Grassland biodiversity indicators in the Western Swiss Plateau – Modelling possible impacts of climate vs. management changes

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Abstract

Agricultural intensification and climate change are among the main causes for current biodiversity losses. The effects of environmental changes on species richness may be assessed with statistical modelling approaches. In this study, a two-part hurdle model was implemented to predict present and future distribution patterns of plant richness in grasslands within the catchment of the Broye river, an intensively managed area in the Western Swiss Plateau. This approach allowed identifying environmental factors affecting significantly the presence and/or abundance of selected species. Mean winter temperatures and the intensity of pasture management were very significant drivers over all groups of species. These predictors were thus used to define future climatic and land use scenarios. An extensification of grasslands (20% of pastures area from intensive to extensive) under warmer conditions (+ 2° C in mean winter temperature) resulted to be a particularly profitable strategy for the highland of the Broye region in terms of species richness. Moreover, we conclude that the incorporation of land use data and stakeholder-based scenarios in species richness modelling approaches could substantially improve the identification and implementation of future biodiversity conservation areas.

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1. Introduction

1.1 Research Motivation

Biodiversity at a global scale is changing rapidly due to climate change and human activities. Loss, degradation and fragmentation of natural habitats, overexploitation of natural resources, increasing nutrient inputs, invasive alien species and global warming are some of the major causes for biodiversity loss (Secretariat of the Convention on Biological Diversity, 2014). Modern agriculture striving maximisation in productivity, requires the homogenization of the environment's structure over vast areas and depends only on a handful of varieties (for its major crops) and on external nutrients inputs (Altieri, 1999). This type of intensive agriculture is one of the main forms of pressure on biodiversity. On the other side, species diversity plays a key role in agroecosystems (Reidsma et al., 2006). Biodiversity loss in agricultural landscapes affects not only the production of food, but also a wide range of ecological services (ESS). High levels of biodiversity in agroecosystems provide a large variety of beneficial ESS such as pollination, soil formation, invasion resistance, and human well-being in general due to microclimate regulation, water purification, cultural values, etc. (Altieri, 1999; Herzog et al., 2012, BAFU, 2017a). However, modern intense agricultural management has been growing worldwide during the past decades and considering the actual population growth, it is likely to continue (Reidsma et al., 2006).

Since the post-war period, agriculture policies in Switzerland support production growth and rationalization in order to ensure national food security. Technical progress (e.g. mechanization, mineral fertilizers, pesticides etc.) and economic development led to an intensification of grass- and arable land (BAFU & BLW, 2008). This evolution reduced the richness in plant and animal species especially in the lowlands, where suitable habitats have been strongly reduced. Population sizes have fallen and today, almost half of the habitats and one third of the plant and animal species are endangered (BAFU & BLW, 2008; BAFU, 2017a). Since the 1990's, the conservation and promotion of biodiversity in agriculture has become an explicit target of the Swiss agrarian policy (BAFU & BLW, 2013). Nowadays, protection of biological diversity is stipulated in the Swiss federal constitution and in international treaties (BAFU, 2017a). On the 6th of September 2017, the Federal Council adopted the action plan of the Swiss Biodiversity Strategy, which aims to ensure the long-term conservation and promotion of biodiversity, ecosystem services and habitats (BAFU, 2017b). This highlights the social awareness for past, present and future efforts in preserving biodiversity.

Conservation strategies aiming to maintain high levels of diversity in the future, need to consider the changing climatic conditions evolving from anthropogenic greenhouse gas emissions. Biodiversity will get into additional pressure through climate change at all stages, from organism to biome (Bellard et al, 2012). In order to develop adequate adaption strategies, a better understanding of the response of species richness to changing temperature and precipitations regimes is needed (BAFU, 2017a). To efficiently invest the available resources for conservation, it is crucial to foster the knowledge of how ecosystems and species diversity will respond in future to different land management and climate change scenarios.

