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Are Swiss protected areas suitable for mammal's conservation now and in the future? A spatial modeling and prioritization approach.

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Résumé

Les réserves naturelles jouent un rôle important pour la conservation de la biodiversité et ont pour but principal d'éviter l'extinction des populations des espèces déjà en danger. Les réserves naturelles, ou aires protégées, préservent la diversité des espèces à l'échelle régionale, nationale et mondiale. Cependant et à cause du réchauffement climatique, leur efficacité est mise en danger. Leur frontière actuellement fixes pourraient être modifiées pour répondre à des buts de conservation futurs. Afin d'anticiper ces changements et limiter une future perte de biodiversité, des outils de modélisation et de priorisation sont de plus en plus utilisés par les responsables politiques, dans le but de répondre à des problématique actuelles et futures. Dans cette étude, une approche à deux échelles pour modéliser la distribution des mammifères a été créée et utilisée pour évaluer l'intégration des espèces dans le réseau de réserves actuel dans des conditions actuelles et futures (RCP 4.5 et RCP 8.5), dans le but d'optimiser ce réseau dans le temps. Trois analyses ont été ensuite réalisées à l'aide du logiciel Zonation et ont permis de 1) identifier les potentiels hotspots de biodiversités en Suisse sans prendre en compte le réseau de réserves naturelles actuelles ; 2) d'évaluer l'efficacité du réseau actuel pour la protection des espèces de mammifères étudiées, et d'explorer les potentielles possibilités d'extension ; 3) Evaluer la distribution des espèces au sein du réseau d'aires protégées en fonction de leur degré de priorité nationale et de leur statut taxonomique pour le présent et pour le futur. Cette étude est concentrée sur trois classes d'aires protégées : le Parc National Suisse ainsi que les réserves régionales, les réserves Pro Natura et les aires protégées Emeraude ainsi que le réseau de réserves naturelles dans son entièreté. Dans l'ensemble, nous avons constaté que les aires protégées existantes ne sont pas situées dans les endroits les plus appropriés pour maximiser la richesse des espèces au sein du groupe taxonomique des mammifères et sont donc moins efficaces que prévu. En outre, pour certaines espèces, le réseau actuel d'aires protégées pourrait devenir encore moins optimal dans les deux scénarios futurs envisagés, même si l'occupation des sols reste inchangée. Cependant, les réserves Pro Natura et les sites Emeraude, dont le but principal est de protéger des espèces ciblées, resteraient bien situées et efficaces même dans un scénario peu optimiste. Cette étude n'a pas tenu compte des changements d'utilisation du sol et des paysages, ni des habitats spécifiques ou d'autres groupes taxonomiques qui auraient pu être inclus lors de la conception du réseau d'aires protégées existant. Nous concluons que, afin que les espèces de mammifères soient suffisamment protégées dans des conditions actuelles et futures, le réseau de réserves naturelles devrait mieux prendre en compte le changement climatique, en particulier pour les réserves nationales et régionales. Pour approfondir cette étude, nous pensons qu'il pourrait être intéressant d'inclure d'autres groupes taxonomiques également importants pour la préservation de la biodiversité.

Abstract

Protected areas (PAs) play a major role in biodiversity conservation and aim to avoid population extinction of threatened species. PAs are preserving species diversity in many countries around the world, but with climate change their efficiency is threatened. Their currently fixed boundaries could have to be modified to account for future conservation goals. To anticipate these changes and limit future biodiversity loss, modelling tools and prioritization analyses are increasingly used by policy makers, under current trends and future scenarios. In this study, a two scales approach to model mammal species distribution, was used to assess how integrating species richness from stacked species model predictions under three climatic change scenarios can help optimize the design of current and future PA networks. The three types of analysis, implemented within the Zonation software allowed for 1) the identification of potential mammalian biodiversity hotspots (BDs) in Switzerland without prior consideration of the current PA network; 2) the evaluation of the efficiency of the current PA network to preserve mammals, and explore possibilities to extend it; and 3) the evaluation of the species' distributions within PAs as a function of their national priority and taxonomic status, now and in the future. This analysis focused on three classes of PAs: National and Regional reserves, Pro Natura reserves and Emeraude sites and the whole PA network. Overall, we found that existing PAs are currently not situated in the most environmentally suitable locations for maximizing mammalian species richness and are thus less efficient than originally expected. Furthermore, for some species the current PA network could become even less optimum under the two future scenarios considered, even with an unchanged land-use. However, Pro Natura reserves and Emeraude sites, whose main aim is to protect targeted species, would remain well located and efficient even in the worst scenario. This study did not account for land-use changes, or for specific habitats or other taxonomic groups that could have been included when designing the existing PA network. We conclude that future Swiss conservation planning should better account for climate change, especially regarding national and regional PA, and future studies could be conducted with the same approach as used here but including all important groups of the general biodiversity.

Glossary

All-PA network: All protected areas network

EM-PN network: Emeraude Pro Natura network

PAs : protected areas

SCP: Spatial Conservation Prioritization

SDMs: Species Distribution Modelling

SP network: Swiss parks network

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Keywords: SDMs – conservation – spatial prioritization – Zonation – biodiversity – climate change – reserve

1. Introduction

For the past 100 years, global biodiversity loss has been an international concern (Butchart *et al.*, 2010). Growing anthropogenic activities have caused increasing threats to biodiversity(Niemelä *et al.*, 2000).Temperature rises, intensive farming and the introduction of invasive species are affecting natural ecosystems, reducing the habitat of endemic species and causing species extinctions and biodiversity loss (Souza and Prevedello, 2021a). The effects of climate change have already influenced species ranges, shifting them northwards and to higher altitudes causing some species to move away from current protected areas (I. C. Chen *et al.*, 2011; Melles, M. J. Fortin, *et al.*, 2011). The fast rate of climate change might limit the capacity of species to adapt locally or to migrate to suitable areas and cause additional extinctions (Hannah *et al.*, 2002). There is thus an urgent need to find better ways to protect biodiversity against these different threats (IPBES 2019; Mace, 2014), for instance through protecting land.

According to the IUCN, a protected area (PA) is a clearly defined geographical space which is managed through legal or other effective means and recognised as dedicated, to achieving the long-term conservation of nature with associated ecosystem services and cultural values (IUCN Definition 2008). PAs are classed by the IUCN in six categories from strict protection with limited human access to protected landscapes and seascapes in relation with human activities regulation but free access (Dudley, 2008). They are a mainstay of biodiversity conservation while contributing to people's good environment quality. PAs are thus the cornerstone of global conservation efforts and offer practical and tangible solutions to the problems of both species' loss and adaptation to climate change (Hannah *et al.*, 2002). However, PAs generally have fixed boundaries, and as such might not fulfil their initial conservation goal if species are driven out of them by changing climate (Araújo *et al.*, 2004, 2011). Being able to reshape current reserve networks accordingly would therefore be key to improve future connectivity, slow down biodiversity loss and maintain ecosystem integrity (N Lopoukhine *et al.*, 2012). Although some studies show the good efficiency of current reserve networks (Naughton-Treves *et al.*, 2005; Farashi *et al.*, 2017), others showed contrasted result with less than a half of the species remaining (Stuart H.M. Butchart *et al.*, 2012).

In Switzerland, the reserve network is a mosaic of areas managed by private and governmental organisations (P.Galland, IUCN, 2004). The Swiss National Park was created in 1914 and was followed much later by the establishment of Parks of National Importance (2007-2011). Unique landscapes and natural monuments are protected in 162 sites with a surface area of 7800 km^2(18.9% of the country). This inventory is complemented by 3 natural sites of the UNESCO World Heritage, by habitats of national importance, Federal Hunting reserves, water and migratory birds' reserves (Ramsar sites, international and national importance sites), parks of national importance and the National Park (*Appendix 1*). Conservation biology confirms the need to protect large areas and maintain connectivity along altitudinal gradients. However, as the case of Switzerland is showing, natural ecosystems are becoming increasingly fragmented and many protected areas have become areas within more intensively used production lands (N Lopoukhine *et al.*, 2012).

A problem however when designing PAs is to have the appropriate spatial coverage of data on species, as many existing databases are incomplete and biases (Meyer *et al.*, 2015; Anderson *et al.*, 2016). Species distribution modelling (SDMs, Guisan and Zimmermann, 2000; Franklin, 2010; Peterson *et al.*, 2011; Guisan *et al.*, 2017), is a major tool used to derive spatially-explicit predictions of environmental suitability for species, and accordingly allow spatial generalization of lacunar data to entire regions. In

conservation, SDMs were used for conservation decisions (Guisan *et al.*, 2013), for instance to anticipate biological invasions (Petitpierre *et al.*, 2016), to identify, and protect critical habitats (Titeux *et al.*, 2007), to support conservation planning (Tulloch *et al.*, 2016) and the selection of potential PAs (Underwood *et al.*, 2010). Furthermore, SDMs allow for the modelling of future projections under changing environmental conditions (Guisan *et al.*, 2017), for instance under climate change (Wiens *et al.*, 2009). A problem however can arise if the SDMs are fitted on a too restricted geographic extent that causes a truncation of the climatic niche, potentially affecting future projections (Chevalier *et al.*, In press). A solution to this niche truncation approach is to use a nested hierarchical approach combining the regional and global scales as used in this study (Mateo *et al.*, 2019; Chevalier *et al.*, In press).

To optimize the delimitation of PAs and to identify a set of complementary areas that could maximize biodiversity conservation, systematic conservation planning approaches were proposed (Alagador, Cerdeira and Araújo, 2014). As initially presented, the effectiveness of systematic conservation is highlighted by using limited resources to achieve conservation goals, by defending and being flexible in the face of competing land-uses, and by accounting in allowing decisions to be critically reviewed (Margules and Pressey, 2000). Including land-use further allows improving conservation planning to reach a balance between costs of conservation related to human conservation and the benefits to wildlife (Newburn *et al.*, 2005). However, PAs have often been established in order to be efficient in the current situation to maintain high biodiversity richness and protecting threatened species, but they should also be designed in such way that they can be adapted to changing conditions (Tulloch *et al.*, 2016).

This is because climate change and habitat fragmentation push species to move to other territories and species distributions are not static anymore (Fischer and Lindenmayer, 2007; Raphael K Didham, 2010; Hetem *et al.*, 2014). To be able to identify where suitable habitats will be located in the future, SDMs under different future scenarios can be used (Kariyawasam *et al.*, 2021; Riley *et al.*, 2021). To evaluate, and potentially modify (e.g. extend) current reserve networks and find the best conservation solution for the studied species, prioritization tools can be used such as the Zonation software, which allows for the identification of important areas to retain habitat quality and connectivity for a number of species, and as a way to plan species' long-term persistence (Moilanen *et al.*, 2005). Zonation can incorporate diverse tools such as, the current PA network, cost map, future landscape changes, species interactions and connectivity to ultimately propose the most optimal PA network based on the parameters selected for specific conservation goals (Moilanen *et al.*, 2011). This type of prioritization software is increasingly used in studies across the world (F. N. Robinne *et al.*, 2020), but is still not very often used in combination with SDM predictions (Tulloch *et al.*, 2016). A such Combined SDM-Zonation approach was recently tested in a restricted area of the Swiss Alps (Vincent, Fernandes, Cardoso, Broennimann, Di Cola, D'Amen, Ursenbacher, Schmidt, J. N. Pradervand, *et al.*, 2019; Ramel, P. L. Rey, *et al.*, 2020), but was never applied so far to the whole territory of Switzerland.

Here, we aim to fill this gap. We were particularly interested in the criteria to create protected areas at the Swiss scale. Based on previous work, we supposed that as in many parts of the World, protected areas were established with the aim to include the largest number of threatened species according to the IUCN red list (IUCN, 2021). We also assumed that some protected areas were designed to protect emblematic and charismatic species (Marris, 2013). Due to human/wildlife conflicts, we were also curious to assess what the proportion of large predators such as wolves could potentially be in the Swiss reserve network. The same questions can be addressed for micromammals, although far more rarely assessed (Morand *et al.*, 2006). As shown in previous studies (Araújo *et al.*, 2004; Thuiller *et al.*, 2014), we also anticipate that protected areas might not have been initially designed to efficiently

protect species in a climatically changed future, and accordingly how alternative PA networks could be more optimally designed.

To achieve these prospects, we modelled the current and future spatial distribution of 68 mammal species in Switzerland by using a two scales hierarchical modelling approach and tested two different ways to combine models at the two scales. The predicted species were then used in an existing prioritization framework and compared to the actual Swiss reserve network to evaluate how it contributes to protect potential mammalian biodiversity, today and in the future, and propose an improved network, corresponding to various prioritization options and subgrouping of the species (by Orders). Additionally, we finally investigated the effects of climate change on optimal conservation solutions and the efficiency of current and future reserve. We finally discussed possible improvements and further studies that could complement this analysis.

2. Methods

2.1. General framework

We developed a framework (Fig.1) combining species distribution modelling (SDM) and spatial conservation prioritization (SCP) using the Zonation software (Lehtomäki and Moilanen, 2013) and applied it to a selection of mammals over Switzerland. For each species, we first built hierarchical SDMs using two strategies to combine the two scales (European and national) (cf 2.3.2). The resulting spatial predictions were then used as inputs in SCP analyses (cf 2.4) to identify current hotspots, evaluate their matching with the current reserve network, and propose a possible expansion of the protected areas (PAs) to improve mammal conservation. We compared the outcomes of the different SCP scenarios from the different SDM methods to each other and to the existing protected areas (PAs) network. Lastly, the same analyses were also carried out for the future change using different climate change scenarios (cf. 2.3.2).

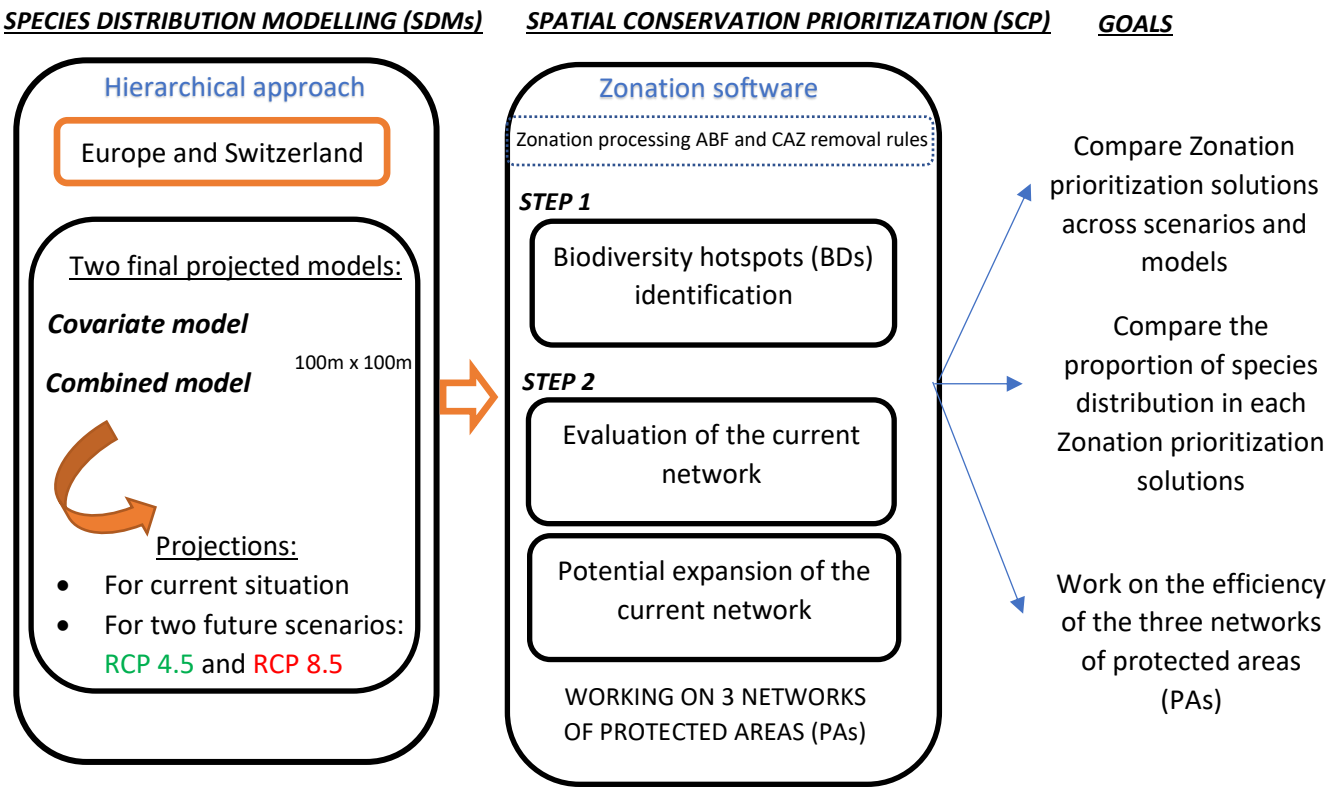


Figure 1 : Conceptual framework representing the major steps and goals of this study. 1. Species distribution modelling (SDMs) by using a hierarchical approach at European and Swiss scale. The final models obtained were then projected at a resolution of 100m x 100m for the current situation and for two future scenarios with low and high carbon concentration respectively RCP 4.5 and RCP 8.5. 2. Spatial conservation prioritization (SCP) using the Zonation software to identify the Biodiversity Hotspots (BDs) in Switzerland and to evaluate and propose a potential expansion of the current network. The analyses were done on three networks of protected areas and for both current situation and future scenarios. The major goals of this study were 1) Compare Zonation prioritization solutions across scenarios and models; 2) Compare the proportion of species distribution in each Zonation prioritization solutions; 3) Work on the efficiency of the three networks of protected areas (PAs).

2.2. Study area

The study area is the whole territory of Switzerland. Extending across the north and south side of the Alps in west-central Europe, Switzerland encompasses a great diversity of landscapes, ecosystems and climates (J. M. Fallot, 2021). With a large range of elevation (193m for Lake Maggiore in Ticino to 4634m for Dufour peak in Valais), the country is divided into three topographical areas: the Swiss Alps, the Plateau and the Jura mountains.

2.3. Modelling approaches

The modelling approach is built on the methodological framework (Fig.2).

2.3.1. Species' occurrence data

We worked on the distribution of 68 mammal species from 6 orders (*Appendix 3*), using presence data gathered from observations stored in the Global Biodiversity Information Facility (GBIF.org (2020), GBIF Home Page. Available from: https://www.gbif.org) and Info Species platforms (www.infospecies.ch). The coordinates of observations are initially in the WGS84 projection system for European data and CH1903 for national data and they cover a time range from 1900 to 2020 depending on the species. To ensure a minimum sample size sufficient for accurate model fitting (van Proosdij *et al.*, 2016), only species with a minimum of 30 occurrences between 1970-2020 (temporal range of environmental variables) in the study area were considered. The Swiss data corresponds to the aggregation of one observation only by species per pixel of 100 m x 100 m (*Appendix 3*). The single data restriction was such that, due to the origin of the project, only mammal species occurring in the Vaud Alps were selected for this study in order to be re-use in the future for the "RechAlp area"(RechAlp (unil.ch)). The brown bear (*Ursus arctos*), the racoon (*Procyon lotor*), the Italian water vole (*Arvicola italicus*), the sika deer (*Cervus nippon*) and the forest dormouse (*Dryomys nitedula*) were therefore not considered here.

2.3.2. Species distribution models (SDMs)

A two scales approach was used in this study. SDM studies integrating multiple geographical scales are still limited. However, recent studies (Fearnside, 1996; Di Febbraro *et al.*, 2019; Rubén G Mateo *et al.*, 2019). have shown that multiscale approaches provide better results than regional SDMs when the purpose is to derive future climate change projections. As this was the case here, we used a two-scales strategy to predict mammal's distributions in Switzerland.

