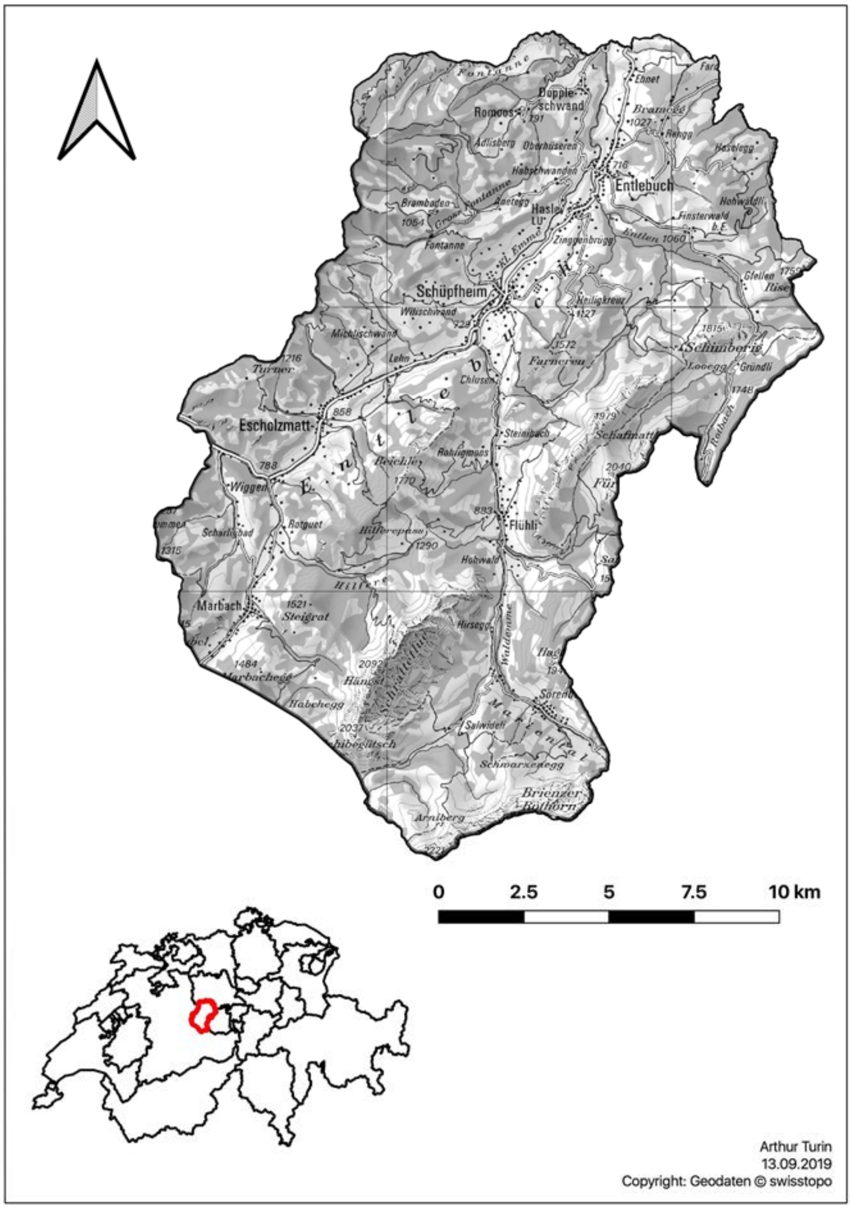
Applying Systematic Conservation Planning in the UNESCO Biosphere Entlebuch



Arthur Turin
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Master's Thesis
Master of Environmental Science
Major in Landscape and Forest Management

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Abstract

Due to the increasing pressure on ecosystems, species extinctions occur at an unprecedented rate all around the globe. Protected area networks are an effective means to halt biodiversity loss. There is thus a strong incentive to evaluate and increase the number of protected areas in Switzerland. In this Master's Thesis, the concept of Systematic Conservation Planning was used to answer the following research questions for the UNESCO Biosphere Entlebuch: i) Where should protected areas be optimally situated, and with regards to land use restrictions? ii) Is the current network of protected areas suitable for the conservation of the species analysed? and iii) How could the current network be modified to increase its performance?

114 species were assessed, including nesting birds, vascular plants, fauna, fungi and mosses. Maxent software was used to produce species distribution models to distribute species occurrences across the UNSECO Biosphere Entlebuch to reduce the effect of sampling bias. Then, Marxan software was used for the spatial prioritization phase. It has generated networks of protected areas that achieved user-defined biodiversity conservation objectives. Based on modeled distributions, several scenarios of protected area networks were produced: 1) optimal scenario; 2) scenario considering land-use restrictions; 3) scenario evaluating the current network of protected areas; 4) scenario expanding the current network of protected areas.

This project has shown that Systematic Conservation Planning is an effective procedure for evaluating the performance of the current protected area network in the UNESCO Biosphere Entlebuch. It has been shown that the current network of protected areas has not achieved conservation targets for 19 species. By defining the optimal distribution of protected areas, as well as their distribution according to the existing land use restrictions, modifications to improve the efficiency of the current network have been proposed.

Table of contents

List of illustrations

Figures

Tables

Equation

Appendices

List of abbreviations

AUC	Area Under the Curve
BFF	Biodiversitätsförderflächen (Biodiversity Promotion Areas)
BLM	Boundary Length Modifier
BR	Biosphere Reserve
CBD	Convention on Biological Diversity
DTM	Digital Terrain Model
IUCN	International Union for Conservation of Nature
NT	Near Threatened
VU	Vulnerable
EN	Endangered
CR	Critically Endangered
MTSPS	Maximum Training Sensitivity Plus Specificity threshold
NPF	Natural Priority Function
NUMITNS	Number of Iterations for annealing
NUMREPS	Number of Repeated runs for each scenario
PA	Protected Area
PU	Planning Unit
SDM	Species Distribution Model
SCP	Systematic Conservation Planning
SPF	Species Penalty Factor
UBE	UNESCO Biosphere Entlebuch
UNESCO	United Nations Educational, Scientific and Cultural Organization

1 Introduction

Due to the increasing pressure on ecosystems, species extinctions occur at an unprecedented rate all around the globe (Hooper et al. 2012). The effects of civilization on the atmosphere, the land, or the oceans are transforming these habitats at an alarming rate, making them increasingly less suitable for sustaining life (Brooks et al. 2002). As a result, the parties to the Convention on Biological Diversity (CBD) agreed in 2010 on 20 new targets to be met by 2020 to halt biodiversity loss, which are known as «Aichi biodiversity targets» (www.cbd.int/sp/targets/). Target 11 requires setting 17% of terrestrial land and inland water areas inside a network of protected areas (PAs) worldwide. Currently, only 9.99% of Switzerland's land area is being protected (UNEP-WCMC 2019). There is thus a strong incentive to increase the number of PAs in the country. Unfortunately, this is not a simple procedure. The classic top-down conservation approach which excludes local residents from the PAs is being criticized and faces resistance (Holmes, 2007).

UNESCO's Man and the Biosphere program is an attempt to bridge conservation and sustainable management (Stoll-Kleemann, De La Vega-Leinert, and Schultz 2010). As a core item of the program, the concept of a Biosphere Reserve (BR) was created in the early 1970's. The goals of BR's are multiple: 1) conservation of landscapes, ecosystems, species and genetic diversity; 2) sustainable development and 3) support for research and education. To implement these integrative goals in BR, a zoning strategy has been developed (Stoll-kleemann and Job 2008). Core zones represent PAs strictly essential for conservation. Buffer zones surround core zones allowing research or educational activities. Transition zones are the areas of a BR allowing socio-cultural and economical activities which are ecologically sustainable (Batisse 2003).

In Switzerland, following the adoption of the Rothenthurm Moorland Protection Initiative in 1987 calling for constitutional conservation of Swiss peatlands and mire landscapes, the inhabitants of the Entlebuch valley started a bottom-up approach to establish a BR during the late 1990's. Hosting a wide variety of endangered species and unique ecosystems such as moorlands and karst areas, there was a strong incentive to protect the area while allowing local communities to pursue sustainable development (Hammer 2007). In September 2001, Entlebuch was defined as the first BR of Switzerland in accordance with the Seville Strategy (Hammer 2007). With the creation of the UNESCO Biosphere Entlebuch (UBE) core, buffer and transition zones have been implemented. The core zones and other areas that are protected by law represent 17.1% of the total area of the UBE (Frei and Knaus 2017). Although the 17% goal is met, it is not clear whether the network of conservation areas is functioning. Indeed, in order for PAs to fulfill their roles, two objectives need to be met. Firstly, that the network of PAs needs to represent the entire spectrum of biodiversity. The second is persistence, which means that the network needs to insure the long-time survival of biodiversity (Margules and Pressey 2000). Fulfilling these objectives requires PAs to allow migration among them, represent a broad range of biodiversity features, and be well designed to safeguard species persistence. Thus, parameters such as connectivity, complement, and size must be taken into account.

To tackle these issues from a planning perspective and to facilitate the implementation of effective PAs, the concept of Systematic Conservation Planning (SCP) was developed (Margules and Pressey 2000; Pressey 1993). SCP has as its main goals to locate, design, and manage PAs that best represent biodiversity occurring in the study area while maximizing representation and persistence (Mace and Possingham 2006; McIntosh et al. 2017). It requires applying a transparent process to select a PA network that meet region-wide conservation goals. By proposing a framework consisting of several stages SCP process provides decision-support for conservationists and tends to increase the defensibility of the created PA network. Since it is such a widely used procedure for designing new PA networks, the six-stages process has evolved into eleven stages. In the context of this Master's thesis, the 11-stages framework proposed by McIntotsh et al. will be followed, which can be seen in Figure 1b (McIntosh, Pressey, Lloyd, Smith, & Grenyer, 2017).

Figure 1: a) early six-stages of SCP and b) the current 11-stages framework. The orange stages represent the spatial prioritization stages, often including an optimization software (McIntosh et al. 2017).

Stages 1 to 2, corresponding to designing the scope and costs of the planning process and identifying relevant stakeholders were not assessed in this Master's thesis for several reasons. They have already been assessed during the implementation of the UBE, and the time-frame of this work is too short to identify relevant stakeholders. The SCP framework was followed from stage 3 until stage 9. The context for implementing PAs was described, clear conservation goals were defined, relevant data was gathered, and finally a stage of spatial prioritization was completed. In the end, the resulting PA network was analysed and compared to the existing network. More specifically, the following questions were addressed for the UBE:

- Where should PAs be optimally situated, and with regards to land use restrictions?
- Is the current network of PAs suitable for the conservation of the species analysed?
- How could the current network be modified to increase its performance?

2 Method

2.1 Study region

The UBE is situated in the southern part of the canton of Lucerne (Figure 2). Covering 394 km^2 with an elevation range of approximately 590m to 2350 m, the site is known for its marshy and karst landscapes of the Pre-Alps. The UBE is home to several protected areas of national importance: 12’100 hectares (ha) of landscapes of national importance, 10’400 ha of mire, 1’765 ha of fen, and 170 ha of bog (Hammer 2007). The wetlands in Laubersmad-Salwidili were evaluated as an internationally important site in 2005, designating 1’376 ha of moorland to be included in the Ramsar Convention on Wetlands of International Importance, one of only 11 Ramsar sites in Switzerland (www.ramsar.org). A great variety of flora and fauna flourish in these areas thanks to their large and diverse moorlands and wetlands. The UBE consists of eight municipalities: Doppleschwand, Romoos, Entlebuch, Hasle, Escholzmatt, Flühli, Marbach, and Schüpfheim, with a total population of around 17,000 people. PAs were mostly designated before the BR was created. They currently encompass 17,1% of the UBE area for a total area of 67,55 km^2 (Frei and Knaus 2017). Thus, in hosting such a diversity of biodiversity, it is extremely important that the UBE's PA network be as effective as possible.

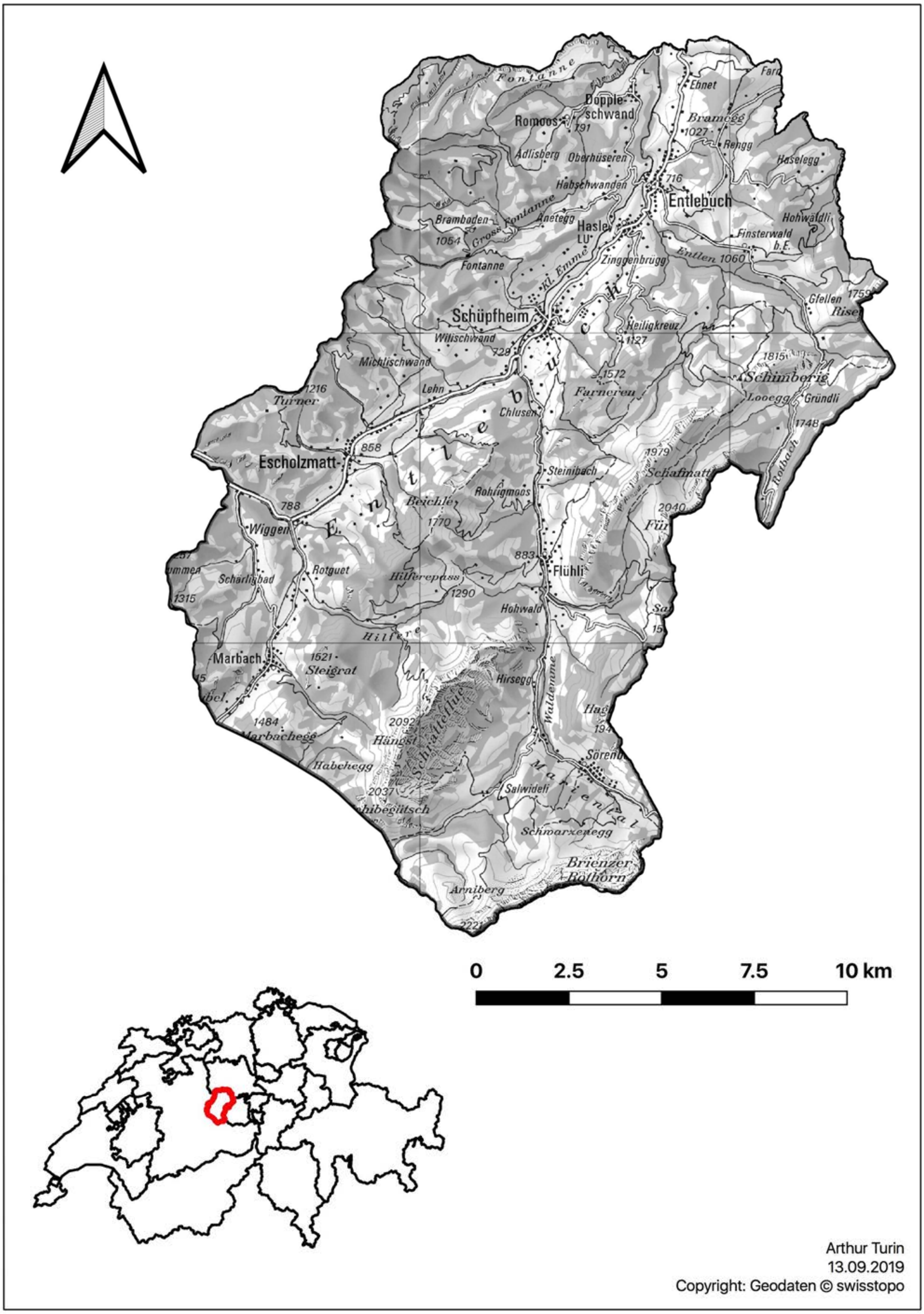

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Figure 2: Location of the UNESCO Biosphere Entlebuch

2.2 Collecting and processing data

2.2.1 Occurrence data

To protect biodiversity as a whole, every occurring species should ideally be included in an SCP-analysis, but for reasons of practicality biodiversity surrogates need to be used (Grantham et al. 2010). In this work surrogates represent every species occurring inside the UBE registered as a priority or threatened species.

The species occurrence data represented in the study area were obtained from the Swiss Species Information Center, Info Species (www.infospecies.ch). Raw occurrence data has been provided for several species groups from their respective institutions inside Info Species: nesting birds from the Swiss Ornithological Institute Sempach; vertebrate and invertebrate fauna from the Swiss Centre for Wildlife Mapping (CSCF-Info Fauna); vascular plants from the National Data and Information Centre for Flora in Switzerland (Info Flora); mosses from the National Data and Information Centre on Swiss Mosses (Swissbryophytes); fungi from the National Data and Information Centre on mushrooms in Switzerland (SwissFungi).

These occurrence data were then selected using the following requirements:

- Resolution in hectare (ha)
- Latitude and longitude values
- Species identification
- International Union for Conservation of Nature (IUCN) Red List status, either: near threatened (NT), vulnerable (VU), endangered (EN), or critically endangered (CR)
- When the observation years were available, only the observation from 1984 until today were kept.

All species groups were treated equally in order to guarantee consistency between them. All processes were made using the statistical computing R-software (R Core Team 2019). The used occurrence data have to be used with care. Most of these data are biased as they have been collected along walking paths, near cities, inside scientific plots or completely randomly from haphazard observations. As these data collections do not cover the entire reserve it can be assumed that many species have gone undocumented within the reserve itself, likewise, those regions unobserved may also contain observed species. Additionally, the used data are in the form of presence-only data, which means that we lack information where the species does not occur. The bias and weakness in the data requires that a step of species distribution modelling be performed in order to get an understanding of the presence and absence of each of the selected species for the whole UBE. Species distribution models (SDM) evaluate the relationships between a species record and the environmental characteristics at its observation point (Franklin 2009). To build such a model all environmental factors potentially influencing species distribution are identified, with a required minimum of five observations per species to allow for good performance of the species distribution model. The following section describes exactly how those variables are taken into account.

2.2.1.1 Explanatory variables

To get information on the environmental characteristics of each species occurrence, GEOSTAT points picturing surface area statistics of Switzerland for the period 2013-2018 were downloaded from the Federal Statistical Office (www.bfs.admin.ch). These points provide land-use information at a hectare scale in the form of 17 aggregated classes. In order to produce explanatory variables, a raster covering the entire UBE at a hectare scale was created. Since the GEOSTAT points were providing land-use information at the corner of each raster cell, each point was distributed in the four neighboring raster cells. It was then possible to calculate the proportion of a specific land-use class in each hectare (Figure).

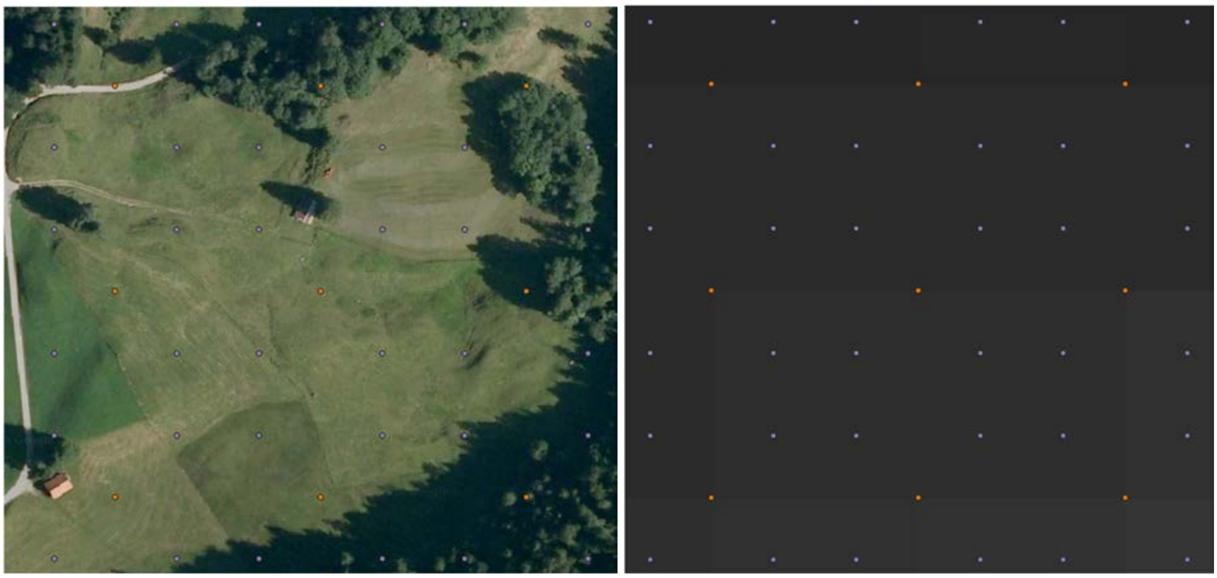


Figure 3: Each GEOSTAT points (orange) were duplicated to occur in each of the four neighboring raster cells. Thus, four different GEOSTAT points (purple) are available in each 100mx100m raster cells.

From the 17 available GEOSTAT classes fifteen were used (Figure 4, blue) and aggregated to six explanatory variables (Figure 4, green). Two GEOSTAT classes were not used; the land-use classes representing lakes and glacier did not apply.

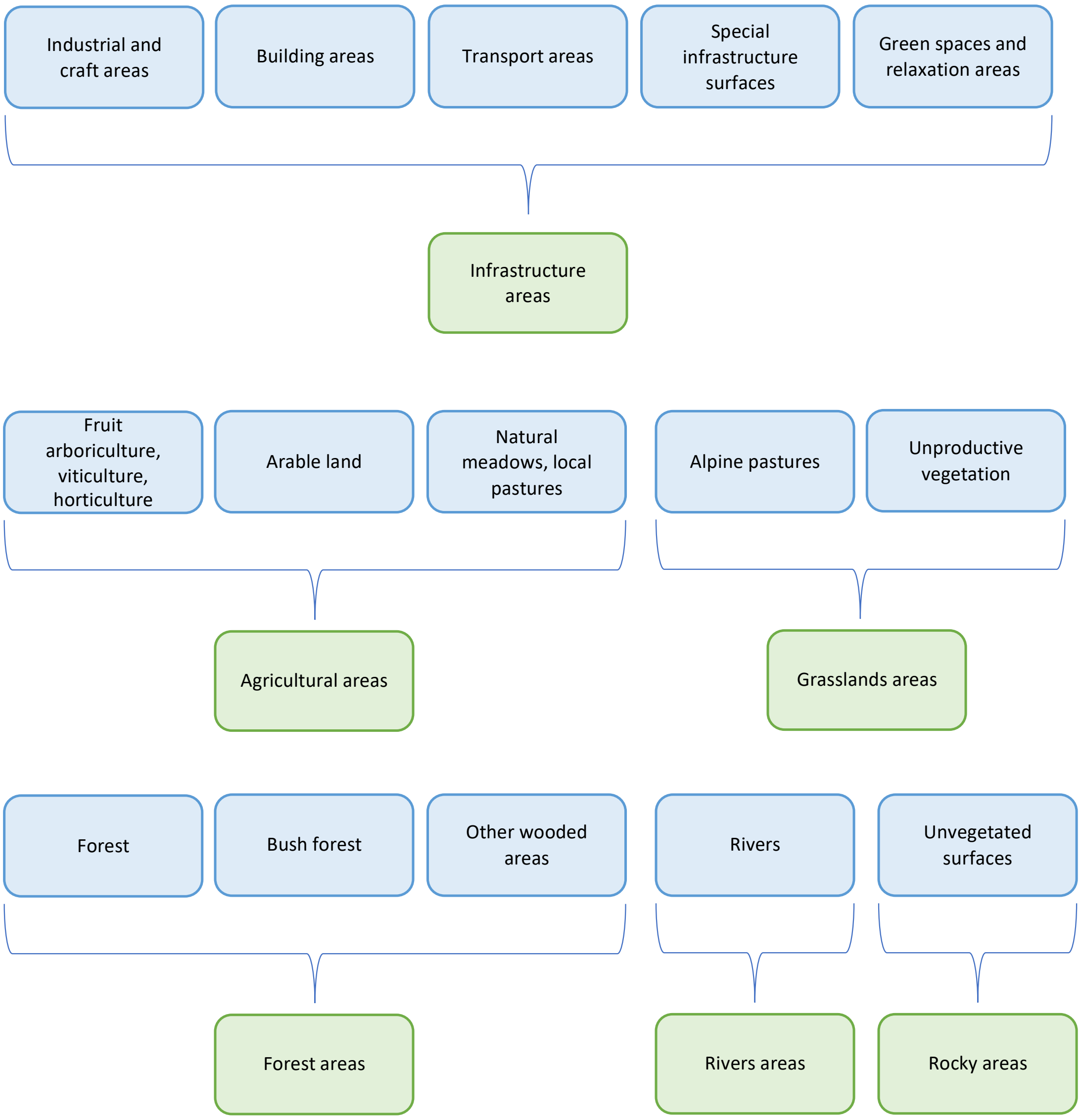


Figure 4: In blue, the 15 GEOSTAT classes that have been gathered into six land-use groups (green). Two GEOSTAT classes representing lakes and glaciers do not appear here, as they have not been used.