One of the main goals in conservation ecology research is to understand and model factors and processes generating patterns in species composition, so that if conditions alter, changes in the patterns can be predicted (D'Amen et al., 2017). In recent years, many studies investigated the effects of climate change on future biodiversity, mostly at coarser (global or continental) spatial scales (i.e. Root et al., 2003; Adler et al., 2009; Bellard et al., 2012). Furthermore, impacts of agriculture on species richness has been studied by McLaughlin & Mineau, 1995; Plantureux *et al*., 2005; Reidsma *et al*., 2006. Although several studies already investigated the response of species richness to both climate and land use changes (Pearson et al., 2004; Pompe et al., 2008; Steinmann et al., 2009), less efforts have been put into the prediction of biodiversity shifts at regional, landscape or community scale (Shoyama, & Yamagata, 2014; Mossman et al. 2015; Schirpke et al., 2017). Research in this field provides important tools for implementing biodiversity conservation strategies, as these decisions are in many cases a matter of regional political stakeholders. This study focusses on the consideration of this aspects and aims to assess current and future biodiversity distribution within a regional agroecosystem as function of climate and land use factors.

1.2 TALE Project

In 2015, the interdisciplinary research project TALE (Towards multifunctional Agricultural Landscapes in Europe – Assessing and governing synergies between food production biodiversity and ecosystem services) was started. The TALE project aims to unravel and quantify synergies between agricultural production, biodiversity, and ESS in different European landscapes. Human population, market globalization, dietary shifts, and urbanization are increasing the pressure on natural resources. The demand driven land use changes come at a cost in form of trade-offs between food or bioenergy production, biodiversity conservation and other ESS. TALE aims to deepen the knowledge regarding these trade-offs and to help developing policy strategies by assessing and governing synergies between these factors. The end-product of TALE should provide a platform that supports the design and evaluation of policy options helping to reconcile conflicting demands, while at the same time ensuring conservation of biodiversity and the provision of ESS within a changing environment. The project is accompanied by local involvement to achieve a high level of policy coherence (UFZ, 2015). Agroscope, the Swiss centre for agricultural and sustainability research, is conducting the TALE case study for Switzerland. The main project of this case study consists of an analysis and prediction of changes in water supply under future social-economic and climatic scenarios. This master's thesis serves as an additional input and focuses on biodiversity responses to climate and land use scenarios by investigating dependencies of different biodiversity indicators on habitat characteristics.

1.3 Biodiversity Indicators

Ideally, conservation planning is based on a complete and detailed knowledge of the distribution of all different components of biodiversity (genes, populations, species communities, ecosystems) in the region of interest. In reality, the knowledge of biodiversity and its single aspects, is far from complete (Ferrier, 2002). The complexity and multidimensionality of biodiversity does not allow to measure it as a single entity. However, it is possible to characterise some aspects of biodiversity using surrogate measures, the so-called *biodiversity indicators* (Büchs, 2003). In general indicators are defined as "pieces of information that provide insight into matter of larger significance and make perceptible trends that are not immediately detectable" (Hammond et al., 1995).

Indicators are used to face the complexity of biodiversity. In the case of biodiversity, do not measure directly the change within the biological system, but rather reveal information about the change of a phenomenon or activity, that if left unaltered, will lead to impacts on biodiversity (Duelli & Obrist, 2003). For this study, indicators should express biodiversity as a whole and be sensitive to environmental conditions and to agricultural activities. However, it is very complicated to find indicators that fulfil all these requirements (Herzog et al., 2012). The huge number of species and the complexity of ecological processes within agricultural habitats, complicates the choice of appropriate indicators that can robustly represent the link between biodiversity, environment and agricultural management (Duelli & Obrist, 2003;

Herzog et al., 2012). In the agricultural landscape, biodiversity can be divided into three levels: genetic, species and ecosystem diversity, each with its respective indicators (see Figure 1).

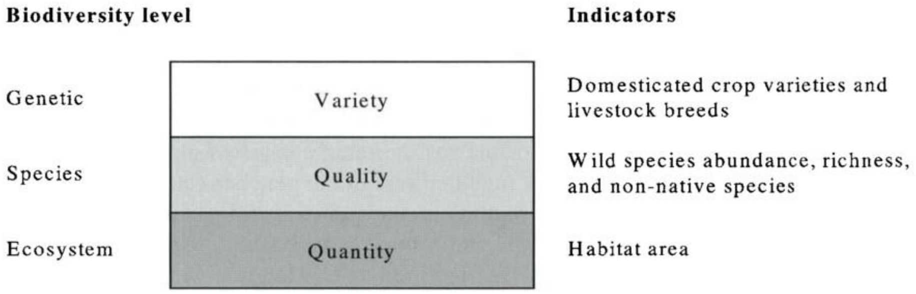


Figure 1: Biodiversity indicators in relation to agriculture (OECD, 2001)

