
654	*Taraxacum palustre* aggr.	1	LC
655	*Taraxacum schroeterianum*	1	LC
656	*Teucrium chamaedrys*	6	LC
657	*Teucrium montanum*	3	LC
658	*Thalictrum aquilegiifolium*	3	LC
659	*Thesium pyrenaicum*	19	LC
660	*Thlaspi arvense*	1	LC
661	*Thlaspi perfoliatum*	1	LC
662	*Tofieldia calyculata*	20	LC
663	*Traunsteinera globosa*	12	LC
664	*Trichophorum cespitosum*	2	LC
665	*Trifolium alpestre*	4	LC
666	*Trifolium alpinum*	3	LC
667	*Trifolium campestre*	15	LC
668	*Trifolium dubium*	2	LC
669	*Trifolium montanum*	21	LC
670	*Trifolium pallescens*	1	LC
671	*Trisetum distichophyllum*	19	LC
672	*Tussilago farfara*	20	LC
673	*Urtica dioica*	6	LC
674	*Valeriana dioica*	16	LC
675	*Valeriana tripteris*	18	LC
676	*Valerianella carinata*	2	LC
677	*Valerianella locusta*	2	LC
678	*Verbascum lychnitis*	1	LC
679	*Veronica agrestis*	1	LC

#	Plants	Occ.	CH-RLs
680	*Veronica beccabunga*	2	LC
681	*Veronica fruticans*	3	LC
682	*Veronica fruticulosa*	2	LC
683	*Veronica montana*	1	LC
684	*Veronica officinalis*	26	LC
685	*Veronica spicata*	2	LC
686	*Veronica teucrium*	2	LC
687	*Veronica urticifolia*	3	LC
688	*Viburnum opulus*	1	LC
689	*Vicia sylvatica*	6	LC
690	*Vincetoxicum hirundinaria*	5	LC
691	*Viola calcarata*	28	LC
692	*Viola hirta*	30	LC
693	*Viola palustris*	8	LC
694	*Viola reichenbachiana*	2	LC
695	*Viola riviniana*	2	LC
696	*Viola tricolor*	1	LC
697	*Lathyrus latifolius*	4	LC
698	*Oxalis fontana*	1	LC
699	*Prunus armeniaca*	1	LC
700	*Veronica filiformis*	2	LC
701	*Veronica persica*	23	LC
702	*Agrostis canina*	2	NT
703	*Androsace pubescens*	5	NT
704	*Aquilegia alpina*	1	NT
705	*Centaurea cyanus*	1	NT
706	*Centaurea triumfettii*	1	NT
707	*Crepis pygmaea*	2	NT
708	*Dracocephalum ruyschiana*	1	NT
709	*Eleocharis uniglumis*	1	NT
710	*Fourraea alpina*	1	NT
711	*Galeopsis ladanum*	1	NT
712	*Gentiana schleicheri*	1	NT

#	Plants	Occ.	CH-RLs
713	*Hieracium schmidtii* aggr.	1	NT
714	*Inula salicina*	1	NT
715	*Koeleria eriostachya*	1	NT
716	*Linum alpinum*	14	NT
717	*Muscari racemosum*	1	NT
718	*Narcissus radiiflorus*	11	NT
719	*Ornithogalum pyrenaicum* s.str.	8	NT
720	*Peucedanum austriacum*	8	NT
721	*Pulmonaria mollis* aggr.	1	NT
722	*Rosa micrantha*	1	NT
723	*Salix pentandra*	1	NT
724	*Salix repens*	1	NT
725	*Serratula tinctoria* subsp. *macrocephala*	8	NT
726	*Silaum silaus*	1	NT
727	*Stachys pradica*	3	NT
728	*Taraxacum aquilonare*	1	NT
729	*Trifolium rubens*	4	NT
730	*Viola canina* s.str.	17	NT
731	*Viola cenisia*	3	NT
732	*Viola pyrenaica*	2	NT
733	*Crepis foetida*	1	VU
734	*Eryngium alpinum*	1	VU
735	*Gentiana cruciata*	1	VU
736	*Juncus arcticus*	1	VU
737	*Myosotis cespitosa*	1	VU
738	*Potentilla thuringiaca*	1	VU
739	*Rhinanthus angustifolius*	4	VU
740	*Trifolium ochroleucon*	2	VU
741	*Trifolium spadiceum*	2	VU
742	*Chenopodium vulvaria*	1	EN
743	*Orobanche major*	1	EN
744	*Valeriana pratensis*	1	EN
745	*Woodsia pulchella*	1	EN