However, some particular ecosystems occurring in the UBE, which are important for biodiversity, were not sufficiently represented in the GEOSTAT land-use classes. These were wetlands, marshes, forest having natural priority function (NPF), and agricultural areas promoting biodiversity (BFF). These particular land-uses were available from other spatial data. By assessing the following data from the UBE database, GEOSTAT points distributed over these specific zones were selected and their attributes values were modified in QGIS to the respective explanatory variable:

- *N000049 - Bodenbedeckung* to select marshes (layer attribute *ART* = 12) and rivers (layer attribute *ART* = 15)

- *N000016 - Inventar der Naturobjekte regionaler Bedeutung* to select wetlands (layer attribute *INR_TYP* = F)
- *N000467 - Wälder mit Naturvorrangfunktion* to select forest having natural priority function (NPF)
- *N000453 - Landwirtschaftliche Kulturflächen* to select agricultural areas promoting biodiversity (BFF)

As a result, ten land-use categories are created in total: infrastructure areas; agricultural areas; grassland areas; forest areas; rivers areas; rocky areas; marsh areas; wetland areas; areas of forest having natural priority function; agricultural areas promoting biodiversity.

Each hectare of the UBE has now been attributed four GEOSTAT points providing information on these ten land-use categories. Thus, ten raster layers were produced, depicting the percentage of each land-use category occurring in each 100mx100m cell. These ten raster layers will be used as explanatory variables to calculate the SDMs.

To increase the accuracy a complement of three explanatory variables providing topographic information were produced. A digital terrain model (DTM) picturing elevation at a 25m resolution was obtained from Swisstopo by the ETHZ portal (https://geodata4edu.ethz.ch/index.html). Then, this DTM was used to calculate the layers depicting slope and aspect. These three layers (altitude, slope, aspect) were then aggregated to a resolution of 1 ha to match the resolution of the GEOSTAT points. The produced explanatory variables can be found in Appendix 2.

2.2.2 Maxent modelling and validation

Once the input data were set up for the SDM, they were supplied to the Maxent program (Phillips, Anderson, and Schapire 2006). In the case of the UBE, for which only presence-data were available, therefore preventing the use of regression models, the application of the Maxent software with its maximum entropy method presents itself as the most effective method (Elith et al. 2006). By dividing the landscape as a grid and based on presence data and explanatory variables, the model assessed the suitability of each cell as a function of explanatory variables at this cell (Merow, Smith, and Silander 2013). To do so, Maxent selected a model maximizing entropy by choosing the most spread-out distribution (Moilanen, Wilson, and Possingham 2009). The software produced probability grids where a high value meant that such a location was suitable for the given species (Pawar et al. 2007). Then, by selecting an appropriate threshold on the probability grid, the model can be reclassified to presence/absence predictions.

Maxent version 3.4.1 was used with most of its default parameter settings as they have been validated by previous studies (Elith et al. 2006). The feature selection was set to “auto” to allow the program to select the most appropriate feature for the model, and the maximum iteration was set to 1000. Lastly, the replicates parameter was set to 10, with a replicated run type “crossvalidate” to allow model training and testing. Once Maxent outputs were created, area under the curve (AUC) values were assessed, calculated using the 10-fold cross-validation. Species having an AUC value lower than 0.75 were removed, as values over 0.75 are likely to indicate useful models (Pearce and Ferrier 2000). Thus, 60 species having between 5 and 10 observations caused difficulties for Maxent in its ability to create a robust model and were further removed from the analysis.

At this stage, Maxent models represent the probability of occurrence for each species across the UBE, as a raster grid, at a ha-scale. To reclassify these grids into presence/absence predictions, a threshold needs to be implemented. The threshold represents the minimum probability above which a certain location is defined as suitable enough for a habitat of the analysed species. Maxent produces several thresholds with a specific value for each species, and the Maximum Training Sensitivity Plus Specificity threshold (MTSPS) was used. It maximizes the sum of sensitivity and specificity of the model, where sensitivity is the proportion of presences which were correctly predicted, and specificity is the proportion of absences which were correctly predicted (Liu, Newell, and White 2015). In the case of presence-only data, where no absence data is available to calculate specificity, Liu et al. have demonstrated that the same threshold value is found when using pseudo-absences (Liu, White, and Newell 2013). Thus, they claim that MTSPS threshold is a promising selection method when presence-only data is available. Once these thresholds are applied to the probability of occurrence maps, the areas having a species probability of occurrence lower than the threshold are considered as absences and hence removed. The remaining areas represent the modeled suitable habitats for each species, creating maps picturing the distribution of each species.

2.2.3 Spatial prioritization

Once each species distribution has been projected over the UBE, it is needed to select priority areas which would best protect the species being studied. To select the most appropriate planning units (PUs), version 2.43 of the Marxan software was used (http://marxan.org/software.html). Widely used among SCP practitioners, the software delivers support to reserve system design by solving the minimum set problem. The goal of Marxan is to select the most appropriate PA network to maximize representation of biodiversity features at a minimum cost under several user-defined parameters (Game and Grantham 2008). Marxan's simulated annealing algorithm will prevent the software from stopping at a local minima and instead find the true optima, while minimizing the objective function (Equation 1) (Game and Grantham 2008). The goal of the objective function is to rank each Marxan's run, and to identify how good a solution is at solving a problem (Ardron, Possingham, and Klein 2010). The value given to a solution is a function of total PU costs, the total reserve boundary length, and the penalty when a species does not meet conservation targets. Furthermore, a last parameter can be included, a cost threshold penalty, which was not used in this project. Thus, each Marxan's solution will be attributed a value, a smaller value being optimal.

$$\sum_{PUs} Cost + BLM \sum_{PUs} \text{Boundary} + \sum_{PUs} \text{SPF} * \text{Penalty} + Cost\ Threshold\ Penalty$$

Equation 1: Marxan's objective function, modified from (Ardron et al. 2010).

The first step in applying Marxan is to define PUs across the study area. Defining the shape and size of PUs is critical, as they represent the distribution of conservation features across the UBE. PUs can be regular, like a grid, or irregular, as habitat or property parcels, thereby changing the spatial distribution of PAs and their efficiency in representing the biodiversity features occurring in the region. (Pressey and Logan 1998). Using regular, polygonal PUs has distinct advantages: irregular units can become large depending on the habitat or the landowner, therefore it tends to be more efficient not to protect the whole unit but instead to identify crucial areas within it (Nhancale and Smith 2011). In the case of the UBE, however, a grid of 100mx100m has been used as it corresponds to the resolution of the explanatory variables. Thus, 39'442 cells of 10'000m^2 were defined as PUs. As it makes little sense to use all of them as potential PAs, these PUs were filtered according to the land-use. To do so, the building areas were excluded from the PUs. Finally, 37’374 PUs were used as input in Marxan.

Then, a key stage of Systematic Conservation Planning is the definition of targets for biodiversity features (Margules and Pressey 2000). It represents the amount of a species range that must be included inside the PA network to ensure its persistence. Once defined, these quantitative targets for biodiversity surrogates can be used as inputs for Marxan spatial prioritization software (Pressey, Cowling, and Rouget 2002).

In order to help planners to select appropriate targets, Levin et al. (2015) performed a sensitivity analysis of conservation targets. They found that with low targets, few areas were selected as priority areas, while high targets induced increasing areas selection, resulting in unrealistic outputs. Therefore, they stated that the most efficient scenarios were the ones with targets ranging from 35% to 45% of a species distribution range. Moreover, in a review of conservation targets, it has been reported that evidence-based conservation targets must be set around 30.6 percent ± 4.5 percent of the area being studied (Svancara et al. 2005). In this work, the conservation targets have been set to 30%. This means that 30% of the suited habitats defined by applying the MTSPS threshold on Maxent outputs should be included inside the PA network in order for the species to be defined as protected. This value is slightly lower than what was proposed by Levin et al. (2015) in order to produce a feasible network inside an inhabited study area.

One of the strengths of Marxan is its ability to attribute costs to each PU. Using this option, it will aim to meet all biodiversity constraints for a minimum cost (Ardron et al. 2010). As each PU has the same size, the cost settings will help Marxan to prioritize certain areas over others. These costs may reflect the purchase price of the PUs for inclusion in the reserve network, or they may reflect an environmental issue not to be included.

In the UBE case, as a surrogate of land costs, a land-use intensity map was used, provided by the UBE Geodatabase. It depicts for each parcel of the UBE the amount of biomass extracted in [kg/yr/ha] (Table 1). The regions where intensive land-use occur are located in the main valleys of the UBE (Figure 5). It changes to more extensive land-use the further away the parcels are from these main valleys. As a result, areas where the most extensive land-use occurs are distributed in the first alpine ridges located south-east of the UBE.

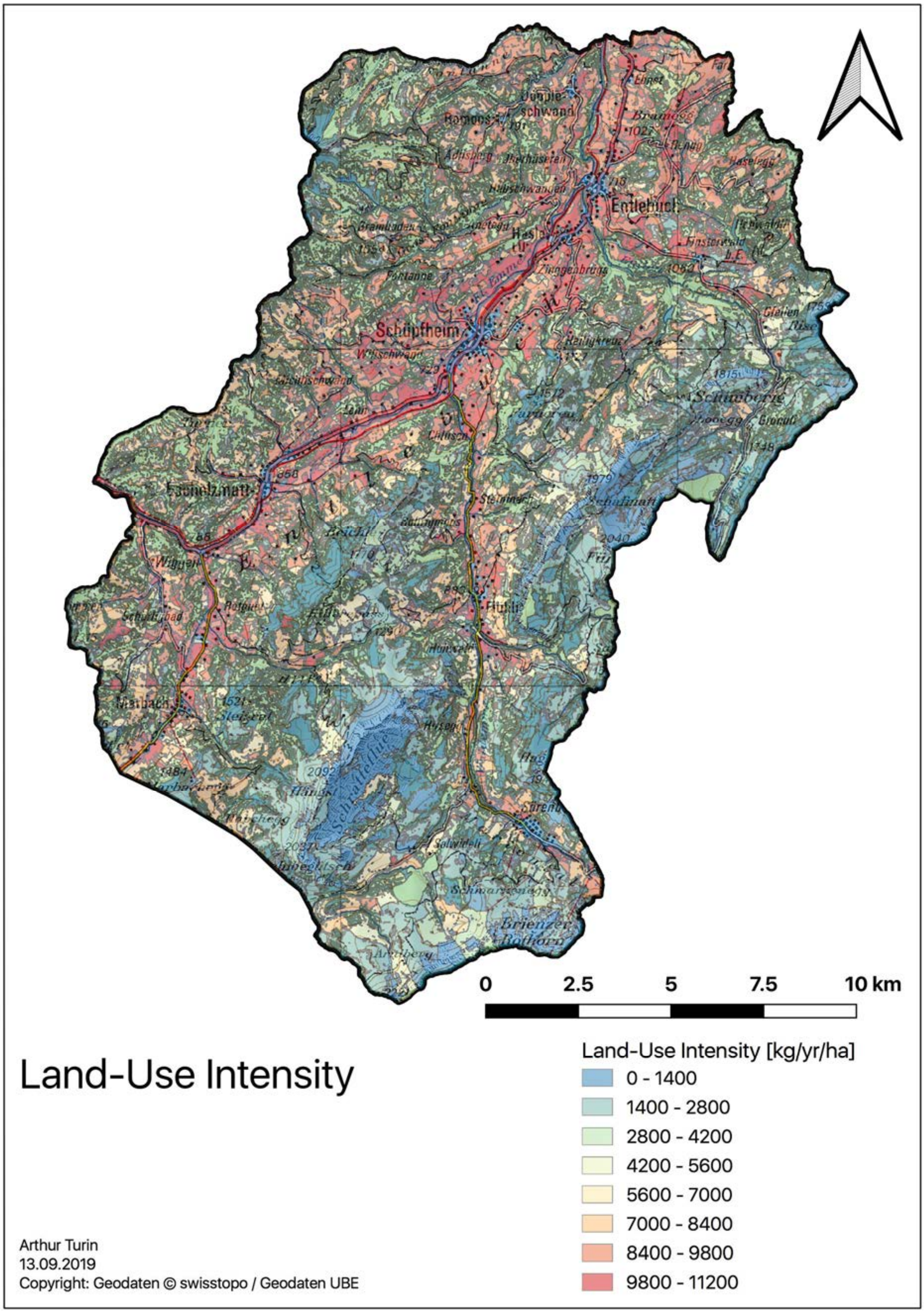


Figure 5: Land-use intensity categories occurring in the UBE (Knaus 2015).

As land-use correlates negatively with biodiversity in the UBE, the PUs where intensive extraction takes place are assumed to be in a more degraded state (Knaus 2015). It is further assumed that these parcels will be harder to acquire as they have higher opportunity costs for the land owner.

Thus, land-use intensity acts as a good surrogate for implementation costs. Identically to the land-use data, for each PU, four points were used to systematically extract the land-use intensity: given the data format, the amount of dry-matter extracted at these locations was used as a proxy for land-use intensity (Table 1).

Table 1: Land-use intensity categories and their distribution in the UBE, modified from Knaus (2015).

Land-use intensity	intensive		medium intensive		little intensive		extensive		Not used
% of area	20%		16%		28%		22%		14%
Used dry matter [kg/yr/ha]	From 11’200	To 9’800	From 8’400	To 7’000	From 5’600	To 4’200	From 2’800	To 1’400	none
% of area	9%	11%	9%	7%	9%	19%	13%	9%	14%

2.2.3.1 Marxan input files

To run Marxan, four input files containing data and parameters for the conservation problem are required.

- The **Input Parameter File** contains every parameter value used to control each Marxan run. Furthermore, it tells Marxan the name of the required files and where to find them.
- The **Conservation Feature File** provides information regarding each species considered. Each species was assigned a name, representation target, and a penalty if the representation is not met.
- The **Planning Unit File** contains information on the PUs. For each of them, an ID number, a cost, and a status (selected to be part of the analysis, or not) were defined.
- The **Planning Unit versus Conservation Feature File** represents the distribution of each species across the PUs. It links each species occurrence with the PU ID it occurs in.

Lastly, an additional input file was created, the **Boundary Length File**. Although it is optional, it allows for an increase in the compactness of the created reserve system by providing information on the length of shared boundaries between PUs.

With the exception of the Input Parameter File, which can be found in Appendix 3,, the following input file variables have been configured using R:

Conservation Feature File

- ID: A unique numerical identifier was attributed for each species being considered.
- Target: The target amount of each species that must be included in the solution. As previously explained, this variable was set to 30%.
- Species Penalty Factor: The penalty that Marxan needs to account for when a certain species does not meet targeted representation in the solution. This variable was defined during the calibration phase, explained in the next section.

Planning Unit File

- ID: A unique numerical identifier attributed to each PU.
- Cost: As previously explained, land-use intensity was used as a surrogate for costs.

Planning Unit versus Conservation Feature File

- Species: It corresponds to the unique numerical identifier defined in the Conservation Feature File, which identifies each species.
- Planning Unit: It corresponds to the unique numerical identifier defined in the Planning Unit File, which identify each PU. Thus, each species occurrence is linked to the PU it occurs in.
- Amount: The occurrence amount of each species in a specific PU. As the species distribution is at a hectare resolution, systematically the value of this variable is 1.

Boundary Length File

- ID1 & ID2: These are two separate variables. They represent the identifiers of two PUs sharing a border. An adjacency matrix was created in order to produce an adjacency list, it was then possible to extract the surrounding PUs for each PU.

- Boundary: This variable represents the length of the shared boundary between ID1 and ID2. In our case, as the boundary length always equals 100m, the variable was systematically attributed the value 1.

2.2.3.2 Marxan calibration

Before running Marxan, the Input Parameter File needs to be set up. It contains the parameters that control how Marxan finds solutions for a specific run. Even though a large number of parameters are part of this file, only a few were modified from their default values: the species penalty factor (SPF); the number of iterations for annealing (NUMITNS); the number of repeated runs for each scenario (NUMREPS); the boundary length modifier (BLM). These parameters need to be calibrated for each specific scenario.

The following calibration phase has been applied under the guidance of the Marxan Good Practice Handbook (Ardron et al. 2010). The first calibrated variable is the Species Penalty Factor (SPF) from the Conservation Feature File. Every species has an SPF value, which represents the penalty when the species does not meet target representation. Since the goal of the Marxan software is to minimize penalties, increasing the SPF value of a species that does not meet target representation will encourage its inclusion in the PA network. SPF needs to be as low as possible so that Marxan's performance is not restricted, but high enough so that each species target is met. In order to find the most efficient SPF value, four test runs were completed, each having a constant SPF value for every species (SPF = 1,2,3,10). These values were chosen to determine whether an optimal SPF value was within this range. Cumulative distribution functions were produced for each scenario to identify the optimal SPF value (Figure 6).

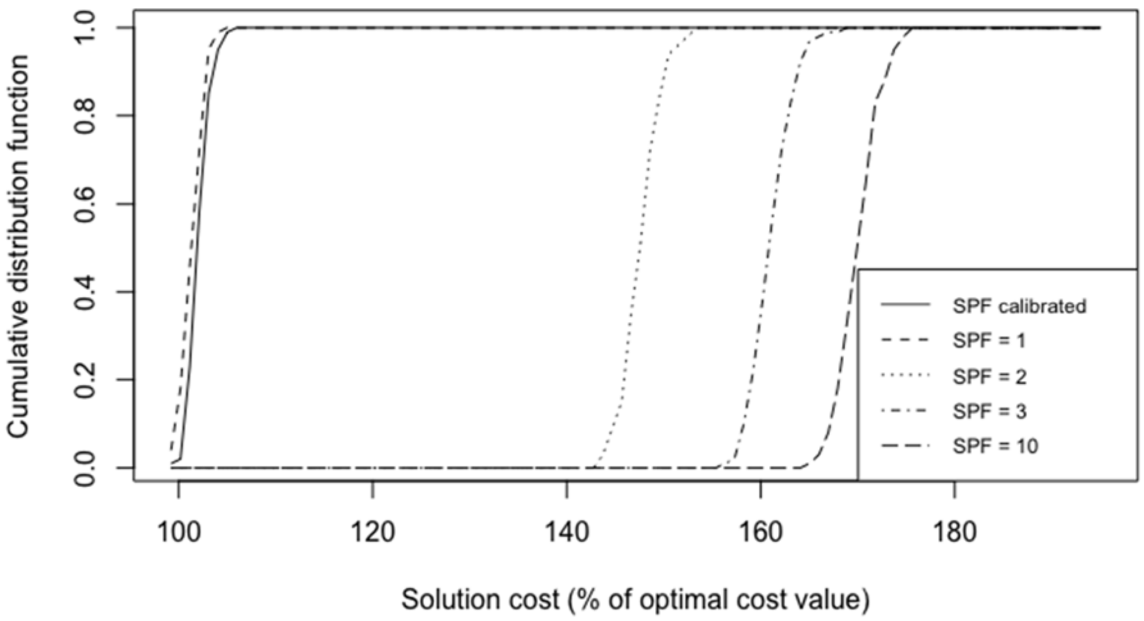


Figure 6: Cumulative distribution functions of solution cost for five test runs using different SPF values. The least-costing scenario has an SPF value of one, but one species does not reach target representation. The SPF values for the species that do not meet target representations were iteratively increased until every species met the targets. The scenario using the calibrated SPF values was tested, and it did not significantly increase the overall costs of the PA network.

Having an SPF value of 1 for every species is the least-costing test run, while increasing the SPF value produced more costly results. Under these conditions (SPF = 1), one species did not achieve target representation. Thus, the SPF value was iteratively increased until Marxan was able to meet target representation for this species. Being sensitive to a change of SPF value, other species were not meeting target representation, their SPF values were also increased iteratively until every species met their representation target while running Marxan.

The next variable to be calibrated is the number of iterations for annealing (NUMITNS). The simulated annealing solver relies on a large number of iterations to find an optimal solution. The larger the number of iterations, the greater the chances Marxan identifies a global optimum. In order to come up with an optimal number of iterations, three test runs were completed in Marxan, with 10^4, 10^5, and 10^6 iterations. Cumulative distribution functions were produced to identify the best scoring test run, which includes the overall costs as well as the penalties. The optimal number of iterations was concluded to be 10^6, as it produces feasible solutions at the lowest score, where the score represents the value of Marxan’s objective function (Figure 7).

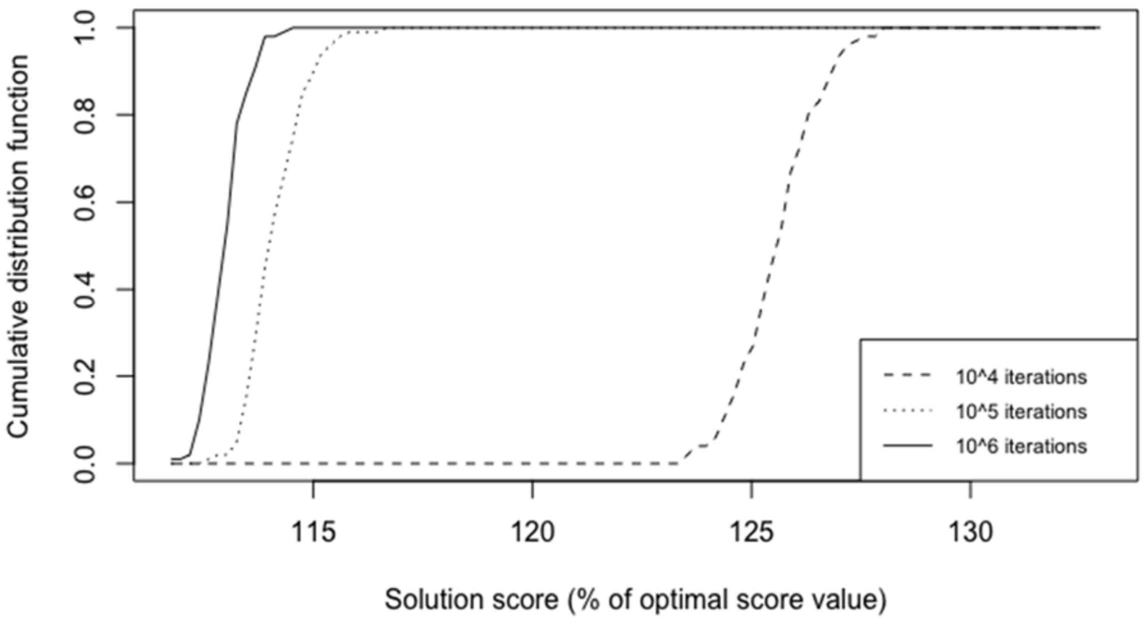


Figure 7: Cumulative distribution functions of solution score for three test runs using different iteration values, 10^4, 10^5, and 10^6. The test run having the lowest score was produced using 10^6 iterations.

Then, the number of repeated runs for each scenario (NUMREPS), was calibrated. For each scenario, there is a very large number of possible solutions and there is no need to identify them all. The idea is to choose a number of restarts where the spatial distribution of the optimal solution does not vary much with a higher number of repeated runs. The spatial pattern of the best run out of one hundred runs was compared to a scenario with the best run out of two hundred runs. No significant spatial differences were observed. A value of one hundred repeated runs was chosen.

Finally, the boundary length modifier (BLM) was calibrated. This variable is used to improve the compactness of the solution but tends to increase the overall cost of the solution (Fischer and Church 2003). In order to find a trade-off between costs and boundary length, a method has been developed to easily find a range of BLM values having a significant impact either on costs or boundary length (Fischer and Church 2005). Two test runs were calculated and plotted, a test run with the BLM = 0, which minimizes costs rather than boundary length, and a test run with the BLM = 1, which optimizes boundary length rather than costs (Figure 8). Then, the slope of the line connecting the two solutions was calculated and used as the calibrated BLM value (BLM = 0.0064). This run using the calibrated value was the estimated trade-off between boundary length and cost (Fischer and Church 2005).