For this study, the focus is set on the species richness as indicator for biodiversity and it refers to the total number of species of a functional group (species that share common characteristics within a community) per site and reflects the quality of an agroecosystem. The subset of species used in this study are selected vascular plants representing the quality of meadows and pastures in the study region (Chapter 3.2). Natural or weakly managed grasslands provide habitat for many plants and animals and are essential for agroecosystems; but their distribution is shrinking (Herzog et al., 2012; BAFU and BLW, 2013; BAFU, 2017). In previous studies, the application of plants richness as general indicator for biodiversity has been valuated as reliable (Duelli et al. 1999; Peters et al. 2016) and grasslands as suitable to assess simultaneously the effect of climate and land use changes on biodiversity (Pearson et al., 2004; Shoyama & Yamagata, 2014; Schirpke et al., 2017). In this study, the selected indicators are used in a statistical modelling approach to first identify regions of high plant diversity in grasslands and second to predict the shift of these hotspots under future climatic and land use scenarios.

1.4 Biodiversity Modelling

To directly measure changes in biodiversity, detailed information on the distribution of different taxa would be necessary. However, this spatial data is rarely available and usually of poor quality (Mossman et al., 2015). By using a selection of indicators and a set of certain modelling techniques, it is possible approximate the assessments and quantification of different aspects of biodiversity and their spatial pattern (Pfestorf et al., 2013, Mossman et al., 2015). Since the mid 1990's, predictive geographical modelling has been increasingly used as a tool to assess the impact of land use and other environmental change on the distribution of organisms, and to prioritize conservation efforts (Guisan & Zimmermann, 2000; Mossman et al., 2015). Today, there exist a variety of different modelling approaches, but the prediction of spatial patterns of species richness remains challenging (D'amen et al. 2017). Among these approaches, statistical modelling provides suitable tools to quantify the relation between biological data and environmental predictors. (Guisan & Zimmermann, 2000; Ferrier & Guisan, 2006). With this method, biological survey data may be linked to easily available environmental variables, and it provides a powerful mean for filling geographical gaps in the coverage of the usually sparse and coarse biodiversity data records (Ferrier et al., 2002; Mossman et al., 2015). After a selection process among different statistical models, a two-part hurdle model for count data has been chosen to be suitable for this study (Chapter 3.5).

The implementation of diversity models in agricultural landscapes is more complicated than in other unaffected environments, because agricultural production and biodiversity conservation often imply contrasting types of land use. Therefore, management strategies need to strike a balance between food production and biological variety considering local socioeconomic constraints and trade-offs (Grau et al., 2013). In order to find the best strategies for optimizing these trade-offs, it is necessary to generate a deep understanding of the complex relationships between species richness, agricultural management and environment.

1.5 Project Aim and Research Questions

The here presented master thesis focuses therefore on the development of a statistical model and attempts to identify current potential biodiversity hotspot regions in the grasslands of the Broye catchment. In addition, it aims to predict their future changes under different climate and land management scenarios. The evolving research questions can be summed in the following points:

- Which climatic and land use factors affect current biodiversity patterns of grasslands within the Broye catchment, and is it possible to predict them with a statistical modelling approach?
- What is the effect of future changes regarding climatic drivers and land use practices on patterns of species richness?
- Is it possible to identify potential regions for conservation or agricultural extensification?

1.6 Project Design

In order to answer the above-mentioned research questions, this master thesis project included the following work steps:

1. **Data Selection:** To compile the set of biodiversity indicators a restricted number of grassland plants was selected. In a next step, the related topographical, climatic, soil and land use explanatory variables, have been chosen to be used as predictors in the statistical model (Chapters 3.2 & 3.3).

2. **Data Preparation:** To model the current distribution of indicator species, the dataset had to be prepared in order to relate their abundances to the predictors. The species were grouped in guilds, their spatial observations and the environmental predictors were merged into a grid (Chapter 3.4).

3. **Model Design:** Once the dataset was prepared, the best possible statistical model had to be chosen based on the characteristics of the explanatory variable, species richness (Chapter 3.5).