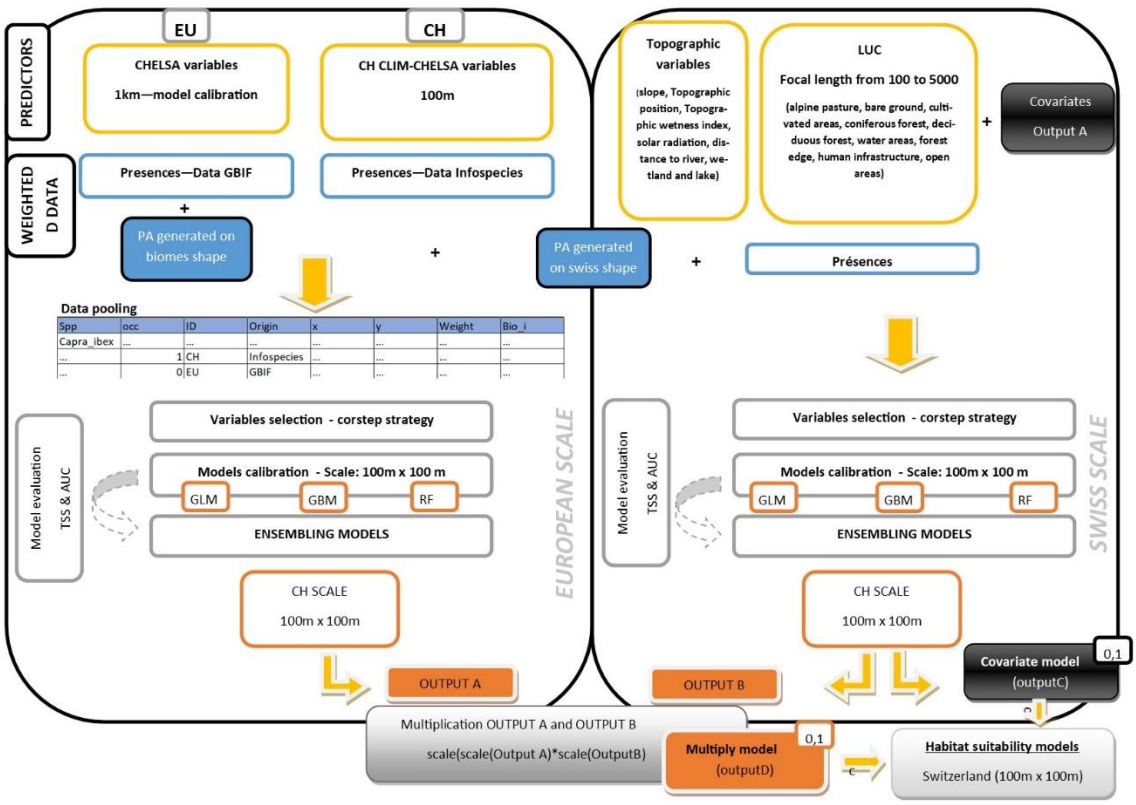


Figure 2: Conceptual framework representing the different analytical steps for part 1 following in this case study. PA=10 000 absences points in background; EU=Europe; CH=Switzerland. The focal lengths of land use and land cover are from 100 meters to 5000 meters at a resolution of 100m and contains alpine pasture, bare ground, cultivated areas, coniferous forest, water areas, forest edge, human infrastructure, open areas (Appendix. 2).

For each species, we used a framework that was based on fitting a first climate-only model at the European scale merging European data at 1 km x 1 km and Swiss data at 100m x 100 m resolutions, the projected at 100 m x 100 m resolution (Fig. 2, output A) and Combined in two possible ways with a model including other non-climatic environmental variables at the Swiss scale (Fig. 2, output B). This allowed us to yield one final European prediction and two alternative national predictions (all taking values between 0 and 1) – (Fig. 2):

i) ***European model***: based only on the bioclimatic variables using the European climatic data of CHELSA (large scale-30 arc-seconds pixel, (Karger *et al.*, 2017) and the Swiss bioclimatic variables (CHclim25 dataset, Broennimann, 2020; fine scale – 100 meters pixel). The CHELSA variables are bioclimatic variables from the monthly mean, max, mean temperature and mean precipitation values developed for species distribution modelling (Karger *et al.*, 2017). A background of 10'000 pseudoabsences data;

ii) ***Covariate model***: fitted only at the Swiss scale, using topographic, land-use land-cover (LULC) variables (*Appendix 2*) and the prediction of the European model as Covariate. The same background pseudoabsences, as used with the European model are included here;

iii) ***Combined model***: fitted only at the Swiss scale, uses topographic and LULC variables but without the European prediction as Covariate. The same background pseudoabsences as in the European model are also used. The predictions of this model are then Combined with the European model's predictions to obtain the second final model predictions at the Swiss scale. The final model is then rescaled with the function rescale0to1 from R package "Climate Stability" (Owens and Robert, 2019). The rescaling is done using the formula (value-min)/(max-min).

Scale (scale(European predictions)*scale(Combined predictions))

The variables selection for the three SDMs is based on the "Corstep strategy" (Adde *et al.*, 2020). To avoid multicollinearity and to select the most appropriate variables regarding our species, we performed bivariate Pearson's correlation coefficients between species occurrences and each of the candidate habitat variables. The variables were evaluated sequentially in decreasing order of the absolute values of the correlation coefficients. The variables were retained if they were "non-collinear" with any previously added variable. The collinearity threshold was defined as a Pearson correlation coefficient of 0.70 in absolute value (Dormann *et al.*, 2013). The three SDMs were generated using the R package *biomod 2*, following an ensemble procedure (Thuiller *et al.*, 2009; Grenouillet *et al.*, 2011), including three modelling techniques: generalized linear models (GLM, (McCullagh and Nelder, 2019)), generalized boosting model (GBM, (Bühlmann and Hothorn, 2007)) and random forest (RF, (Breiman, 2001)). For each of the three modelling techniques, the data were randomly partitioned into 70% for calibration and 30% for validation; this procedure was repeated 10 times. For each species 30 models were generated (10 resampling runs models x 3 modelling techniques).

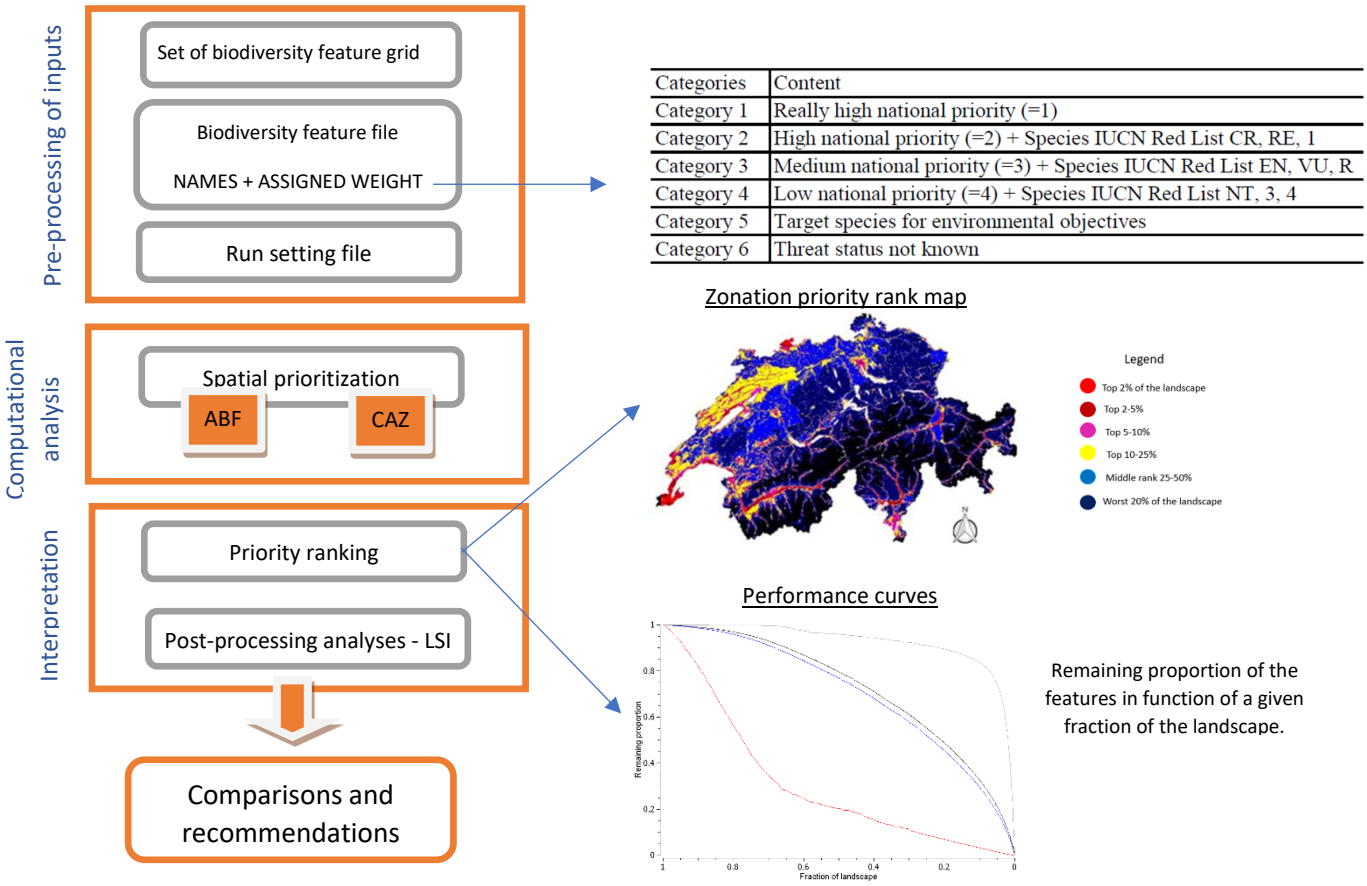
To assess the performance of individual models, we used the maximization of the True Skill Statistic (TSS, (Liu *et al.*, 2005)); i.e. max TSS;(Guisan *et al.*, 2017)) and the Area Under Curve (AUC) of a Receiver Operating Characteristics (ROC) plot (Fielding and Bell, 1997). Max-TSS and AUC are two accuracy complementary accuracy methods widely used to evaluate model's performance (Shabani *et al.*, 2018). The use of max-TSS allowed us to find the optimized threshold that maximizes the metric (Liu *et al.*, 2005; Guisan *et al.*, 2017). The max-TSS is a threshold-dependent measure of accuracy, not sensitive to prevalence (unlike Cohen's Kappa;(Cohen, 1960)) and applied in predictions (Allouche *et al.*, 2006). The AUC is a threshold-independent measure and uses an integrative approach which calculates values of sensitivity and specificity across the whole range of possible thresholds and integrate them into a single evaluation value. The AUC values between 0.5 and 0.7 are considered as "poor" predictions, values between 0.7 and 0.9 as "useful" predictions, and values >0.9 as good to excellent predictions (Swets, 1988; Guisan *et al.*, 2017). As such, all models with maxTSS<0.5 and AUC<0.7 were eliminated and the remaining models were used to generate an ensemble prediction consisting of the mean of the predictions produced by the three modelling techniques. The final ensemble prediction was evaluated with maxTSS.

For the future, we projected the model fitted in the present according to two future scenarios (RCP 4.5 and RCP 8.5, i.e. *Appendix 4*). We also assumed that the LULC is unchanged for the future predictions leading to optimistic solutions.

2.4. Spatial conservation prioritisations with the Zonation software

2.4.1. The Zonation software: general presentation of the analysis

To identify putative PAs based on richness of all and endangered mammals species in Switzerland, we used the software Zonation 4.0 (Lehtomäki and Li, 2013). The software identifies areas that are important for retaining habitat quality and connectivity simultaneously for multiple biodiversity features. It produces a hierarchical prioritization of the landscape meaning that the least useful sites receive the lowest ranks close to 0 whereas areas most valuable for biodiversity conservation receive the highest ranks and are selected for the final solution as extensively documented elsewhere (Moilanen *et al.*, 2005; Moilanen *et al.*, 2011). The Zonation software create a nested ranking meaning that the top 1% of the landscape is included in the best 2% of the landscape. An arbitrary value of 25% is fixed in the Zonation software and corresponds to the fraction of the landscape that includes the top 25% of the landscape for the species studied over the whole territory.



Categories	Content
Category 1	Really high national priority (=1)
Category 2	High national priority (=2) + Species IUCN Red List CR, RE, 1
Category 3	Medium national priority (=3) + Species IUCN Red List EN, VU, R
Category 4	Low national priority (=4) + Species IUCN Red List NT, 3, 4
Category 5	Target species for environmental objectives
Category 6	Threat status not known

Figure 3: Conceptual framework of classic Zonation analysis including 3 steps: i) Pre-processing of inputs; ii) Computation analysis; iii) Interpretation. For the "Pre-processing of inputs" step, three files are required: i) a set of biodiversity feature grid; ii) A biodiversity feature file including names of the species and their corresponding weight; iii) a run setting file including the main commands. The "Computational analysis" step is corresponding to the spatial prioritization by using two cell removal rules : i) Additional Benefit Function (ABF) and ii) Core-Area-Zonation (CAZ). The "Interpretation" step is corresponding to the analyses of results by using Zonation priority rank maps and performance curves and the post-processing analyses files.

The Zonation analyses were divided in three parts (Fig.3). The first step is the "Pre-processing of inputs" and include the preparation of a i) a set of biodiversity feature grid; ii) A biodiversity feature file including the names of the species and their assigned weight; iii) a run setting file (Moilanen *et al.,* 2005). The second step is the "Computational analysis" corresponding to the spatial prioritization process by using two removal rules : i) the additive benefit function (ABF) that emphasizes species richness and ii) Core Area Zonation (CAZ) (Minin *et al.*, 2014) that emphasizes rarity (i.e. endangered species). The third step is the interpretation by working on the priority ranking step and the post-processing analyses. To do so, we created an automated post-processing file describing the post-processing analysis that is called after the main computations. In this study we used the "Landscape identification analysis, identified by analysis type LSI". This post-processing analysis allowed us to obtain statistics related to the biodiversity features (i.e. species).

2.4.2. Specificity of the biodiversity hotspots (BDs) identification analysis

First, we identified the major biodiversity hotspots (BDs) in Switzerland. The goal of this analysis was to identify the top 25% most valuable areas of the landscape to form a potential conservation area network (Moilanen *et al.*, 2005). The hotspots identification analysis was conducted on all mammal's species, on orders (i.e. *Artiodactyla*, *Carnivora*, *Eulipotyphla*, *Chiroptera*, *Lagomorpha*, *Rodentia*). We

called the output of this analysis "unconstrained BD hotspots solution". This analysis was conducted to get a general idea about what the output looks like and was used as a reference analysis. To run this analysis, and as said in the previous section, we used i) a set of biodiversity feature grid layers (i.e. the outputs from the previous distribution models for each species); ii) a biodiversity feature list file, including all the names of the species and their attributed weights; iii) a run settings file with appropriate settings (i.e. specifying the cell removal rules, warp factor, edge removal, use of ecological corridors…).

To include the importance of the threatened species in this analysis, each feature was assigned a weight corresponding to their national priority. To be consistent with our study area, all statutes were assessed at a national scale. First, we listed the status of the 68 species regarding the species national IUCN Red List (IUCN 2021) with its 6 categories (critically-endangered (CR) species, endangered (EN), vulnerable (VU), near threatened (NT), least concerned (LC) or deficient data (DD)). Then we looked at the National Priority level given by Swiss legislation with a scale of 1 (=high priority) to 4 (=low priority) referenced in the legislative documents of OFEV (Bafu, 2010). Finally, we looked at the specific species that are part of the environmental Swiss objectives. To do so a prioritization scale containing 6 categories (Table 1) inspired by Cindy Ramel (Ramel *et al.*, 2020) was used. One of the six categories, represented by numbers from one to six, was given to each species. The corresponding weight was assigned in descending order with a high priority (=1) corresponding to a higher weight (=6) (Appendix 3). Since categories attributed to the species studied correspond to the degree of importance, only results including these weights are presented in the results part.

Categories	Content
Category 1	Really high national priority (=1)
Category 2	High national priority (=2) + Species IUCN Red List CR, RE, 1
Category 3	Medium national priority (=3) + Species IUCN Red List EN, VU, R
Category 4	Low national priority (=4) + Species IUCN Red List NT, 3, 4
Category 5	Target species for environmental objectives
Category 6	Threat status not known

Table 1: Prioritization scale with 6 categories of national priority (WWF project (2020), not published, Ramel et al., 2020). Category 1 included species with a really high national priority (=1); Category 2 was created for species of high national priority (=2) and species from IUCN Red List that are Critically Endangered (CR) or Extinct (RE); Category 3 included species of Medium national priority (=3) and species from IUCN Red List that are Endangered (EN), Vulnerable (VU) and Rare (R); Category 4 is composed by species of low national priority (=4) and species from IUCN Red List that are Near threatened (NT); Category 5 corresponded to species that are target species for environmental objectives; Category 6 was created for species with a threat status not known.

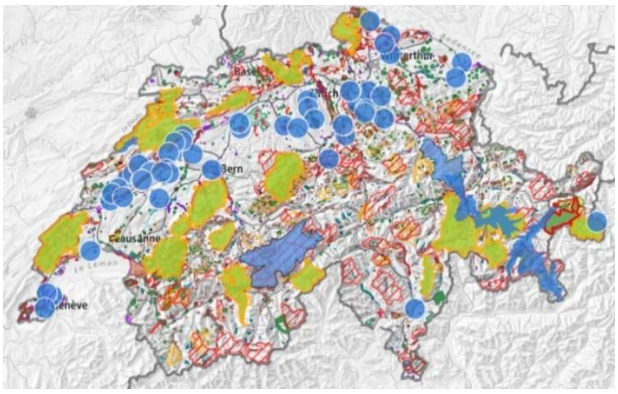
2.4.3. Specificity of expanding conservation areas analysis

Secondly, we identified areas that would best complement the already existing protected areas (PAs) network (Vincent *et al.*, 2019). We focused on the quality of the new areas and the overall connectivity of the PA network. Our PA ranking, used to create then our three networks, was inspired by IUCN categories (Dudley, 2008). We assigned a high value to the Swiss national park (Cat. 1), followed by Pro Natura and Emeraude areas (Cat.2), then Regional parks (Cat.3), Habitat species management areas (Cat. 4) and UNESCO sites (Cat.5). From these categories, we created three masks to be used in the analyses. The study was thus conducted on three different networks created as following: 1) the "All Protected Areas Network" (All-PA network), including all the different types of reserves except the cantonal reserves; 2) the "Emeraude sites – Pro Natura reserves network" (EM-PN network), with only the reserves created to protect biodiversity, specific species or taxonomic groups (FOEN, 2012;

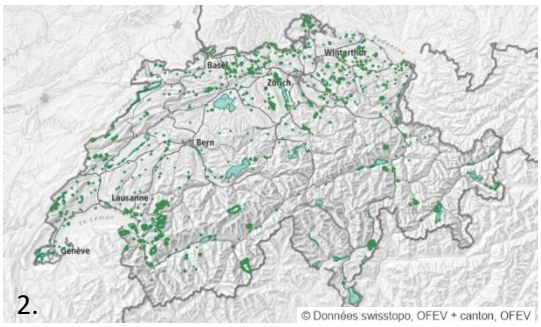
www.pronatura.ch) ; 3) the “Swiss Parks network”, including only the regional nature parks made to protect landscape and ecosystem services (FOEN, 2014) and the National Park (Fig. 4).

During the analysis, the highest pixel value was given to the areas included in the masks (e.g. Protected areas). In this analysis, the existing PAs were already included in the top 25% of the landscape. Thus, the Zonation software is constrained to include the existing PAs in the final solution that we called “constrained solution”. In other words, in this latter analysis, the current PA network was complemented to see which sites could be integrated or removed to optimize the overall BD conservation. To identify these sites, the Classic Zonation colour scheme was used indicating the biological value of the site as following: 1) Red = the best 2% of the landscape; 2) Dark red = the best 2-5% of the landscape; 3) Magenta = the best 5-10% of the landscape; 4) Yellow= the best 10-25% of the landscape.

All Protected Areas network (All-PA)



Emeraude Sites – Pro Natura reserves network (EM-PN)



Swiss Parks network (SP)

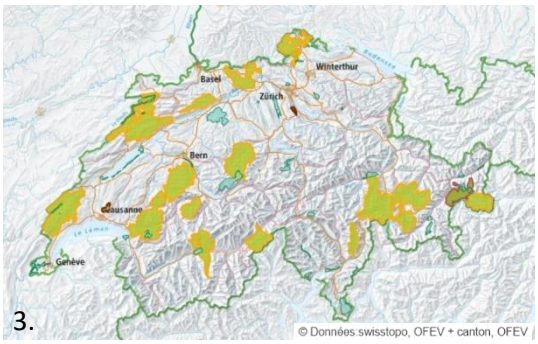


Figure 4: Presentation of the three networks studied. 1) All Protected Areas network, including all types of reserves in addition to Emeraude sites, Pro Natura reserves and Swiss parks; 2) Emeraude Sites and Pro Natura reserves network; 3) Swiss Parks network, including regional nature parks and the national park.

2.4.4. Specificity of evaluating existing versus proposed conservation areas analysis

This step was made at the same time than the previous one by using the three networks (Fig. 4) and the identified biodiversity hotspots from the first step of Spatial Conservation Prioritization (SCP). We evaluated the conservation value of existing/proposed PA networks in terms of spatial representation.