#	Plants	Occ.	CH-RLs
746	*Veronica acinifolia*	1	CR
747	*Crepis vesicaria s.str.*	14	CR
748	*Cuscuta epilinum*	1	RE
749	*Bromus racemosus* subsp. *commutatus*	1	NA
750	*Campanula alpestris*	1	NA
751	*Carex atrata* aggr.	22	NA
752	*Galium pusillum*	1	NA
753	*Lapsana communis* s.l.	6	NA
754	*Luzula nutans*	1	NA
755	*Satureja montana*	1	NA
756	*Serratula nudicaulis*	1	NA
757	*Thlaspi rotundifolium* aggr.	24	NA
758	*Aconitum napellus* aggr.	15	NA
759	*Aconitum variegatum* s.l.	5	NA
760	*Aconitum vulparia* aggr.	4	NA
761	*Arctium minus* s.l.	1	NA
762	*Bupleurum falcatum* s.l.	2	NA
763	*Bupleurum ranunculoides* s.l.	10	NA
764	*Campanula glomerata* s.l.	12	NA
765	*Carex muricata* aggr.	3	NA
766	*Centaurea scabiosa* s.l.	28	NA
767	*Cerastium arvense* s.l.	23	NA
768	*Erigeron annuus* s.l.	3	NA
769	*Festuca arundinacea* s.l.	15	NA
770	*Galium verum* s.l.	7	NA
771	*Geranium phaeum* s.l.	1	NA
772	*Geranium robertianum* s.l.	3	NA
773	*Juniperus communis* s.l.	14	NA
774	*Koeleria pyramidata* aggr.	8	NA
775	*Luzula luzuloides* s.l.	2	NA
776	*Luzula spicata* s.l.	12	NA
777	*Ononis spinosa* s.l.	1	NA
778	*Oxytropis campestris* s.l.	6	NA

#	Plants	Occ.	CH-RLs
779	*Pastinaca sativa* s.l.	1	NA
780	*Picris hieracioides* s.l.	11	NA
781	*Rubus fruticosus* aggr.	1	NA
782	*Saxifraga biflora* s.l.	15	NA
783	*Saxifraga exarata* s.l.	28	NA
784	*Scabiosa columbaria* s.l.	16	NA
785	*Sempervivum tectorum* s.l.	3	NA
786	*Sonchus arvensis* s.l.	1	NA
787	*Stachys officinalis* s.l.	26	NA
788	*Stachys recta* s.l.	4	NA
789	*Stellaria media* aggr.	10	NA
790	*Stellaria nemorum* s.l.	4	NA
791	*Thalictrum minus* s.l.	1	NA
792	*Thymus serpyllum* aggr.	3	NA
793	*Trifolium hybridum* s.l.	2	NA
794	*Valeriana officinalis* aggr.	10	NA
795	*Vicia sativa* s.l.	23	NA