4. **Model Implementation:** The hurdle model for every guild was run and cross-validated to produce values for current distribution maps (Chapter 3.6)

5. **Predictions:** In order to predict future species richness maps, two climate and four land use scenarios were defined, applied to the dataset and new prediction maps were produced (Chapter 3.7).

6. **Results Description:** The model outputs were used to investigate the effect of the predictors on the guilds, and the prediction maps to identify present and future biodiversity hotspots (Chapters 4.1 & 4.2)**.**

7. **Discussion and Outlook:** In this section, the whole study is reviewed from the original data to the models' outputs. The strength and weaknesses of the applied approach and the results of this study are discussed and some improvements for future applications are proposed (Chapter 5).

2. Theoretical Background

To arrange the choice of the best suitable model for the type of data used in this study, a short technical review has been integrated in the thesis. First, different modelling approaches for species richness at community-level are introduced and then regression models for count data are briefly described.

2.1 Modelling Approaches

There are two broadly used strategies to model species richness. The most popular way, is to model the distributions of the species one by one, in relation to predictors, and then assemble the results. This method is referred to as cumulative approach. The output allows the reconstruction of community composition and some attributes from single species. The second method is called macroecological approach and it first combines the data from multiple species, e.g. by building groups of species with similar properties. Then, the distribution within these groups of species are modelled in relation to the explanatory variables. The outputs consist of cumulative community attributes, usually richness prediction, but they do not provide any information on the single species. (Guisan & Zimmermann, 2000; Ferrier, 2002; Ferrier et al., 2002; Ferrier & Guisan, 2006; Guisan & Rahbek, 2011; D'Amen et al., 2017).

Both approaches have their strength and limits. The cumulative approach allows to take into account the properties of the single species and thereby to model their distribution more precisely. The results should hence reflect a more realistic distribution (Guisan & Zimmermann, 2000). Additional difficulties evolve if the aim is to predict species richness distribution. Modelling individual species is only possible if enough spatial data is available. Rare species are infrequently surveyed and not a lot of information is given about their occurrence. Furthermore, modelling single species can be a very time-consuming process (Ferrier, 2002; Ferrier & Guisan 2006).

On the other hand, the macroecological approach allows to include multiple species in the modelling, process which is an advantage if the species are recorded infrequently. Moreover, the computational effort is lower and it simplifies the detection of environmental responses of rarely recorded species and makes complex data more comprehensive (Ferrier & Guisan, 2006). A main argument against this approach is the fact that plant species assemblages or communities are very variable over time due to changing environmental conditions and interactions between the species. Therefore, it is difficult to predict future distributions of communities in case they are treated as one entity (Guisan & Zimmermann, 2000).

2.2 Regression Models for Count Data

Due to previous personal knowledge and the widespread use in conservation biology, this study focuses on statistical models, more precisely on linear regressions. These types of models are frequently used to quantify the relationship between species richness and environmental variables (Guisan & Zimmermann, 2000; Lehmann, 2002; Potts & Elith, 2006; Steinmann et al., 2009; Zuur et al. 2009).

The knowledge about the species as well as the characteristics of the available raw data define the choice of the suitable statistical model (Latimer et al., 2006). It this study, the focus is set on the analysis of the interactions between grassland plant richness in agricultural landscapes and the environmental/land-use factors. The dependent variable to be modelled in this study is the abundance of species, which means the number of species observed in a defined area and is usually given as count and discrete data (only non-negative integer values). This type of response variable follows a Poisson or a negative binomial distribution and their respective models are special types of generalized linear models (GLM) (Guisan & Zimmermann, 2000; Zeileis et al., 2008; Zuur et al., 2009).

2.2.1 Generalized Linear Models

Linear regression relates a response variable to a combination (multiple regression) of predictors (or explanatory variables). In case of a simple linear regression, the response variable must be normally distributed and the variance does not change as a function of the mean (homoscedasticity). The GLM is a more flexible type of regression model, which allows to model also response variables with other distributions than normal and with non-constant variance functions (heteroscedasity) (Guisan & Zimmermann, 2000).

To maintain the predictions within the range of coherent values for the response variable, the link function in the regression, is used for the transformation to linearity (Zuur et al.,2009). If the response variable is non-linear with a predictor, a transformed term of the latter can be included in the model. This characteristic of GLM allows to model data with Gaussian, Poisson, Binomial or Gamma distribution (Guisan & Zimmermann, 2000). Since in this study the response variable (species richness) consists of a count data, the following sub-chapters cover only model specifications for this type of data.