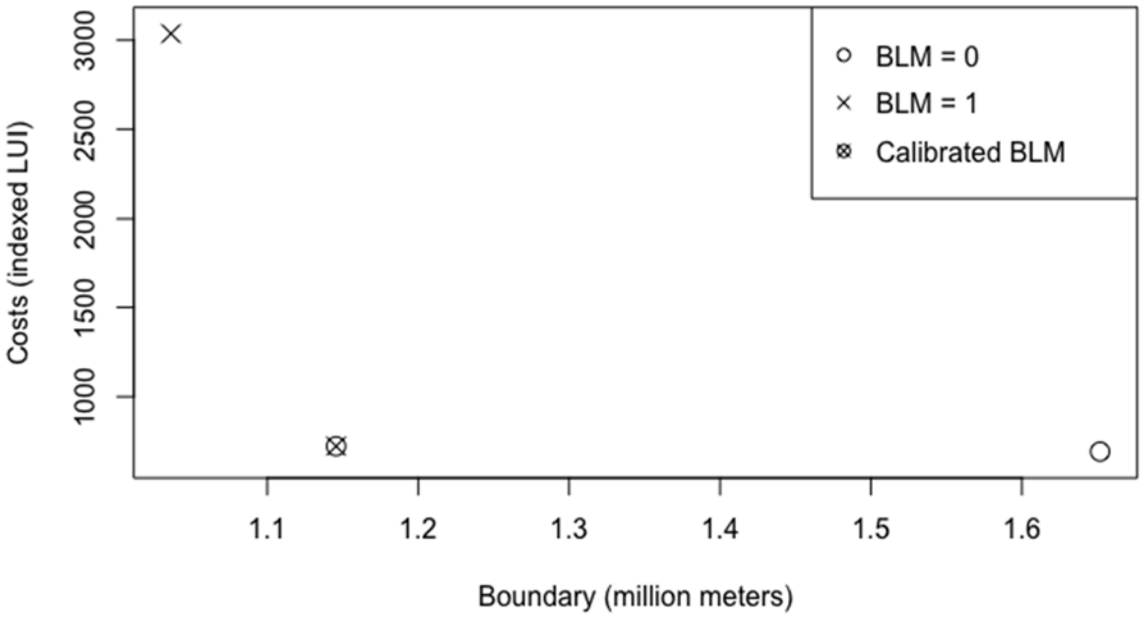


Figure 8: Calculation of trade-off between minimizing cost and minimizing boundary length. Marxan's run using BLM = 0 minimizes costs, and Marxan's run using BLM = 1 minimizes boundary length. Using the calibrated BLM value, corresponding to the slope of the line connecting the two previous runs, achieved a large reduction of boundary length at almost no increase to cost (BLM = 0.0064).

These calibration steps were done for four reserve network scenarios: 1) using a value of 1 for each PU cost, in order to focus only on species distributions without taking into account human activities. A value of 1 was used so that Marxan still tried to minimize the number of PUs; 2) using land-use intensity as a surrogate for PUs costs; 3) using existing PAs as PUs; 4) using existing PAs as PUs and expanding the PA network to include every species inside it.

3 Results

3.1 Data cleaning

From a total number of 4394 reported species, only 602 occur across the UBE perimeter (Table 2). From these, only 174 species fulfill the requirements to be used as input in Maxent. Finally, 114 species were kept for the spatial prioritization phase, as the others did not produce useful SDM, their AUC values being below 0.75. The list of the 114 species, as well as their IUCN category, AUC values, MTSPS thresholds and conservation targets can be found in the Appendix 1.

Table 2: Species groups and the number of species before and after data filtration

Species groups	**Nesting birds**	**Vascular plants**	**Fauna**	**Fungi**	**Mosses**	Total
Total number from Info Species database	42	356	92	3176	728	4394
Occurrences across UBE	25	135	49	269	124	602
After filtration	20	59	23	39	33	174
AUC above 0.75	**15**	**46**	**13**	**17**	**23**	**114**

3.2 Species Distribution Models

Maxent produced a raster layer picturing a probability grid of species distribution for each species (Figure 9). Once the Maximum Training Sensitivity Plus Specificity threshold (MTSPS) was applied to the raster layer, only the areas defined as suitable enough to host the species were kept (10). Each species' SDMs can be found in the Appendix 2. The smallest area defined as a habitat is represented by one PU, which is one hectare.

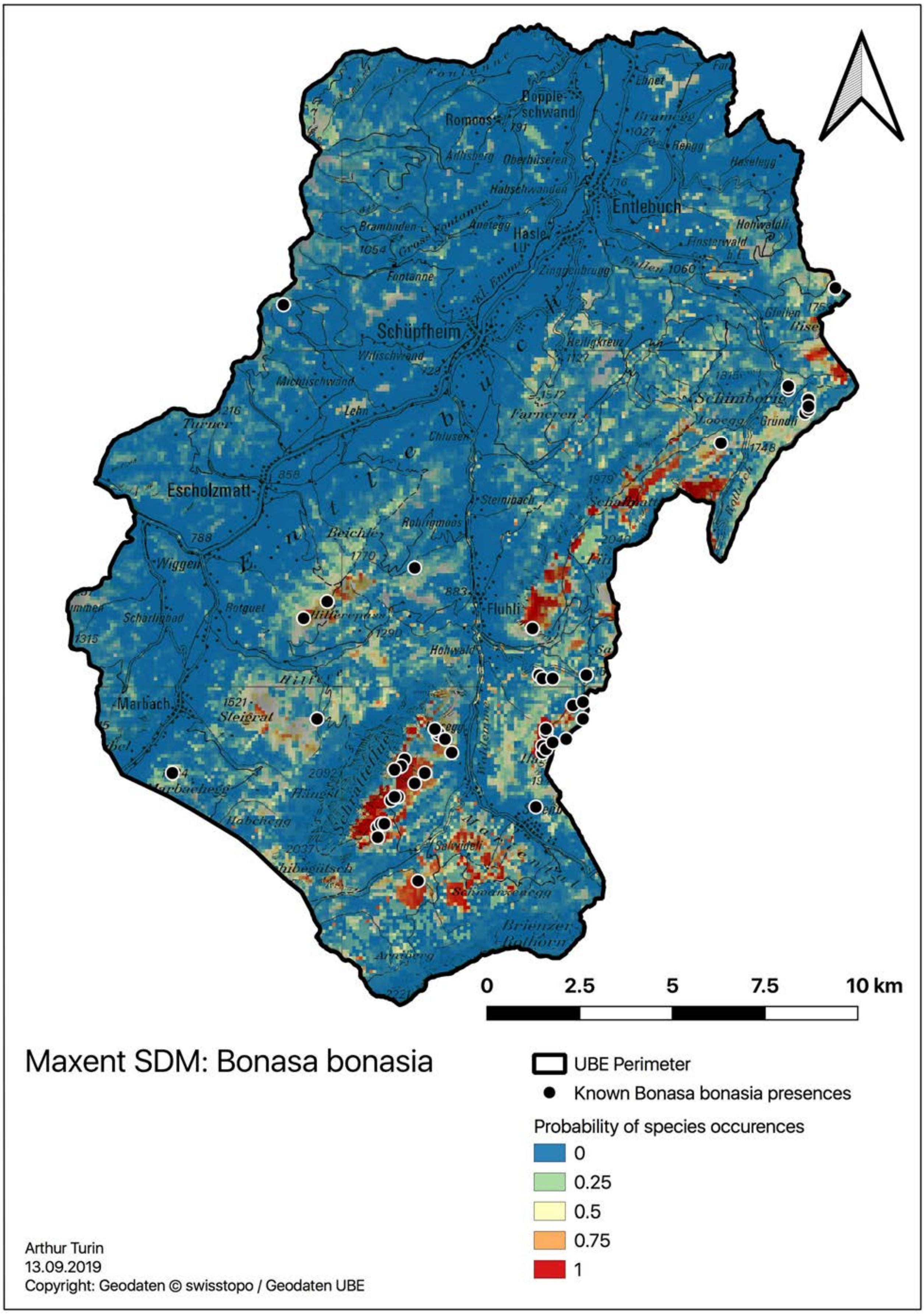


Figure 9: Distribution of Bonasa bonasia *presences data across the Unesco Biosphere Entlebuch, and its distribution model, represented as a probability of occurrence map resulting from Maxent.*

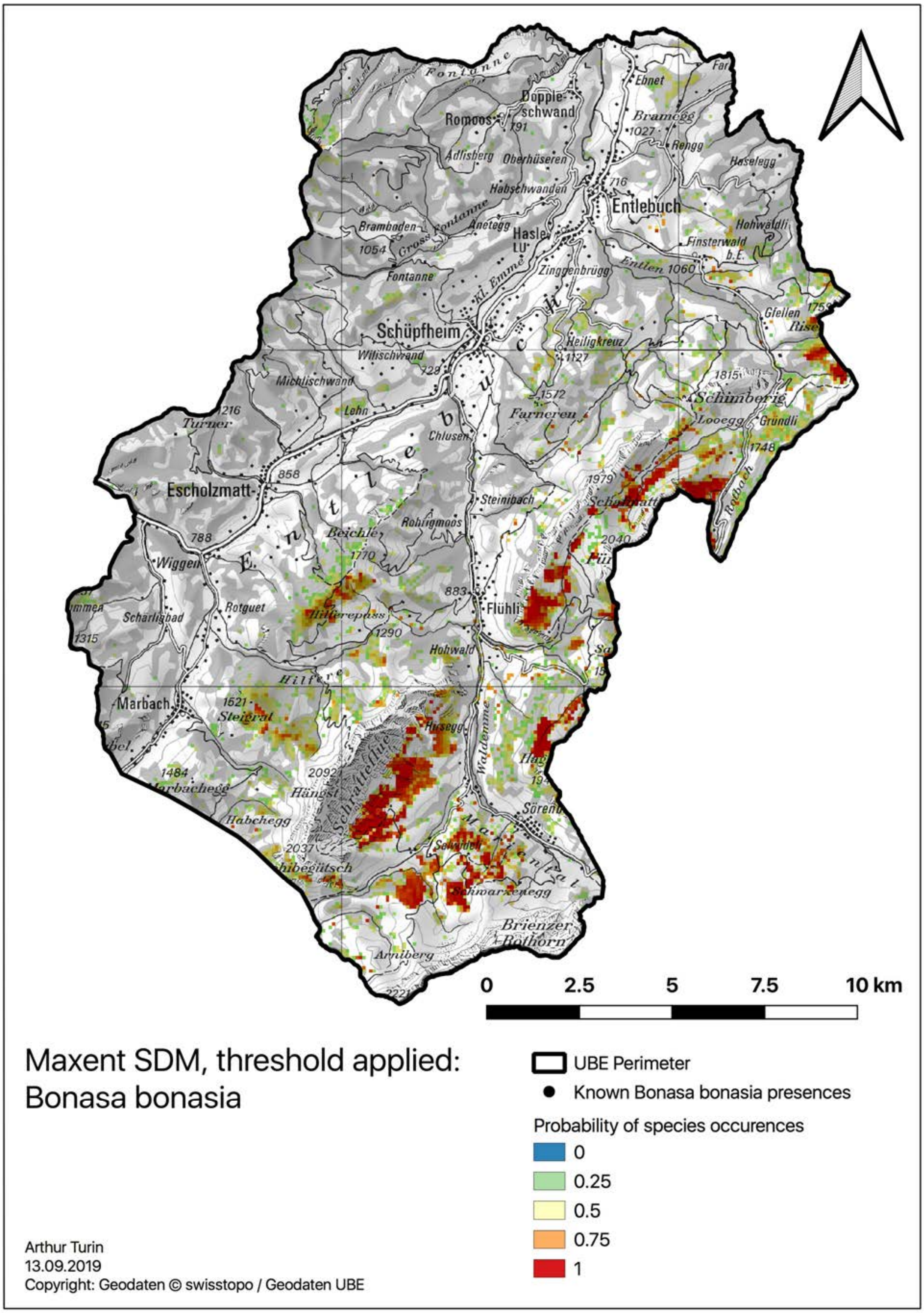


Figure 10: Modeled suitable habitats for the species Bonasa bonasia*, created by applying a Maximum Training Sensitivity Plus Specificity threshold (MTSPS threshold = 0.2616 for this species) on its probability of occurrence map.*

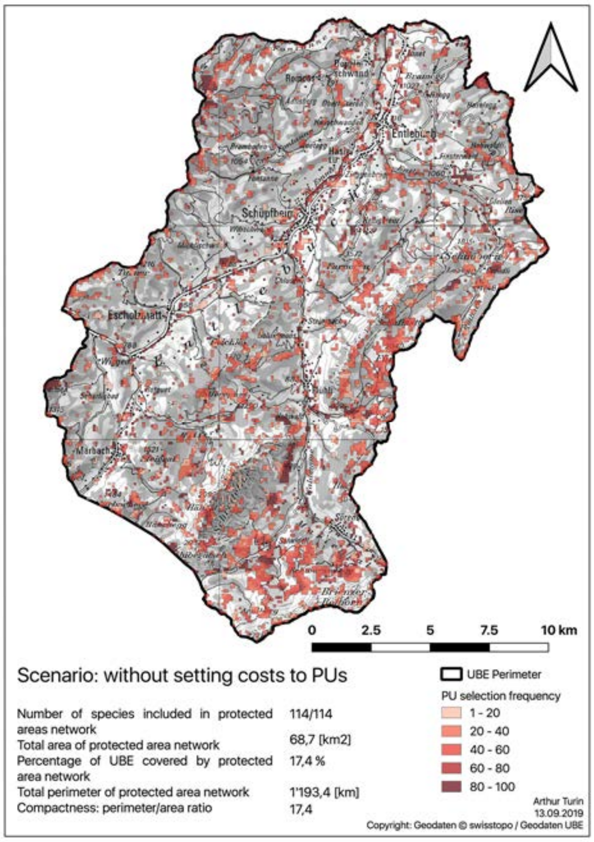
3.3 Protected area networks

Marxan was run for each scenario. The best run out of one hundred produced the following protected reserve networks: 1) using a value of 1 for each PU cost (Figure 11); 2) using land-use intensity as a surrogate for PUs cost (Figure 12); 3) using existing PAs as PUs (Figure 13); 4) using existing PAs as PUs and expanding the PA network to include each of the 114 species inside it (Figure 14). These maps show the resulting network of PAs needed to include 30% of Maxent's modelled habitats for each 114 species. As a proxy for irreplaceability, each PU was attributed its selection frequency, representing the amount of times each PU was selected over one hundred runs and showing the importance of each PU in creating an efficient network (Ardron et al. 2010). Moreover, using the total network area and the total network perimeter, an interesting parameter can be calculated, that of the perimeter over area ratio, providing information on the compactness of the reserve network. A compact network has indeed several advantages as it has a smaller number of reserves, leading to smaller management costs, and less suffering from perturbations that could happen in the borders of a reserve.

The particularities of each scenario can be seen in Table 3. Every scenario successfully included 30% of suitable habitats for each of the 114 species of interest except for that scenario using the existing PAs as PUs.

Table 3: Particularities of each protected area network scenarios

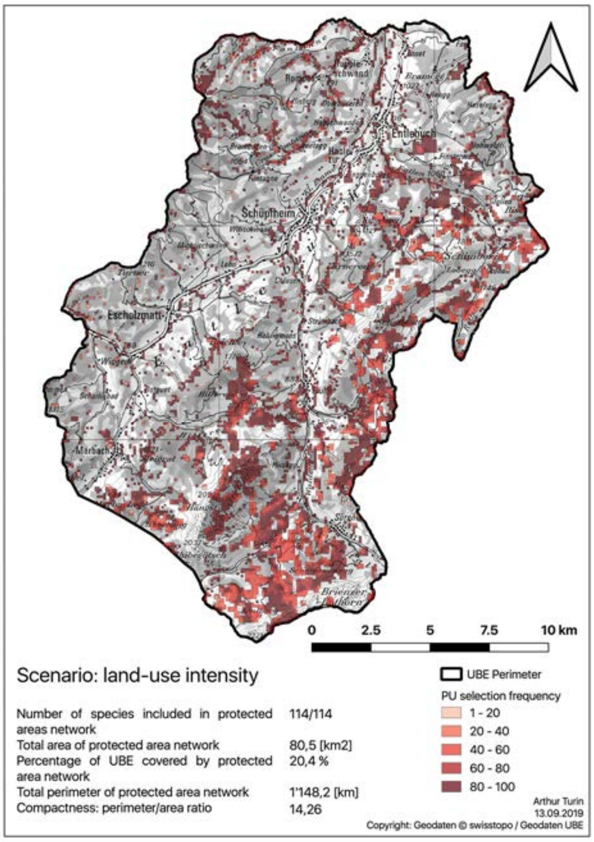
Scenario name	Number of species covered	Total network area [km^2]	% of the UBE covered	Total network perimeter [km]	Perimeter over area ratio
Without costs	114/114	68,7	17,4	1'193,4	17,4
Land-use intensity	114/114	80,5	20,4	1'148,2	14,26
Existing PAs	95/114	66,5	16,9	677,2	10,2
Expanding PAs	114/114	105	26,6	1'362,6	12,98



Scenario: without setting costs to PUs

Number of species included in protected areas network	114/114
Total area of protected area network	68,7 [km2]
Percentage of UBE covered by protected area network	17,4 %
Total perimeter of protected area network	1'193,4 [km]
Compactness: perimeter/area ratio	17,4

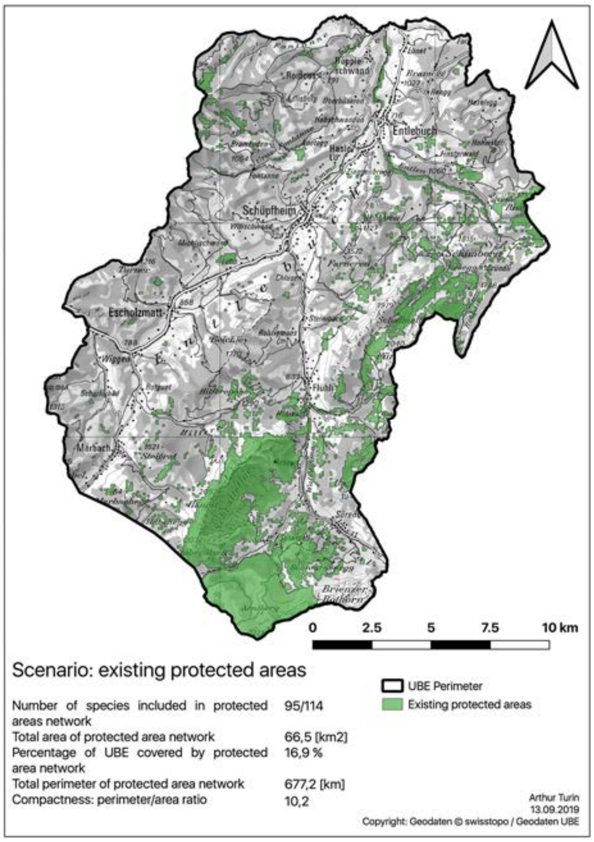
Figure 11: Scenario of PA network without implementtation of costs for PUs.



Scenario: land-use intensity

Number of species included in protected areas network	114/114
Total area of protected area network	80,5 [km2]
Percentage of UBE covered by protected area network	20,4 %
Total perimeter of protected area network	1'148,2 [km]
Compactness: perimeter/area ratio	14,26

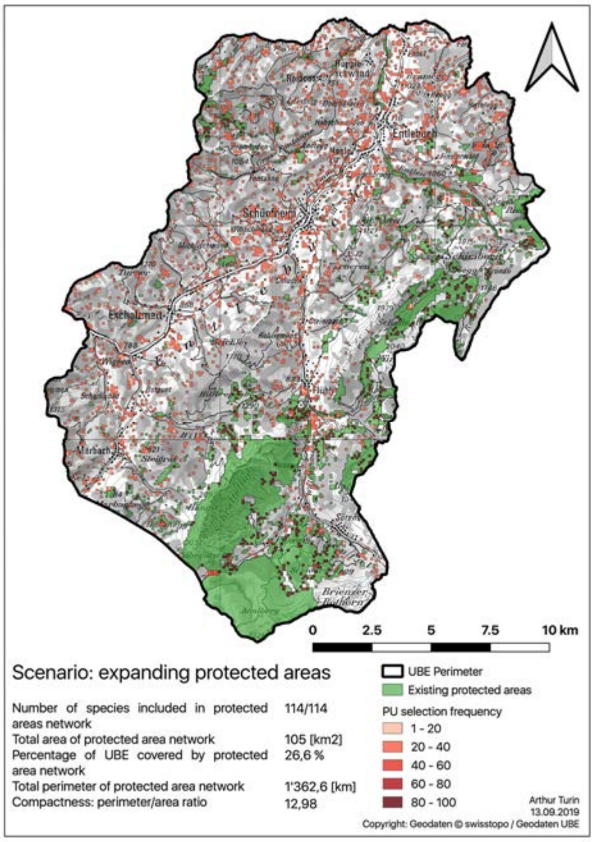
Figure 12: Scenario of PA network using land-use intensity as a surrogate for PUs costs.



Scenario: existing protected areas

Number of species included in protected areas network	95/114
Total area of protected area network	66,5 [km2]
Percentage of UBE covered by protected area network	16,9 %
Total perimeter of protected area network	677,2 [km]
Compactness: perimeter/area ratio	10,2

Figure 13: Scenario using strictly the existing PAs as PUs.



Scenario: expanding protected areas

Number of species included in protected areas network	114/114
Total area of protected area network	105 [km2]
Percentage of UBE covered by protected area network	26,6 %
Total perimeter of protected area network	1'362,6 [km]
Compactness: perimeter/area ratio	12,98

Figure 14: Scenario expanding the existing PAs to meet conservation targets for the 114 species of interest.

The first two scenarios were created without taking into account the existing PAs in the UBE (Figure 11 & Figure 12). Where the land-use intensity was not taken into account, the scenario needed 68,7 km^2 to achieve target representation. By contrast, the scenario using land-use intensity as a surrogate for PUs costs, selected an area of 80,5 km^2 to achieve target representation for each of the 114 species. Indeed, since the first scenario had no land-use intensity constraint on the selection of PUs, it was able to select a more efficient network of PUs even if it corresponded to parcels having high land-use intensity. This has an impact on the spatial configuration of the two scenarios. By being limited by land-use intensity, the second scenario selected PUs that are distributed in the south-eastern regions of the UBE. If the first scenario had also an incentive in selecting PUs in the south and east of the UBE, its network of PUs is much sparser and more located preferentially in valleys where land use is more intensive.

Moreover, the scenario without costs had a network perimeter of 1'193,4 km, longer than the 1'148,2 km of the land-use intensity scenario. This is due to the selected PU-areas being smaller so less connected and more dispersed. This has an impact on the perimeter over area ratio, as it has a value of 17,4 for the scenario without costs and a value of 14,26 for the land-use intensity scenario, which make the latter a more compact network.

Figure 13 shows Marxan's scenario using the existing PAs as PUs. The distribution of these PAs shares some similarities with the land-use intensity scenario. They are also distributed in the south-eastern regions of the UBE, but they cover larger area at these locations. Having a total area of 66,5 km^2 and a total perimeter of 677,2 km makes it the most compact PA network with a perimeter over area ratio of 10,2. Meanwhile, by using the modelled suitable habitats of the 114 species of interest, this scenario was able to meet conservation targets for only 95 species. Table 4 shows the 19 species which are not covered by the existing PAs. The table depicts their targets which represent the number of PUs needed to cover 30% of their modelled suitable habitats. Moreover, it shows how much of these targets are included in the existing PAs, and how much are missing.