The method of replacement cost (Cabeza and Moilanen, 2006) was used to determine the cost of including or excluding a specific site from the PA network. Replacement cost analysis was used to evaluate the effects of forced inclusion or exclusion of biological entities (Moilanen *et al.*, 2009). In this study, we supposed that the budget would be constant. The exclusion costs of a site were calculated as the loss of the network’s conservation value that follows when sites that would belong to the optimal solution have to be excluded from the reserve network. Conversely, the inclusion of a site is the loss in conservation value that must be accepted if a suboptimal site is forced into the reserve network (Moilanen *et al.*, 2005). The output of this analysis is also considered as “constrained solution” as the current PAs are forced into the solution.

2.5. Comparison analysis

To compare the results in function of the model, network and scenario studied, three comparison analyses were done. The first one, mostly applied for Combined and Covariate models comparison, is a statistical comparison using a Wilcoxon test to compare maxTSS and AUC of both models with R. The second one was performed on a GIS program such as ESRI's ArcMap (ESRI, Redlands, CA). For each analysis two outputs - from the Combined or Covariate models respectively - were loaded in ArcMap to highlight the major differences between the identified BD hotspots and the Pro Natura, Emeraude network, Federal reserve network and the entire Swiss reserve network. The same comparisons were done by comparing the results between current and future scenarios (RCP4.5 and RCP8.5). To do so, we performed a range detection analysis by computing the difference between the two raster layers studied through pixel-over-pixel comparison ("Difference" function in ArcMap). The differences were highlighted when the two images are not perfectly aligned or identical. Finally, the third comparison analysis was done by working on the post-processing analysis computed with the Zonation software while solutions were created. The post-processing analysis gave text files with percentages of the proportion of species remaining in the PAs network. The post-processing file was computed for all solutions for both Combined and Covariate models. The percentages were then entered per species in Excel file and were compared between output solutions.

To know which should be most included in the current and future PA networks and to compare the different outputs, we defined a ranking of priority for orders, regarding the number of species in category 1 and category 3 of national priority, and the total number of species. Six orders were included in this study: *Artiodactyla*, *Carnivora*, *Eulipotyphla*, *Chiroptera*, *Rodentia*, *Lagomorpha*. As shown in Table 2, some orders include species from category one and three with national priority. To know which order should be more protected, they were ranked in function of their proportionality of threatened species. The three top-ranked orders according to their proportion of higher priority species are: Chiroptera, Carnivora and Lagomorpha (i.e. Table 2). Less weight was given to Eulipotyphla and Rodentia because of the lower number of species included in this study. Artiodactyla was the only order without any threatened species.

Orders	Number of species from Category 1	Number of species from Category 3	Proportions of species with national interest
Artiodactyla	0	0	0
Carnivora	2	1	0.27
Chiroptera	9	2	0.5
Eulipotyphla	0	2	0.2
Lagomorpha	0	1	0.33
Rodentia	0	2	0.12

Table 2: Proportion of threatened species by order. The number of species from category one and three containing the species with highest priorities was given for each order. Then we calculated a proportion for each order allowing to rank their priority. The calculation for the last column was the following one: number of species threatened/ number of species within the order. More importance was given to species form category 1.

3. Results

3.1. Analysis under current situation

3.1.1. Efficiency of the Covariate and Combined models regarding hotspot identifications

For the first analysis, the best hotspots covering 25% of the area were identified, the maps present the 25% most valuable areas for the studied species. For both models the principal biodiversity hotspots are located near the main cities of Switzerland (Geneva, Lausanne, Zurich, Berne, Lugano, Basel), in large valleys (Rhone Valley, Scuol and Zuoz valleys, Bellinzone, Biasca, Lugano valleys), near lakes (Lake Geneva, Neuchatel Lake, Zurich Lake and Obersee, Zoug lake, Lucerne lake), and on the Jura Plateau (Fig. 5).

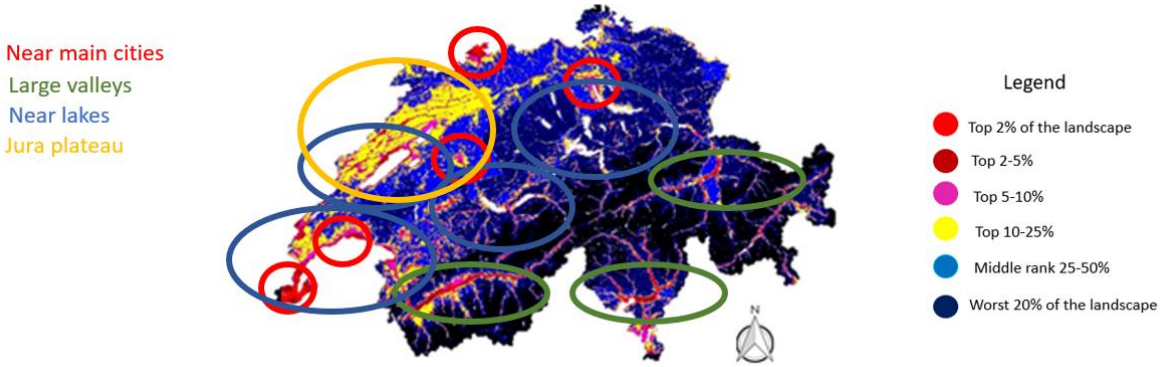


Figure 5: Main biodiversity hotspots identified for the Combined models. The main biodiversity hotspots are representing the top 25% fraction of the solution and are represented by red, dark red, magenta, and yellow colours. They are mainly located near main cities, in large valleys, near lakes and on the Jura Plateau.

The hotspots identified in this analysis are corresponding to urbanized areas. These results should be taken with cautions regarding the possible sampling biases related to the species. Indeed, as explained in the previous section, the Zonation analysis is based on SDMs built on presences and pseudo-absences. In the Zonation analysis, weight is given to the species in function of their national priority. Thus, if we are comparing the maps corresponding to the presences of the 11 most threatened species in Switzerland to the possible hotspots identified in this section, we could see a similar trend between the two (Fig.6). These results are going to be discussed later (c.f. 4.6).

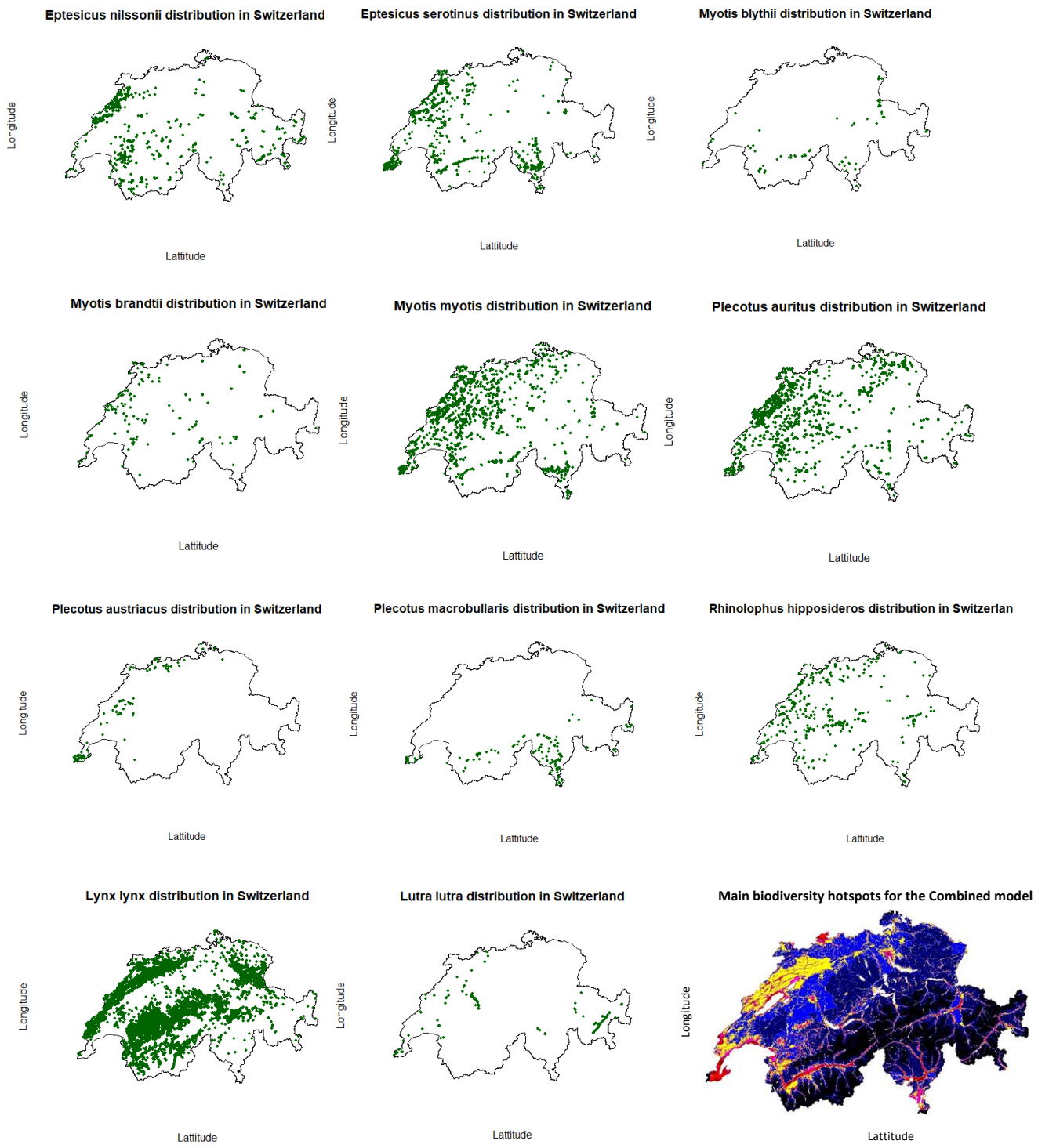


Figure 6 : Distribution of the 11 most threatened species in Switzerland, based on presences from InfoSpecies and GBIF compared to the Main biodiversity hotspots identified in the first step of Zonation analysis. The biodiversity hotspots (BDs) are highlighted by red, dark red, magenta and yellow colours and are representing the top 25% fraction of the solution.

Moreover, models differ between them. Differences between the Combined and Covariate models are highlighted by red areas (Fig. 8). Going from West to East, the Combined model gives more importance to the Jura Vaudois natural regional park, including the top 2-10% of the priority ranking and covers a larger surface south of the Joux Lake, including Mont Tendre and north of the Berolle region (Fig.7). For the Covariate model, the best PAs are suggested to be in the Western part of the Jura regional park

Chappelle-des-Bois (FR) and Bois d'Amont (FR). This pattern is repeated in other regions of Switzerland such as Central Switzerland (near Lucerne lake for example), and in Ticino. In general, the Combined models predict larger areas than the Covariate models, the latter highlighting more but smaller areas.

The Combined models include 45.79% of the species studied against 43.86% for the Covariate models. For all categories of national priority, from one to six, Combined models incorporate more species than the Covariate models with a difference of 4.33% for category one for example. For both models, species included in the solution are mainly species with medium national priority. Those from category three, are the most included in the solution with proportions of 63,76% for Combined model and 61,03% for Covariate models. Species with high national priority, such as those from category one are less included in the solutions (0.6101, 0.5618), followed by species from category four that present a low national priority (0.5816, 0.5519).

The results of the statistical comparison between the maxTSS and AUC values for both models showed that the differences between the two maxTSS values for the two models vary significantly (p=0.0097). However, the AUC values for the Combined and the Covariate models are not significantly different (p=0.123) (i.e. *Appendix 5*).

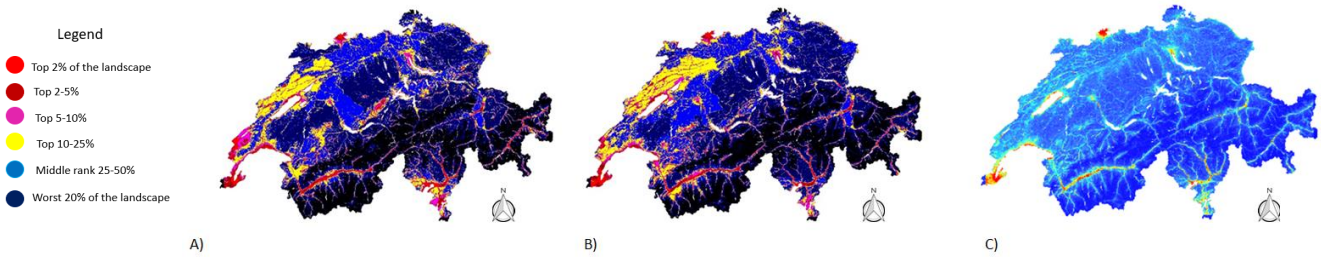


Figure 7: A) Main biodiversity hotspots in Switzerland for the Covariate model. B) Biodiversity hotspot for the Combined model. C) Mammals' species richness in Switzerland. Red: The top 2% of the priority ranking (landscape), Dark red: the top 2-5%, Magenta: The top 5-10%, Yellow: the top 10-25%, Light blue : middle ranks 25-50%, Dark blue: below average 50-80%, Black: the lowest ranked 20%.

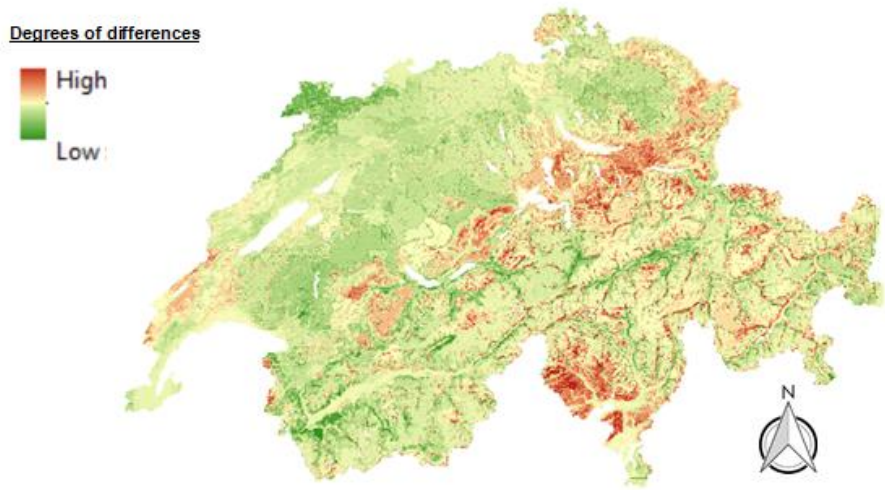


Figure 8: Major differences, highlighted in red, between the priority ranking maps for the Covariate and Combined models, for the first step of Zonation analysis. The superposition of the two priority ranking maps was done by using the "difference" function in ArcMap.

3.1.2. Efficiency of current PA network for mammals' species

We report below results for the three subsets of protected areas (PAs) considered.

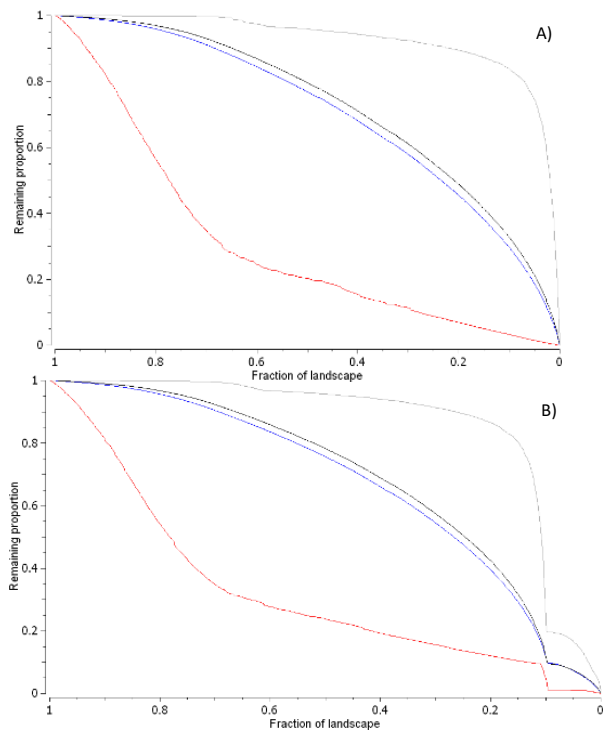
3.1.2.1. Swiss parks PA network (SP-Network)

To work on the efficiency of this PA network, national and regional parks were obligatorily included in the solution as explained in the methods part. As expected, the best 2-10% of the landscape is included in the existing PA areas and is complemented by the hotspots identified in the hotspot analysis. Using this method, hotspots previously identified as being in the last section are less included in the Zonation prioritization solution and are assigned to the background. When comparing unconstrained hotspots and constrained solutions that incorporate national and regional parks (called "SP solution"), the main biodiversity hotspots are not included in the 5-10% of the solution. However, for both models, large valleys, areas near lakes and cities are included in the best 10-25% of the landscape. The actual reserve network could be extended to the yellow parts of Zonation solution. As seen previously in the methods part, we worked on the potential expansion of current PA networks. This Zonation prioritization shows that the federal protected areas (i.e. the National Park and regional parks) would be extended to include the BD hotspots represented in the top 10-25% fraction of the landscape.

The main difference between SP solutions for the Combined and Covariate models and the hotspot zonation solution is observable in the eastern part of Switzerland. As shown in Fig.5c, the eastern part of SP network is mostly coloured in red meaning that federal protected areas do not include the BD hotspots identified in the first analysis.

Zonation software provides performance curves (Fig. 9) representing the remaining proportion of species as a function of the fraction of landscape. By comparing the constrained (Fig 9.b) and unconstrained curves (Fig 9.a) at the same priority fraction of the landscape, changes at the end of the curves are noticeable for a fraction of landscape at 10% which clearly demonstrate that the PAs that were forced in the Zonation prioritization solution are not what one would have ideally chosen. Indeed, only about 15% of the species are present within the forced area, whereas in the unrestricted solution, more than 35% of the distribution would be protected within a similar area.

In terms of percentage of species integration in the top 25% fraction of the SP solution, the results for both models were the same with a reduced efficiency of reserves for mammals, estimated at 3,47% for the Combined model and 3,78% for the Covariate model by comparison with the unconstrained solution, i.e. hotspot solution (0.4232,0.4009). Regarding the species most included in the top fraction, the same ranking is observable as for the unconstrained hotspot solution. However, results showed a lower species' distribution proportion for national priority categories three (0.5991, 0.5586), one (0.5622, 0.5149) and four (0.5355, 0.5045) for the Combined and Covariate models.



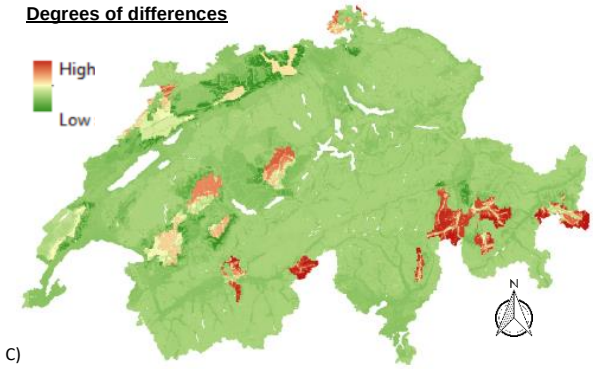


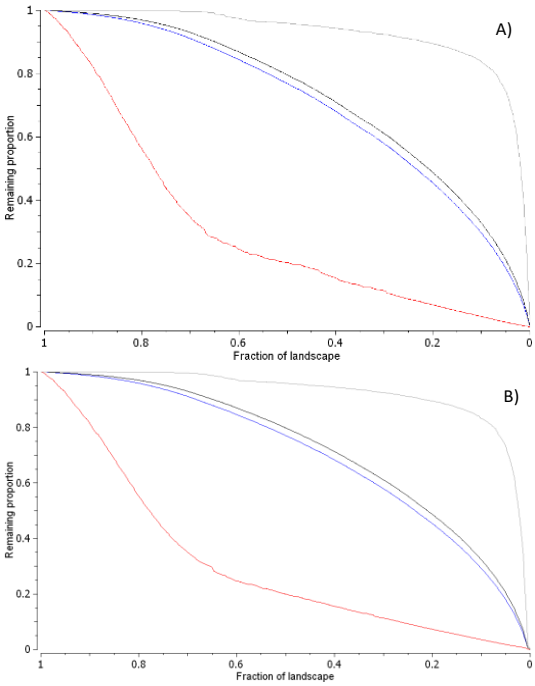
Figure 9: Highlighted differences between constrained SP-solution and unconstrained hotspot solution for the Combined model. Results for the Covariate model is provided in Appendix 6. A) Performance curves for the unconstrained solution. B) Performance curves for constrained SP-solution. The red line represents the biodiversity feature with the lowest distribution remaining, the blue line represents the average over all the features, the black line represents the weighted average over all the biodiversity features, the grey line represents the biodiversity feature with the highest distribution remaining. C) Highlighted spatial differences by red pallet colours, using the "Difference" function in ArcMap, between Swiss parks (SP) and hotspot (BD) priority ranking maps within the reserve network.