2.2.1.1 Poisson

Poisson is the simplest and most common model specified for count data. The Poisson distribution is a special case of GLM, where variance in the data is equal to the mean. This characteristic is called equi-dispersion ($\varphi = 1$). The link between response variable and predictors is a log-linear relationship:

$$\log(p) = \ln(p) = \beta_0 + \beta_1 X_1 + \ldots + \beta_n X_n \tag{1}$$

where p is the probability of an event occurring, X_n the *n*th independent variable and β_n the regression coefficient (Potts & Elith, 2006). The regression coefficients are estimated with a maximum likelihood function (Cameron & Trivedi, 1999). The classical Poisson regression model for count data is often limited, especially for empirical count data sets. This modelling method is not able to address two properties that often occur in ecological data sets: First, the variance is often bigger than the mean (overdispersion) and second, if there exists an excess number of zeros (zero-inflation) (Zeileis et al., 2008).

2.2.1.2 Quasi-Poisson

To address the issue of overdispersion, the Poisson regression model can be modified by estimating the dispersion parameter θ (= variance/mean) from the data instead of being fixed at 1 (Zeileis et al., 2008). The dispersion parameter can be modified to be larger than 1 if overdispersion is present. Let Y be a random variable such that

$$\begin{gathered} E(Y) = \mu \\ var(Y) = v_{Poi}(\mu) = \theta\mu \end{gathered} \tag{2}$$

where $E(Y) = \mu$ is the expected mean of Y and $var(Y)$ the variance (Ver Hoef & Boveng, 2007). The model coefficients (E and var) and the log-link function remain the same as the standard Poisson model (Zeileis et al., 2008). The advantage of the quasi-Poisson model is, besides accounting for overdispersion, leaving the parameters in a natural and easy interpretable state (Ver Hoef & Boveng, 2007).

2.2.1.3 Negative Binomial

A second way of modelling overdispersed count data is to assume a negative binomial (NB) distribution of the random variable Y. This model is the standard parametric model to account for overdispersion (Potts & Elith, 2006). Here, the overdispersion is a multiplicative factor $1 + k\mu^2$ which is dependent on the mean of Y. The model coefficients look like the following:

$$E(Y) = \mu$$
$$var(Y) = v_{NB}(\mu) = \mu + k\mu^2 \quad (3)$$

In case the original data has far more zeros, than it would be expected from a Poisson or NB distribution, there is a strong indication for zero-inflation. When using zero-inflated data with one of the former models, it may cause biased parameters, standard errors or overdispersion (Zuur et al., 2009). Zero-inflated models are a set of methods capable of dealing with this issue.

2.2.2 Zero-Inflated Models

It is a common problem for ecological data collected in the field, to have high portion of zero values in the dataset. In Zuur et al. (2009), the causes for zeros in species abundance observations are divided into four types of potential errors:

1) Structural errors: Species is not present because the habitat is not suitable.
2) Design error: Inaccurate experimental design or sampling practices.
3) Observer error: Mismatch or omission of species by the observer.
4) Species error: The habitat is suitable, but the species is not present.

The last three types of zeros are also called ‘false negatives’, whereas a structural error is also referred to as ‘true negatives’. Zero-inflated models are divided into mixture models and two-part models, which differ in how they deal with the different types of zeros.

2.2.2.1 Mixture Models: ZIP and ZINB

The term, two-component mixture models evolves from their ability to represent two or more ecological processes by combining probability distributions. The modelled zeros come from two different processes, a binomial process and the count process. The count process can also model zeros, which are true negatives, whereas the binomial process only generates false negatives (point mass at zero) and measures their probability. The count model is normally a Poisson GLM, also called Zero-Inflated Poisson (ZIP) or a Zero-Inflated Negative Binomial (ZINB) (Potts & Elith, 2006; Zeileis et al., 2008; Zuur et al., 2009).

If Yi is assumed to be the expected number of species on the *i*th area, the model specification

$$Y_i \begin{cases} 0, & with\ probability\ p_i \\ Poisson\ (\lambda_i), & with\ probability\ 1 - p_i \end{cases} \quad (4)$$

implies that zero observations may arise with the probability p_i, signifying that the zero is a true negative observation. Otherwise, the zero observation may arise from the parametric distribution (e.g $Poisson$) with probability 1 – p_i, implying that the observed zero is a false negative observation, it means the habitat is suitable, but not occupied (Potts & Elith, 2006).