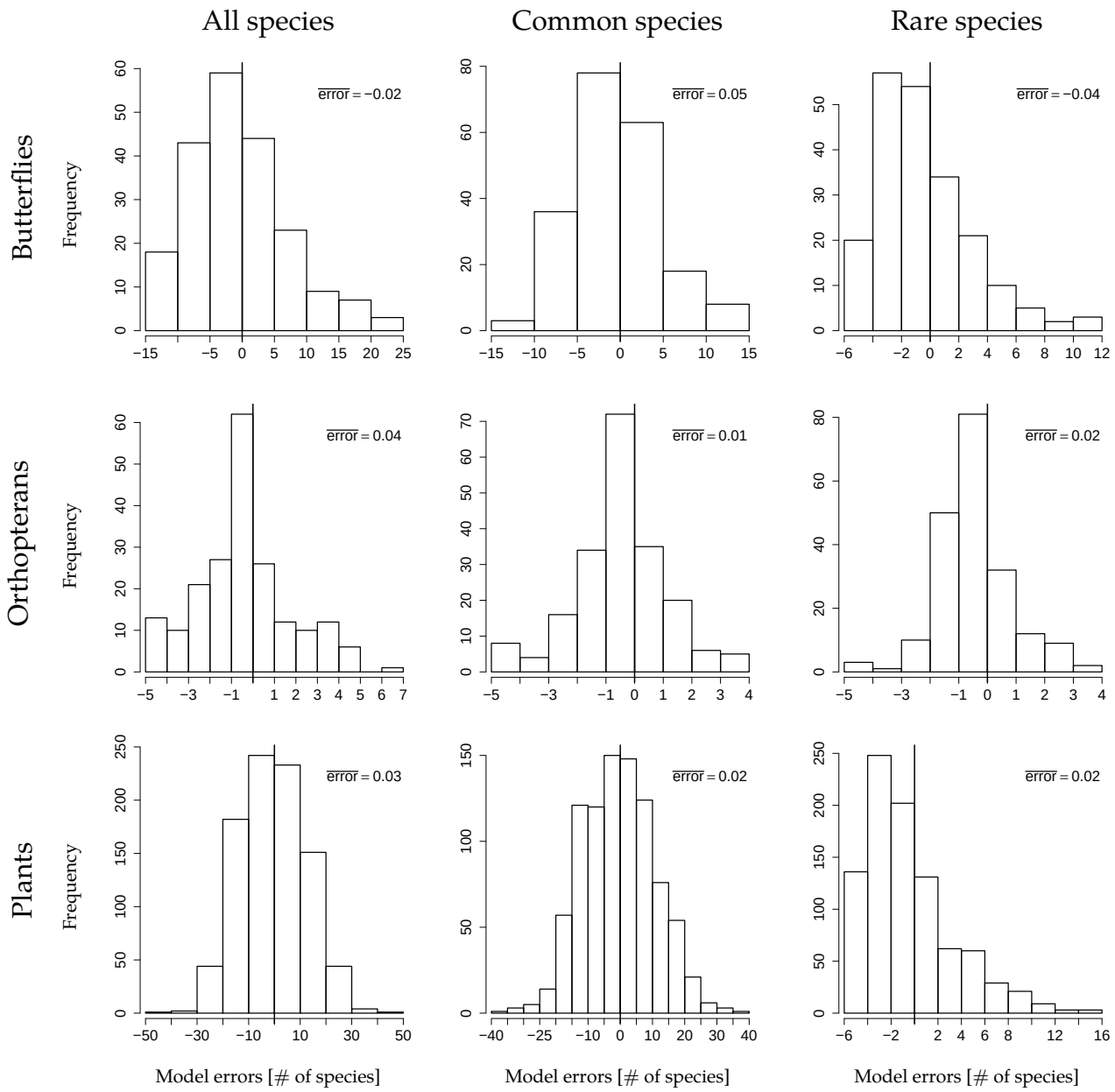

Figure S1: Prediction error distribution (*observed richness - predicted richness*) across the sampling sites. The bars below zero correspond to overprediction and those above zero, to underprediction. The mean prediction error is also indicated.