3.1.2.2. Emeraude-ProNatura PA network

The second PA network, the Emeraude-Pro Natura PA network, is composed of small areas in Switzerland. The maps obtained for the constrained EM-PN and unconstrained solutions are visually similar but small differences are located near the Jura regional park, La Côte aux Fées, the west side of Bienne Lake, Montfaucon and near Bale region, Thal regional natural park, Pre-Alps and Gruyere regional natural park for both models, as highlighted in Fig. 10c by the red color. The Emeraude-Pro Natura PA network is mostly situated in areas with biodiversity hotspots. However, some areas are in the dark and blue parts of the unconstrained hotpot zonation prioritization solution corresponding to the least valuable areas for the species studied. Among them, Grundberg-Almagellertal (Pro Natura), Alp Untersteinberg (Pro Natura) und Breitlauenen (Pro Natura), Saint Moritz Bald (Pro Natura), Oberaargau (Emeraude) are located in places that are not included in the most suitable areas for the species studied. The Emeraude-Pro Natura PA network could be extended to include the other hotspots, near the current Emeraude and Pro Natura sites and included in the top 10-25% fraction of the Emeraude-Pro Natura zonation prioritization solution (EM-PN solution).

Compared to the Swiss parks zonation prioritization solution, no changes at the end of the curves are noticeable for both Combined (Fig. 10b) and Covariate models (i.e. Appendix 6), which is consistent with the previous observation. Moreover, the efficiency of the Emeraude-Pro Natura PA network is greater by two percent than for the unconstrained hotspot zonation prioritization solution with 55% of predicted species included in the solution with similar area prioritized for both models.

In the top 25% fraction for EM-PN solutions, 45,90% species in the Combined model and 44,03% from the Covariate models, are included. The efficiency of the Emeraude-Pro Natura network rose by 3,58% for the Combined model and 3,94% for the Covariate model when compared to the Swiss parks PA network and by 0,11% for the Combined model and 0,17% for the Covariate model compared to the unrestricted hotspot prioritization zonation solution. As mentioned before, the same ranking is observable for the national priority categories three (0.6406, 0.6112), one (0.6085, 0.5618) and four (0.5841, 0.5543) for both the Combined and Covariate models.



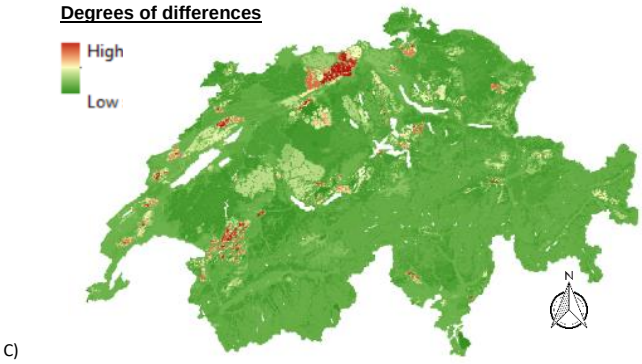


Figure 10: Highlighted differences between unconstrained hotspot solution and constrained EM-PN-solution for the Combined model. Results for Covariate model is provided in Appendix 6. A) Performance curves for the unconstrained solution. B) Performance curves for the constrained EM-PN solution. The red line represents the biodiversity feature with the lowest distribution remaining, the blue line represents the average over all the features, the black line represents the weighted average over all the biodiversity features, the grey line represents the weighted average over all the biodiversity features, the grey line represents the biodiversity feature with the highest distribution remaining. C) Highlighted spatial differences by red paller colours, using the "Difference" function in Arc Map, between Emeraude-Pro Natura (EM-PN) and hotspot (BD) priority ranking maps within the reserve network.

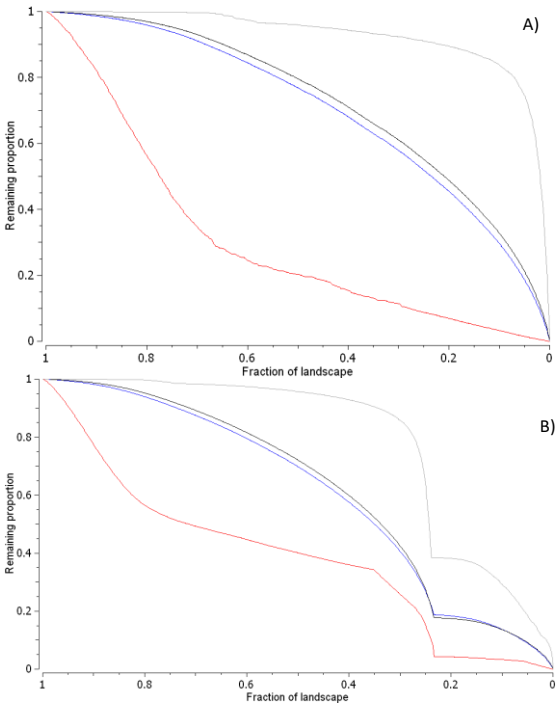
3.1.2.3. All protected areas network

The last network composed by all the PAs in Switzerland (hereafter all-PA solution) includes Swiss Parks and Emeraude-Pro Natura networks together with all other PAs.

As expected regarding results obtained for constrained SP solution, most of the protected areas forced into the solution do not match the biodiversity hotspot of the unconstrained solution. The best 2-10% of the landscape is included in the west part of reserve areas, in Ticino and in large valleys of eastern Switzerland. The following 10-25% of the most suitable areas are attributed to the east part of the reserves. The top 25% fraction of the landscape is mostly included in the reserve network except for small areas near Bâle, Geneva and in Rhone Valley. A mismatch between unconstrained and constrained solution is thus observed.

Performance curves for both models show once again changes at the end of the curves for a fraction of landscape about 23% (Fig.11), showing that this solution does not include the most suitable areas. For the constrained PA solution, less than 20% of the predicted species are within the forced area, whereas in the unconstrained solution, more than 55% of the potential distributions would be protected with a similar conservation cover.

Compared to the unconstrained solution, a decrease of 21,03% for the Combined and 22% for the Covariate model is obtained here. Indeed, only 24,76% of the species for the Combined and 21,86% for the Covariate models are included in the top 25% fraction of all-PA zonation prioritization solution. This trend has an impact on national priority categories with lower proportions of potential species include in the all-PA solution. However, the ranking is the same with species' categories three (0.3714, 0.3000), one (0.3237, 0.2728) and four (0.2891,0.2649) being the most included in the top 25% fraction of the all-PA prioritization solution.



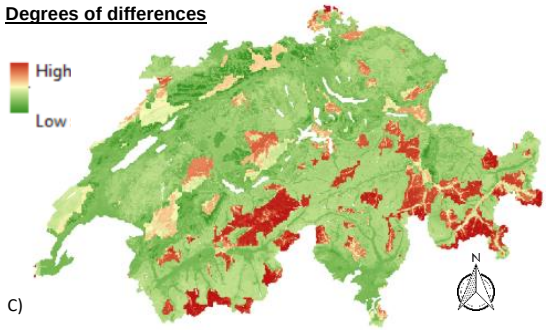


Figure 11: Highlighted differences between the unconstrained hotspot solution and constrained PA-solution for the Combined model. Results for the Covariate model is provided in Appendix 6. A) Performance curves for the unconstrained solution. B) Performance curves for the constrained All-PA solution. The red line represents the biodiversity feature with the lowest distribution remaining, the blue line represents the average over all the features, the black line represents the weighted average over all the biodiversity features, the grey line represents the biodiversity feature with the highest distribution remaining. C) Highlighted spatial differences by red pallet colours, using the "Difference" function in ArcMap, between all protected areas (All-PAs) and hotspot (BD) priority ranking maps within the reserve network.

3.1.3. Protected areas for which orders and species?

3.1.3.1. Orders

As presented in the previous section, this study was conducted on three types of networks: Swiss parks (SP) network, Emeraude-Pro Natura (EM-PN) network and all protected areas (all-PA) network. By comparing the results obtained for the three reserve networks, common points and differences are highlighted regarding species themselves and corresponded distribution proportion in each solution (Fig.12).

For the constrained SP zonation prioritization solution, the order most included in the solution was *Chiroptera* with a distribution proportion equal to 58,81% and 53,53% for the Combined and Covariate models. *Eulipotyphla* presents a distribution proportion of 52,37% and 48,14% for the Combined and the Covariate models respectively, followed by *Lagomorpha* with 50,19% and 48,67% of species included in the top 25% fraction of the constrained SP zonation solution. For the constrained EM-PN zonation prioritization solution. *Chiroptera* was also the most included in the top 25% fraction of the constrained EM-PN solution (0.6383, 0.5919). However, the Covariate and Combined models did not give the same importance to the different orders. Indeed, for the Combined model *Eulipotyphla* (0.5651) and *Rodentia* (0.5362) were the two best. For the Covariate model, positions two and three were inverted, with 52,92% of *Rodentia* species included and 52,25% for *Eulipotyphla*. For the last constrained all-PA zonation prioritization solution, the top three categories also differed from the two previous networks, and all distribution proportions were lower for all orders except *Artiodactyla*. The most included order in the top 25% fraction of all-PA constrained solution is *Lagomorpha* for both the Combined and Covariate (0.4021, 0.3889), followed by *Chiroptera* for the Combined model (0.3185) and *Rodentia* for Covariate model (0.2771). The third position is given to *Eulipotyphla* order for both the Combined and for the Covariate models with distribution proportion equal to 31,23% and 26,86% respectively (*Appendix 8*).

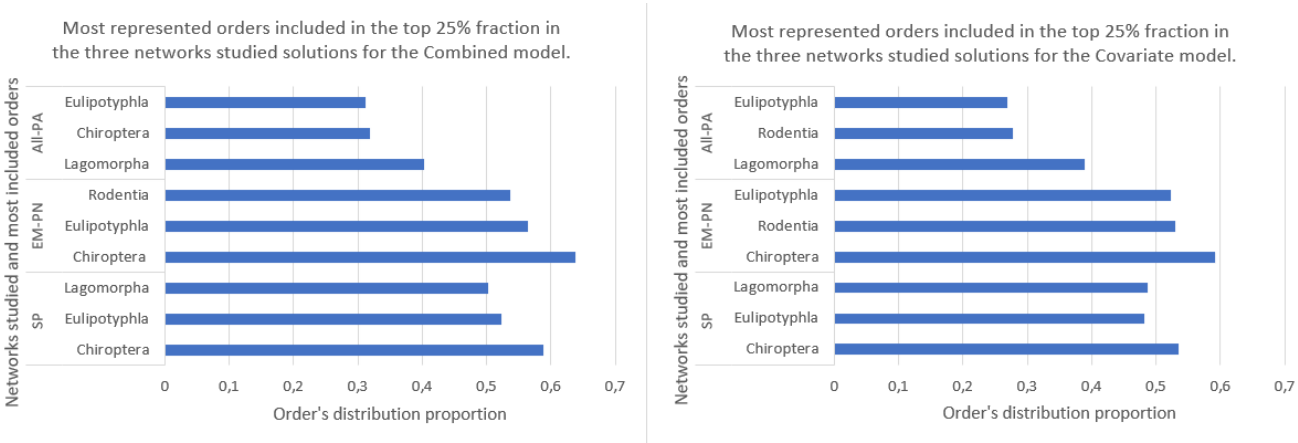


Figure 12: The three most represented orders included in the top 25% fraction within the three networks studied i) All protected areas network (All-PA); ii) Emeraude-Pro Natura network (EM-PN); iii) Swiss parks (SP) network, for the Combined (left) and Covariate (right) models.

3.1.3.2. Threatened species

3.1.3.2.1. *Chiroptera* species

Chiroptera is the most threatened order in Switzerland. Eleven out of 23 species are threatened and are of national priority. Nine of the eleven threatened species are included in the first category, the remaining two are in category three (i.e. *Appendix 3*).

In the constrained SP solution, the most represented species in the top 25% fraction was *Plecotus macrobullaris* (0.8722, 0.7317), a species from category one, followed by *Pipistrellus khulii* (0.8352, 0.7193), for both the Combined and Covariate models (Fig. 13). The third position was given to *Tadarita teniotis* for the Combined model (0.7091) and *Nyctalus noctula* (0.6955) for the Covariate model. Representativeness of threatened species from category one in the Combined model was mostly superior to 50%, except for *Myotis brandtii* (0.3717), *Myotis myotis* (0.4645) and *Plecotus auritus* (0.4104). For the Covariate models, the proportion of threatened species in this solution was lower and most of the species were included at more than 40% in the solution, except for *Myotis blythii* (0.3552). *Barbastella barbastellus* and *Myotis bechsteinii*, from category three, were included at 49% in the top 25% fraction of the constrained SP solution.

In the constrained EM-PN solution, results are more contrasted compared to previous network and between the Combined and the Covariate models. For the Combined model, *Plecotus macrobullaris* was still the most represented species in the 25% fraction of the constrained EM-PN solution with a proportion of 90.47% (Fig. 13) but the second and third positions differ, occupied by *Hypsugo savii* (0.8872) and *Pipistrellus khulii* (0.8827). For the Covariate model, the first position was attributed to *Pipistrellus khulii* (0.7829) followed by *Plecotus macrobullaris* (0.7771), and *Nyctalus noctula* (0.7461). Overall, proportions of species included in the top fraction were higher and most of the threatened species are represented above 50% in this solution except for *Plecotus auritus* (0.4658, 0.4772) and *Myotis brandtii* (0.4055, 0.4449) for the Combined and the Covariate models.

In the constrained all-PA solution, the proportion of species included in the top 25% fraction of the solution were much lower with a decrease of 26.96% for the Combined and 27.41% for the Covariate model compared to the constrained SP solution. The same trend is observable by comparing constrained all-PA solution with constrained EM-PN solution with a decrease of 31.98% for the Combined and 33.07% for the Covariate models. Once again results differed across models with a top three constituted of *Myotis blythii* (0.5317), *Plecotus macrobullaris* (0.5174) and *Hypsugo savii* (0.4641) for the Combined model and *Tadarita teniotis* (0.3784), *Plecotus macrobullaris* (0.3519) and *Nyctalus*

noctula (0.3388) for the Covariate model. The majority of threatened species are included at 30% in the top 25% fraction of all-PA zonation prioritization solution for both models.

3.1.3.2.2. *Carnivora* species

In the order of *Carnivora,* three species out of eleven are threatened. In the constrained SP solution, the most included species in the top 25% fraction of the solution is *Lutra lutra* with a proportion of 73.06% and 75.89% for the Combined and the Covariate models respectively. Results differed across models with a top three complemented by *Mustela nivalis* (0.4670) and by *Canis lupus* (0.4083) for the Combined model and by *Canis aureus* (0.4609) and *Martes martes* (0.4219) for the Covariate model. *Lynx lynx*, the second most threatened species, from category one, was represented in the top 25% fraction of the solution at approximatively 30% by both models (0.3353, 0.3373) (Fig.13).

In the constrained EM-PN solution, *Lutra lutra* was still the most included species in the top fraction for both models (0.7901, 0.8051). For the Combined model *Mustela nivalis* (0.4851) was the second most represented species in the top fraction followed by *Canis aureus* (0.4484). For the Covariate model, *Canis aureus* (0.5028) had a higher distribution in the top 25% fraction of the solution compared to the previous network and was followed by *Martes martes* (0.4678). The same trend was observed for *Lynx lynx* compared to the constrained SP solution (Fig. 13).

As expected, species in constrained all-PA solution were less included in the top 25% fraction of the solution with a decrease of 16.10% for the Combined and 19.75% for the Covariate model, compared with the constrained SP solution. Decreases were even more highlighted when comparing with the constrained EM solution as observed for *Chiroptera* in the previous section. However, for the Covariate model, all the threatened species were the most distributed in the top 25% fraction of the solution including *Lutra lutra* (0.3735), *Canis lupus* (0.3047) and *Lynx lynx* (0.2757). For the Combined model, the most included species in the top 25% fraction were *Canis lupus* (0.3221) at the top position followed by Mustela nivalis (0.3008) and *Lutra lutra* (0.2987).

3.1.3.2.3. *Lagomorpha* species

In the order of *Lagomorpha* one species out of three is threatened, from category three of national priority. *Oryctolagus cuniculus* was well included in the top 25% fraction of the constrained SP solution with a percentage of species of 94,5% for the Combined model and 89,36% for the Covariate model in the solution. The two other species, *Lepus europaeus* and *Lepus timidus* were less represented with a percentage of distribution around 30% and 20% respectively for both models in the top 25% fraction of the solution. In the constrained EM-PN solution, the same trend was observed but with higher proportion. For both the Combined and the Covariate models *Oryctolagus cuniculus* (0.9576, 0.9123) was the species most included in the top 25% fraction of the solution followed by *Lepus europaeus* (0.3545, 0.4084) and *Lepus timidus* (0.2305, 0.1856). In the constrained all-PA solution, the decrease of effectiveness of the network was less important than for *Chiroptera* and *Carnivora* orders. Compared to the constrained SP solution, a decrease of 9,98% for the Combined and 9,78% for the Covariate models was observed. As expected, the PA's effectiveness decreased by 11,21% for the Combined and 11,32% for the Covariate models compared to the constrained EM-PN solution.

3.1.3.2.4. *Eulipotyphla* species

In the order of *Eulipotyphla*, two species out of nine are threatened. In the constrained SP zonation prioritization solution, *Neomys anomalus* and *Neomys fodiens*, the two threatened species from category three, were the species most included in the solution. *Neomys anomalus* was included in the top fraction with a distribution proportion of 73,46% for the Combined and 66,05% for the Covariate

models followed by *Crocidura russula* (0.6132, 0.5886) and *Neomys fodiens* (0.5957, 0.5554). In the constrained EM-PN zonation prioritization solution, the same species were the most included in the top 25% fraction of the solution with higher proportion. *Neomys anomalus* was the species most included in the top fraction at 77,32% for the Combined and 70,35% for the Covariate models followed by *Crocidura russula* (0.6901, 0.6693) and *Neomys fodiens* (0.6616, 0.6030). In the constrained all-PA zonation prioritization solution, the efficiency of the studied network (i.e. all-PA) decreased by 21,14% of species in the top 25% fraction of the solution for the Combined and 21,28% for the Covariate models compared to the constrained SP solution and 25,28% for the Combined and 23,39% for the Covariate models compared to EM-PN restricted solution. For the Combined model, *Neomys anomalus* (0.4689) was the species the most included in the top 25% fraction of the constrained all-PA solution followed by *Sorex minutus* (0.3597) and *Neomys fodiens* (0.3363). For the Covariate model, *Sorex araneus* (0.3521) was the species most included in the top 25% fraction of the solution followed by *Sorex alpinus* (0.3332) and *Neomys anomalus* (0.3234).