This type of model is a good option to account for zero-inflation, but it does not explicitly account for overdispersion and the interpretation of the parameters (e.g. average plant richness) is less straightforward than in the two-part models (Martin et al., 2005; Potts & Elith, 2006).

2.2.2.2 Two-Part Models: Hurdle

Another model that accounts for overdispersion and zero-inflation within the data set is the hurdle model. This type of model was developed in 1971 and published in an econometrics journal, research field where it is still mostly used (Cameron & Trivedi, 1999). The hurdle model is a two-part model that specifies one process for zeros and another process for positive counts. The zero part can be either a binomial or a censored count distribution. The second part models the probability of a count value with a truncated count model (zeros cannot occur), such as Poisson or negative binomial. The advantage of fitting the model for two different parts allows to have more possibilities shaping the model structure. The idea is that positive counts occur only once a threshold is crossed. If the hurdle cannot be overcome, the count will be 0. The main difference to ZIP and ZINB is that there is no discrimination between the four types of zeros, they are all simply seen as zeros (Martin et al., 2005; Potts & Elith, 2006; Zeileis et al., 2008; Zuur et al., 2009).

The model specification may be resumed by the following example of a probability function:

$$f_{hurdle}(y) \begin{cases} f_{bin}(0) & if\ y = 0 \\ \dfrac{1 - f_{bin}(0)}{1 - f_{poi}(0)} f_{poi(y)} & if\ y \geq 1 \end{cases} \tag{5}$$

The model is divided in zero part with binomial function $f_{bin}(0)$ and the count part, where the ratio is the probability of a non-zero from the first process $(1 - f_{bin}(0))$ divided by the probability of a non-zero in the second untruncated process $(1 - f_{poi}(0))$, and then multiplied with the conditional mean $f_{poi(y)}$ from the Poisson distribution (Cameron & Trivedi, 1999).

In the case of species richness modelling, a grid-cell needs to cross a hurdle to produce a non-zero value and the count process has to exclude the probability of zero values. The zero part models the probability for presence or absence of the species and the count part gives the probabilities of the species counts.

3 Materials and Methods

3.1 Study Site

For the TALE project, five different case study regions in Europe were selected in Switzerland, Germany, Netherlands, Spain and Austria. For Switzerland, the region of the Broye catchment on the western plateau was chosen due to the catchment scale, its intense and diverse agricultural management, the presence of different habitats, and because of a previous study focussing on water supply in the same region; see Fuhrer *et al.*, 2013. The catchment covers an area of 598 km^2 and the elevation goes from 400 to approx. 900 m.a.s.l. It is crossed by the Broye river, which discharges into Lake Morat (Figure 2). The region can be divided into a rather flat, more intensively used area in the north (lowland), and a hilly, less intensively used area in the south (upland). In the lowland, land use is dominated by arable crop production (potato, maize, tobacco, sugar beat), and some of the water of the Broye is used for irrigation. In the upland a dairy farming dominates, which is why coverage with meadows and pastures is more frequent (Fuhrer et al., 2013). Environmental conditions differ slightly between the two regions: In the lowland, the annual average temperature is 9.6 °C and the annual precipitation is 886 mm (Payerne weather station), whereas in the upland it is slightly colder and moister (7.1 °C and 1,535 mm, Semsales weather station - MeteoSchweiz, 2016).