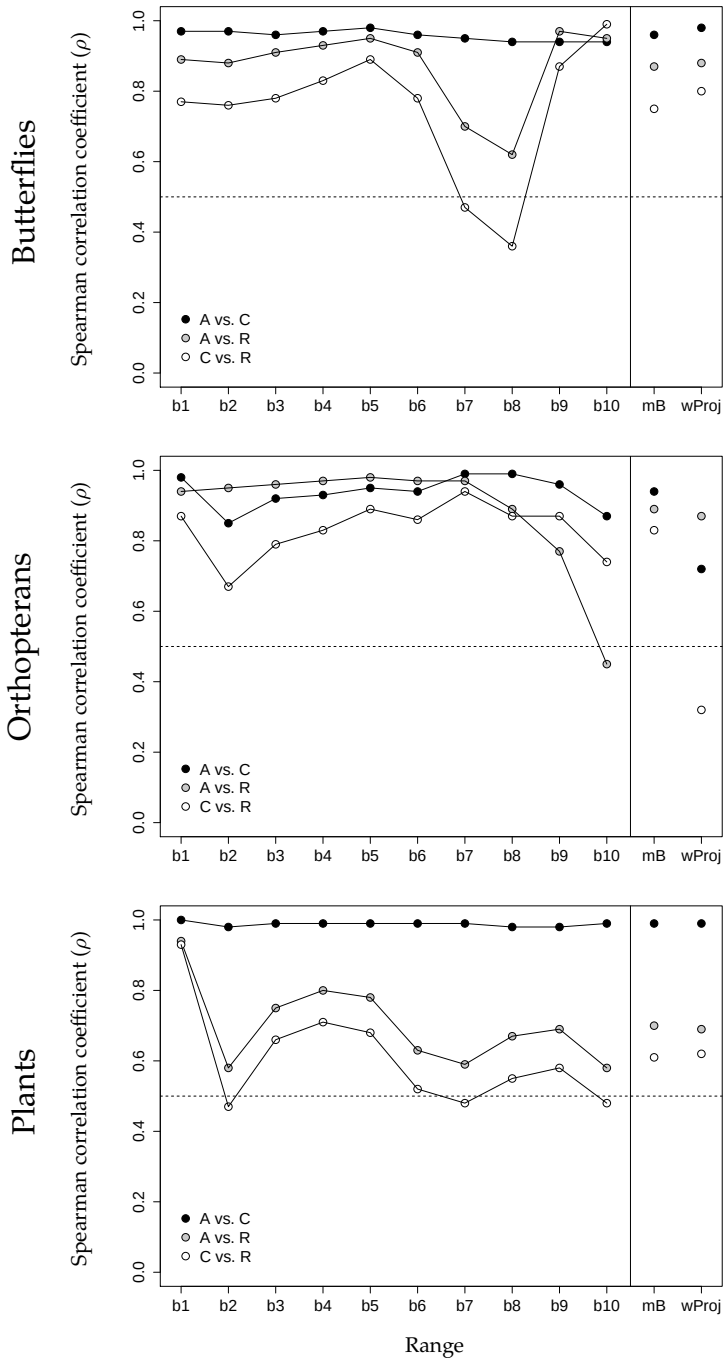

Figure S2: Spearman correlation values (ρ) between the predicted richness of the subgroups of each taxon. For each band of elevation (*b1* to *b10*), the correlation coefficients were computed using the richness values from the same set of 200 random points extracted from the projections of the groups compared (same data sets used for boxplots). The mean across bands is also given (*mB*). The whole projections were used to calculate the overall correlation coefficient (*wProj*). Only significant correlations (ie. $p \leq 0.05/30$) are presented.