Table 4: Species non-meeting targets under the scenario using the existing PAs as PUs

Species groups	Species names	Targets [# of PUs]	Target amounts included in ECZ [# of PUs]	Target amounts missing [# of PUs]
Nesting birds	*Alauda arvensis*	1628,4	1434	194,4
	Apus apus	2567,7	155	2412,7
	Delichon urbicum	1848	158	1690
	Phylloscopus sibilatrix	1495,8	110	1385,8
	Sylvia borin	1746,9	1040	706,9
Vascular plants	*Chrysosplenium oppositifolium*	1058,4	113	945,4
	Euonymus atifolius	964,5	269	695,5
	Linaria alpina	1158,9	684	474,9
	Orchis morio	606,3	187	419,3
	Orchis ustulata	1225,2	896	329,2
	Pleurospermum austriacum	398,4	308	90,4
	Saxifraga mutata	1634,7	678	956,7
Fauna	*Brachyptera seticornis*	1236	907	329
	Cottus gobio	977,4	186	791,4
	Lacerta agilis	1425	347	1078
	Salamandra salamandra	1088,4	198	890,4
	Salmo trutta	2047,2	893	1154,2
Fungi	*Lactarius repraesentaneus*	2133,6	1945	188,6
Mosses	*Frullania tamarisci*	2531,4	655	1876,4

This has been tied to the fact that the majority of the PAs are distributed in the southern wetlands of Laubersmad-Salwidili and over the Schrattenfluh mountain. The way these PAs are designed greatly contributes to the compactness of the PA network but fails to protect 19 species that have suitable habitats outside these areas.

For this reason, the expansion scenario for the existing PAs has been developed (Figure 14). In this scenario, the PUs representing the existing PAs were excluded to focus on the PUs which can expand the PA network to cover each of the 114 species. As conservation targets, the amounts missing in Table 4 were used in Marxan, and the software selected appropriate PUs to complete the existing PAs. This scenario successfully produced a network covering each of the 114 species. However, the PA network has a total area of 105 km^2 for a total perimeter of 1’362,6 km, making it at least 25% larger than the previous scenarios. Moreover, even if the perimeter over area ratio seems low compared to the other scenarios (12.98 compared to

17.4 and 14.26 for the first and second scenario respectively), this is largely due to the compactness of the existing PAs.

Finally, Marxan's most realistic output has been compared with the existing PA network (Figure 15). The PUs that were selected in the land-use intensity scenario have been differentiated: they have been depicted in orange when the PUs were covered by the existing PAs; in red when they were not covered. From a PUs network of 80,5 km^2, 29,9 km^2 of selected PUs are covered by the existing PAs, but there are regions defined as important by Marxan that are uncovered. For example, the northern part and western part of the UBE are underrepresented by the existing PAs, while the southern part of the UBE is overrepresented.

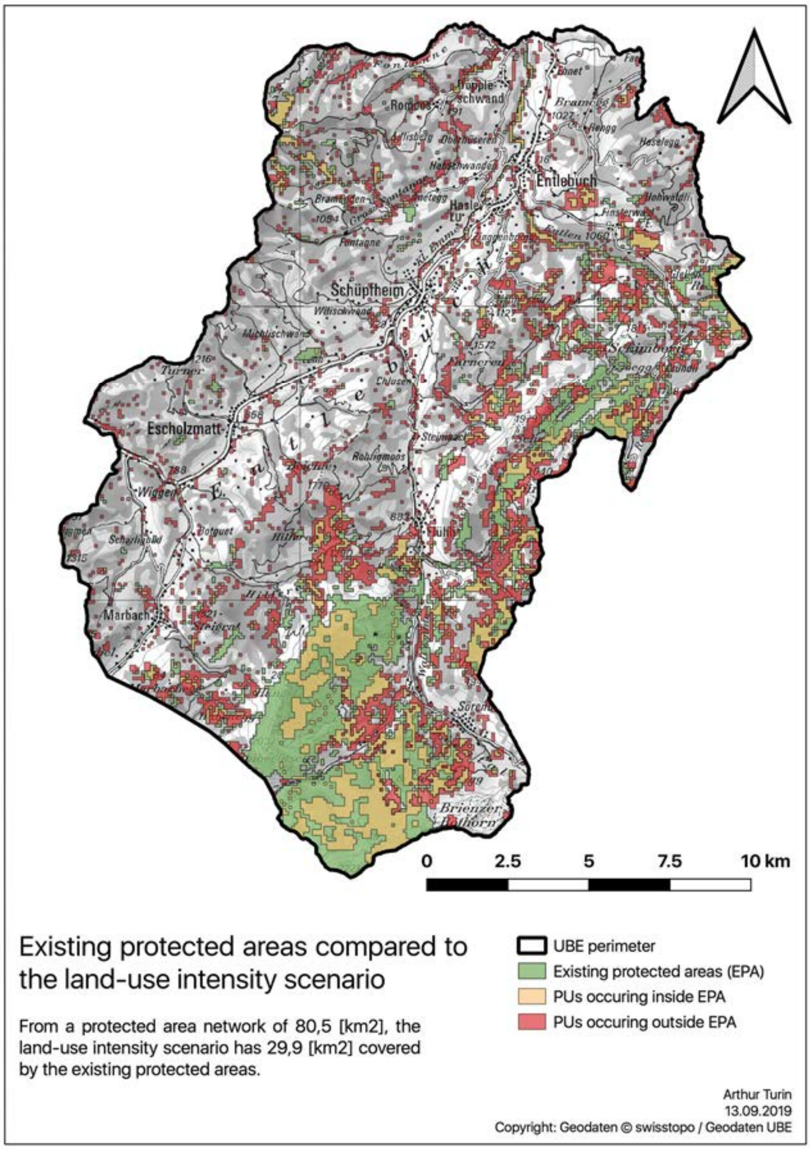


Figure 15: Comparing the existing PAs with the land-use intensity scenario.

4 Discussion

4.1 Marxan outputs

By looking at Figure 11 & Figure 12 we can see that, without taking into account the existing PAs, Marxan successfully created PA networks including each of the 114 species of interest. Focussing on the scenario without costs (Figure 11) Marxan selects PU more efficiently as the total area is smaller than that of the land-use intensity scenario. By contrast, the PA network is less compact as it selects smaller areas in strategic locations to augment biodiversity. Moreover, we can see that the selected PUs are less correlated with extensively managed parcels, thus they represent less elevated areas, often situated in the main valleys of the UBE. Additionally, the selection frequencies of selected PUs are lower than in the land-use intensity scenario. In this case, Marxan is free to choose from a variety of potential PUs, making the scenario without costs much more flexible. It can be modified more easily when taking into account stakeholders' points of view, as less PUs are irreplaceable (Stewart and Possingham 2005). This is important especially since land-use intensity is not taken into account. Some selected PUs will be difficult to acquire as a part of the PAs network as they could represent a high opportunity cost for landowners, leading to piqued resistance from farmers to change the form of land-use, or an exorbitant cost to a nature conservation NGO looking to buy the parcels in question.

In the case of the scenario with land-use intensity as implementation costs (Figure 12), we see that the best scenario out of 100 runs includes PUs having generally high selection frequencies. Because of cost constraints Marxan does not have much liberty to choose any PU as it has to minimize its objective function (Equation 1). The software then tends to choose mostly the same PU in each run. The spatial distribution of the selected PUs correlates with land-use intensity. We see that it represents mostly elevated areas that are well distant from infrastructure areas.

The strength of this scenario is that it selects PUs that could be easier to acquire than in the scenario without costs, as it takes land-use intensity as a surrogate for opportunity costs to landowners. However, since many PUs are irreplaceable, this scenario does not allow much room for variation. Moreover, it has a lower perimeter over area ratio than the scenario without costs, which means that it keeps the PA network more compact. Therefore, it increases the resilience of the network by reducing the disturbances which occur mostly in the border of PAs, as many species are sensitive to edge effects (Fischer and Church 2003).

For the scenario using existing PAs only, Marxan fails to protect 30% of the suitable habitats for 19 of the 114 species (Figure 13). When comparing this scenario to the first two a noteworthy difference is its limitation of PAs mostly to the Schrattenfluh mountain, the wetland landscapes of Laubersmad-Salwidili associated to the Sörenberg moorlands. These PAs have a total area of 35,84 km^2, which represents 53,9% of the existing PA network, the largest PAs in the UBE.

By looking at the modelled results, we see that Marxan does not select such a large area at that location. Thus, we could assume that these PAs are not effective in protecting the analysed species, and that other PUs are more important in order to cover 30% of the habitats suitable to the selected species. The strength of having such large PAs relies in its compactness. This scenario has the lowest value for the perimeter over area ratio, making it the best at mitigating potential perturbations affecting PAs. This is indeed a strength as conservation biology theory shows that larger PAs might be more effective in protecting some species than having the same area under protection from several unconnected PAs (Reid and Murphy 1995).

In reality, the existing PA network covers 17,1% of the UBE, and only 16,9% in this analysis. To keep consistency in the analyses, the design of the PUs was kept for this scenario as well. To best represent the existing PAs, only the PUs having their centroids intersecting a core zone were selected, creating slight differences. But we will assume that the 0.2% difference in coverage will not have a significant impact on the results.

In the last scenario (Figure 14), we can see that the most frequently selected PUs occur near existing PAs as they are the most suited to expanding the existing network while keeping it compact. Coupled with them, however, we see that Marxan selects a large number of isolated PUs to achieve conservation targets, even if a high BLM value is chosen. This is understandable as Marxan cannot create large PAs covering a large number of species because 95 species are already covered by the existing PAs. So, it first selects areas where PUs can form a compact group, but soon after needs to select isolated PUs to achieve conservation targets. Even if this network has a low perimeter over area ratio, it represents the scenario covering the largest area in order to protect each of the 114 species. It makes this scenario unsuitable, as such small and isolated PUs would be difficult to set up and to manage.

Overall, in order to improve the existing network of PAs, the existing ones need to be kept as much as possible. Indeed, creating a brand-new network such as in the first two scenarios is unrealistic. Regardless, we saw that expanding the existing PAs to cover 30% of the modelled suitable habitats of the 114 species would be unsuccessful. A better option would be to modify existing PAs to make them more effective at covering the analysed suitable habitats. In order to provide decision support, the land-use intensity scenario will be compared to the existing PAs (Figure 15). As it has been pointed out, the northern and western part of the UBE are underrepresented by the existing PAs, while the southern part of the UBE is overrepresented. This is why, based on Marxan's results, a modification of the spatial distribution of the existing PAs needs to be discussed.

Nevertheless, we need to keep in mind that the PAs in the Laubersmad-Salwidili region, the southernmost PAs, has been defined as a Ramsar Site. This consideration underlines the international importance of these wetlands. Marxan chose many of these unique wetlands but prioritized other areas above the entirety of the Laubersmad-Salwidili wetlands. Still, having such large PAs implemented over these wetlands is important as it represents different types of peatland providing habitats for a great diversity of flora and fauna. However, the Schrattenfluh mountain, for example, does not offer such a diversity of habitats, and yet is still covered by a PA of approximatively 18 km^2, while the Laubersmad-Salwidili Ramsar Site is reported to be 13,75 km^2 (www.ramsar.org). Based on these facts, the PA covering the Schrattenfluh mountain represents the best option to modify the current network of PAs in order for them to cover 30% of the modeled suitable habitats of the 114 species analysed here. Fuller et al. (2010) have shown that replacing underperforming PAs achieve better conservation outcomes than by expanding an existing PA network. Therefore, a reduction in the size of the PAs in the Schrattenfluh region should be considered in order to make space for the protection of other, more important regions. However, it is important to take into account that the 114 species considered represent mainly species living in mire and peatlands ecosystems. As a result, suitable habitats may be correlated uniquely to these types of environments, neglecting environments for species not considered in this analysis.

Moreover, these suitable habitats should also be assessed taking into account climate change. Strategic locations where species can survive climate change should be defined (Reside and Adams 2018). In the UBE, most species will see their habitats shifted to more elevated areas. It is of great importance that connectivity analyses be carried out to ensure that the species occurring in the UBE will be able to migrate to these future suitable regions (Loyola 2013).

Finally, it is important to keep in mind that Marxan outputs should not be seen as one final network to be implemented, but rather as decision support. Such maps as Figure 15 should be used as discussion material to inform a dialogue between those people with a stake in the decision on PAs distribution. Nevertheless, these results highlight the limitations of the existing PAs and how they can be improved.

4.2 Strengths and limitations

One of the great opportunities of this Master's thesis was the wide range of data available: including the Geodata provided by the UBE Geodatabase and the species occurrences from the Info Species database. However, of the 174 species that were selected after being filtrated and had their distribution modelled (Table 1), only 114 had an AUC value over 0.75. As a result, more than a third of the species that could have been used in the spatial prioritization phase were rejected. More effort should be spent analyzing each SDM individually, in order to find out why they have been producing results that could not be trusted. This issue is also due to explanatory variables that could have been more precise. Indeed, they were built by extracting land-use occurring in the UBE at only four locations per hectare. Moreover, the SDMs would ideally also provide information on species distribution occurring in a buffer around the UBE. In this work, all the thirteen explanatory variables were restricted to the perimeter of the UBE to avoid creating bias, as some habitat information was only available for the study area.

Furthermore, the quality of the species occurrence data left something to be desired, as has already been highlighted. They were available in the form of presence-only data and contained bias as they were not thoroughly sampled across the entire study region. Even though producing SDM effectively partially corrects sampling biases, the biases found in the data are propagated in the models (Fourcade et al. 2014). In addition, species occurrence data were provided at a ha resolution, which could result in SDMs locating some species in unlikely regions. In order to highlight these biases, the uncertainties associated with SDMs should ideally be taken into account, especially as SDMs bring further uncertainties in the planning process (Reside and Adams 2018). To limit the effects of biases, the most feasible option would be that biodiversity experts inspect each SDM and investigate in the field to clear any outstanding doubts. By doing so, it would greatly increase the accuracy of the spatial prioritization phase.

Furthermore, it should be noted that the modeled habitats were produced by analyzing the occurrence data available in the Info Species database. Protecting 30% of a species' habitat could be sufficient if the natural range of the species is taken into account. In the case of this project, the habitat considered does not reflect the full range of habitat of a particular species. Thus, when the conservation objectives were set at 30%, they did not correspond to 30% of the habitat required for any given species. This means that these results could have produced a non-viable PA network for some species.

Finally, while being able to model species distribution and optimize PAs spatially, I certainly lack ecological skills to correctly analyze and assess the studied species. The outputs created in this project are greatly influenced by ecological and environmental processes specific to the UBE which were difficult to consider due to my limited knowledge about the specific species.

4.3 Recommendations

By comparing the four scenarios that were produced during the spatial prioritization phase, it would be ideal to identify larger areas that would be truly worth setting aside for conservation. These areas would be composed of multiple PUs, each representing a location where suitable habitat occur for one or several species. While each PU has a resolution of one hectare, it does not mean that the whole hectare should be protected. Analyses in the field should be carried out in order to identify the specificity of the selected PUs. Then, choices should be made on which portion of the PU should be included in the PA network.

Moreover, if the existing PAs were to be modified by such an approach, a strong incentive should be given to integrating the stakeholders in that process as much as possible. By producing PA networks depicting the selection frequency of each selected PU, it would be possible to identify PUs that could potentially be exchanged with other ones. Then, a new solution could be produced by locking conflicting PUs in or out of the network. Despite the fact that such a process would be time consuming, it has the ability to produce a PA network that would be better understood, accepted, and chosen by the local population.

Finally, one principal issue with the produced PA networks is that they have been obtained using static biodiversity data points, whereas biodiversity features adapt to a changing world (Moilanen et al. 2009). Species' range are expanding or shifting because of environmental changes (Chen et al. 2011). Since climate change needs to be factored into any prediction model of species distribution to best ensure species persistence, using explanatory variables to adequately model the future climate becomes imperative.

5 Conclusion

This project has shown that SCP is an effective procedure to spatially define PAs that best represent biodiversity occurring in the UBE. SCP allowed to define the optimal distribution of PAs, as well as their distribution according to the existing land use intensity. In addition, it was possible to evaluate the performance of the current network, while proposing revisions to improve its efficiency. By providing clearly defined stages, SCP is of great help to carry out comprehensive conservation assessments while considering all relevant factors. The combined use of Maxent and Marxan has proven to be a good strategy for making the most of biased data. By prioritizing areas during the frequency analysis, Marxan provided decision-support outputs to critically evaluate how a current conservation network can be improved. Furthermore, using real land-use restrictions as inputs allows it to produce PA networks that reduce the potential resistance from local stakeholders.

To help this approach be further implemented in Switzerland or in other parts of the world, it is important to keep sampling biodiversity features thoroughly while minimizing biases and making these records accessible. Even though the use of SDMs mitigated the biases in this project, they propagated uncertainties and reduced the produced PA network's precision. This is why it is important to increase the quality of the available distribution data in order to increase the quality of PA networks produced. Moreover, managing such a great amount of data requires an automatization of the analysis requiring strong computational knowledge. In order to reduce the gap between data analysts and conservationists, source code sharing should be incentivized alongside the provision of research outputs.

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7 Appendices

	SPECIES NAME	IUCN CATEGORY	AUC VALUES	MTSPS THRESHOLD	CONSERVATION TARGET
NESTING BIRDS	*Alauda arvensis*	1	0,901	0,473	1628,4
	Anthus pratensis	2	0,941	0,258	1123,2
	Apus apus	1	0,885	0,179	2567,7
	Bonasa bonasia	1	0,872	0,262	1475,1
	Cuculus canorus	1	0,751	0,489	3785,4
	Delichon urbicum	1	0,892	0,311	1848
	Lagopus muta	1	0,986	0,219	322,8
	Linaria cannabina	1	0,818	0,304	2601
	Lyrurus tetrix	1	0,9	0,242	2096,1
	Phoenicurus phoenicurus	1	0,887	0,164	1384,8
	Phylloscopus sibilatrix	2	0,759	0,597	1495,8
	Phylloscopus trochilus	2	0,821	0,131	1383,6
	Saxicola rubetra	2	0,856	0,611	1021,5
	Sylvia borin	1	0,827	0,368	1746,9
	Turdus torquatus	2	0,879	0,362	2643
VASCULAR PLANTS	*Agrostis canina*	1	0,973	0,139	782,1
	Andromeda polifolia	1	0,978	0,076	594,6
	Carex ericetorum	1	0,967	0,524	252,3
	Carex lasiocarpa	2	0,921	0,277	626,4
	Carex limosa	1	0,988	0,139	240,9
	Carex pauciflora	1	0,973	0,128	567,6
	Carex paupercula	1	0,989	0,239	254,7
	Carex pulicaris	1	0,9	0,341	1017,9
	Carex vaginata	2	0,763	0,688	368,1
	Chrysosplenium oppositifolium	1	0,828	0,65	1058,4
	Dactylorhiza incarnata	1	0,804	0,604	665,4

Drosera anglica	2	0,932	0,7	110,1
Drosera rotundifolia	1	0,983	0,091	464,4
Drosera xobovata	2	0,987	0,033	536,1
Epipactis palustris	1	0,854	0,184	1266,9
Eriophorum vaginatum	1	0,964	0,068	1265,4
Eryngium alpinum	2	0,797	0,841	32,4
Euonymus latifolius	1	0,918	0,303	964,5
Juncus acutiflorus	1	0,794	0,585	597,6
Juncus squarrosus	3	0,95	0,7	386,1
Juncus stygius	4	0,867	0,616	167,4
Linaria alpina	1	0,898	0,508	1158,9
Listera cordata	1	0,986	0,153	429
Lycopodiella inundata	2	0,947	0,194	775,2
Lycopodium clavatum	1	0,773	0,697	824,4
Orchis militaris	1	0,92	0,993	0,6
Orchis morio	2	0,918	0,553	606,3
Orchis ustulata	1	0,836	0,461	1225,2
Papaver occidentale	1	0,973	0,381	517,8
Pedicularis palustris	1	0,954	0,088	786,3
Pedicularis sylvatica	2	0,94	0,123	1360,5
Petrocallis pyrenaica	1	0,987	0,61	188,1
Pinguicula vulgaris	1	0,892	0,129	1847,1
Pleurospermum austriacum	2	0,786	0,636	398,4
Potentilla palustris	1	0,94	0,535	176,7
Ranunculus flammula	1	0,885	0,194	1733,7
Rhynchospora alba	1	0,993	0,488	77,4
Salix repens	2	0,976	0,173	190,2
Saxifraga mutata	1	0,909	0,252	1634,7
Scheuchzeria palustris	2	0,979	0,046	582,6

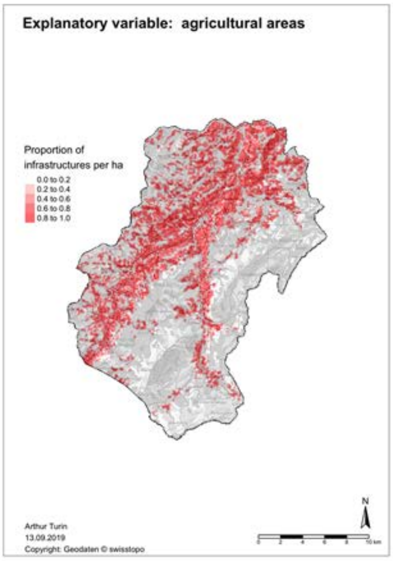
	Spiranthes spiralis	2	0,928	0,839	4,2
	Swertia perennis	1	0,938	0,065	1497
	Trichophorum alpinum	1	0,793	0,282	992,1
	Vaccinium oxycoccos	1	0,96	0,208	357,9
	Vaccinium uliginosum	1	0,949	0,517	200,7
	Viola pyrenaica	1	0,962	0,249	630,9
FAUNA	*Brachyptera seticornis*	2	0,824	0,288	1236
	Chorthippus montanus	2	0,892	0,155	1703,7
	Colias palaeno	1	0,826	0,503	891,6
	Cottus gobio	1	0,963	0,124	977,4
	Lacerta agilis	2	0,914	0,128	1425
	Lepus timidus	1	0,759	0,22	2010,6
	Leucorrhinia dubia	1	0,975	0,059	451,8
	Phengaris arion	1	0,836	0,423	2345,4
	Rhithrogena dorieri	1	0,799	0,589	876
	Salamandra salamandra	2	0,947	0,121	1088,4
	Salmo trutta s.l.	1	0,854	0,232	2047,2
	Somatochlora alpestris	1	0,961	0,053	900,3
	Stethophyma grossum	2	0,894	0,238	853,8
FUNGI	*Aleurodiscus amorphus*	2	0,875	0,672	224,7
	Amanita lividopallescens	2	0,807	0,735	110,1
	Camarophyllus berkeleyi	3	0,968	0,88	41,4
	Cantharellula umbonata	2	0,936	0,43	176,1
	Cortinarius croceoconus	2	0,879	0,372	394,2
	Cortinarius tubarius	1	0,888	0,699	293,7

	Cortinarius pholideus	2	0,871	0,862	21,6
	Entoloma elodes	2	0,762	0,578	188,7
	Galerina sphagnorum	1	0,781	0,591	892,8
	Galerina tibiicystis	1	0,858	0,233	1775,1
	Hygrocybe helobia	2	0,807	0,529	562,2
	Lactarius helvus	2	0,788	0,366	1409,1
	Lactarius repraesentaneus	2	0,793	0,288	2133,6
	Leccinum holopus	2	0,916	0,773	21,6
	Phlebiella vaga	2	0,833	0,861	65,1
	Sarcoleotia turficola	3	0,8	0,641	750,3
	Trichoglossum hirsutum	1	0,827	0,24	2103
MOSSES	*Anastrepta orcadensis*	2	0,933	0,658	697,5
	Cephalozia connivens	1	0,99	0,424	192,3
	Frullania tamarisci	1	0,845	0,418	2531,4
	Hypnum bambergeri	3	0,909	0,654	1030,2
	Hypnum procerrimum	3	0,966	0,7	273,3
	Kurzia pauciflora	3	0,94	0,682	437,1
	Mylia anomala	1	0,972	0,193	562,8
	Odontoschisma denudatum	1	0,953	0,577	264,3
	Odontoschisma fluitans	1	0,953	0,598	242,7
	Polytrichum longisetum	1	0,944	0,748	85,5
	Polytrichum strictum	1	0,981	0,051	570,9
	Sphagnum angustifolium	1	0,943	0,177	709,2
	Sphagnum capillifolium	1	0,951	0,17	1036,8
	Sphagnum cuspidatum	1	0,955	0,117	585,9

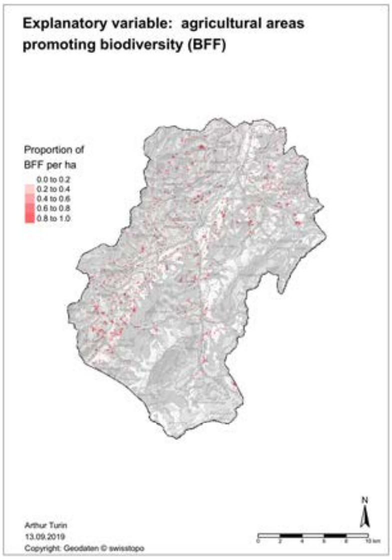
Sphagnum fallax	1	0,932	0,106	937,8
Sphagnum flexuosum	1	0,812	0,346	774,6
Sphagnum magellanicum	1	0,931	0,192	1759,2
Sphagnum papillosum	1	0,967	0,093	988,2
Sphagnum rubellum	1	0,964	0,659	119,7
Sphagnum russowii	1	0,948	0,173	1059
Sphagnum tenellum	1	0,962	0,094	936,3
Splachnum ampullaceum	1	0,982	0,667	127,2
Warnstorfia fluitans	1	0,977	0,374	189,3

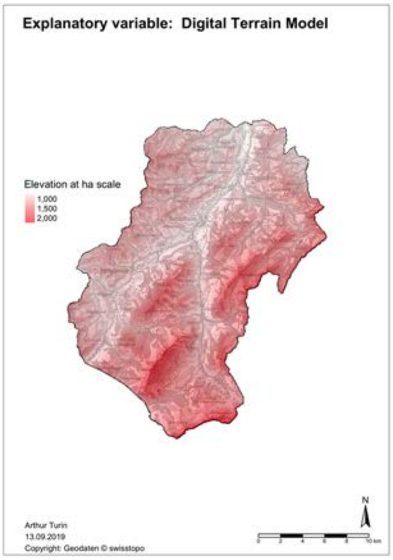
Appendix 1: each of the 114 species names, IUCN category, AUC values, MTSPS thresholds and conservation targets.