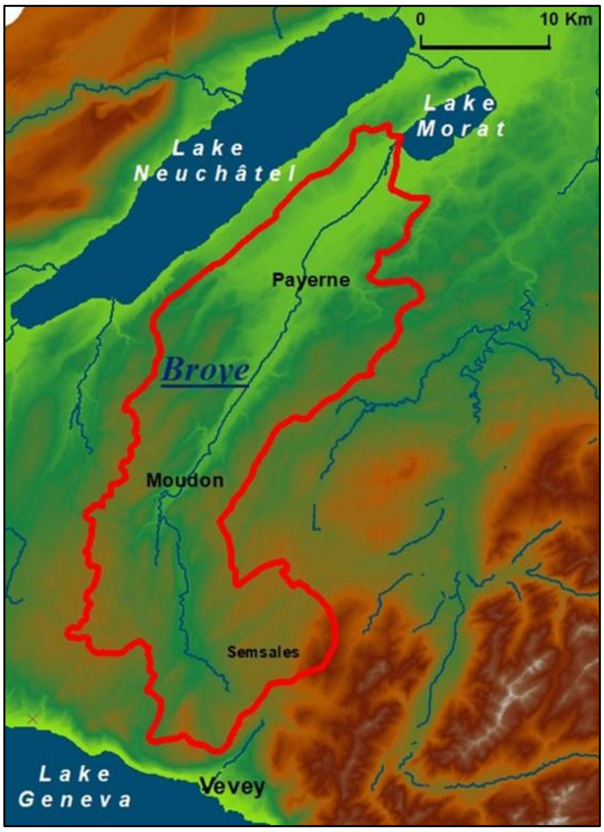


Figure 2: Broye catchment. (Swisstopo, 2001)

3.2 Selection of Biodiversity Indicators

The process of model-building can be divided into two parts: structure and specification. The model structure includes the choice of environmental characteristics (predictors or explanatory variables) that are assumed to affect the species abundances (response variable) and the intended shape of the modelled response (i.e. linear) (Potts & Elith, 2006). This selection process for species and predictors is described in this chapter and chapter 3.3. Chapter 3.4 describes how the selected data has been arranged to be integrated into the model.

Nowadays, more than one third of the Swiss territory is used for agriculture. Grasslands occupy about 75% of this area and can be separated into meadows (unregularly grazed and for production of hay) and pastures (mainly grazing). Especially the less intensively managed grasslands are, besides providing quality food for ruminants, habitat of a high diversity of plants and animals being essential for our ecosystems and for cultural values of the population (Herzog et al., 2012). Due to urban sprawl and agricultural intensification, the species richness and the extent of these habitats are decreasing. Especially highly diverse dry meadows and pastures (*Fettwiesen* and *-weiden*) and the less intensively managed meadows (*Fromentalwiesen*) have drastically shrank during the last decades and are therefore important for future conservation (BAFU, 2017a). Due to the high potential for biodiversity conservation of grasslands in Switzerland and the strong relation to agriculture management, in this study only vascular plants growing in meadows and pastures were selected and used as indicators for species richness.

Spatial extension data of species are often provided by scientific or voluntary surveys. This distributional information can be used for analysing spatial patterns in biodiversity. Here, the spatial information of selected species originates from survey data of plants developed by the National Data and Information Center on the Swiss Flora (25.01.2017 – InfoFlora, 2017), a non-profit foundation that documents and promotes wild plants in Switzerland. Among many other information, it provides a floristic database for research projects promoting conservation and promotion of native plants. The occurrence of the species is given at different resolutions throughout Switzerland or for specific regions. For this project, the most precise floristic data provided by Info Flora was used, given as presence-only data at a resolution of 100x100 m. Unfortunately, no information about the certain absence of species or the number of elements within the parcel is given.

To maintain the multifunctional characteristics of agricultural landscapes, a new policy was put into place for the period 2014-2017 including a system of direct payments to farmers who promote biodiversity (BAFU and BLW, 2013). Farms aiming for such a contribution need to fulfil a certificate of ecological performance, which requires areas for biodiversity promotion (*Biodiversitätsförderflächen*; BFF). The subsidies for improving biodiversity are payed for the quality (divided in level I and II) as well as the interconnection of the BFFs. One part of the quality evaluation consists of the count of a minimum number of species present on specific lists for each habitat (BLW, 2014). Therefore, a first selection criteria was to choose among plants present in the BFF list of meadow and pasture (BLW,2014). Secondly, the species need to possibly grow within the Broye region, wherefore alpine plants were excluded. In order to increase the number of observations, further species being present in the Swiss environmental goals for agriculture (*Umweltziele Landwirtschaft* - BAFU & BLW, 2013) were included. These are mostly species classified as endangered and have therefore a high ecological value. Since the provided floristic data set for the Broye region only was too limited to produce robust models, the input data included also observations from regions around the Broye catchment with similar environmental and land use conditions. The total area (Figure 3) corresponds to the sub-regions 2.5 and 2.6 from BAFU & BLW (2013).