3.1.3.2.5. *Rodentia* species

In the *Rodentia* order, two species out of seventeen are threatened and are in category three. In the constrained SP solution, the species most included in the top 25% fraction of the solution was *Rattus rattus* for both the Combined and the Covariate models (0.8019, 0.7139). For the Combined model, the species most included in the top 25% fraction of the network studied (i.e. SP solution) was *Apodemus alpicola* (0.7464) followed by *Apodemus sylvaticus* (0.5961). For the Covariate model, *Apodemus flavicollis* (0.6285) and *Microtus agrestis* (0.6244) were the two other most included species in the top fraction. For both models, *Muscardinus avellanarius,* a threatened species from category 3 of national priority, was not greatly included in the top 25% fraction of the solution with values species values inferior to 50% (0.4379, 0.4435). In the constrained EM-PN solution, *Rattus rattus* (0.8454, 0.7694) was, as for the constrained SP solution, the most represented species in the top 25% fraction in both models followed by *Apodemus alpicola* (0.7631) and *Mus domesticus* (0.6684) for the Combined model and by *Apodemus flavicolis* (0.6998) and *Apodemus sylvaticus* (0.6943) for the Covariate model. Once again *Muscardinus avellanarius* was not included among the species most represented in the top 25% fraction of the solution but its distribution was above 50% in the network studied (i.e. EM-PN solution) for both models. In the constrained all-PA solution, the decrease of distribution proportion was close to the results obtained for *Eulipotyphla* with minus 21.16% for the Combined and 20.33% for the Covariate models, compared to the constrained SP solution, and minus 25.54% for the Combined and minus 25.21% for the Covariate models, compared to the constrained EM-PN solution. Differences were also visible regarding the species most included in the solution with *Apodemus alpicola* (0.4670, 0.3949) as the species most included in the top 25% fraction of all-PA solution. *Rattus rattus* (0.4419) and *Chionomys nivalis* (0.3616) came in second and third for the Combined model. For the Covariate model, the second species most included in the top fraction was *Chionomys nivalis* (0.3759) and the third one was *Eliomys quercinus* (0.3479). The same trend was observed, as the two other constrained solutions, for *Muscardinius avellanarius.*

3.1.3.2.6. *Artiodactyla* species

In the order of *Artiodactyla*, no species are threatened in Switzerland. As a reminder, this order was also the least included in the solution. In the constrained SP zonation solution, for both models, *Sus scrofa* (0.3466, 0.3292) was the most represented species in the top 25% fraction of the solution with *Cervus elaphus* (0.3313, 0.3167) and *Capreolus capreolus* (0.2997, 0.3125). In the constrained EM-PN solution, *Sus scrofa* (0.3964, 0.3851) was still the species most included in the top 25% fraction of the EM-PN solution followed by *Cervus elaphus* (0.3435) and *Capreolus capreolus* (0.3254) for the Combined model. For the Covariate model *Capreolus capreolus* was the second most included species

and *Cervus elaphus* the third. In the constrained all-PA solution, there was no decrease of distribution proportion for both models. However, the results were surprising with *Capra ibex* (0.3551, 0.3468) as the species most included in the top 25% fraction of the all-PA solution followed by *Cervus elaphus* (0.2892, 0.2732) and *Rupicapra rupicapra* (0.2749, 0.2860). Once again, results differ from models and networks studied.

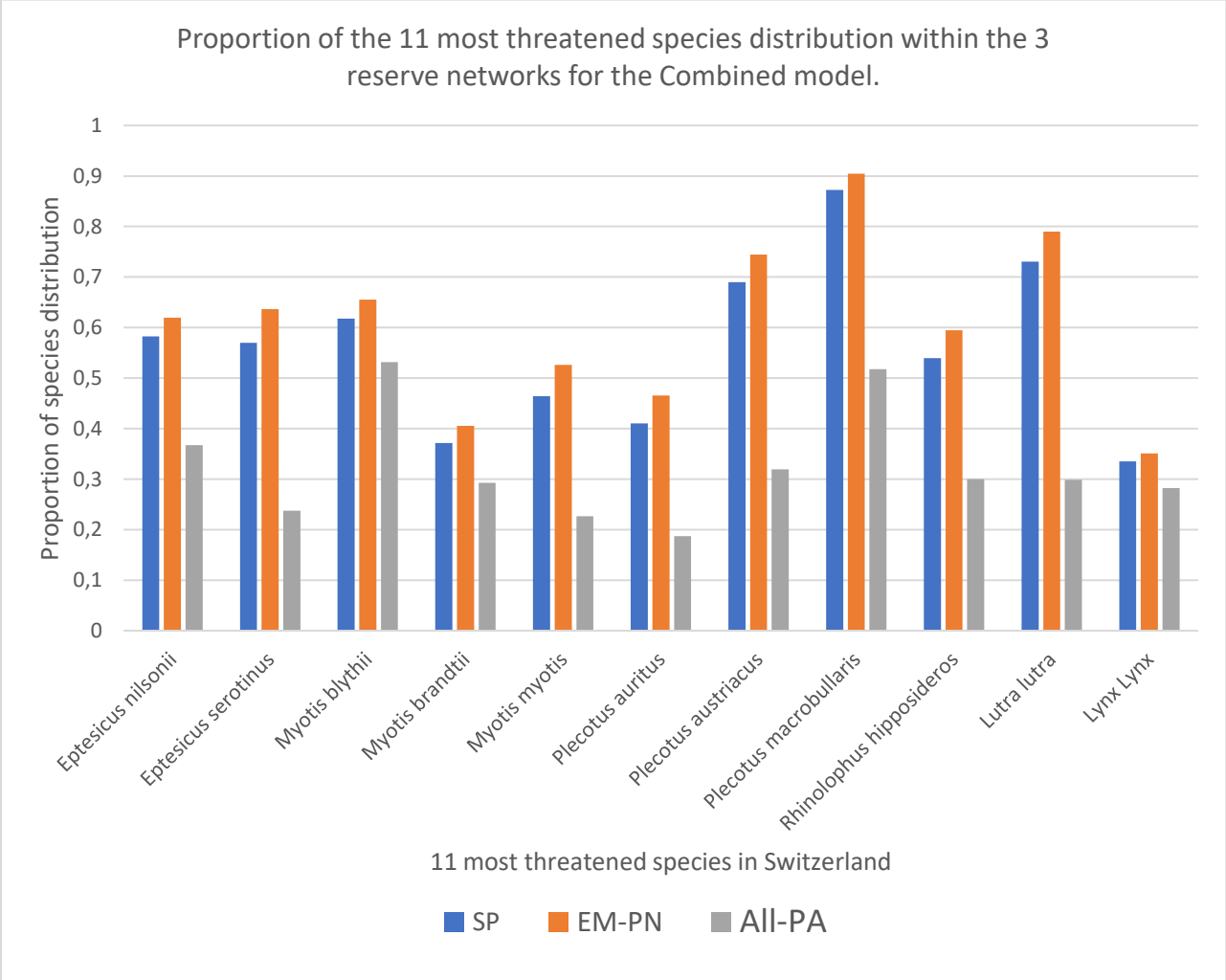


Figure 13: Proportion of the 11 most threatened species distribution within the 3 studied networks : i) Swiss parks (SP) network; ii) Emeraude-Pro Natura (EM-PN); iii) All protected areas (All-PA) network. The network that includes the highest proportion of threatened species proportion is the EM-PN network followed by SP network and finally by All-PA network.

3.2. Analysis under future conditions

For this part, the results from future predictions compared with analysis under present conditions, highlight major differences between current and future predicted scenarios. As we did before for the current situation, we identified the main BD hotspots in Switzerland based on our future projections, and then looked at the efficiency of the current reserve network in the far future (2060-2080) and its potential expansion or improvement if needed.

3.2.1. Identifying future hotspots

Differences between current patterns and both the RCP 4.5 and the RCP 8.5 scenarios can be seen on comparison maps. As shown in Fig.14, the red colour highlights the major changes between the two possible future scenarios studied and the current situation. Indeed, for RCP 4.5, for both the Combined

and the Covariate models, a loss of suitable areas was mainly visible on the sides of major valleys, for example for Rhone Valley at the south-east side near Nendaz and north side near Crans Montana. Other changes were visible in western and eastern Central Alps and in the southern region of the Alps. Areas in the North side of the Alps, including Pre-Alps and Gruyere Regional Park were also subject to changes related to a predicted increase of Carbon in the atmosphere. At lower elevation, loss of suitable habitats was also visible near lakes and in the Plateau. The shores of the main lakes still have a high level of species richness but the environment near lakes made up of fields and wetlands are no longer suitable for those mammal species. The same trend is observed near Saint Gall. Conversely, certain places are included in the solution were not presented as suitable in the current situation. These areas are located at the south and north sides of the Plateau including north of Bienne lake, between Bienne and Zurich and Thal and Aargau jura natural regional parks (Fig.14).

With RCP 8.5, at +8.5 W/m^2 of greenhouse gases, predicted habitat loss for our mammal' species was higher. As observed on Fig.10, fewer areas are highlighted in the top 2-10% fraction of the BD hotspot solutions, for both the Combined and the Covariate models. Under the high carbon concentration scenario, the north areas of Neuchâtel lake, including Doubs regional natural park, were no longer included in the top 25% fraction of the solution as it was previously observed under the current scenario (Fig.15). The same trend was observed for the middle elevation mountainous areas but at a lower proportion. Under RCP 8.5, the Pre – Alps were not concerned by the loss of predicted habitat suitability for the mammal species studied. As observed with RCP 4.5 scenario, species richness was higher in some areas. Among them, an area under Yverdon-les-Bains had higher species richness compared to current unconstrained BD hotspot zonation prioritization solutions. The same trend is observed in the south-eastern part of Zurich lake (Fig.15).

Overall, for both the Combined and the Covariate models under RCP 4.5 and RCP 8.5, the top 1-10% fraction of the solution were the same than under current conditions. However, the top 10-25% fraction of the solution differs across models and scenarios. A slight move toward the North-West direction was observed under both the RCP 4.5 and the RCP 8.5 scenarios for both models.

A comparative analysis was done using the percentage of species included in the top 25% fraction for both models under RCP 4.5 and RCP 8.5. Under the RCP 4.5 scenario, the Combined model included 45,74% of species compared to 43,58% for the Covariate models. Under RCP 8.5 scenario, The Combined model included 45,88% of the species compared to 43,14% in the Covariate model. As seen in the sections before, differences with current BD hotspot identification analyses are not significant. The national priority categories most included in the network were category three (0.6489,0.6089), category one (0.6067, 0.5452) and category four (0.5887, 0.5293). Once again, differences between results were not significant ($p>0.05$).

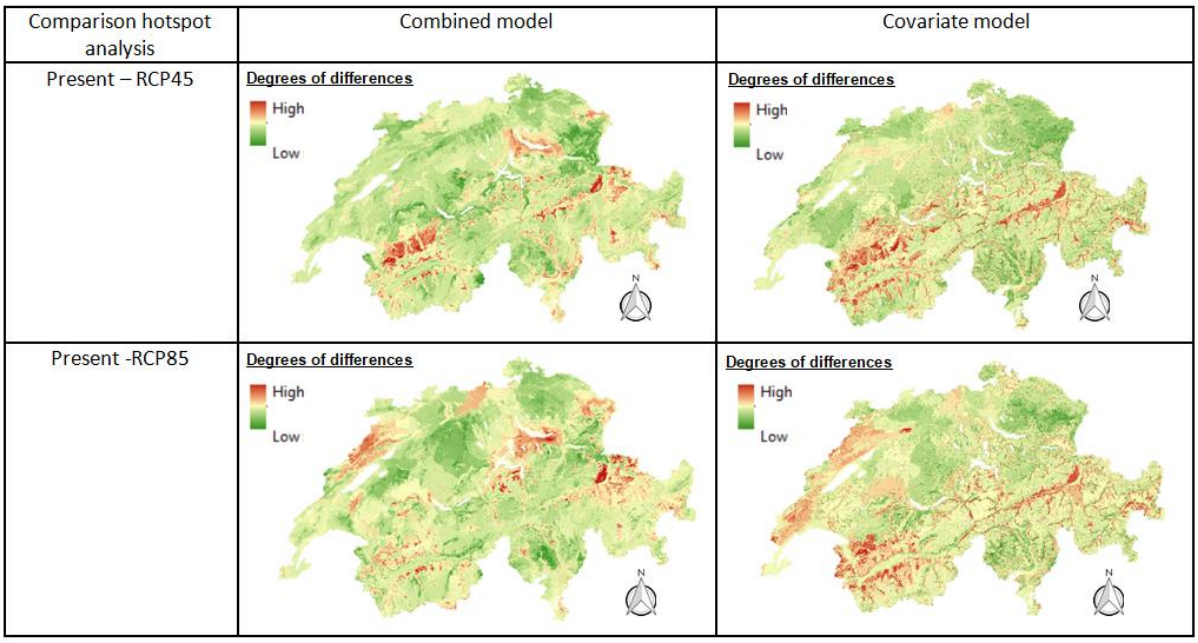


Figure 14: Comparison between priority ranking maps of the current situation unconstrained solutions with unconstrained solutions under RCP 4.5 and RCP 8.5 scenarios for the Combined and Covariate models. The main differences were highlighted by red pallet colours, using the "Difference" function in ArcMap.

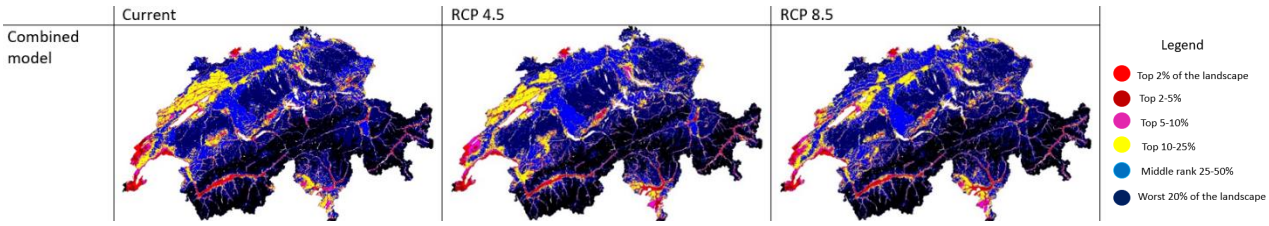


Figure 15: Comparison between future scenarios (i.e. RCP 4.5, RCP 8.5) with current situation for the Combined model solutions (Results for the Covariate model are presented in Appendix 7). For both future scenarios, we observed smaller areas included in the top 25% fraction. This phenomenon is even more accentuated for RCP 8.5 scenario (i.e. Jura Plateau).

3.2.2. Efficiency of current protected areas (PAs) network for threatened species in the far future (2060-2080)

3.2.2.1. SP network

Under both scenarios and for both models, the top 2-10% fraction of the constrained and future SP zonation prioritization solution was the same than the one identified for the constrained SP zonation prioritization solutions for both RCP 4.5 and RCP 8.5 scenarios. The SP solution in the future predictions is complemented by the remaining top 10-25% fraction of the solution. As for the analysis under present conditions for the same SP solution, the hotspot identified in the previous section were less included in the top 25% fraction of the solution and were relayed in the background. In more details, the identified hotspots for the future SP solutions were not included in the top 5-10% fraction of the solution but remained in the top 10-25% fraction. Those areas could be considered as potential extension areas of the current PA networks to increase their efficiency in the future. By using map differentiation between present and future scenarios, the same trend as for the BD hotspots identification was observed with a shift towards the North-West direction observed over the rest of the landscape including some parts of the top 10-25% fraction of the future SP solution.

Performance curves for the Swiss parks network with RCP 4.5 scenario showed a similar result than for the current situation. Same changes at the end of the curves for a fraction of landscape at 10% was observed (Fig.16). For the 10% top fraction, only about 12.5% of species were included in the constrained future SP solution whereas in the unconstrained BD solution, about 40% of the distribution would be protected within a similar area. Results for the constrained current SP solution were better than for the future RCP 4.5 scenario with a decrease in efficiency of about 2.5%. Under the RCP 8.5 scenario, the solution included, for the same fraction of the landscape, about 11% of the species, which is lower than under current and RCP 4.5 scenarios.

Efficiency of the constrained SP solution under the RCP 4.5 scenario was also highlighted by the proportion of species included in the top 25% fraction of this solution with 42,12% of species for the Combined and 39,17% for the Covariate model. Once again, as observed under the current situation, differences between the unconstrained BD hotspot solution and the constrained SP solution were observed with a decrease of 3,61% of species in the top 25% fraction of the solution for the Combined model and 4,41% for the Covariate model. For the constrained SP solution under the RCP 8.5 scenario, the 25% top fraction includes 41,13% of species for the Combined and 39,06% for the Covariate models. Moreover, species proportion was lower for the RCP 4.5 and even more for RCP 8.5 scenarios compared to the constrained current SP solution with a decrease of efficiency of 1.19% for the Combined and 1,03% for the Covariate models. For both scenarios, RCP 4.5 and RCP 8.5, category three of national priority was still the most included in the top 25% fraction of the solution followed by category one and category four. The same trend is observed for RCP 8.5 with a higher proportion.

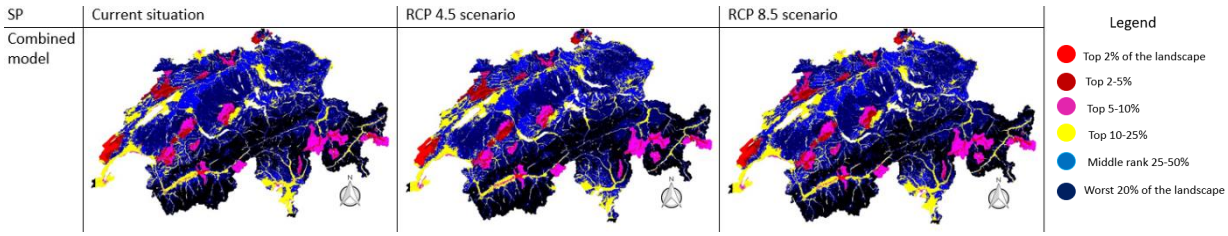


Figure 16: Comparison of the constrained SP zonation prioritization solution between future scenarios and current situation for the Combined model solutions (Results for the Covariate model are presented in Appendix 7).

3.2.2.2. EM-PN network

As seen in the under analysis under current conditions, constrained EM-PN and unconstrained solutions share a lot of similarities. The same thing was observed for future RCP 4.5 and RCP 8.5 with a switch toward the North-East direction (Fig.17).

Looking at performance curves allowed us to show that constrained EM-PN solutions under RCP 4.5 and RCP 8.5 scenarios were as well as efficient than unconstrained current and future solutions. For the unconstrained RCP 4.5 scenario for both models, 35,36% of species were included in the top 10% fraction compared to 37% in the constrained EM-PN solution. The same thing was observed under the pessimistic RCP 8.5 scenario, in a lower proportion, with 36,61% of the species included in a 10% fraction compared to about 36% in the constrained EM-PN solution. However, an important decrease of about 20% was observed when comparing with the current situation.

Percentages of species integration in the top 25% fraction of zonation solution, under the RCP 4.5 scenario, were not significantly different from the results observed for unconstrained solution with a species proportion of 45,81% for Combined and 43,54% for Covariate models. The same trend is observed for the constrained EM-PN solution under the RCP 8.5 scenario, with 45,63% of species included in the top 25% fraction for the Combined model and 43,12% for the Covariate model.

Compared to the analysis under present conditions for the same network (i.e. EM-PN solution), we observed a slight decrease of 0,09% of species for the Combined and 0,49% for the Covariate models. Category three of national priority was still the category most included in the top fraction of the solution under both scenarios and for both models.

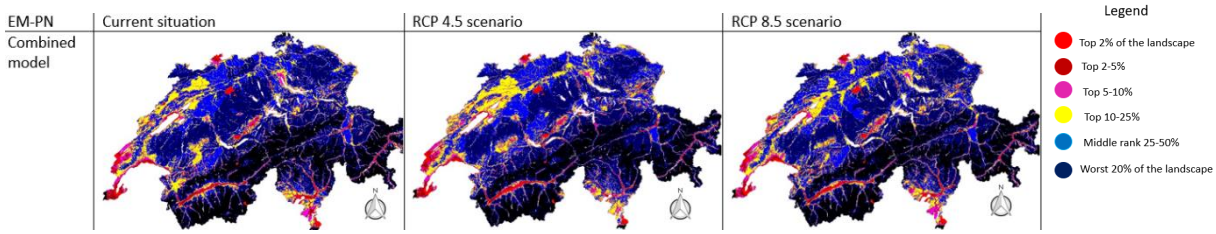


Figure 17: Comparison of the constrained EM-PN zonation prioritization solution between future scenarios and current situation for the Combined model solutions (Results for the Covariate model are presented in Appendix 7).

3.2.2.3. All-PA network

As in the analysis under current conditions for all-PA networks, the top 2-10% fraction of the constrained future all-PA solution was included in the western part of Switzerland, in Ticino and in large valleys of eastern Switzerland under both scenarios and for both models. However, larger parts of western Swiss area were included in this top fraction due to the northern shift compared to the constrained current all-PA solution. The top 10-25% of the fraction was in the eastern part of Switzerland (Fig.18).

Performance curves for both models showed the same trend as the under present conditions analysis. Under the RCP 4.5 scenario, changes were observed for a fraction of the landscape representing about 24%. For this area, about 20% of species were included in the solution compared to 58,04% for the unconstrained RCP 4.5 solution. Under RCP 8.5, for the same fraction of landscape about 19,5% of species were included in the solution against 57,32% for the unconstrained RCP 8.5 solution. By comparison with analysis conducted under present conditions, the all-PA network in Switzerland was more efficient in the future under the RCP 4.5 scenario but not under the RCP 8.5 scenario.