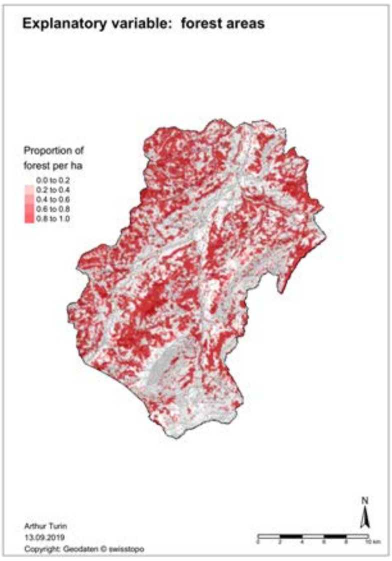
Appendix 2: Explanatory variables

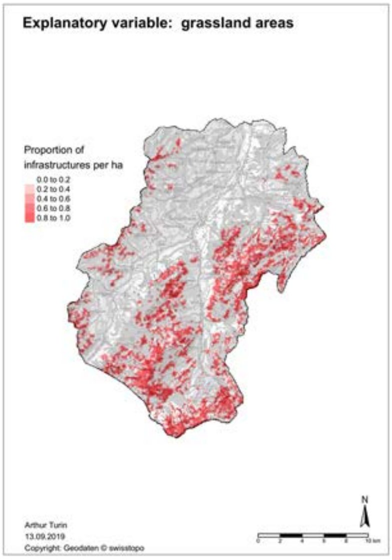

Explanatory variable: agricultural areas

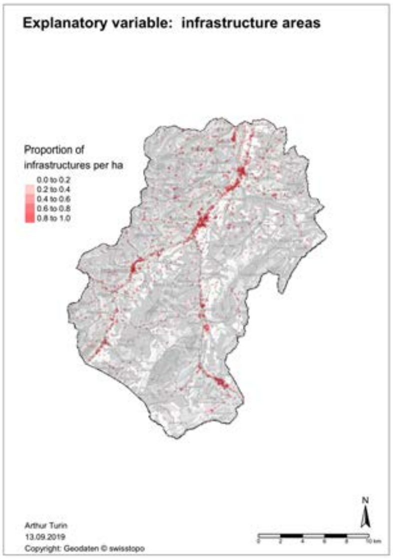

Explanatory variable: aspect

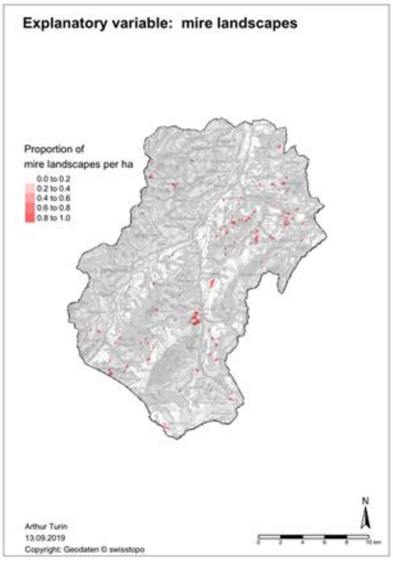

Explanatory variable: agricultural areas promoting biodiversity (BFF)

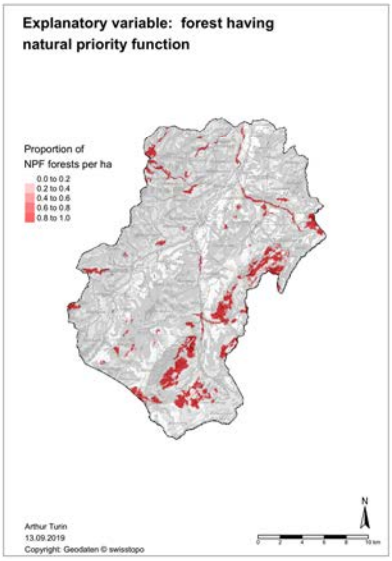

Explanatory variable: Digital Terrain Model

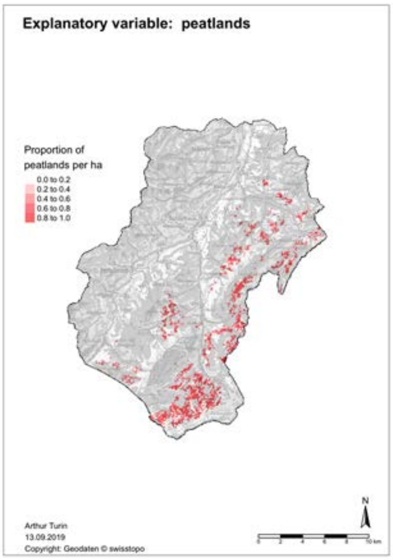

Explanatory variable: forest areas


Explanatory variable: grassland areas


Explanatory variable: infrastructure areas


Explanatory variable: mire landscapes


Explanatory variable: forest having natural priority function


Explanatory variable: peatlands
Proportion of peatlands per ha
0.0 to 0.2
0.2 to 0.4
0.4 to 0.6
0.6 to 0.8
0.8 to 1.0
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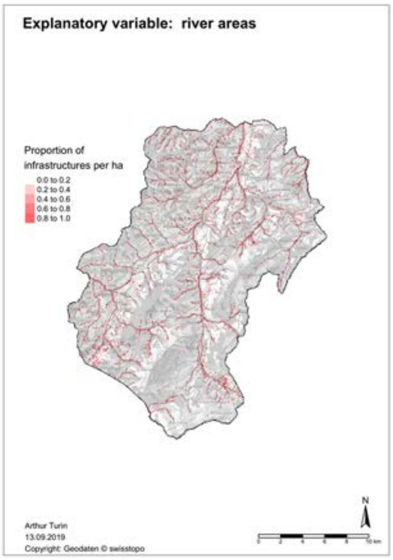
13.09.2019
Copyright: Geodaten © swisstopo
N
0 2 4 6 8 10 km


Explanatory variable: river areas
Proportion of infrastructures per ha
0.0 to 0.2
0.2 to 0.4
0.4 to 0.6
0.6 to 0.8
0.8 to 1.0
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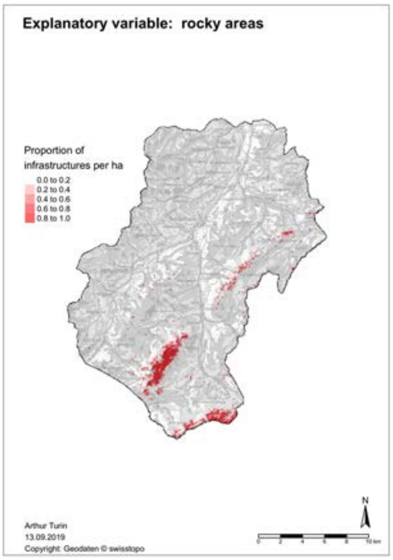
N
0 2 4 6 8 10 km


Explanatory variable: rocky areas
Proportion of infrastructures per ha
0.0 to 0.2
0.2 to 0.4
0.4 to 0.6
0.6 to 0.8
0.8 to 1.0
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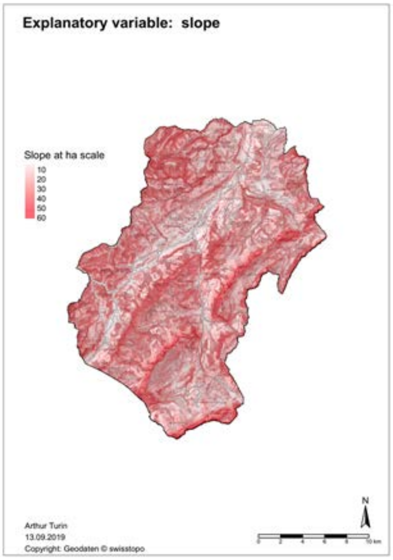
N
0 2 4 6 8 10 km


Explanatory variable: slope
Slope at ha scale
10
20
30
40
50
60
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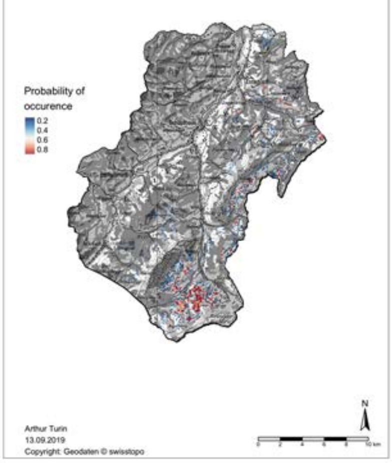
N
0 2 4 6 8 10 km

Appendix 3: Each of the 114 species SDMs.

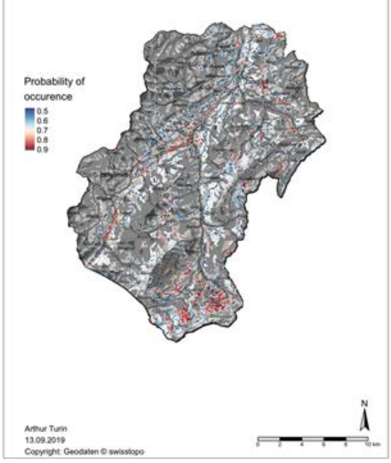
SDM for the species Agrostis canina

MTSPS threshold = 0.1393



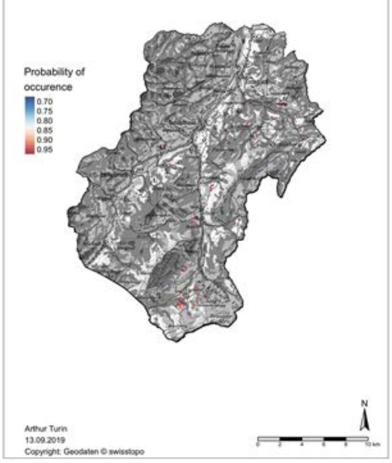
SDM for the species Alauda arvensis

MTSPS threshold = 0.473



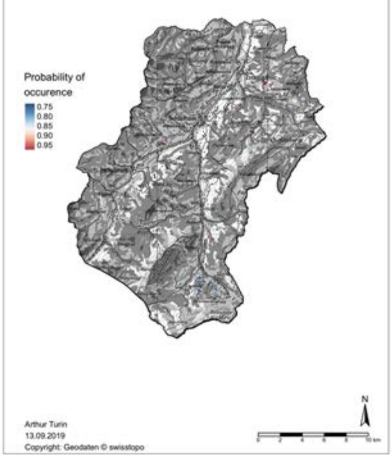
SDM for the species Aleurodiscus amorphus

MTSPS threshold = 0.6719



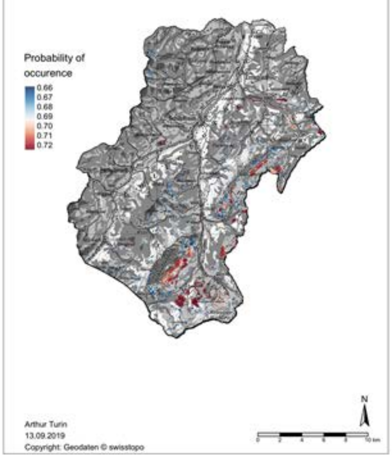
SDM for the species Amanita lividopallescens

MTSPS threshold = 0.7354



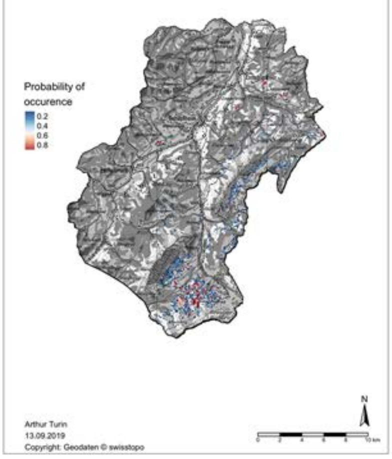
SDM for the species Anastrepta orcadensis

MTSPS threshold = 0.6579



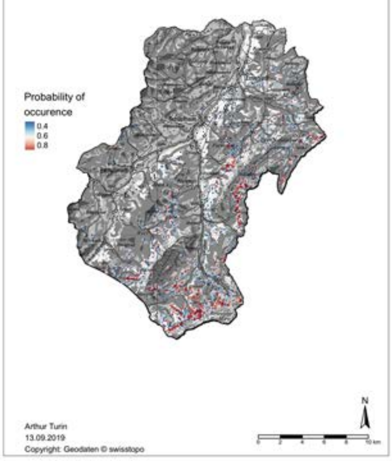
SDM for the species Andromeda polifolia

MTSPS threshold = 0.0759



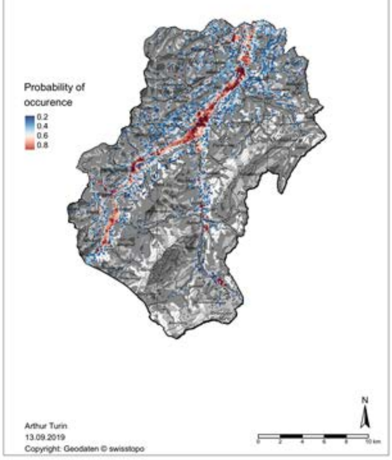
SDM for the species Anthus pratensis

MTSPS threshold = 0.2575



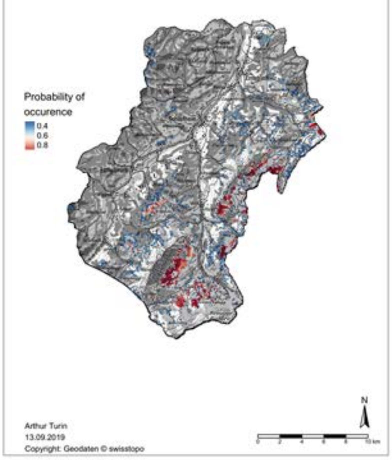
SDM for the species Apus apus

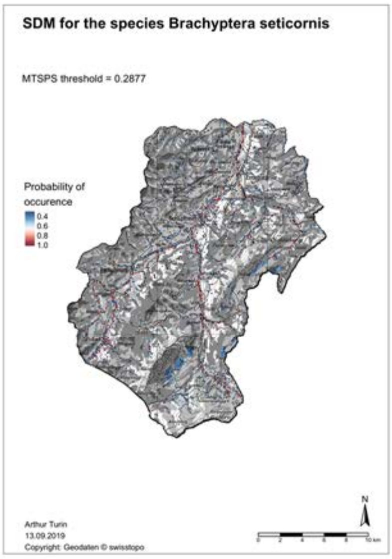
MTSPS threshold = 0.1792



SDM for the species Bonasa bonasia

MTSPS threshold = 0.2616




SDM for the species Brachyptera seticornis

MTSPS threshold = 0.2877

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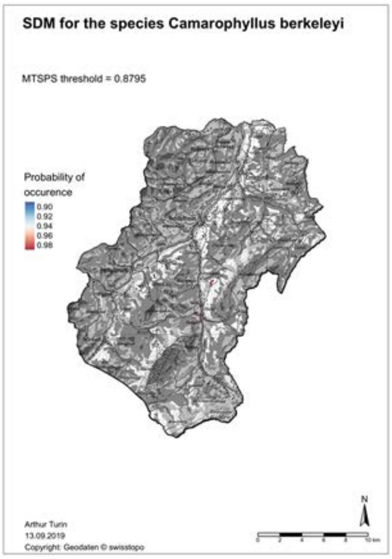
SDM for the species Camarophyllus berkeleyi

MTSPS threshold = 0.8795

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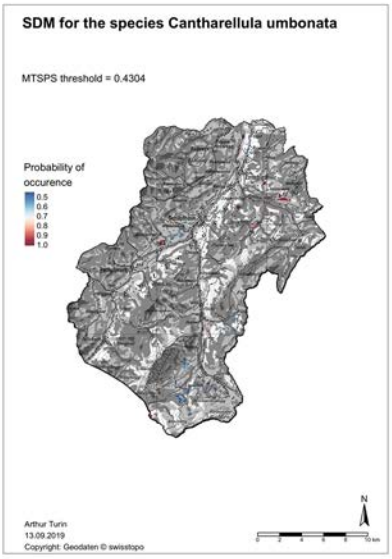
SDM for the species Cantharellula umbonata

MTSPS threshold = 0.4304

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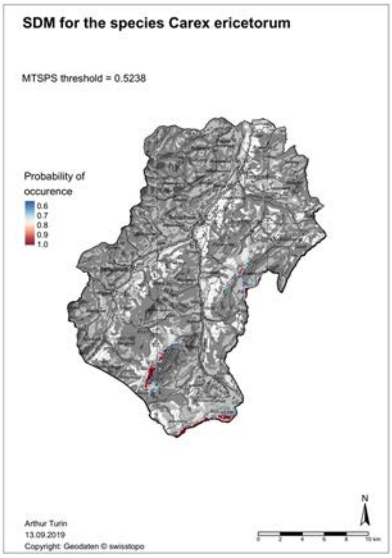
SDM for the species Carex ericetorum

MTSPS threshold = 0.5238

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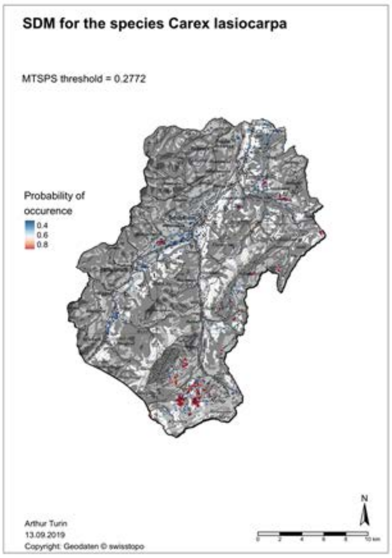
SDM for the species Carex lasiocarpa

MTSPS threshold = 0.2772

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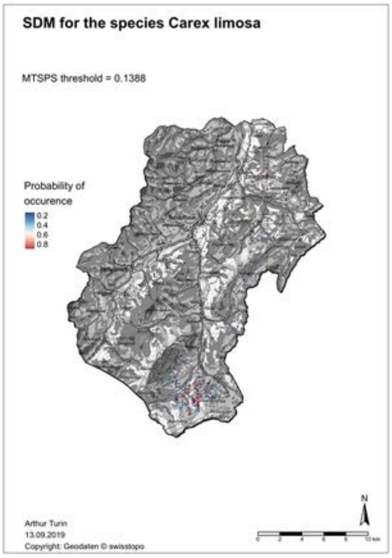
SDM for the species Carex limosa

MTSPS threshold = 0.1388

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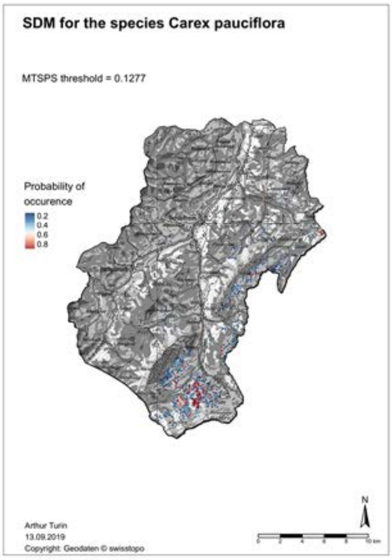
SDM for the species Carex pauciflora

MTSPS threshold = 0.1277

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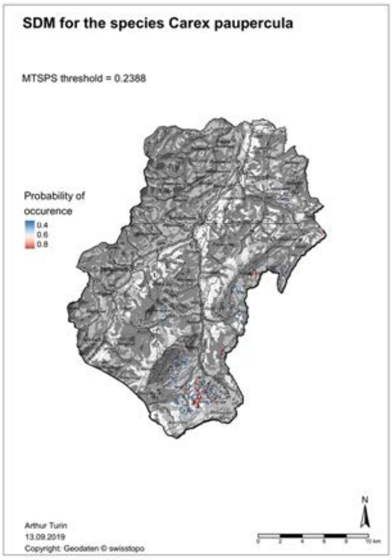
SDM for the species Carex paupercula

MTSPS threshold = 0.2388

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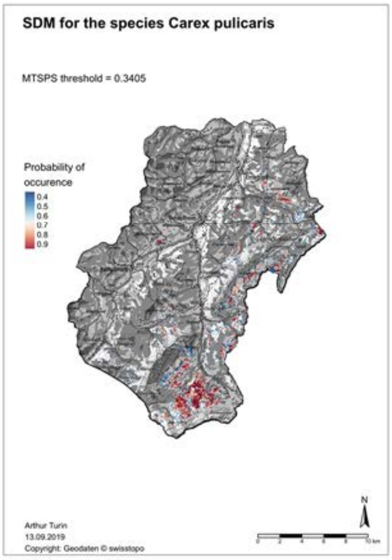
SDM for the species Carex pulicaris

MTSPS threshold = 0.3405

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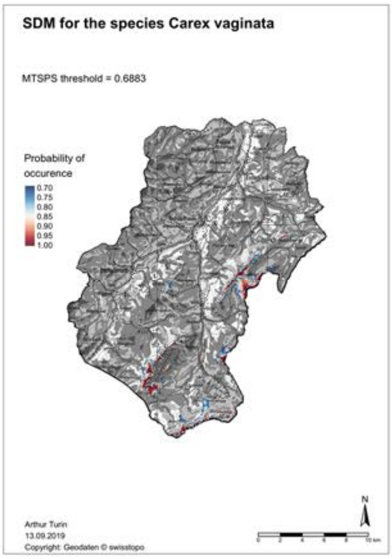

SDM for the species Carex vaginata

MTSPS threshold = 0.6883

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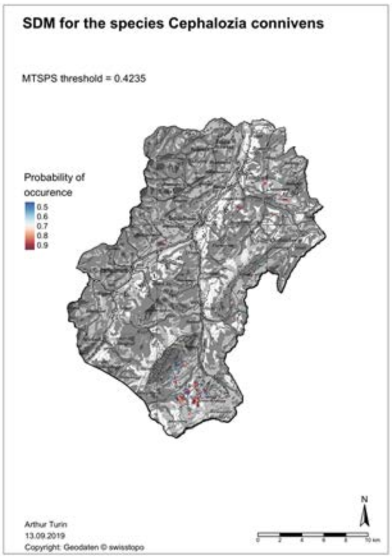