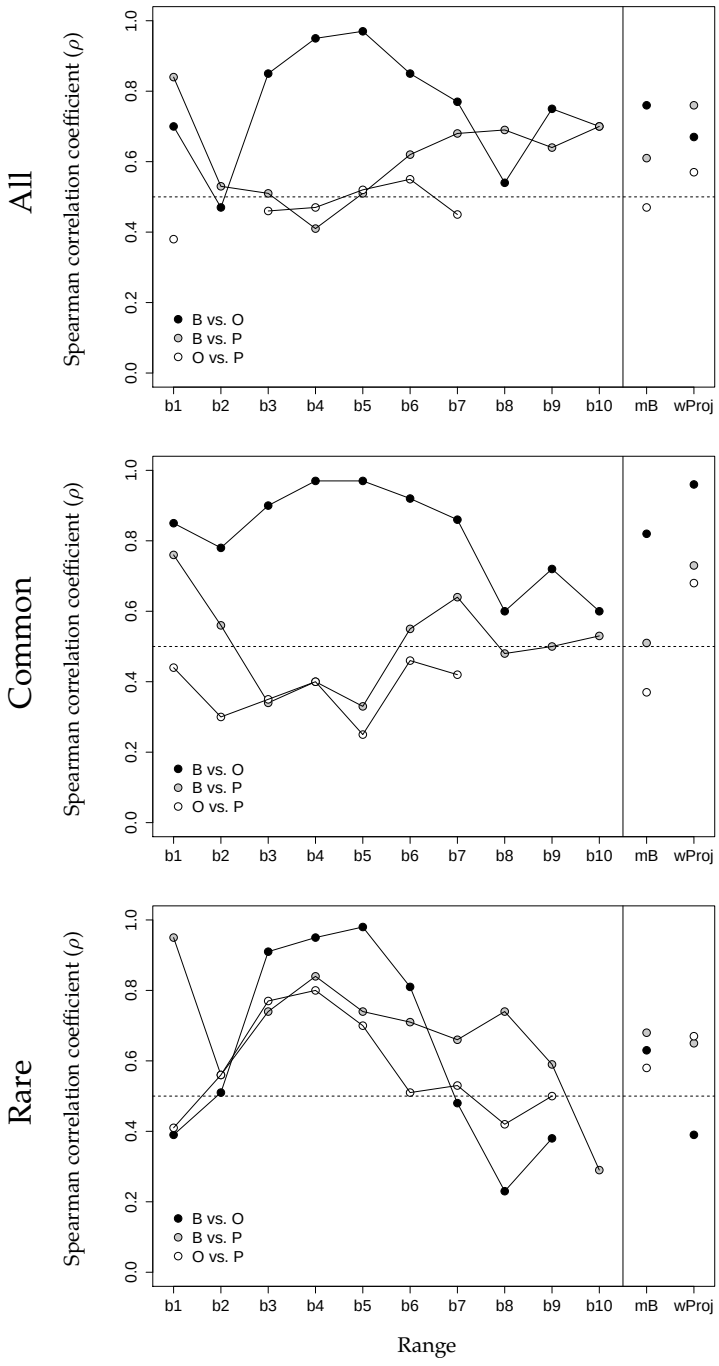

Figure S3: Spearman correlation values (ρ) between the predicted richness of a given subgroup of a taxon and that of it's counterpart in another taxon. For each band of elevation (*b1* to *b10*), the correlation coefficients were computed using the richness values from the same set of 200 random points extracted from the projections of the groups compared (same data sets used for boxplots). The mean across bands is also given (*mB*). The whole projections were used to calculate the overall correlation coefficient (*wProj*). Only significant correlations (ie. $p \leq 0.05/30$) are presented.

Table S4: Evaluation metrics of the models built for the subgroups of plants at a 25 m-resolution: the mean index of deviance reduction (mD^2) and the mean Spearman correlation coefficient ($m\rho$) derived from the 100 models generated in the cross-validation process.