For the top 25% fraction of the constrained PA solution under RCP 4.5, 24,78% of species for the Combined and 20,97% for the Covariate models were included. Constrained PA solution under RCP 8.5 included 24,66% of species for the Combined and 21,08% for the Covariate models. Surprisingly, results were close to those during the current conditions analysis. For categories of national priority, species from category three were most included in the top fraction followed by category one and category four.

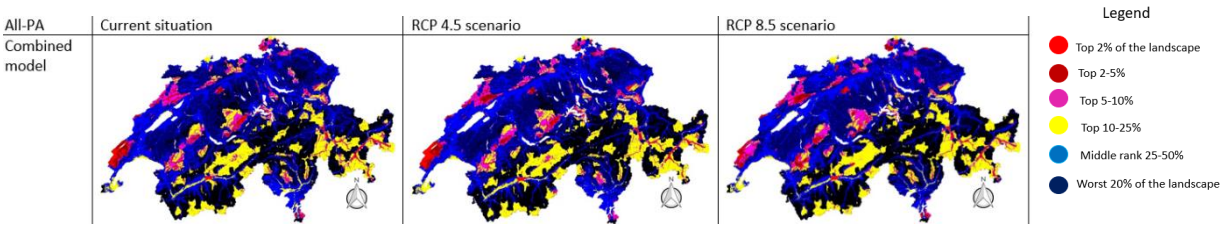


Figure 18: Comparison of the constrained All-PA zonation prioritization solution between future scenarios and current situation for the Combined model solutions (Results for the Covariate model are presented in Appendix 7).

3.2.3. Orders and threatened species.

For this part, only global results are presented. We focused on the distribution of the order in the top 25% fraction under both RCP 4.5 and RCP 8.5 scenarios and of the 11 most threatened species from category one among the three networks studied.

3.2.3.1. Orders

For the constrained future SP solution under the RCP 4.5 scenario, the orders most included in the top 25% fraction of this solution were *Chiroptera* (0.5698), *Eulipotyphla* (0.5109) and *Rodentia* (0.4916) for the Combined model. For the Covariate model, *Chiroptera* (0.5156) were still the most included in the same top fraction, followed by *Lagomorpha* (0.4497) and *Eulipotyphla* (0.4473). For the constrained SP solution under the RCP 8.5 scenario, orders most included in the solution for both Combined and Covariate models were *Chiroptera* (0.6347, 0.5794*), Eulipotyphla* (0.5727, 0.5119) and *Lagomorpha* (0.4902, 0.4610). Compared to the results from the analyses under current conditions, the three orders most included in the top 25% fraction of the solution differed, giving more importance to *Rodentia* and less to *Lagomorpha*.

To highlight the differences between current and future scenarios regarding species proportion, only results from *Chiroptera* were taken as an example. For constrained SP solution under RCP 4.5, a decrease of 1,83% for the Combined and 1,97% for the Covariate models was observed. However, results from constrained SP solution under RCP 8.5 contrasted with previous observation. Indeed, this last solution included more species from *Chiroptera* with an increase of 4,66% for the Combined and 4,41% for the Covariate models.

Concerning the constrained EM-PN solution under RCP 4.5, *Chiroptera* was still the order most included in the solution (0.6279, 0.5801) followed by *Eulipotyphla* (0.5498) and *Rodentia* (0.5297) for the Combined model. For the Covariate model, second position was attributed to *Rodentia* (0.4994) and *Eulipotyphla* (0.4903). For the other scenario, RCP8.5, the three orders most included in the top 25% fraction of the solution were *Chiroptera* (0.6370, 0.5794), *Eulipotyphla* (0.5727, 0.5119) and *Rodentia* (0.5233, 0.4993) for both models. Compared to the current constrained SP solution, results were close to each other even if the current solution is a little bit more efficient than the future ones according to the species proportion included in the top 25% fraction of the solution.

For constrained all-PA solutions under both RCP 4.5 and RCP 8.5 scenarios, lower proportions of species were included in the top 25% fraction of the constrained all-PA solutions. For constrained all-PA solution under the RCP 4.5 scenario, Lagomorpha (0.3974) was the order with species more included in this top fraction followed by *Chiroptera* (0.3063) and *Eulipotyphla* (0.3047). For the Covariate model, *Lagomorpha* was also the most represented order in the top fraction (0.3593) followed by *Artiodactyla* (0.2707) and *Rodentia* (0.2580). Under the pessimistic scenario, the three orders most included in the top fraction were *Lagomorpha* (0.3925), *Chiroptera* (0.3138) and *Eulipotyphla* (0.3216). For Covariate model, the three most included order in the top fraction were *Lagomorpha* in higher proportion than for the RCP 4.5 scenario, followed by *Rodentia* and *Artiodactyla* in lower proportion. Compared to current results, no major differences were observed.

3.2.3.2. Threatened species

To highlight the efficiency of the Swiss PAs network in the far future (2060-2080), a last comparison analysis was done on the 11 threatened species with national priority from category one across the three networks studied. For the SP network, the constrained solution under RCP 8.5 included for most of them a higher species proportion in the top 25% fraction except for *Eptesicus nilsonii*, represented in higher proportion in constrained solution under RCP 4.5 scenario and *Lynx lynx*. For the EM-PN network, results were more contrasted with half of the threatened species better represented in the

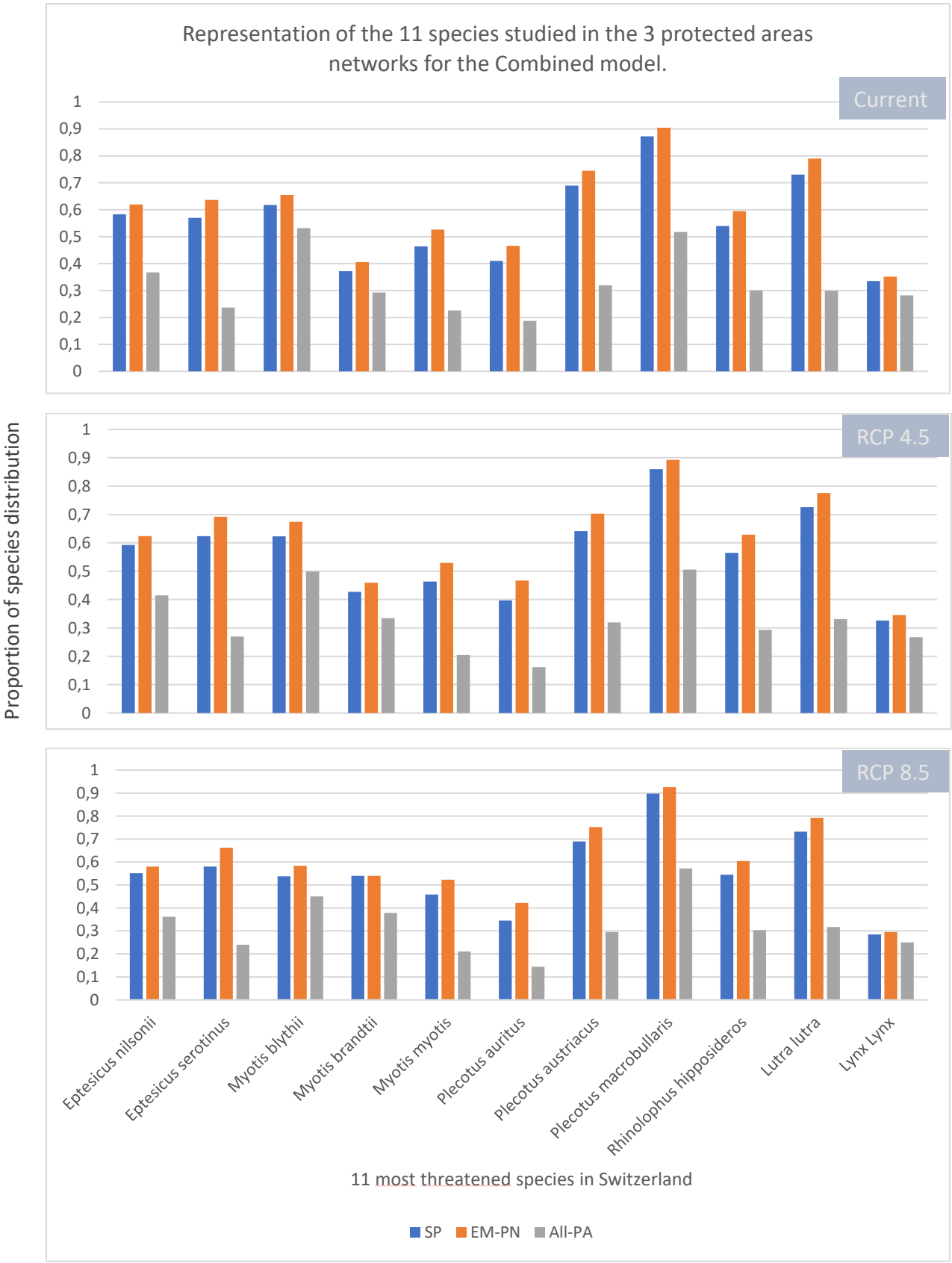


Figure 19: Proportion of species distribution proportion for the 11 most threatened species in Switzerland within the 3 networks studied : i) Swiss parks (SP) network; ii) Emeraude-Pro Natura (EM-PN) network; iii) All protected areas (All-PA) network; under current situation, and two future scenarios: RCP 4.5 and RCP 8.5. For some species, we can see that the proportion of the species is decreasing across the situations (i.e. Lynx lynx), remaining stable (i.e. Myotis myotis) or increasing (i.e. Myotis brandtii).

constrained solution under RCP 4.5 and the other half by the constrained solution under RCP8.5 scenario. *Lynx lynx* was the only species better represented in the current situation with a decrease of distribution in the top fraction for all networks studied across the scenarios. For all protected areas network, a greater number of species were included in the top 25% fraction of the solution in current or RCP 4.5 solutions. Only three among eleven species were better included in constrained RCP 8.5 solutions (Fig.19).

4. Discussion

4.1. Efficiency of the models

As showed in previous studies, the choice of combining species distribution models (SDMs) at two scales enables us to obtain good and accurate results for predicting future distributions rather than using a regional single-scale SDM (Fearnside, 1996; Di Febbraro *et al.*, 2019; G. Mateo *et al.*, 2019). Here, we mainly compared two ways of building such hierarchical models, by multiplying predictions of a fine (Switzerland) and large-scale (Europe) model (Combined models) or by using the large-scale predictions as Covariates in the fine-scale model (Covariate models) and observed significant differences in TSS and AUC between them. This major difference is likely due to the different ways of combining the two scales. Indeed, the Combined model gives equal importance to the Europe and Swiss models, whereas the Covariate model uses the European model as an additional predictor variable. Combining the two scales models should theoretically provide higher predictive performance (Mateo *et al.*, 2019), as the large-scale model can consider a larger part of the climatic niche of the species and accordingly reduce the risk of niche truncation and biased predictions (Chevalier *et al*., In press). These models reflect either global and local ecological processes which are responsible for species distribution across the landscape at the two scales. Using two-scale SDMs thus allows us to include data collected across wide environmental gradients, capturing the full realized niche of species (Elith *et al.,* 2008) and to better conserve niches through time and space (Wiens and Graham, 2005). Thus, the Combined and Covariate models are two possible approaches for these multi-scale models. In this study, as we cannot validate the models in the future, and thus we could not decide which model projections would be better than the other, and simply consider that they are providing alternative information, which can both be considered as providing possible options.

4.2. Forecasting species habitat suitability and hotspot biodiversity identification

This study generated an important prediction dataset for mammal species' distribution in Switzerland, as a supporting tool to evaluate the effectiveness of the current protected areas (PAs) network – for this group. Recent conservation studies were conducted on mammals' at country level in Iran or China (Farashi et al., 2017),or at local scales, for instance in the Western Swiss Alps for plants, reptiles, amphibians, insects and some isolated order or species (Scherrer and Guisan, 2019; Vincent *et al.*, 2019; Ramel *et al.*, 2020). However, based on our literature reviews, no complete analysis including most mammal species present in Switzerland has ever been performed for the whole country. Moreover instead of the hierarchical approaches used in previous studies (Gallien *et al.*, 2010; Gastón and García-Viñas, 2010; Hattab *et al.*, 2014), we tested here two new approaches to combine the Swiss and European scales (partly inspired by Mateo *et al*., 2019 and Chevalier *et al.*, In press), for modelling mammal's distributions. Although the effectiveness of PAs in biodiversity management and conservation is often debated (Moilanen *et al.*, 2005; Fleishman *et al.*, 2006; Vincent *et al.*, 2019), no research was conducted yet to evaluate how Swiss PAs performed in species based protection on potential distributions for important taxonomic groups such as mammal species in Switzerland.

Biodiversity hotspots (BDHs) are defined as areas particularly rich in species, especially rare and threatened species or some combination of these attributes (Walter V. Reid, 1998). BDHs have been

widely used in conservation planning (Ceballos and Ehrlich, 2006; Singh *et al.*, 2021) even if they are not efficient alone for proper conservation planning (Fleishman *et al.*, 2006). Here, by selecting the top 25% fraction of the landscape for conservation prioritization, we found potential (i.e. predicted) BDHs to be localized in valleys, near lakes and cities, and in open areas. Surprisingly, at first sight, all potential hotspots are located near human installations, such as cultivated areas or human infrastructures. These results could be consistent with the studied species ecology. Indeed, the majority of our species are rodents (*Rodentia*) and bats (*Chiroptera*), the latter being the second largest order of mammals. Previous studies have shown that bats are generally found at low elevation in land use categories related to forest, meadows, pastures (Scherrer *et al.*, 2019), along streams and roads (Kerbiriou *et al.*, 2018). Depending of the species, their distribution can be strongly related to human activities such as for *Myotis blythii*, an insectivorous bat living mostly in human infrastructure (No et al., 2021). However, the most threatened bat species tends to be mostly confined to less urbanized areas along the mountain slopes bordering the main lowland valleys (e.g. along the Rhone valley; Scherrer et al., 2019).

Rodents are the largest group of mammals. They are diverse in their ecology and can be found in nearly all types of terrestrial habitats, including anthropogenized environments. For example, common volves are found mainly in grasslands, meadows, along streams at low – to mid – elevation whereas alpine species such as *Apodemus alpicola*, *Chionomys nivalis* or *Marmota marmota* prefer high elevation in rocky and snowy alpine and nival areas. For the rodent species studied here, many are linked to human activities and settlements. Indeed, fields and human infrastructure, such as houses or farms ensure food provision during their breeding season (Allainé and Yoccoz, 2003) or shelter them during cold winters (Naderi *et al.*, 2016). The same trend was observed for the other orders, such as *Artiodactyla* or *Carnivora*, with a strong link with human and low elevation except for alpine species such as *Capra Ibex* or *Canis lupus*.

4.3. Efficiency of current reserve networks

This study has shown that the Swiss' PAs network, including all types of reserves, might not be best suited for the conservation of all mammal species studied in Switzerland, according to the species predictions of the models used. The solutions from the spatial conservation prioritization schemes including all current PAs suggest that they are not currently optimally located to protect high levels of species richness as already reported at local scales in the Western Swiss Alps (Vincent *et al.*, 2019). Currently, the Swiss PA network represents 18.9% of the country (P. Galland, IUCN, 2004) and many of the existing PAs are established for other purposes, e.g. the conservation of landscape, cultural sites, conservation of species-poor habitats, target species, sensitive meadows, wetlands, or target habitats of concerns,…. However, our results highlighted the importance of distinguishing between the different types of PA networks studied. For the Swiss parks (SP) network, results showed that SPs, as well as the overall Swiss all-PA network, are not optimally located, to protect high levels of mammal species richness. For the Emeraude-Pro Natura (EM-PN) network, the opposite is observed, with a performance as good as the (PA-independent) biodiversity hotspots analysis. The differences in results between the two kinds of PAs is consistent with the policy and legislation behind their establishment. Although the Swiss national parks aim to provide unspoiled habitats for flora and fauna, the Swiss regional nature parks, based on the Environmental Protection Act (FOEN, 2013, Swiss Environmental Law) are not only focussed on nature conservation but also on regional development (FOEN, 2014, "Manuel de creation et de gestion de Parcs d'importance Nationale").

The label "park" is given by federal institute with regards to two criteria : i) high natural and scenic value; ii) inhabitants and local authorities' full commitment to the project (www.parks.swiss). They are mainly established to conserve, promote high quality landscapes and sustainable development in rural areas, encourage democratic processes in the regions and guarantee high quality standards (P.Galland,

IUCN, 2004). The main goal of FOEN is to prevent the extinction of indigenous plant species by maintaining adequately large and connected habitats (biotopes) (FOEN, 2013) while maintaining ecosystem services (Ramel et al., 2019). The Emeraude network is the Swiss implementation of the Natura 2000 Network, created to protect rare and threatened species and natural environments in Europe. They are based on Resolutions 4 and 6 of the Bern Convention that lists the European species and habitats that require special protection measures. These areas are less accessible to the public and are made for conservation of habitats and target species. Ecosystem services are not directly included in the creation of those sites. Pro-Natura reserves are one of the major networks of protected areas with 724 reserve sites to protect habitats and associated animal and plant species. Pro Natura reserves are managed by private collaborators and are subject to strict rules. Half of the sites are open to the public and are managed to try to avoid strong human interactions whereas the other half is not accessible to public to let nature take over (www.pronatura.ch). Diversity of the reserve types are well represented in this study, explaining the differences in efficiency for the studied networks.

4.4. Important and threatened species in Switzerland, status and incorporation into reserve networks.

Switzerland has a rich wildlife (Graf et al., 2021) composed of emblematic and important species. Emblematic species were already identified by experts in other studies on the European Alps (Schirpke, *et al*., 2018) and are Alpine ibex, chamois and marmot. In addition to them, two species of large carnivores are added to the list, i.e. wolf and lynx according to the European Convention. Ecology of the species is adapted to a mountainous environment, such as forests and rocks, and are thus neither included in the hotspot solution proposed by Zonation or in most of the protected areas, except for areas located at middle-high elevation (i.e. Swiss national parks). In Switzerland, these species are protected by protecting their habitat and efforts to reduce consanguinity by increasing genetic diversity. These species and especially Alpine ibex, chamois and marmots are also concerned by the increase of outdoor activities which increase the pressure on populations. Human-wildlife and more especially human-predators conflicts are a problem in Switzerland(Glenz *et al.*, 2001; Behr *et al*., 2017) and their protection is regulated with NHCA and Hunting Act (HuntA) including specific regulations for protecting individual animal species. It is also important to note that proposed zonation solutions were done by attributing weight to the most threatened species in Switzerland. In this list of species, lynx and wolf are threatened species from category one and three respectively. Nevertheless, emblematic species are under-represented in the Swiss reserve network.

Over the past century, many animal and plant species have been decreasing in numbers, becoming extinct or much rarer in the world. In Switzerland, the same trend was observed with 11 threatened mammal species from category one of national priority and 8 from category three among 68 species studied.