SDM for the species Cephalozia connivens

MTSPS threshold = 0.4235

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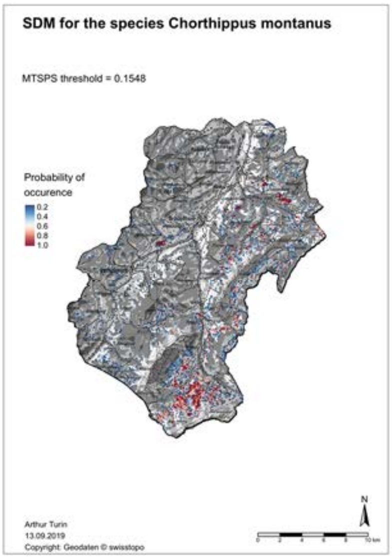

SDM for the species Chorthippus montanus

MTSPS threshold = 0.1548

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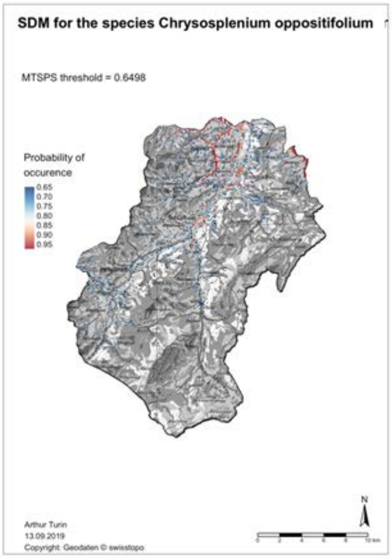

SDM for the species Chrysosplenium oppositifolium

MTSPS threshold = 0.6498

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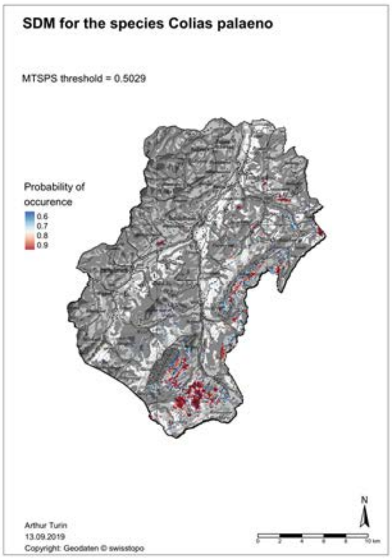

SDM for the species Colias palaeno

MTSPS threshold = 0.5029

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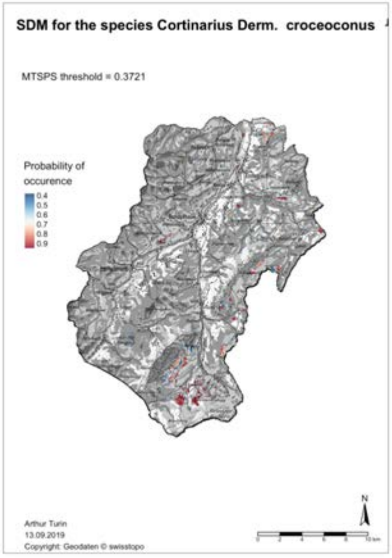

SDM for the species Cortinarius Derm. croceoconus

MTSPS threshold = 0.3721

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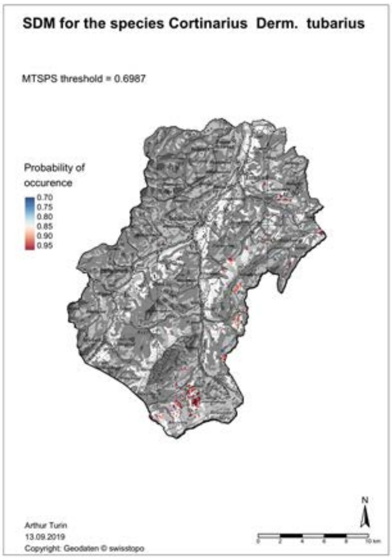

SDM for the species Cortinarius Derm. tubarius

MTSPS threshold = 0.6987

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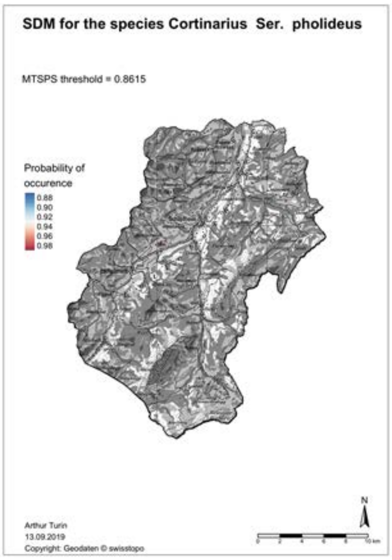

SDM for the species Cortinarius Ser. pholideus

MTSPS threshold = 0.8615

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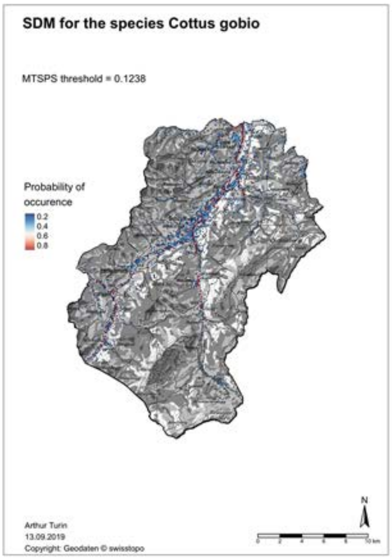

SDM for the species Cottus gobio

MTSPS threshold = 0.1238

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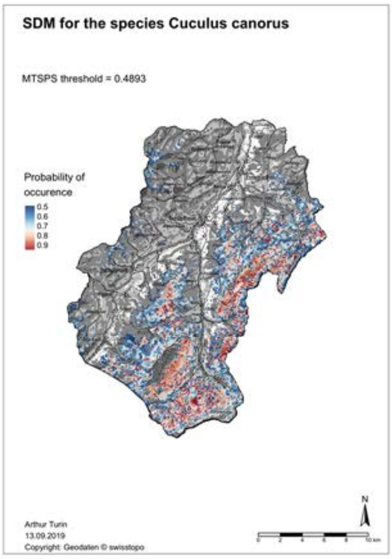
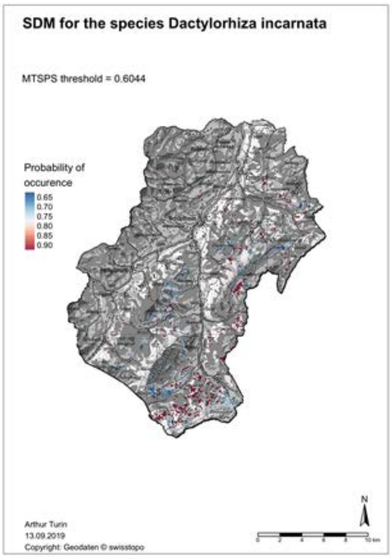
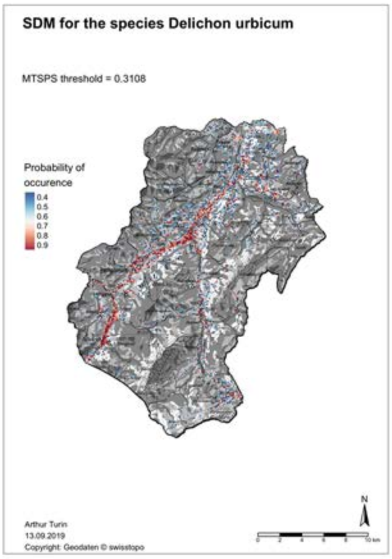

SDM for the species Cuculus canorus

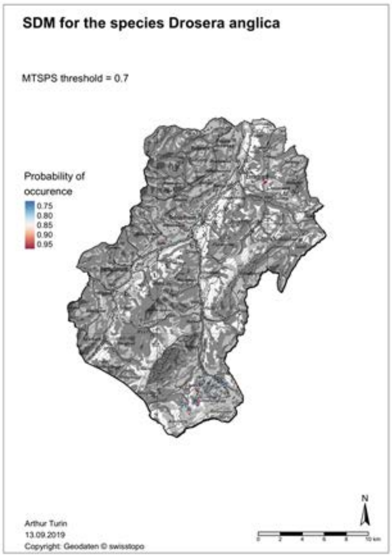
MTSPS threshold = 0.4893


SDM for the species Dactylorhiza incarnata

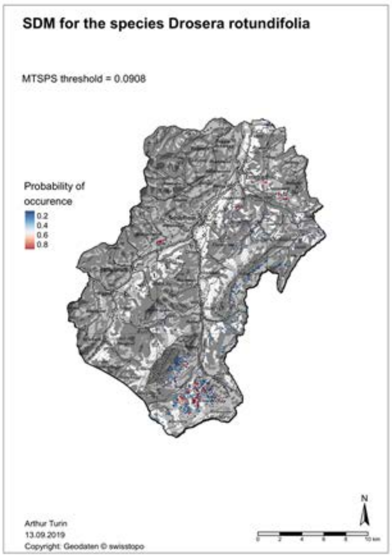
MTSPS threshold = 0.6044


SDM for the species Delichon urbicum

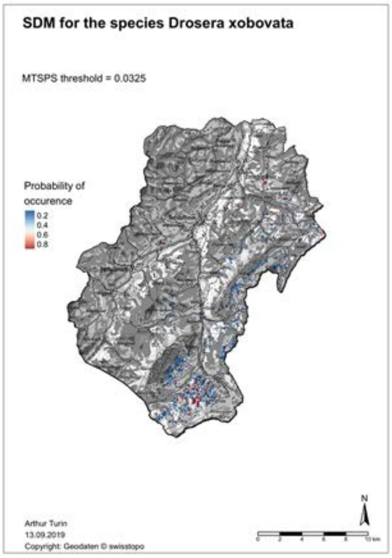
MTSPS threshold = 0.3108


SDM for the species Drosera anglica

MTSPS threshold = 0.7


SDM for the species Drosera rotundifolia

MTSPS threshold = 0.0908


SDM for the species Drosera xobovata

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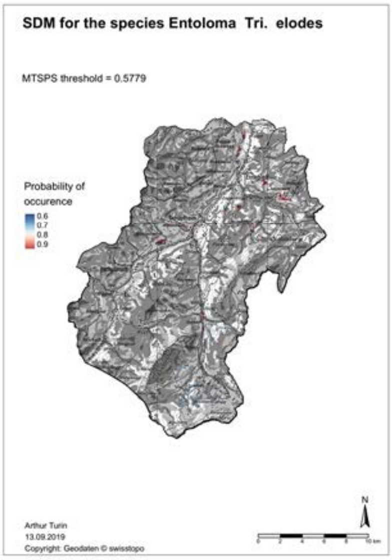
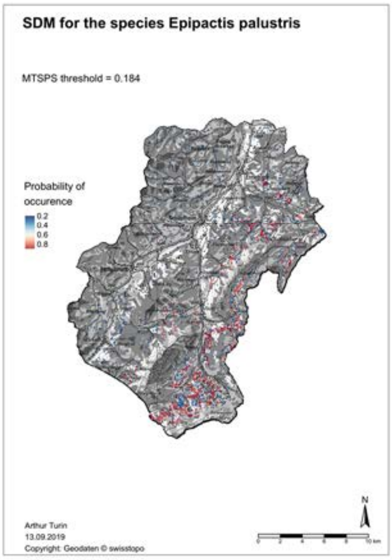

SDM for the species Entoloma Tri. elodes

MTSPS threshold = 0.5779


SDM for the species Epipactis palustris

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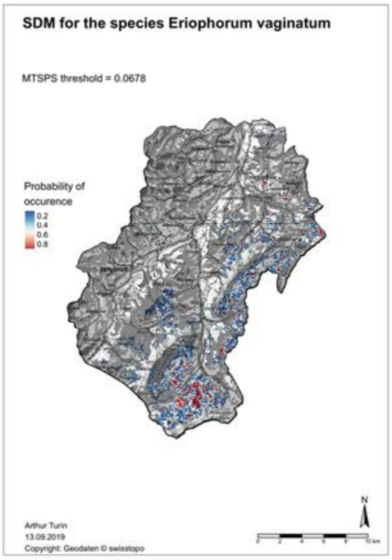
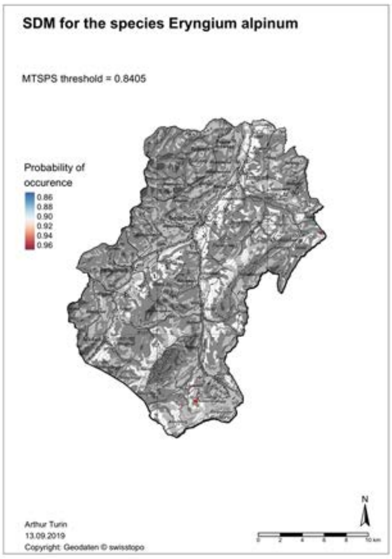
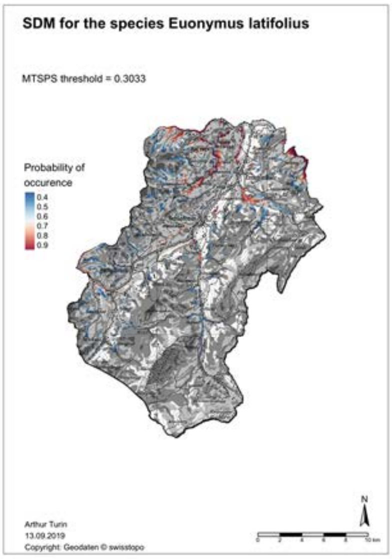

SDM for the species Eriophorum vaginatum

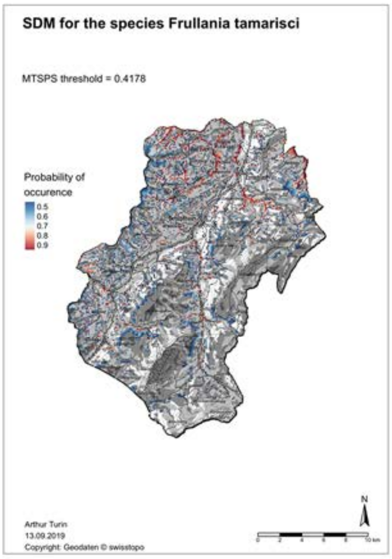
MTSPS threshold = 0.0678


SDM for the species Eryngium alpinum

MTSPS threshold = 0.8405


SDM for the species Euonymus latifolius

MTSPS threshold = 0.3033


SDM for the species Frullania tamarisci

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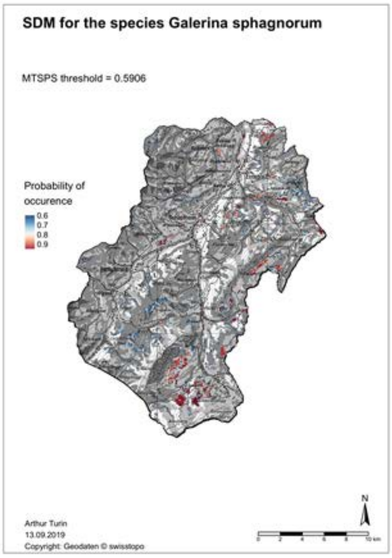
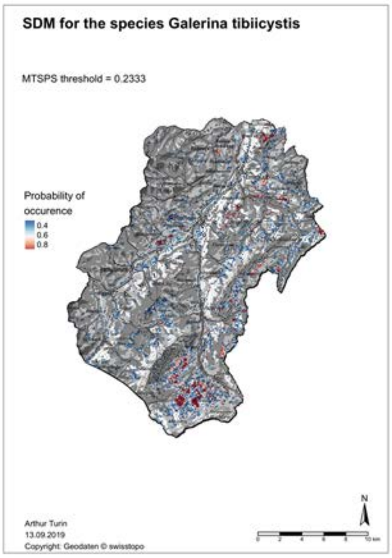
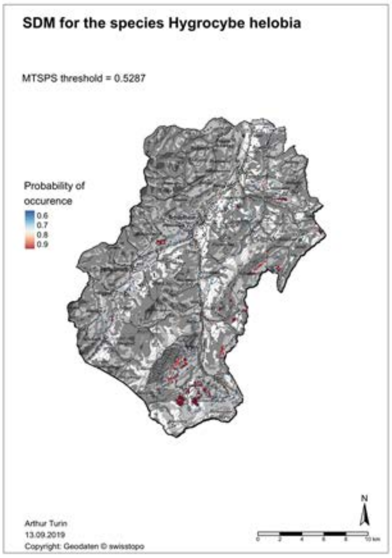

SDM for the species Galerina sphagnorum

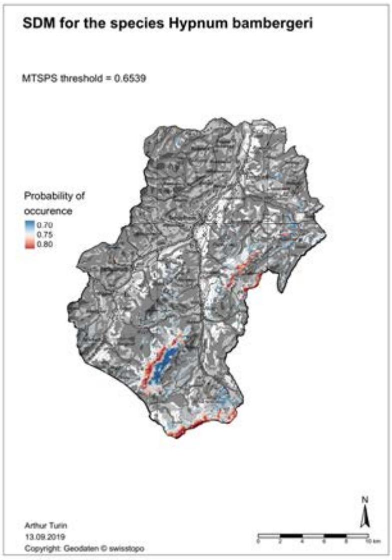
MTSPS threshold = 0.5906


SDM for the species Galerina tibiicystis

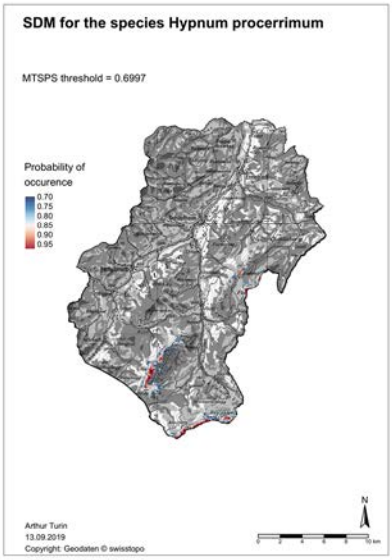
MTSPS threshold = 0.2333


SDM for the species Hygrocybe helobia

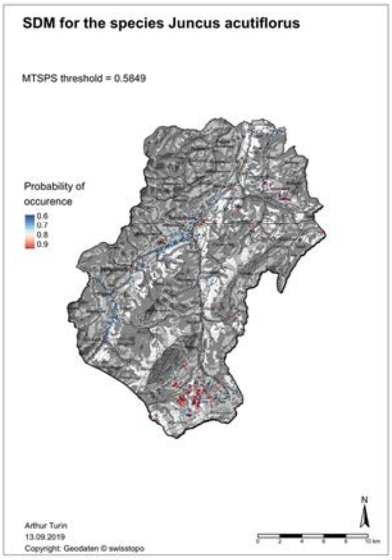
MTSPS threshold = 0.5287


SDM for the species Hypnum bambergeri

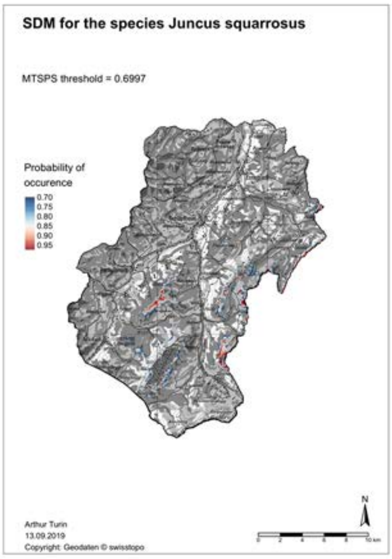
MTSPS threshold = 0.6539


SDM for the species Hypnum procerrimum

MTSPS threshold = 0.6997

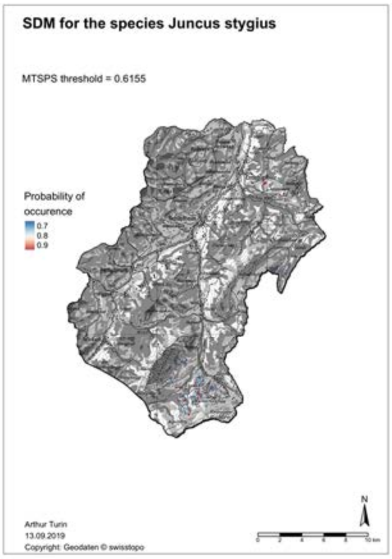

SDM for the species Juncus acutiflorus

MTSPS threshold = 0.5849



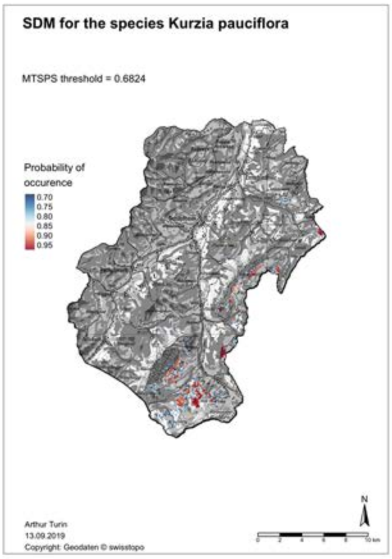
SDM for the species Juncus squarrosus

MTSPS threshold = 0.6997



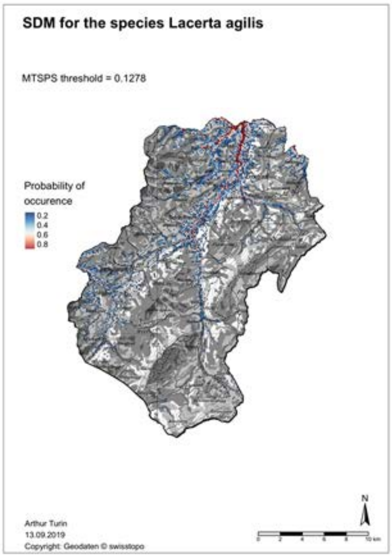
SDM for the species Juncus stygius

MTSPS threshold = 0.6155



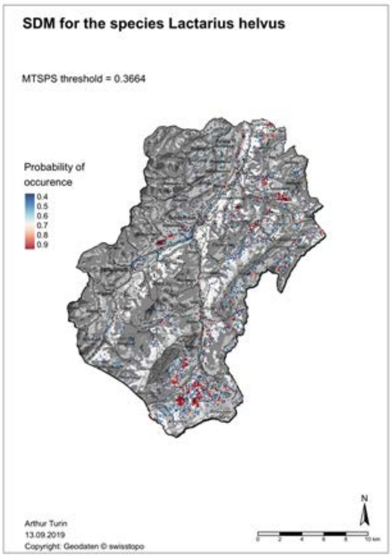
SDM for the species Kurzia pauciflora

MTSPS threshold = 0.6824



SDM for the species Lacerta agilis

MTSPS threshold = 0.1278



SDM for the species Lactarius helvus

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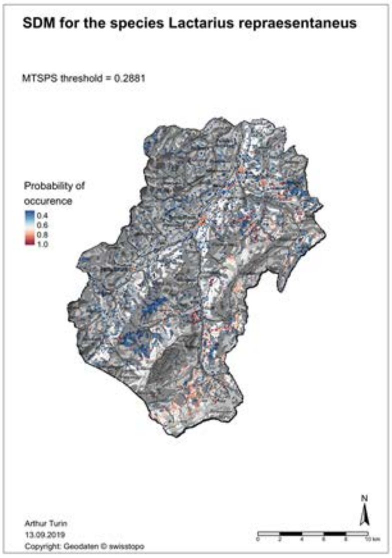
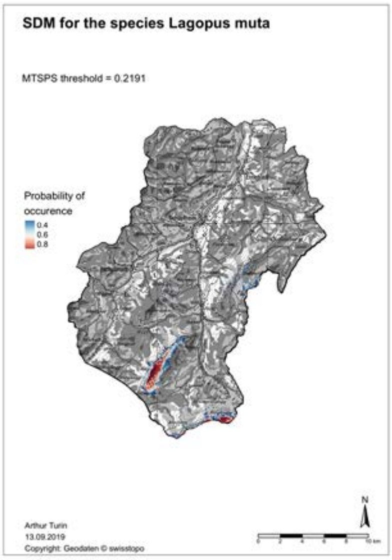