a) Explicative power of the models

mD^2	Plants – 25m
All species	0.278
Common species	0.295
Rare species	0.068

b) Predictive power of the models

$m\rho$	Plants – 25m
All species	0.509
Common species	0.540
Rare species	0.239

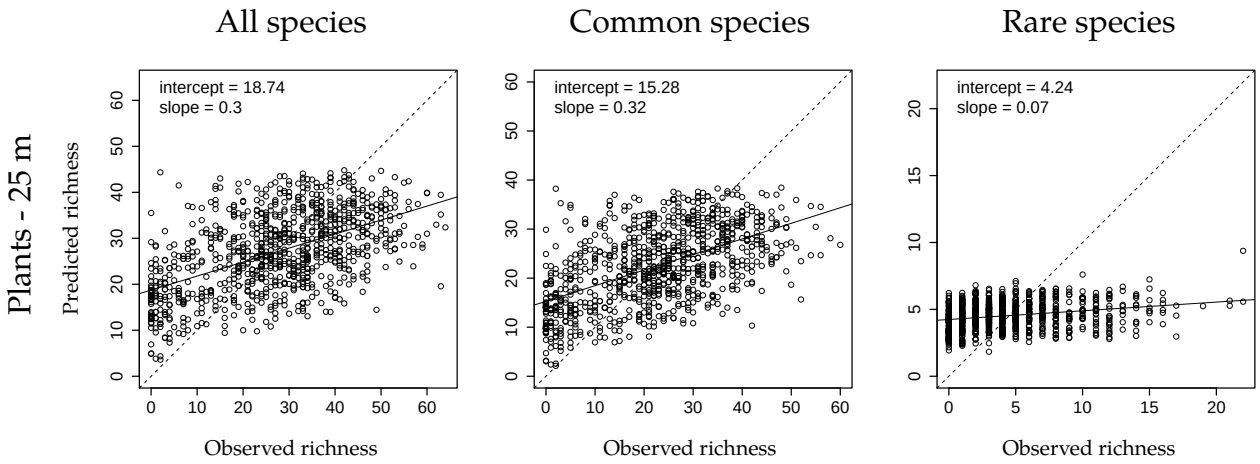

Figure S4: Predicted against observed species richness for plants at a using predictors at a 25m resolution. The linear regression (—) and the perfect correspondence line (- - -) are also represented allowing to visually assess over- and underprediction.

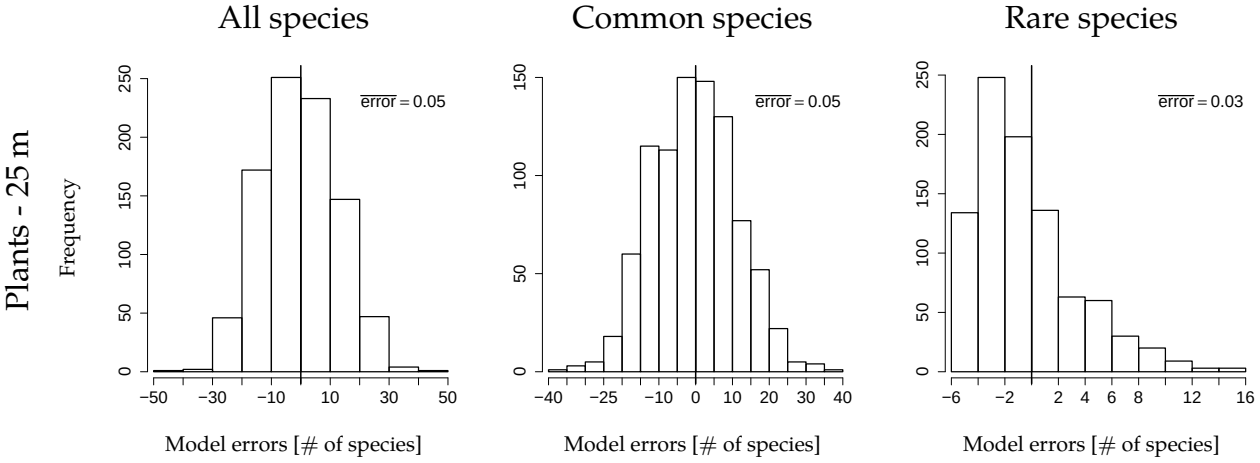

Figure S5: Prediction error distribution (*observed richness - predicted richness*) across the sampling sites for the model of plant species richness using predictors at a 25 m resolution. The bars below zero correspond to overprediction and those above zero, to underprediction. The mean prediction error is also indicated.