Most of the threatened species are from *Chiroptera*, *Carnivora* and *Eulipotyphla* orders. In Switzerland, bats are all protected (Scherrer *et al.*, 2019). As they use many types of habitats, they are facing threats such as increasing deforestation of landscapes, intensification of agriculture, use of plant protection products, road construction, uncontrolled development of human settlements, light pollution.... In our Zonation solution for SP, EM-PN and PA networks, depending on the model, some threatened species are well represented, such as *Plecotus macrobullaris*. This species is restricted to European mountainous areas but can live either at low or high altitudes above 2800m. It uses human infrastructure for nurseries and is therefore vulnerable to renovation work and needs structured environment with ecological corridors suitable for flight made up of shrubs and small forests (Alberdi *et al.*, 2015a). The current reserve network includes suitable environments for this species. However, other threatened species inhabiting forest and human related areas are less included in the solution, i.e. *Myotis brandtii*, *Myotis myotis*, *Plecotus austriacus*, *Barbastella Barbastellus*. *Myotis brandtii* is a

tree species linked to mountainous forests and marshy areas with small streams that provide food. As shown in previous studies, target protection could be established (Kerbiriou *et al.*, 2018). *Barbastella barbastellus*, more threatened than *Myotis brandtii*, is affected by deforestation, light pollution and mostly live in mixed deciduous and pine forest (Zeale, 2011). *Myotis myotis* and *Plecotus austriacus*, one of the rarer species in Switzerland, are two species linked to human infrastructure, dark environments like caves. These two species are threatened by the increase of agriculture, building renovations and deforestation. In general, bat species are locally protected and more targeted than other species due to their ecology. For boreal species, nesting boxes are set up to enhance breeding, nesting, and sheltering. For caves species, such as *Myotis myotis*, only the concerned area is subject to protected regulation. However, protected areas including old buildings and protected villages could have a positive impact on some species (Graf et al., 2021). The second order with a high proportion of threatened species are carnivores. Among them, *Lutra lutra* and *Lynx Lynx* are from category one of national priority and *Canis lupus*, from category three. As seen in the previous section about charismatic species, the situation of carnivores, known as great predators is controversial (Glenz *et al.*, 2001; Graham *et al.*, 2005). Due to human-wildlife conflicts, many were persecuted, leading to the extinction of the species. Today most of them are protected even if some of them are subject to management and hunting plans. Regarding the results, carnivores are divided in two groups in the current protected areas network. Indeed, *Lutra lutra* is the most included Carnivora species in the top 25% fraction even for the constrained PA solution. The otter is linked to streams, rivers, peat dogs, marshes but can also be present in all kinds of habitats, even in heavily urbanised areas, while providing food (Jo *et al.*, 2017). However, the most suitable habitat remains streams, rivers and lakes with natural vegetation and covered shores. This species is threatened by the modification of streams, artificial and brutal alteration of water levels in dams, warming of water temperature, construction of hydroelectric barrier, pollutants and microplastics. The current protected areas included a lot of areas suitable to otter's, explaining the obtained results. It is also important to note that the species is even more included in Emeraude and Pro Natura networks as these are even more consistent with the ecology of the species and our findings. The two studied threatened species are considered as large carnivores. *Lynx lynx* is a boreal species divided in two populations in Switzerland and separated by the Plateau region. Lynx are threatened by habitat fragmentation, genetic depletion, and consanguinity problems. Lynx have limited dispersion and need specific protection measures such as ecological corridors and a decrease in illegal hunting supplemented by stronger legal actions (Basille *et al*., 2008). However, our results show for all solutions that the lynx is the least represented species in the protected areas network and thus the least protected in Switzerland according to the solutions obtained with Zonation software. As said before, *Canis lupus* is the species that arouses anger or fascination. In Switzerland the wolf is mostly found in large forest areas of mid elevation and covers a surface area of 20 000 km^2. The species is mostly present in the Alps, Jura and Prealps. The main threats are related to humans through illegal actions, cars, or train accidents. Even if the species is protected, the wolf is subject to the "wolf concept" set up in Switzerland (FOEN, 2004, "Concept Loup Suisse"), controverted politic decision and socio-economic questions. This controverted climate is also represented by the percentage of species include in the protected areas which is a little bit higher than the lynx in the solutions.

In the *Lagomorpha* order, *Oryctolagus cuniculus* is the only species threatened in Switzerland from category three and is also the species most included in all the solutions of all mammal species. The wild rabbit is not an endemic species and originates from the Iberian peninsula (Carvalho and Gomes, 2003). The first population derived from the domestic rabbit. This species is adaptable and able to colonise a large type of different habitats, but they prefer firm, dry and sandy soils in open landscapes with low bushy vegetation and hedges and avoid agricultural areas. As a non-endemic species, no

specific measures of conservation are recommended even if they are threatened by genetic depletion and disease. Regarding the results, this statement is surprising with such a high percentage of distribution in the current protected network.

The *Eulipotyphla* order includes two threatened species as well but is not a threatened order regarding the ratio of number of species to number of threatened species. *Neomys anomalus*, Miller's shrew, is mainly found in wet habitats with a thick layer on the ground, stream shores, wet grasslands, wetlands and wet forests. It is also possible to see them near urban areas. The decrease of wetlands for the benefit of agricultural areas is the major threat for this shrew living in considerably reduced habitat (Churchfield and Rychlik, 2006). *Neomys fodiens*, the aquatic shrew, inhabits the same type of areas as Miller's shrew but is more related to water areas (Churchfield and Rychlik, 2006). This species is a good indicator of intact aquatic environment with natural shores. These two threatened species of shrew are among the species the most included in Zonation solutions even if the species depends on the network studied. As observed for other species previously, the most represented species in the top fraction of the solutions are species that are related to water or wetlands. This trend is consistent with the need to protect those habitats endangered by intensive farming, extension of urban areas…

4.5. Impact of climate changes

Climate in Switzerland is characterised by large fluctuations. Since 1864, the average annual temperature has increased by around 2°C in the last few decades. Changes are also visible through snow quantity associated with a shorter winter season, changes in precipitation and humidity. To be able to assess the problem climate changes scenarios have been established and used in this study to predict the future suitable habitats of mammals. By using RCP4.5 and RCP8.5, differences in suitable habitats have been highlighted. Due to the increase in greenhouse gas emissions by humans since the industrialisation, changes have an impact on the habitats of the species studied. Even if the main BD identified with Zonation are situated in the same area as in the current situation, changes are observable under both scenarios. A loss of suitable habitats is highlighted in the south of Switzerland in the Western and Eastern Central Alps and the South side of the Alps. This observation is consistent with studies demonstrating a shift of latitude of about 16,9 km per decade to the north and 11.0m per decade in elevation (Chen *et al.*, 2011). Moreover, in mountainous areas, recent studies have shown that temperatures increased by 0.12 to 0.20°C per decade over the last 100 years with an increase since 1980s. This recent Alpine warming occurred at about three times the rate of the global average (Brönnimann *et al.*, 2014). Temperatures at high altitude resembling temperatures found in the lowlands with regional precipitation temperatures induced important changes in environmental boundaries such as snow or tree lines and thus ecological modifications for the species inhabiting those regions. As shown in the results part, the Plateau is one of the areas that will become unsuitable for mammal species. This region of Switzerland is composed of cities, cultivated areas, meadows, pastures and is the swiss part with the most of aquatic and wetlands areas. This observation is thus important for conservation analysis. Wetlands are playing an important role in carbon cycle. However, due to the rise of temperature, intensification of agriculture, and habitat fragmentation, wetlands are threatened. They would be transformed into carbon sources instead of carbon sinks and will therefore have an impact on habitat suitability and species. In the pessimistic scenario, the top 2-10% fraction is considerably reduced due to the high concentration of carbon in the atmosphere and its dramatic consequences (Huston and Marland, 2003). Climate and land cover modify the spatial distribution of mammal species and biodiversity richness in Switzerland.

Concerning the three types of reserve networks, results are surprisingly close to the solutions proposed by the current situation even if a slight decrease of efficiency is observed for all of them. As under the current situation, the EM-PN network is still the most efficient for the studied mammal species

followed by the SP and PA networks under both scenarios. This finding was not necessarily expected as recent studies showed that established reserves network in other countries are included less species in the future than under current situation (Thuiller *et al.*, 2014). However, as the efficiency is decreasing and the performance curves for SP and PA networks show interesting results, the role of protected areas (PAs) in Switzerland questioned as species are moving and are able to acclimate to novel climates especially under future climate scenarios. Because most PAs have fixed borders, they may lack the flexibility to maintain populations of species whose distributions move in response to climate change and other environmental drivers (Monzón *et al.*, 2011). As the differences found in the first analysis about BD identification between current and future scenarios showed, BD hotspots can move from an area to another adapting to new conditions. The same trend is observed in other modelling studies that have shown that species are likely to move out of individual reserves, as attested by the previous results with less species included in the solutions for all networks (Leach *et al*., 2013). However, some species are also probably able to switch their distributions between reserves (Thomas and Gillingham, 2015) but such species are not visible in our study. As a lack of efficiency is observed for the PA network that included all protected areas in Switzerland, questions of area prioritisation are also raised. Indeed, many PAs across the world are found in mountain ranges at relatively high elevations. This is the case for the eastern part of Switzerland in the Eastern and Western central Alps and South side of the Alps. In the future scenarios, those areas do not include a high level of species diversity as they become less suitable for most of the studied species.

The distribution of species is dynamic and has become increasingly so over the past years as they respond to land use change, pollution, invasive species, climate change and other anthropogenic drivers. If species were not yet impacted by these drivers, they might change biological communities in the future. As some will collapse and disappear, other can thrive and expand their ranges. In this study, it was shown that species are either most represented in the protected areas under RCP4.5 or either under the most pessimistic one, RCP8.5. As observed, only on species, the lynx, is decreasingly represented across the two scenarios. The results here are consistent with previous findings about the ecology of the species. Biodiversity in its entirety is threatened by the rise of temperatures, however, some species, such as currently threatened species, montane or water related species, require specific attention as explained before i.e. *Capra ibex*, *Rupicapra rupicapra*, *Marmota marmota*, chiropters… Depending on which side of the aspect we worked on, - i.e. species richness or specific threatened species -, results and decisions regarding protected areas can be modified.

4.6. Biases

Species distribution modelling (SDMs) for biodiversity is based on species observations that are used to determine their potential distribution. The problem of potential biases is increasingly discussed in recent studies because of their bad consequences on the accuracy of the models (Beck et al., 2014) and thus on potential species distribution.

Yet, in this study, we cannot exclude the possibility that the identified potential hotspots could also be the result of sampling biases. Indeed, our models are based on information recorded by various types of observers (volunteers or professionals), which are then fed into the InfoSpecies and GBIF databases, resulting in very heterogeneous species occurrences datasets (Graham *et al.*, 2004; Anderson *et al.*, 2020). The sampling biases can result of the observation type. It depends how and by whom the data have been collected in the areas where citizen observations are widespread. As shown in recent studies, countries with more human observations have a higher percentage of records within 2.5 km of roads (Hughes *et al*., 2021). The status of observers has also its importance in observations biases. explaining the high numbers of easily observed common species (Hugues et al., 2021) such as *Capreolus capreolus* in our study or *Sus Scrofa.* This kind of observations leads to an exacerbating bias

and increases the representation of some taxonomic group as observed in this study. It could thus overcome the observations of some threatened or rare species made by scientists or observers from a less-urbanized areas. Topography and ecosystem accessibility could also result in non-negligible sampling biases. It has been shown that observations near roads, cities, and other easy-access environments are consistently greater in number than expected from a spatially random distribution (Kadmon *et al*., 2004). This finding contrasts with the lack of observations in some ecosystem such as high mountains or marine ecosystems. The swiss population is concentrated in large valleys, near main cities and lakes (*Appendix 9*), where our hotspots were identified. According to OFS (Federal Office of Statistics), the Alps, including high mountains, are not well populated. The sampling is thus limited by elevation and mostly accessibility. Thus, the observers are fewer in number, and less observations are recorded for these areas even if the species could be present.

Such findings could have bad consequences on the main conclusion of this study. The models obtained with Species Distributions Modelling (SDMs) and thus the priority ranking maps made with Zonation software show and include the anthropogenic impacts and biased the information on species and their habitat (Bowler *et al*., 2020; Hugues *et al*., 2021). The main consequences of these biases are to obtain results with spatial gaps (Amano *et al*., 2016). In this study, our selection of 68 species could be underestimated and we possibly over-evaluated or under-evaluated their conservation status depending on the species. However, considering the consistency of the results regarding the species' ecology and as we were not able to use any other observations for Switzerland, these results are predictions for use in further analyses that could be improved by overcoming these information gaps.

4.7. Conclusion and Perspectives

This study showed the difference of efficiency between two types of protected areas: large and specific areas. Results showed that small and targeted areas, - i.e. Pro Natura and Emeraude sites -, have higher biodiversity richness than large areas, i.e. Federal reserves such as the National park or regional parks. Another major finding is that the percentage of species between current and future network is close and does not differ much between the three scenarios. Threatened species are not equally represented in the reserve networks and that could be explained by their specific ecology. To answer the main question of this study, we can say that mammal species are not a good indicator of reserve efficiency in Switzerland even if the Pro Natura reserves and Emeraude sites are more efficient for protecting mammals under current conditions and future scenarios.

However, caution may be required when interpreting these results. Indeed, we worked only here with mammals' species including threatened species but did not consider other taxonomic groups. Although mammals have already been used to assess protected areas efficiency (Ceballos and Ehrlich, 2006; Wiersma and Nudds, 2009), our solutions were established by including only few parameters linked to mammals. Connectivity, habitat fragmentation and relations between species were not included in this study. A complementarity analysis could be done including those parameters and additionally could be conducted on plants, insects, and other taxonomic groups for a complete overview of the current situation in Switzerland. Moreover, this study does not consider the possible acclimation of species (Beniston *et al.*, 1994) as shown in other studies on insects (Bujan *et al.*, 2021) that could lead to a different final pattern. Another critical question is whether models successfully predict current species. Although the results of the models are relatively high compared to other studies, all biases must be reminded as such predictions biases can give truncated solutions (Chevalier *et al.*, In press), as discussed in the previous section...

To conclude, this study represents an improvement of species distribution modelling upon previous methods and a first conservation planning analysis for mammals in Switzerland. The application of

these methods and potentially the implementation of the above suggestions could create solutions and give more information about Swiss conservation goals, both at global or local levels, with similar data by also considering other economics and political parameters.

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Appendix

Appendix 1 : Protected areas in Switzerland involved in this study

Data/Shp	Availabili	link
Parks		
Regional Nature Park	Y	https://www.bafu.admin.ch/bafu/fr/home/themes/paysage/info-specialistes/conserver-et-developper-la-qualite-du-paysage/paysages-d_importance-nationale/parcs-d_importance-nationale.html
Federals inventory		
Batrachians itinerants obje	Y	
Batrachians fixes objects	Y	
Batrachians sites (Annexe	Y	
PPS (meadows and dry pa	Y	
PPS (Annexe2)	Y	
MarshySites	Y	https://www.bafu.admin.ch/bafu/fr/home/themes/paysage/info-specialistes/conserver-et-developper-la-qualite-du-paysage/paysages-d_importance-nationale/sites-marecageux-dimportance-nationale.html
Low-marsh	Y	
Regional Low-marsh	N	
High-marsh	Y	
Alluvial Zones	Y	
Alluvial Zones (annexe 2)	Y	
All.Z out of inventory	N	
Alp.All.Z. out of federal inve	Y	
Alp.All.Veg	Y	
Waters birds Reserves	Y	
Francs districts	Y	
IFP	Y	https://map.geo.admin.ch/?topic=bafu&lang=fr&bgLayer=ch.swisstopo.pixelkarte-grau&catalogNodes=766&layers=ch.bafu.bundesinventare-bln&layers_opacity=0.75&E=2833405.93&N=1195845.43&zoom=0
Protected areas		
Ramsar	Y	
National Park	Y	
Unesco_BiosphereReserv	Y	https://www.bafu.admin.ch/bafu/fr/home/themes/paysage/info-specialistes/conserver-et-developper-la-qualite-du-paysage/paysages-d_importance-nationale/les-reserves-de-biosphere---un-modele-de-gestion-raisonnee-des-m.html
Unesco_CulturalSites	Y	https://www.bafu.admin.ch/bafu/fr/home/themes/paysage/info-specialistes/conserver-et-developper-la-qualite-du-paysage/paysages-d_importance-nationale/patrimoine-mondial-de-lunesco.html
Unesco_NaturalSites	Y	https://www.bafu.admin.ch/bafu/fr/home/themes/paysage/info-specialistes/conserver-et-developper-la-qualite-du-paysage/paysages-d_importance-nationale/patrimoine-mondial-de-lunesco.html
Geopark	N	https://www.bafu.admin.ch/bafu/fr/home/themes/paysage/info-specialistes/conserver-et-developper-la-qualite-du-paysage/paysages-d_importance-nationale/unesco-global-geoparks.html
Pro Natura: Forest Reserve	N	
Pro Natura: Natural Reserv	Y	
Emeraude	Y	

Table 2: Swiss protected areas included in the three networks studied.

Appendix 2: Land-Use-Land-Cover (LULC) categories

Focal name	Origin of the data (OFS categories – in French- or NFI)
Alpine pasture	242 – Alpage pastural
Bare ground	51 – Rochers saillants 52 – Pierres meubles 53 – Surfaces pierreuses
Coniferous forest	NFI data
Cultivated areas	201 - Arboriculture 202 – Viticulture 203 – Horticulture 221 – Terres arables
Deciduous forest	NFI data
Human infrastructure	11 - Surfaces compactées 12 - Bâtiments 13 – Serres 14 – Structures des cultures en planches 15 – Gazon 16 – Arbres sur terrains aménagés 17 – Petites structures mixtes

Open area	51 – Végétation herbacée
Water area	61 – Plans d'eau 63 – Biotopes humides 64 – Roselières
Forest edge	42 – Coins de forêt 43 – Bandes de forêt 44 - Peuplements d'arbres clairsemées 45 – Peuplements de forêts boisées 46 – Peuplement d'arbres linéaires 47 – Groupes d'arbres

Table 4 : Land Use Land Cover (LULC) used in this study for the Speciesl Distribution Modelling at the Swiss scale.

Apendix 3 : studied species and their national priority status

	Statut IUCN				Statut Suisse				Code couleur	Statut
Nom de l'espèce	Monde	Europe	Suisse	Degré de priorité	Prio_CH	OEA	de pondération (échelle de 1 à	Poids		RE
Capra ibex	LC	LC	LC				6	1		CR
Capreolus capreolus	LC	LC	LC				6	1		EN
Cervus elaphus	LC	LC	LC				6	1		VU
Rupicapra rupicapra	LC	LC	LC				6	1		NT
Sus scrofa	LC	LC	LC				6	1		LC
Canis aureus	LC	LC	NA				6	1		
Canis lupus	LC	LC	EN		3		3	4		
Lutra lutra	NT	NT	CR		1		1	6		
Lynx lynx	LC	LC	EN		1		1	6		
Martes foina	LC	LC	LC				6	1		
Martes martes	LC	LC	LC				6	1		
Meles meles	LC	LC	LC				6	1		
Mustela erminea	LC	LC	LC			L	5	2		
Mustela nivalis	LC	LC	VU		4	Z	5	2		
Mustela putorius	LC	LC	VU		4		4	3		
Vulpes vulpes	LC	LC	LC				6	1		
Barbastella barbastell	NT	VU	EN		3		3	4		
Eptesicus nilssonii	LC	LC	VU		1		1	6		
Eptesicus serotinus	LC	LC	VU		1		1	6		
Hypsugo savii	LC	LC	NT				4	3		
Myotis bechsteinii	NT	VU	VU		4		3	4		
Myotis blythii	LC	NT	CR		1		1	6		
Myotis brandtii	LC	LC	VU		1		1	6		
Myotis daubentonii	LC	LC	NT				4	3		
Myotis myotis	LC	LC	VU		1		1	6		
Myotis mystacinus	LC	LC	LC				6	1		
Myotis natterei	LC	LC	NT				4	3		
Nyctalus leisleri	LC	LC	NT				4	3		
Nyctalus noctula	LC	LC	NT				4	3		
Pipistrellus khulii	LC	LC	LC				6	1		
Pipistrellus nathusii	LC	LC	LC				6	1		
Pipistrellus pipistrellus	LC	LC	LC				6	1		
Pipistrellys pygmaeus	LC	LC	NT				4	3		
Plectotus auritus	LC	LC	VU		1		1	6		
Plectotus austriacus	LC	LC	CR		1		1	6		
Plecotus macrobullari	LC	NT	EN		1		1	6		
Rhinolophus hipposid	LC	NT	EN		1		1	6		
Tadarita teniotis	LC	LC	NT				4	3		
Vespertilio murinus	LC	LC	VU		1		3	4		
Crocidura russula	LC	LC	LC				6	1		
Erinaceus europaeus	LC	LC	NT				4	3		
Neomys anomalus	LC	LC	EN	4	4		3	4		
Neomys fodiens	LC	LC	VU	4	4		3	4		
Sorex alpinus	NT	NT	LC				6	1		
Sorex araneus	LC	LC	LC				6	1		
Sorex coronatus	LC	LC	LC				6	1		
Sorex minutus	LC	LC	LC				6	1		
Talpa europaea	LC	LC	LC				6	1		
Lepus europaeus	LC	LC	VU		4	4-Z	4	3		
Lepus timidus	LC	LC	NT				4	3		
Oryctolagus cuniculus	EN	NT	EN				3	4		
Apodemus alpicola	LC	LC	LC				6	1		
Apodemus flavicollis	LC	LC	LC				6	1		
Apodemus sylvaticus	LC	LC	LC				6	1		
Arvicola amphibius	LC	LC	LC				6	1		
Castor fiber	LC	LC	LC			1-Z	5	2		
Chionomys nivalis	LC	LC	LC				6	1		
Eliomys quercinus	NT	NT	LC				6	1		
Glis glis	LC	LC	LC				6	1		
Marmota marmota	LC	LC	LC				6	1		
Microtus agrestis	LC	LC	LC				6	1		
Microtus arvalis	LC	LC	LC				6	1		
Microtus subterraneu	LC	LC	LC				6	1		
Mus domesticus	LC	LC	LC				6	1		
Muscardinus avellana	LC	LC	VU		4		3	4		
Myodes glareolus	LC	LC	LC				6	1		
Rattus rattus	LC	LC	EN	3	3		3	4		
Sciurus vulgaris	LC	LC	LC				6	1		

Figure 20: Extract from the 68 species studied summary's table and their corresponded national priority according to the categories created. See Method part.