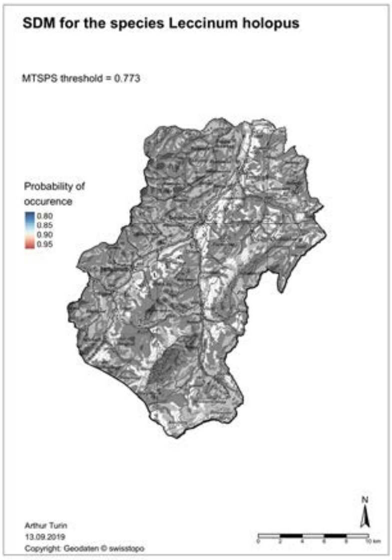
SDM for the species Lactarius repraesentaneus

MTSPS threshold = 0.2881



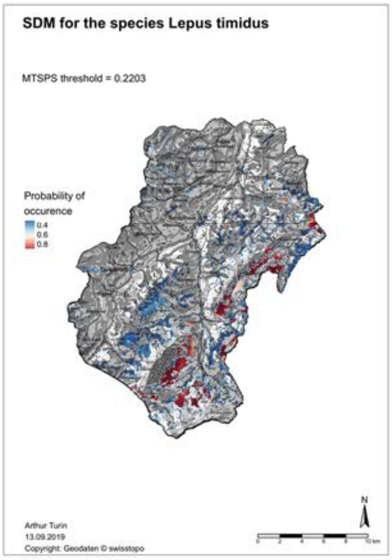
SDM for the species Lagopus muta

MTSPS threshold = 0.2191



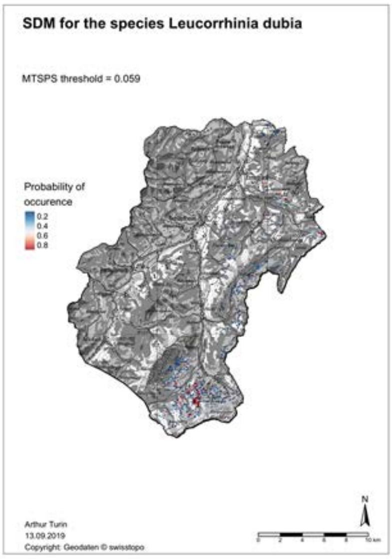
SDM for the species Leccinum holopus

MTSPS threshold = 0.773



SDM for the species Lepus timidus

MTSPS threshold = 0.2203



SDM for the species Leucorrhinia dubia

MTSPS threshold = 0.059

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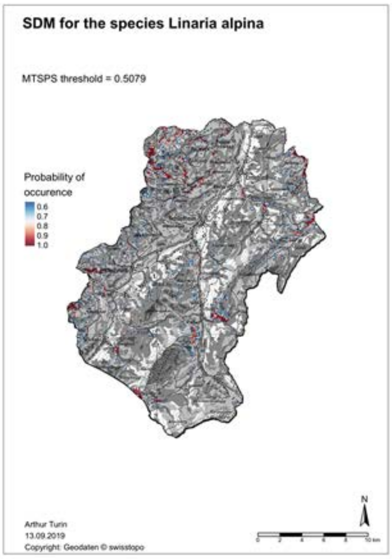

SDM for the species Linaria alpina

MTSPS threshold = 0.5079

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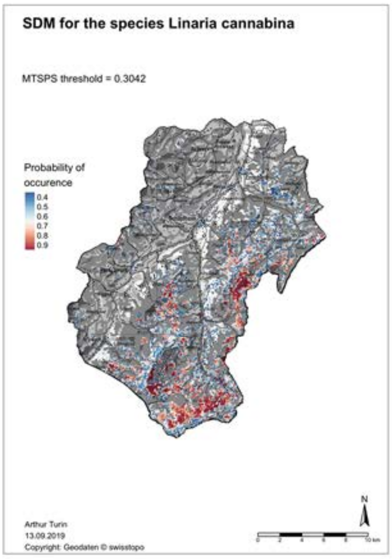

SDM for the species Linaria cannabina

MTSPS threshold = 0.3042

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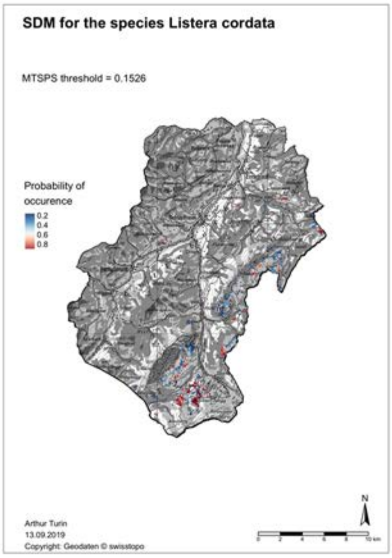

SDM for the species Listera cordata

MTSPS threshold = 0.1526

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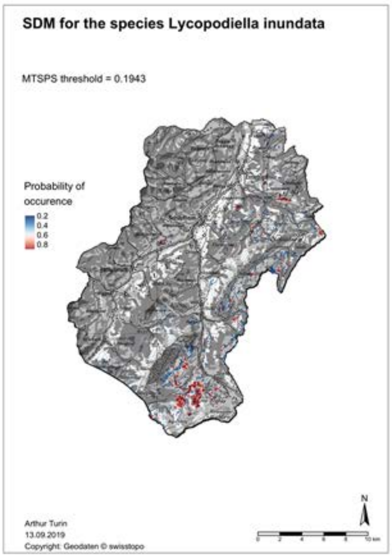

SDM for the species Lycopodiella inundata

MTSPS threshold = 0.1943

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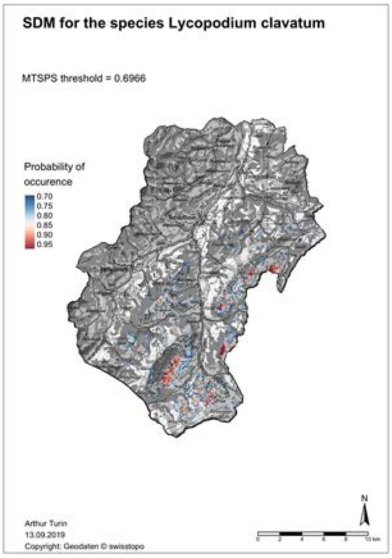

SDM for the species Lycopodium clavatum

MTSPS threshold = 0.6966

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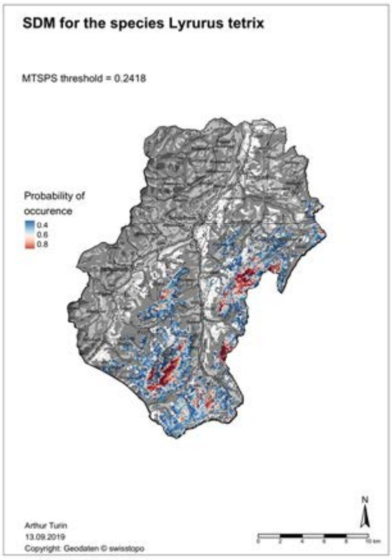

SDM for the species Lyrurus tetrix

MTSPS threshold = 0.2418

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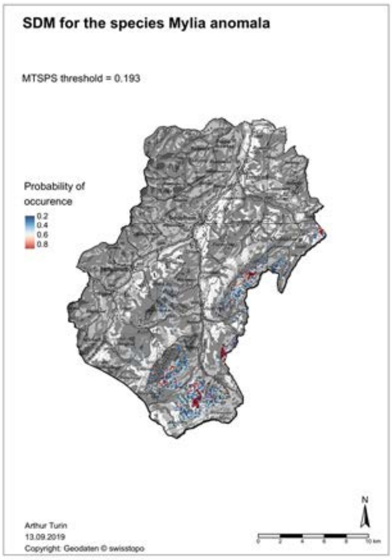

SDM for the species Mylia anomala

MTSPS threshold = 0.193

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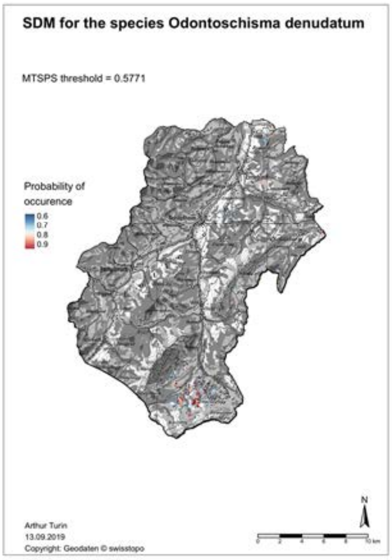

SDM for the species Odontoschisma denudatum

MTSPS threshold = 0.5771

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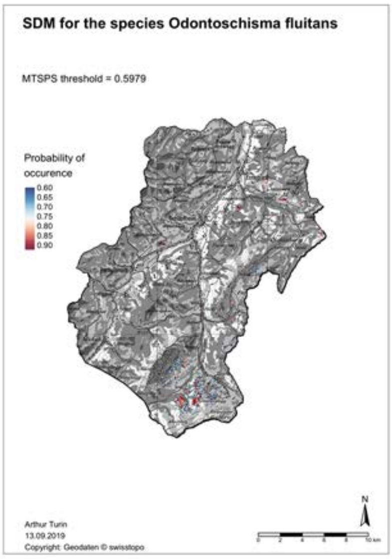
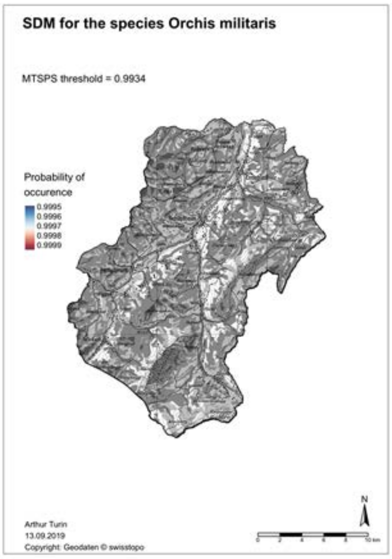

SDM for the species Odontoschisma fluitans

MTSPS threshold = 0.5979


SDM for the species Orchis militaris

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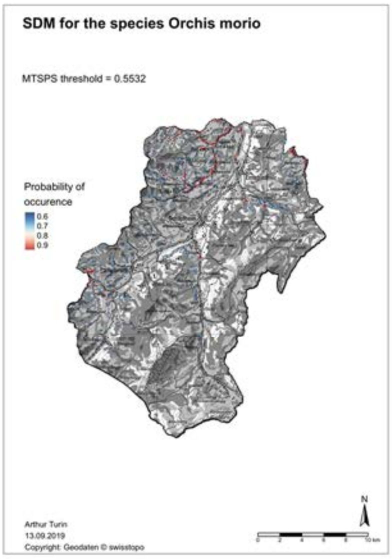
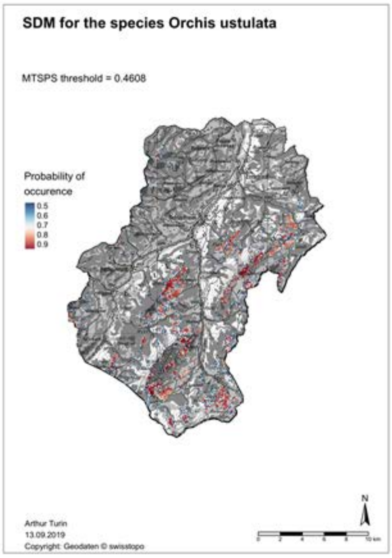

SDM for the species Orchis morio

MTSPS threshold = 0.5532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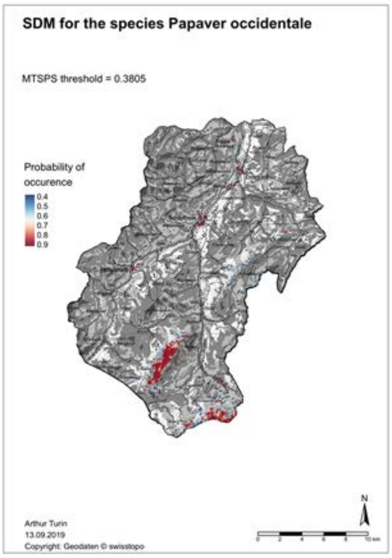
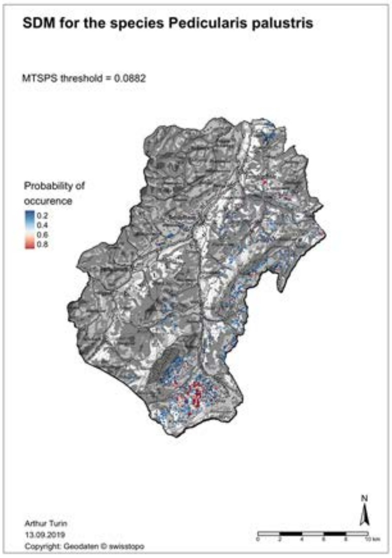

SDM for the species Papaver occidentale

MTSPS threshold = 0.3805


SDM for the species Pedicularis palustris

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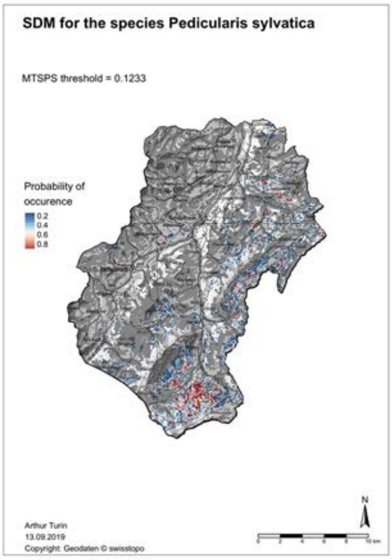
SDM for the species Pedicularis sylvatica

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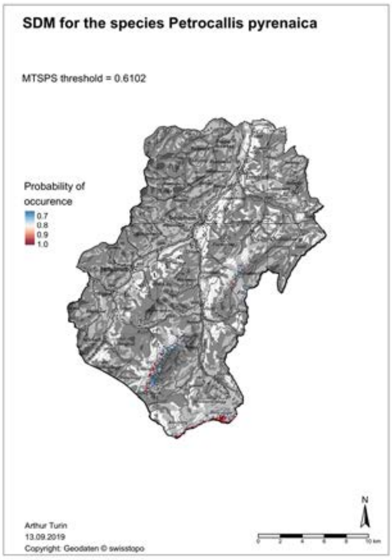
SDM for the species Petrocallis pyrenaica

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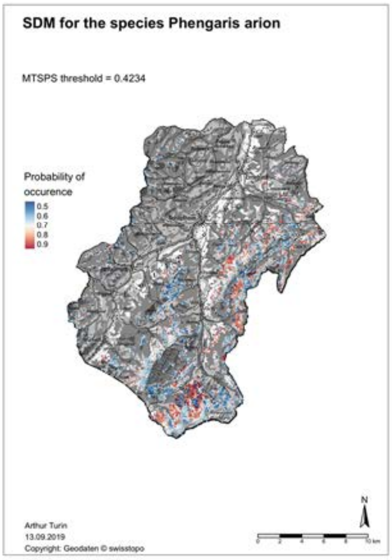
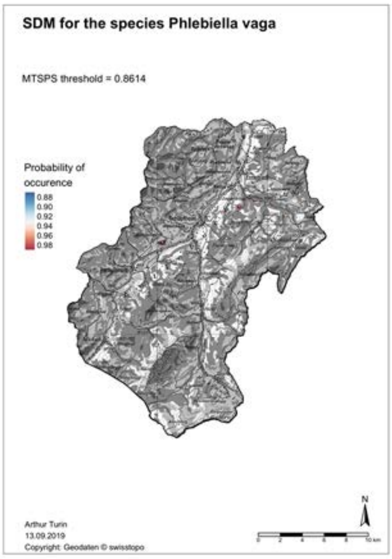

SDM for the species Phengaris arion

MTSPS threshold = 0.4234


SDM for the species Phlebiella vaga

MTSPS threshold = 0.8614

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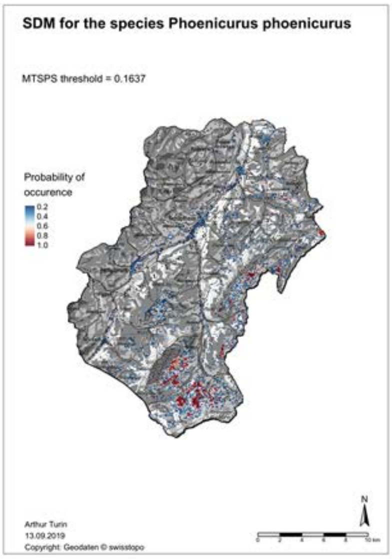
SDM for the species Phoenicurus phoenicurus

MTSPS threshold = 0.1637

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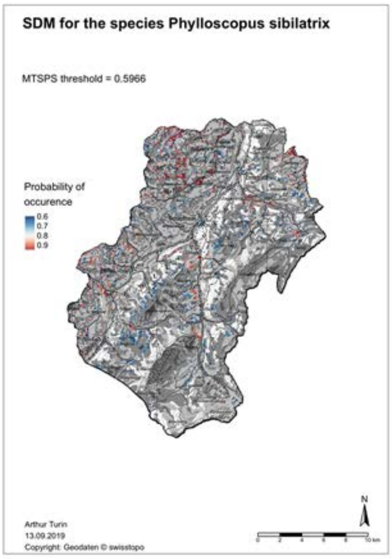
SDM for the species Phylloscopus sibilatrix

MTSPS threshold = 0.5966

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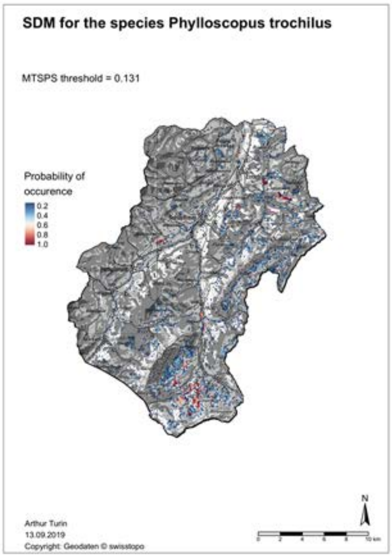
SDM for the species Phylloscopus trochilus

MTSPS threshold = 0.131

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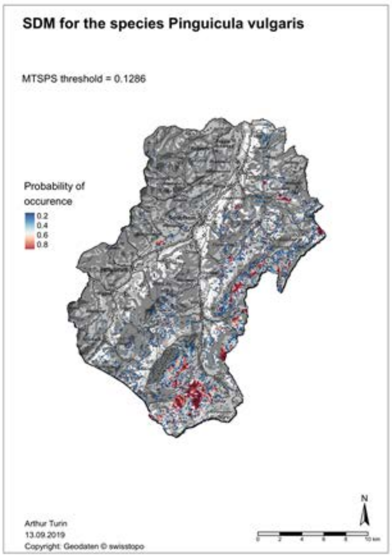
SDM for the species Pinguicula vulgaris

MTSPS threshold = 0.1286

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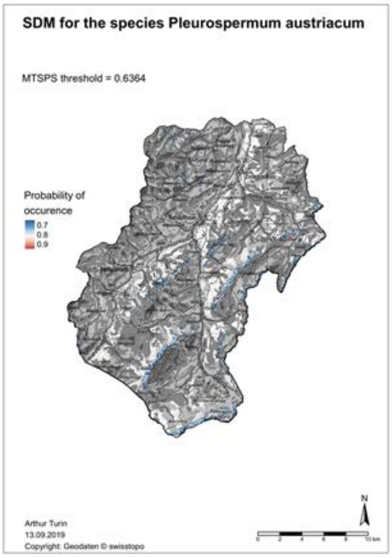
SDM for the species Pleurospermum austriacum

MTSPS threshold = 0.6364

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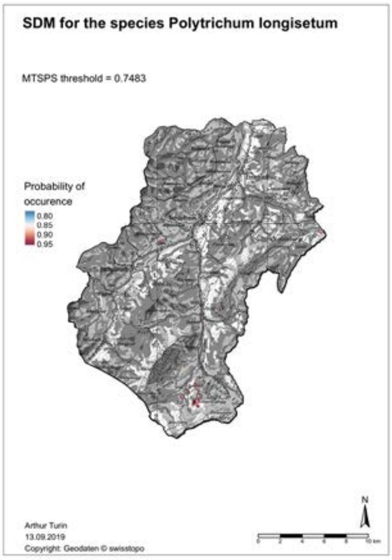
SDM for the species Polytrichum longisetum

MTSPS threshold = 0.7483

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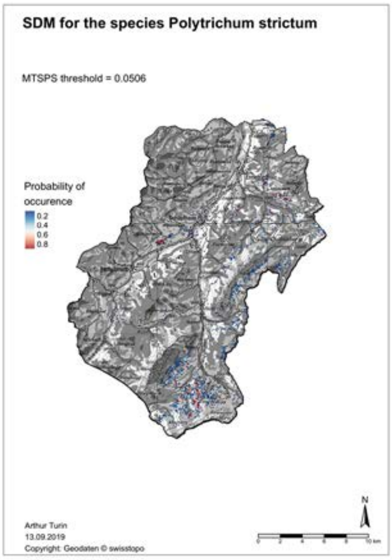
SDM for the species Polytrichum strictum

MTSPS threshold = 0.0506

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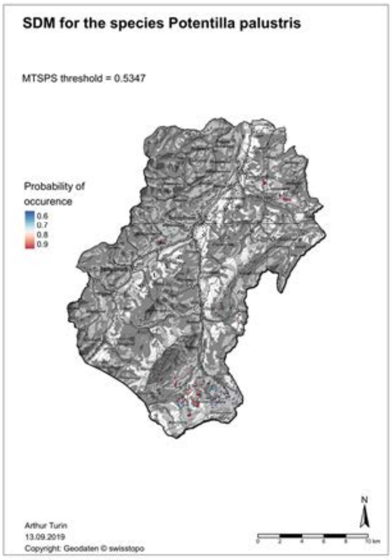
SDM for the species Potentilla palustris

MTSPS threshold = 0.5347

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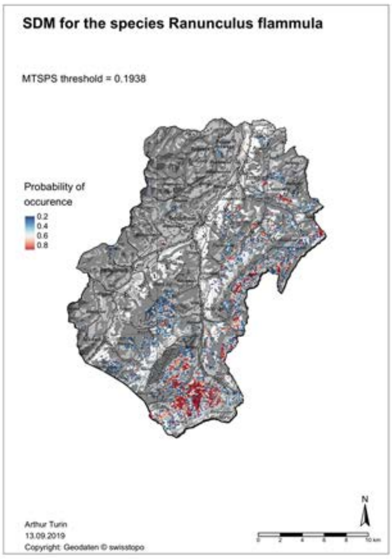

SDM for the species Ranunculus flammula

MTSPS threshold = 0.1938

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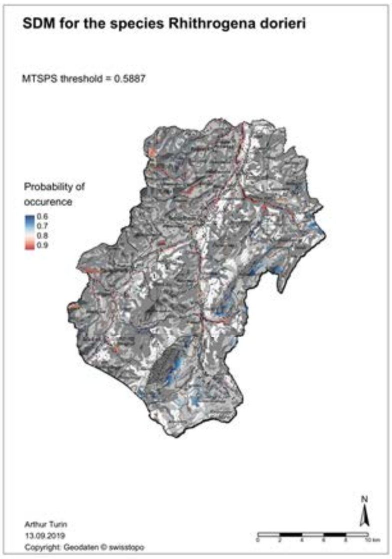

SDM for the species Rhithrogena dorieri

MTSPS threshold = 0.5887

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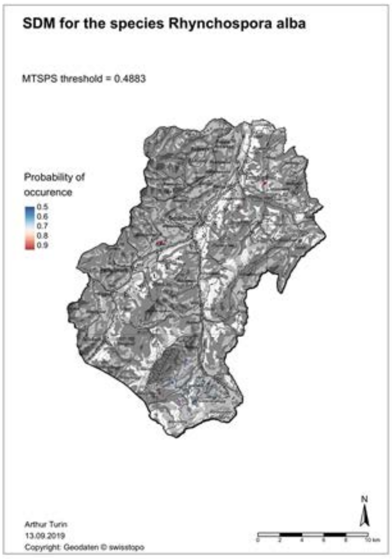

SDM for the species Rhynchospora alba

MTSPS threshold = 0.4883

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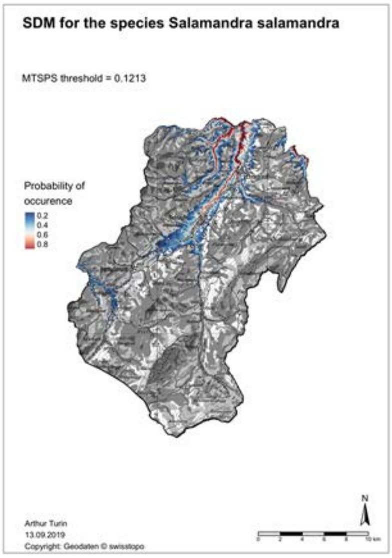

SDM for the species Salamandra salamandra

MTSPS threshold = 0.1213

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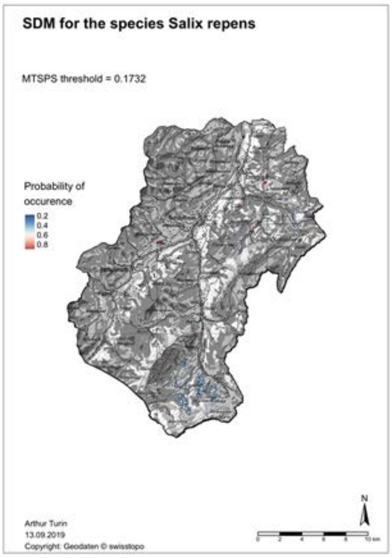

SDM for the species Salix repens

MTSPS threshold = 0.1732

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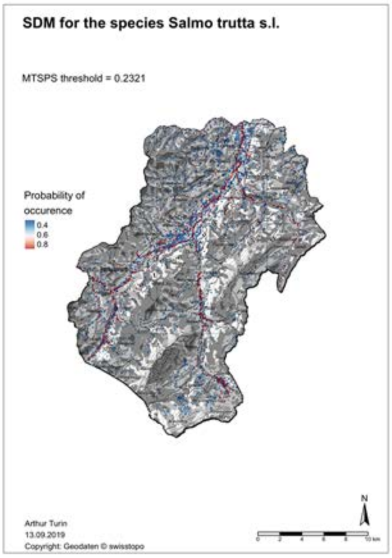

SDM for the species Salmo trutta s.l.