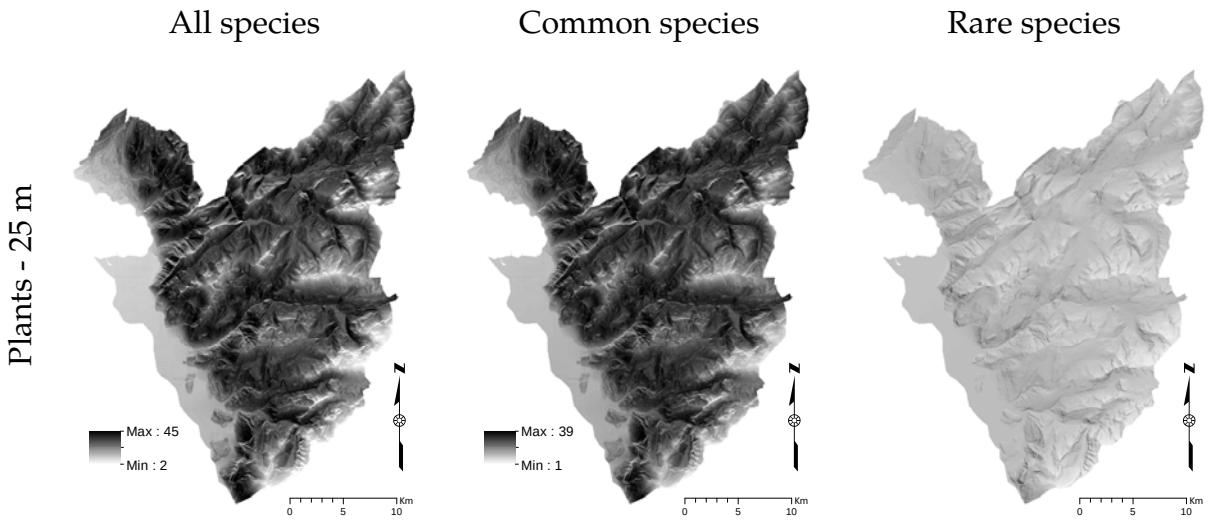

Figure S6: Spatial distribution of the potential richness of each subset of plants across the study area as predicted by the macroecological models using predictors at a 25 m resolution.

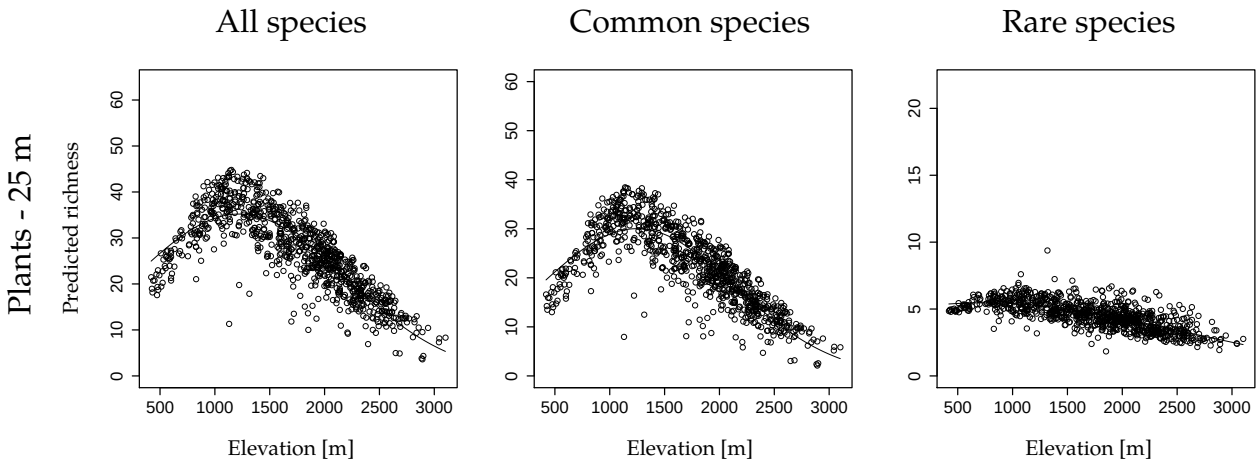

Figure S7: Predicted species richness of plants for *all*, *common* and *rare* species subsets across elevation using predictors at a 25 m resolution. *Circles* represent richness predicted in the sampling plots and the *curve* the corresponding trendline.