Nombreobs	i..DATACENT	TAXONIDCH	SCIENTIFICN	YEAR_MIN	YEAR_MAX	CX	CY	COORDMAXI	ORIGINCH	CLASSIS	ORDO	FAMILIA	ORGANISMALGROUP_DE	ORGANISMALGROUP_FR	RECORDS
1784236	CCO/KOF	infofauna:70	Rhinolophus	1960	2012	487750	117750	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	11
1784237	CCO/KOF	infofauna:70	Rhinolophus	2019	2019	487850	116550	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784238	CCO/KOF	infofauna:70	Rhinolophus	2009	2015	488050	117850	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	6
1784239	CCO/KOF	infofauna:70	Rhinolophus	2019	2019	488450	117850	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784240	CCO/KOF	infofauna:70	Rhinolophus	2019	2019	488950	117250	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784241	CCO/KOF	infofauna:70	Rhinolophus	2019	2019	488950	117450	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784242	CCO/KOF	infofauna:70	Rhinolophus	2011	2019	490150	120750	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	3
1784243	CCO/KOF	infofauna:70	Rhinolophus	2019	2019	490150	120850	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784244	CCO/KOF	infofauna:70	Rhinolophus	1947	1948	490250	114650	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	2
1784245	CCO/KOF	infofauna:70	Rhinolophus	1949	1949	496250	118750	250	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	3
1784246	CCO/KOF	infofauna:70	Rhinolophus	1949	1951	496250	118750	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	13
1784247	CCO/KOF	infofauna:70	Rhinolophus	1905	1954	497450	117550	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	21
1784248	CCO/KOF	infofauna:70	Rhinolophus	1905	1950	498150	117450	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	2
1784249	CCO/KOF	infofauna:70	Rhinolophus	1905	1907	498550	117350	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	50
1784250	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	500950	139950	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784251	CCO/KOF	infofauna:70	Rhinolophus	1968	1983	503250	140650	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	2
1784252	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	503750	130150	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784253	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	504650	131350	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784254	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	506250	143350	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784255	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	507350	140550	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784256	CCO/KOF	infofauna:70	Rhinolophus	1908	1908	508150	153450	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784257	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	510450	144650	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784258	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	512550	146050	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784259	CCO/KOF	infofauna:70	Rhinolophus	1950	1950	514750	166850	250	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784260	CCO/KOF	infofauna:70	Rhinolophus	1948	1951	516050	172650	250	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	2
1784261	CCO/KOF	infofauna:70	Rhinolophus	2014	2014	516050	172650	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784262	CCO/KOF	infofauna:70	Rhinolophus	2015	2015	516250	173750	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784263	CCO/KOF	infofauna:70	Rhinolophus	1968	1968	517650	150350	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	1
1784264	CCO/KOF	infofauna:70	Rhinolophus	2002	2014	518450	172850	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	4
1784265	CCO/KOF	infofauna:70	Rhinolophus	2007	2007	518450	172950	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	3
1784266	CCO/KOF	infofauna:70	Rhinolophus	2002	2014	518550	172850	70.7	INN	Mammalia	Chiroptera	Rhinolophid	FledermÃ¤use	MammifÃ`res: chauves-souris	2

Figure 21: Extract of the table provided by InfoSpecies.

Appendix 4: about the future scenarios

For the future, regional and global climate models are used. The data for Switzerland were already prepared for previous studies and the corresponding regional climate modelling (RCM) are the following ones: CLMCOM-CCLM4, DMI-HIRHAM5, MPI-CSC-REMO2009, SMHI-RCA4. They are transient daily time series of gridded climate scenarios of temperature and precipitations between 1981 – 2099 at 0.02°D (~2.2 km) from the CH2018 initiative (*CH2018-Climate Scenarios for Switzerland Imprint*, no date). They are used to calculate future climatic layers from 4 general circulation models (GCMs) HADGEM, ECEARTH, MPIESM, IPSL (Karger *et al.*, 2017). Only two representative concentration pathways are used: RCP4.5 and RCP8.5. RCP 4.5 scenario is a stabilization scenario which means the radiative forcing level stabilizes at 4.5 W/m2 before 2100 by employment of a range of technologies and strategies for reducing greenhouse gas emissions. RCP 8.5 scenario is characterized by increasing greenhouse gas emissions over time and is representative of scenarios in the literature which result in high greenhouse gas concentration levels. To assess the changes in precipitations and in temperature in the future, simulations of for the 2070-2099 time slice is used of the RCP4.5 and RCP8.5 scenarios (Lee *et al.*, no date).

Appendix 5: TSS and AUC values for both the Combined and Covariate models

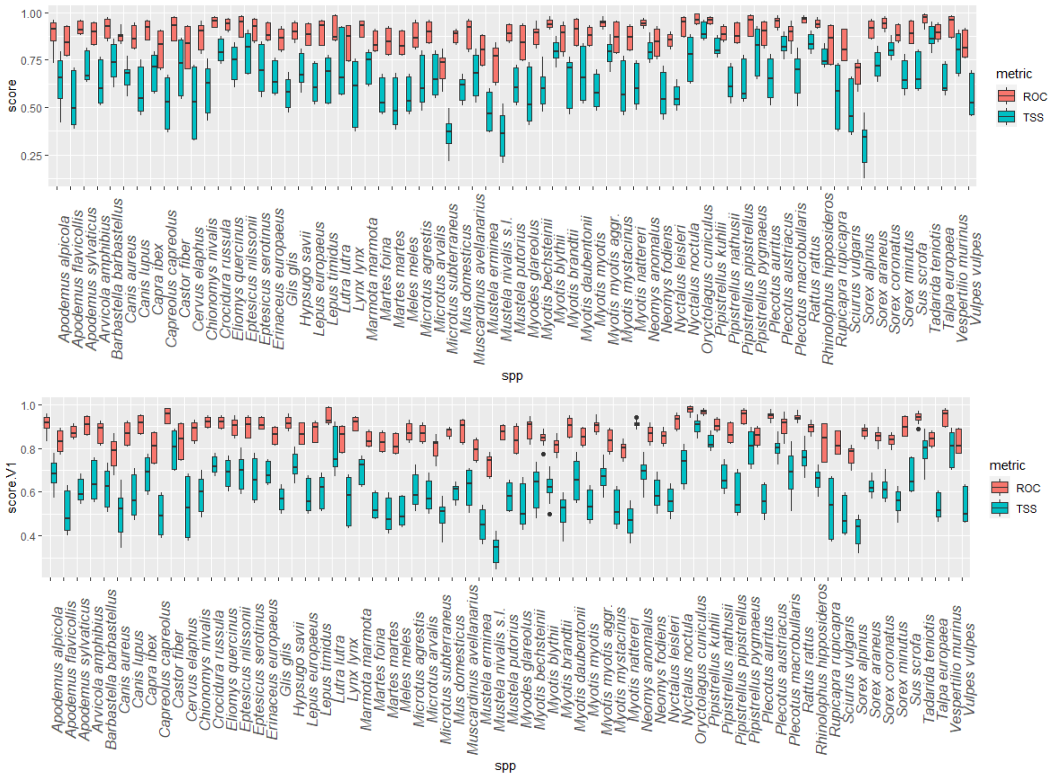


Figure 22: TSS and ROC results for each species for the Covariate (up) and Combined models (down).

Appendix 6: Performances curves for constrained zonation solutions and unconstrained hotspot solution for the Covariate model.

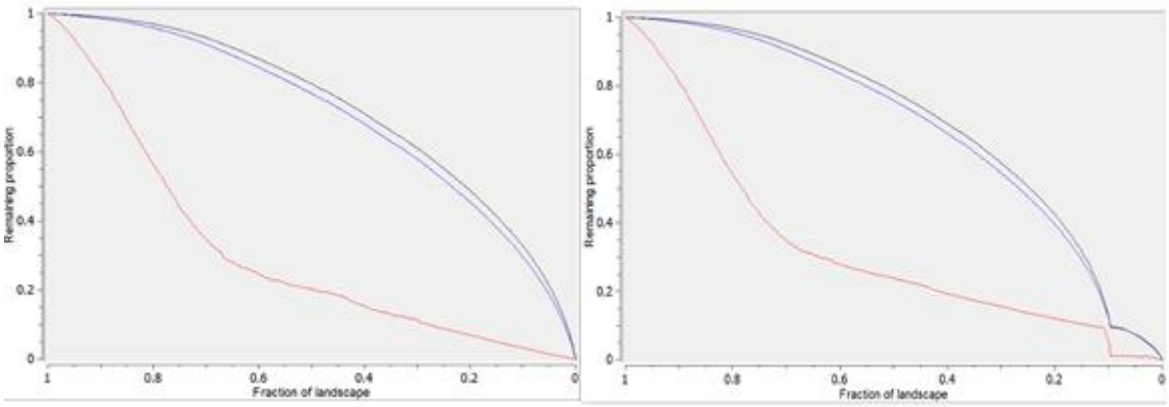


Figure 23: Highlighted differences in performance curves between constrained SP-solution (right) and unconstrained hotspot solution(left) for the Covariate model.

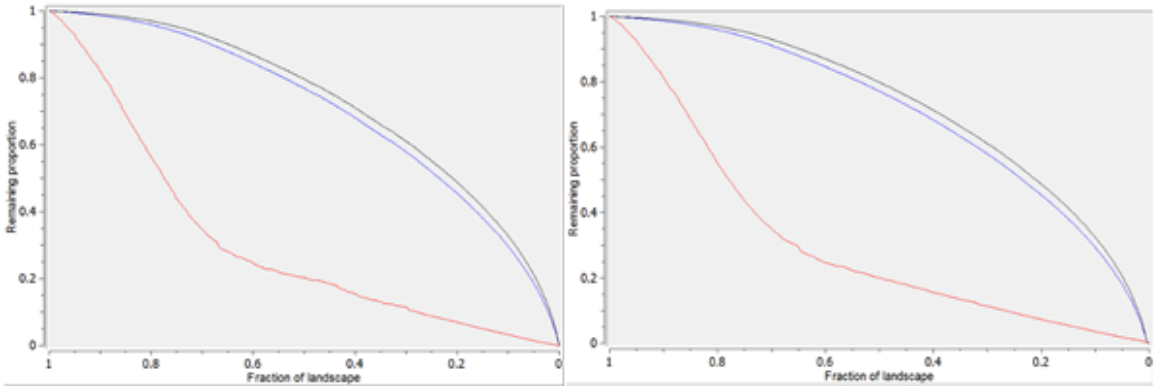


Figure 24: Highlighted differences in performance curves between constrained EM-PN solution (right) and unconstrained hotspot solution(left) for the Covariate model.

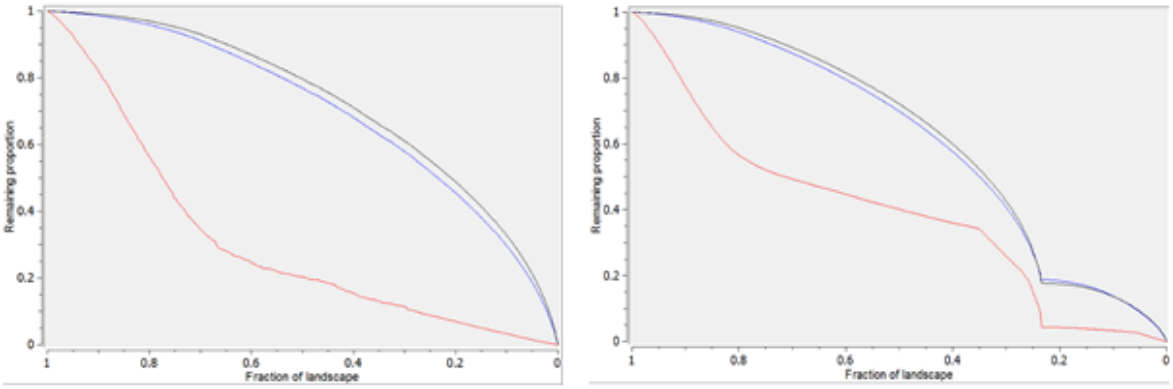


Figure 25: Highlighted differences in performance curves between constrained All-PA solution (right) and unconstrained hotspot solution(left) for the Covariate model.

Appendix 7: Covariate models zonation solution for the current situation and the future scenarios RCP 4.5, RCP 8.5

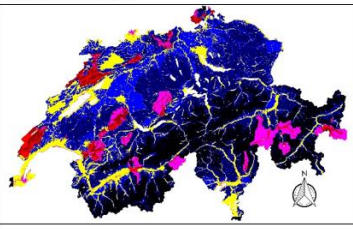
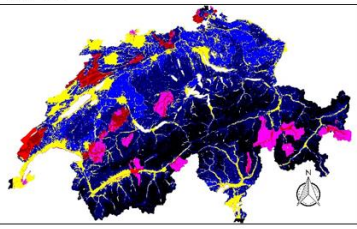
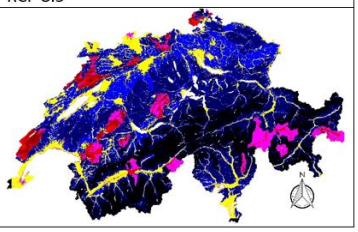
SP	Current situation	RCP 4.5	RCP 8.5
Covariate model			

Figure 26: Constrained SP solution for current, RCP 4.5, RCP 8.5 for the Covariate model.

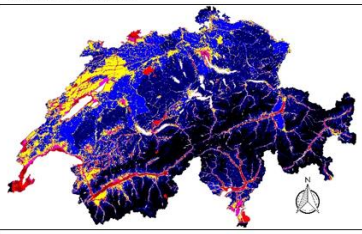
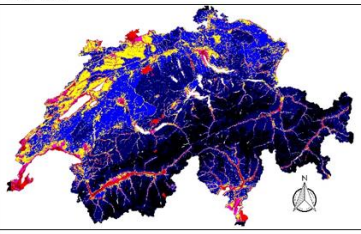
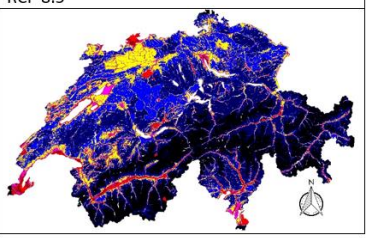
EM-PN	Current situation	RCP 4.5	RCP 8.5
Covariate model			

Figure 27: Constrained EM-PN solution for current, RCP 4.5, RCP 8.5, for the Covariate model.

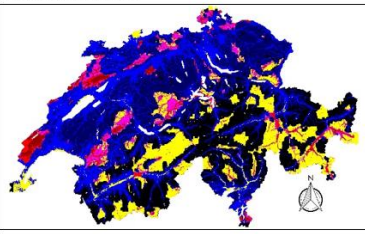
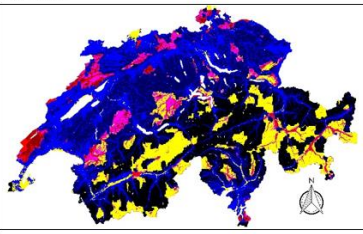
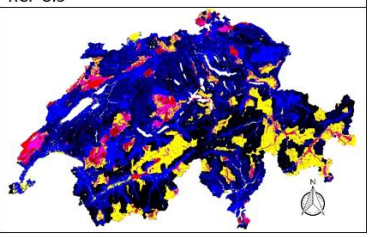
All-PA	Current situation	RCP 4.5	RCP 8.5
Covariate model			

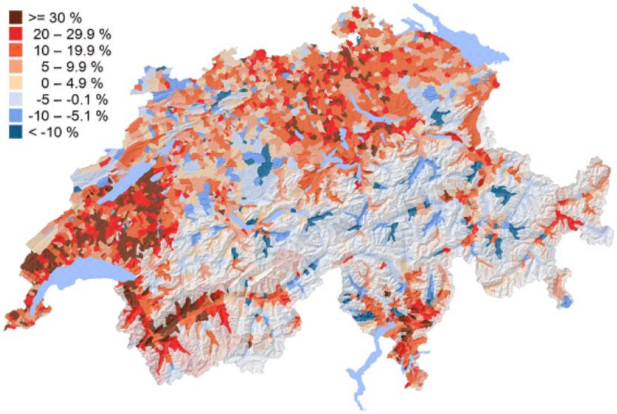
Figure 28: Constrained PA solution for current, RCP 4.5, RCP 8.5 for the Covariate model.

Appendix 8: Top three by orders for both the Combined and Covariate model for the three studied networks for current situation.

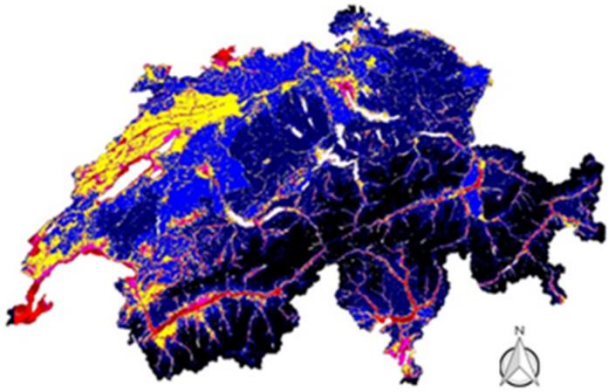
Chiroptera	SP	EM-PN	PA
Combined mode	Plecotus macrobullaris	Plecotus macrobullaris	Myotis blythii
	Plecotus austriacus	Hypsugo savii	Plecotus macrobullaris
	Myotis blythii	Pipistrellus khulii	Hypsugo savii
Covariate model	Plecotus macrobullaris	Pipistrellus khulii	Tadarita teniotis
	Plecotus austriacus	Plecotus macrobullaris	Plecotus macrobullaris
	Rhinolophus hipposideros	Nyctalus noctula	Nyctalus noctula
Lagomorpha			
Combined mode	Oryctolagus cuniculus	Oryctolagus cuniculus	Oryctolagus cuniculus
	Lepus europaeus	Lepus europaeus	Lepus timidus
	Lepus timidus	Lepus timidus	Lepus europaeus
Covariate model	Oryctolagus cuniculus	Oryctolagus cuniculus	Oryctolagus cuniculus
	Lepus europaeus	Lepus europaeus	Lepus timidus
	Lepus timidus	Lepus timidus	Lepus europaeus
Carnivora			
Combined mode	Lutra lutra	Lutra lutra	Canis lupus
	Canis lupus	Mustela nivalis	Mustela nivalis
	Mustela nivalis	Canis aureus	Lutra lutra
Covariate model	Lutra lutra	Lutra lutra	Lutra lutra
	Lynx lynx	Canis aureus	Canis lupus
	Canis aureus	Martes martes	Lynx lynx
Eulipotyphla			
Combined mode	Neomys anomalus	Neomys anomalus	Neomys anomalus
	Crocidura russula	Crocidura russula	Sorex minutus
	Neomys fodiens	Sorex araneus	Neomys fodiens
Covariate model	Neomys anomalus	Neomys anomalus	Sorex araneus
	Crocidura russula	Neomys fodiens	Sorex alpinus
	Neomys fodiens	Sorex alpinus	Neomys anomalus
Rodentia			
Combined mode	Rattus rattus	Rattus rattus	Apodemus alpicola
	Apodemus sylvaticus	Apodemus alpicola	Rattus rattus
	Mus domesticus	Mus domesticus	Chionomys nivalis
Covariate model	Rattus rattus	Rattus rattus	Apodemus alpicola
	Apodemus flavicollis	Microtus arvalis	Chionomys nivalis
	Microtus agrestis	Apodemus flavicollis	Eliomys quercinus
Artiodactyla			
Combined mode	Sus scrofa	Sus scrofa	Capra ibex
	Cervus elaphus	Cervus elaphus	Cervus elaphus
	Capreolus capreolus	Capreolus capreolus	Rupicapra rupicapra
Covariate model	Sus scrofa	Sus scrofa	Capra ibex
	Cervus elaphus	Capreolus capreolus	Rupicapra rupicapra
	Capreolus capreolus	Cervus elaphus	Cervus elaphus

Figure 29: Top three for all the orders regarding the studied network.

Appendix 9 : urbanized/populated areas in Switzerland.



Evolution de la population résidante 2000-2013 par commune (pourcentages). Source: INFOPLAN-ARE, GEOSTAT- OFS, swisstopo, 2014.



Biodiversity hotspots identified for the Combined model.

Figure 30 : Most populated and urbanized areas in Switzerland (left) and the main Biodiversity hotspots identified for the Combined model (right).