MTSPS threshold = 0.2321

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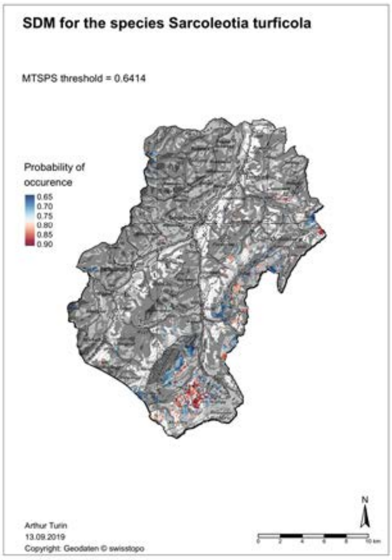

SDM for the species Sarcoleotia turficola

MTSPS threshold = 0.6414

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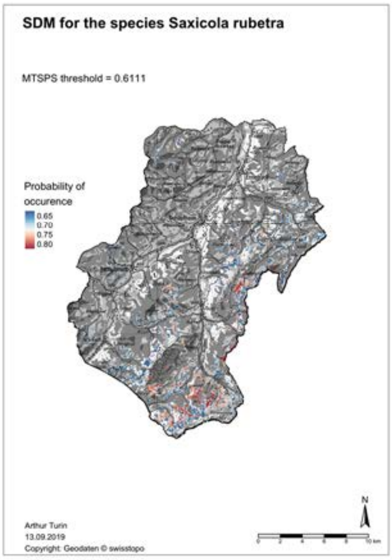

SDM for the species Saxicola rubetra

MTSPS threshold = 0.6111

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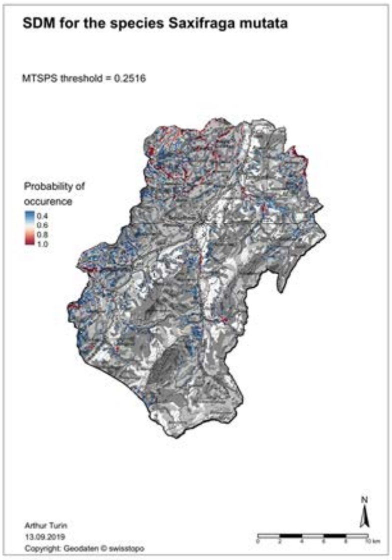

SDM for the species Saxifraga mutata

MTSPS threshold = 0.2516

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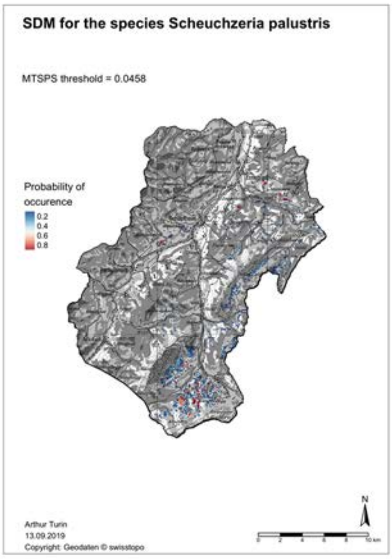
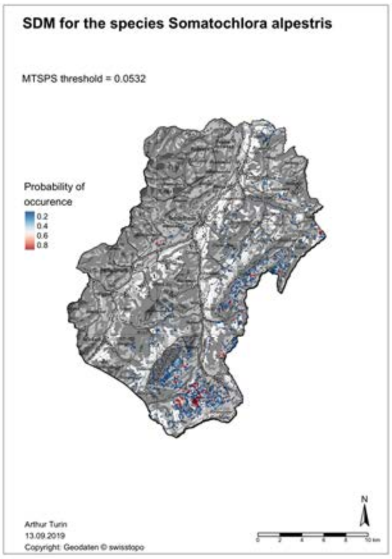


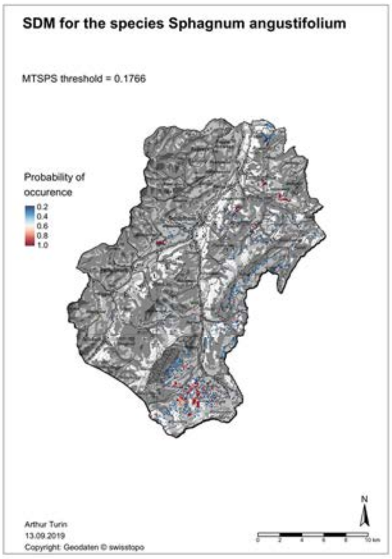
SDM for the species Scheuchzeria palustris

MTSPS threshold = 0.0458



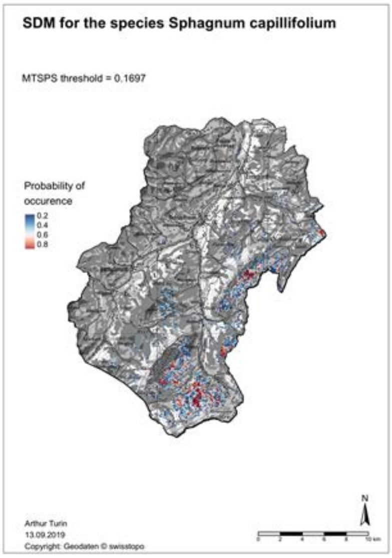
SDM for the species Somatochlora alpestris

MTSPS threshold = 0.0532



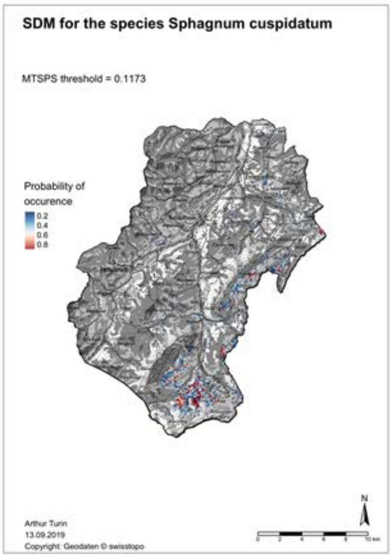
SDM for the species Sphagnum angustifolium

MTSPS threshold = 0.1766



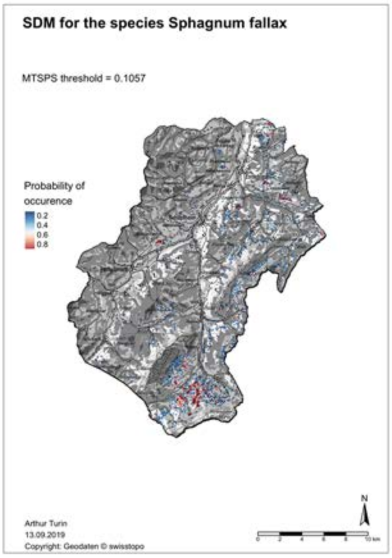
SDM for the species Sphagnum capillifolium

MTSPS threshold = 0.1697



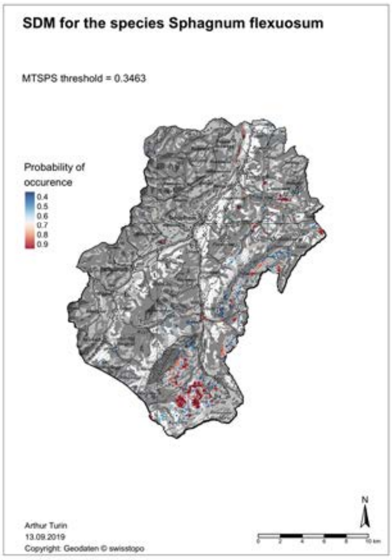
SDM for the species Sphagnum cuspidatum

MTSPS threshold = 0.1173



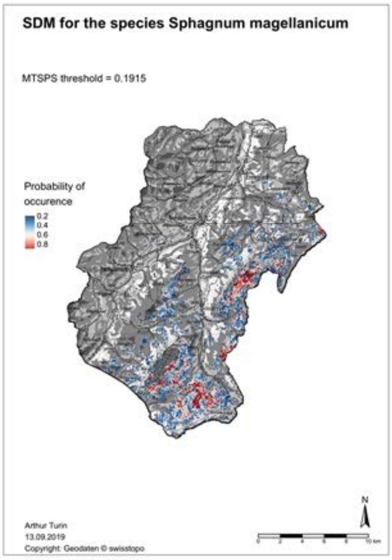
SDM for the species Sphagnum fallax

MTSPS threshold = 0.1057



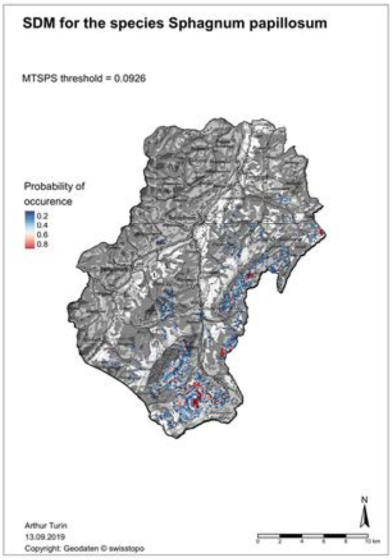
SDM for the species Sphagnum flexuosum

MTSPS threshold = 0.3463



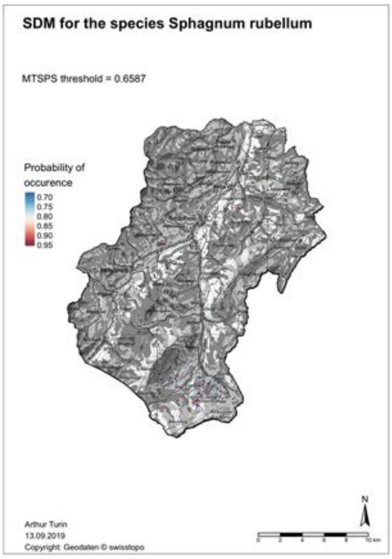
SDM for the species Sphagnum magellanicum

MTSPS threshold = 0.1915

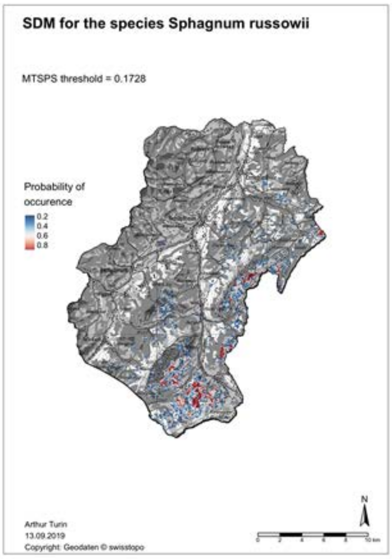


SDM for the species Sphagnum papillosum

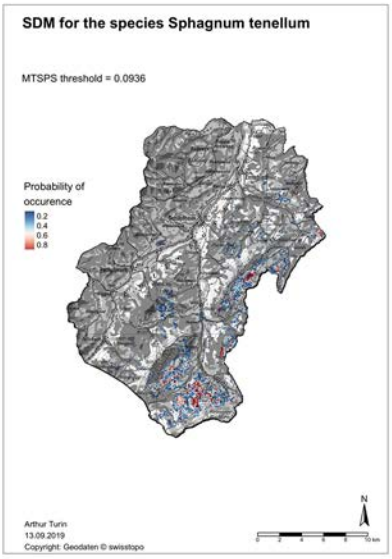
MTSPS threshold = 0.0926


SDM for the species Sphagnum rubellum

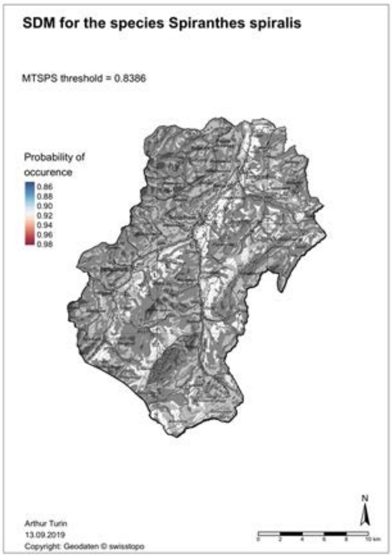
MTSPS threshold = 0.6587


SDM for the species Sphagnum russowii

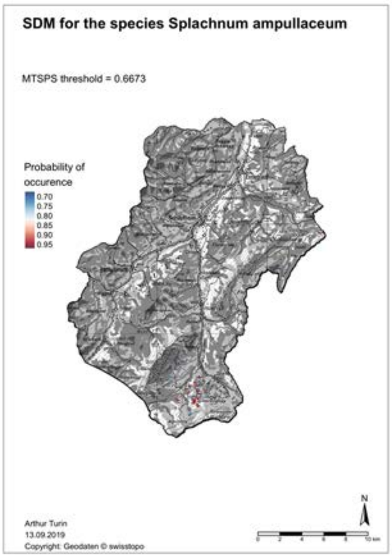
MTSPS threshold = 0.1728


SDM for the species Sphagnum tenellum

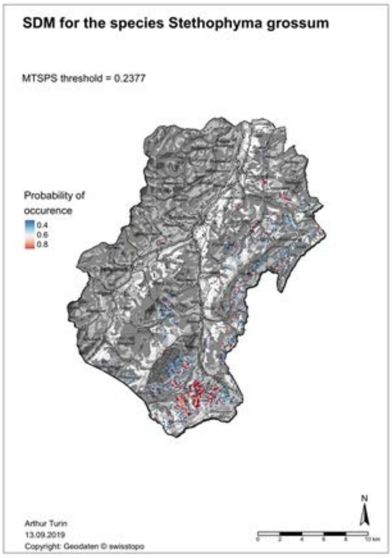
MTSPS threshold = 0.0936


SDM for the species Spiranthes spiralis

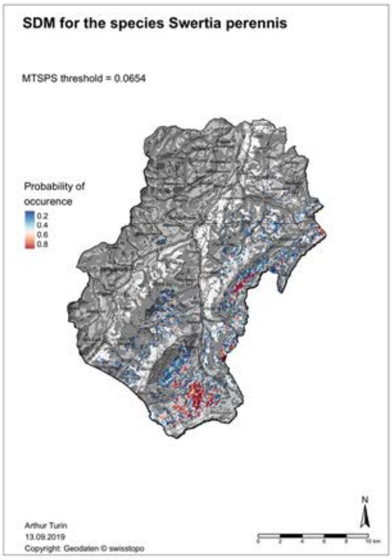
MTSPS threshold = 0.8386


SDM for the species Splachnum ampullaceum

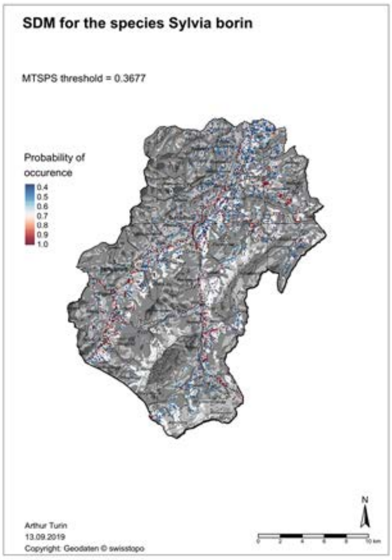
MTSPS threshold = 0.6673


SDM for the species Stethophyma grossum

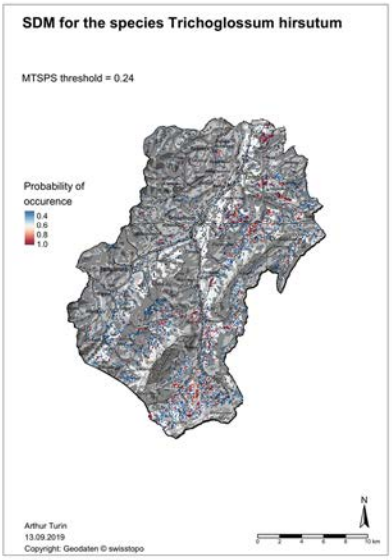
MTSPS threshold = 0.2377


SDM for the species Swertia perennis

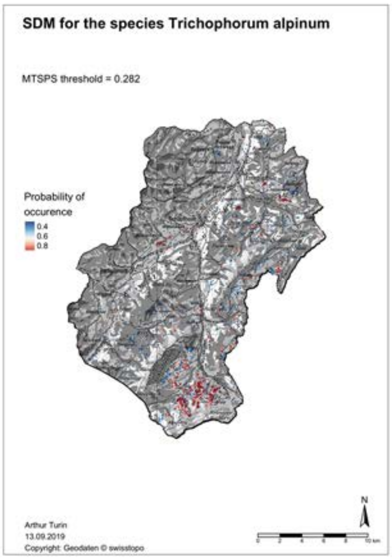
MTSPS threshold = 0.0654


SDM for the species Sylvia borin

MTSPS threshold = 0.3677


SDM for the species Trichoglossum hirsutum

MTSPS threshold = 0.24



SDM for the species Trichophorum alpinum

MTSPS threshold = 0.282

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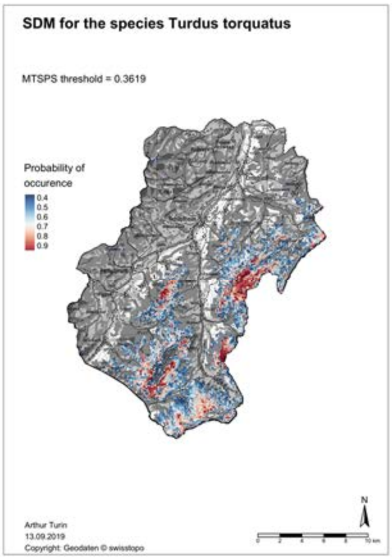

SDM for the species Turdus torquatus

MTSPS threshold = 0.3619

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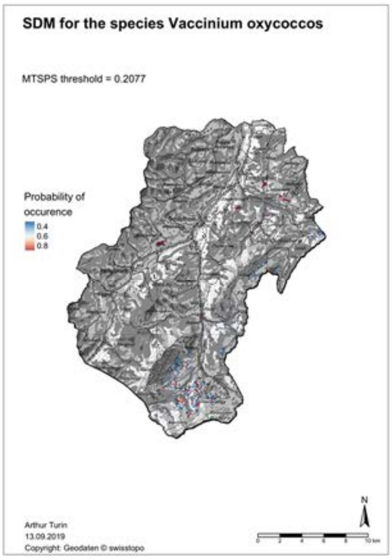

SDM for the species Vaccinium oxycoccos

MTSPS threshold = 0.2077

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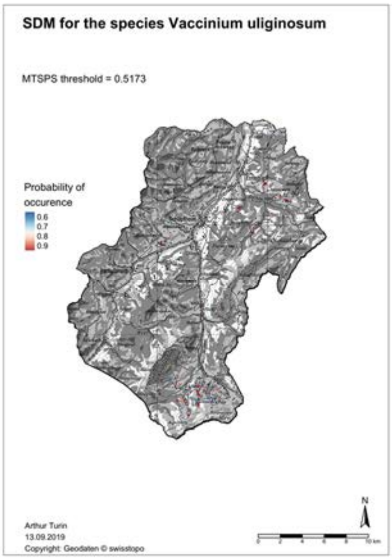

SDM for the species Vaccinium uliginosum

MTSPS threshold = 0.5173

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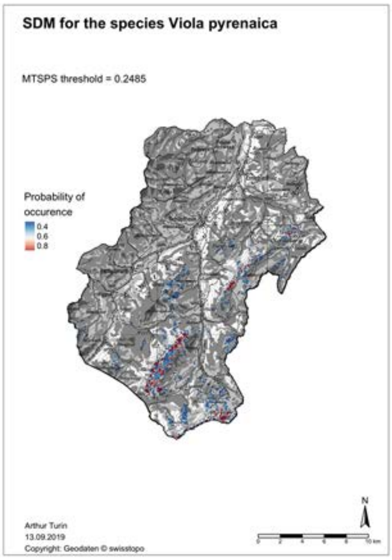

SDM for the species Viola pyrenaica

MTSPS threshold = 0.2485

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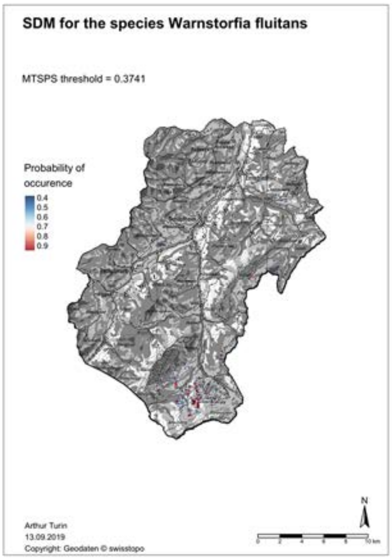

SDM for the species Warnstorfia fluitans

MTSPS threshold = 0.3741

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Appendix 4: Marxan Input File

General Parameters	
VERSION	0.1
BLM	0.006410809
PROP	0
RANDSEED	-1
BESTSCORE	0
NUMREPS	10 0
Annealing Parameters	
NUMITNS	10000000
STARTTEMP	1
COOLFAC	0
NUMTEMP	10000
Cost Threshold	
COSTTRESH	0
THRESHPEN1	0
THRESHPEN2	0
Input Files	
INPUTDIR	input
SPECNAME	spec.dat
PUNAME	pu.dat
PUVSPRNAME	puvspr.dat
BOUNDNAME	bound.dat
Save Files	
SCENNAME	calibrated
SAVERUN	0
SAVEBEST	2
SAVESUMMARY	2
SAVESCEN	0
SAVETARGMET	2
SAVESUMSOLN	0
SAVELOG	0
SAVESNAPSTEPS	0
SAVESNAPCHANGES	0
SAVESNAPFREQUENCY	0
OUTPUTDIR	output
Program control	
RUNMODE	1
MISSLEVEL	1
ITIMPTYPE	1
HEURTYPE	1
CLUMPTYPE	0
VERBOSITY	3