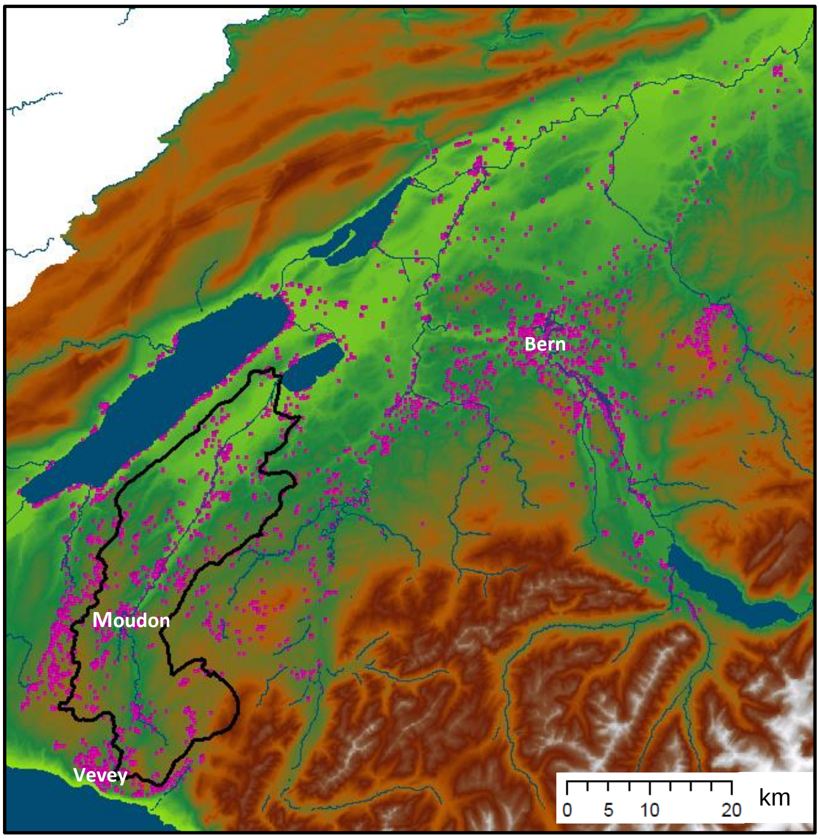


Figure 3: Distribution of observation data from InfoFlora (2017). Pink points represent the 100x100m surveyed cells. (Swisstopo, 2001)

The final subset of indicators is composed by a total of 118 species; 85 of them are species that are valid for the BFF quality contribution, the remaining 33 species are species with high priority for conservation, because rated as vulnerable or endangered. This final set of biodiversity indicators (listed in Annex 1) should represent a balance between target species important for conservation and plants that are easily observed in the agricultural landscape and necessary for the farmers to get the contributions. The observations points (pink points) of the resulting set of species are illustrated in Figure 3. It is possible to see how the dots are concentrated around lakes (e.g. lake Neuchatel), rivers (e.g. Broye), cities (e.g. Bern in the centre-right) and in the natural reserves (e.g. Parc Jorat western Broye). This disparate distribution is due to the patterns of observation. Data from InfoFlora is very heterogeneous, many species, especially the more frequents, are underrepresented, because not part of an inventory like biodiversity monitoring or protected areas. Areas near inhabited zones, places of interest or leisure time are more frequented and species are more surveyed. Once the predictors have been selected, suitable explanatory factors had to be chosen.

3.3 Selection of Predictors

For the predictive modelling of species richness, a set of suitable predictors (or explanatory variables) needs to be selected. They should be able to explain the actual distribution of species but also future shifts under changing climate and land use management. An overview of all factors influencing the geographical distribution of plants is given in Figure 4. For this study, a subset of different parameters was selected, in order to explain the presence and abundance of species in the study region. The set of predictors is composed by variables reflecting topography, climate, soil, and land use conditions in the Broye catchment. The complete initial set of predictors used in this study is shown in Table 1. They are given in form of digital raster data sets at different spatial scales (Table 1). We decided to work with this type of data because it is easily available and already prepared for applications without the need for additional homogenisation and computational efforts. They are provided by different secure and proofed sources. From this initial set of variables, a more specific selection was compiled during the data processing (chapter 3.4)

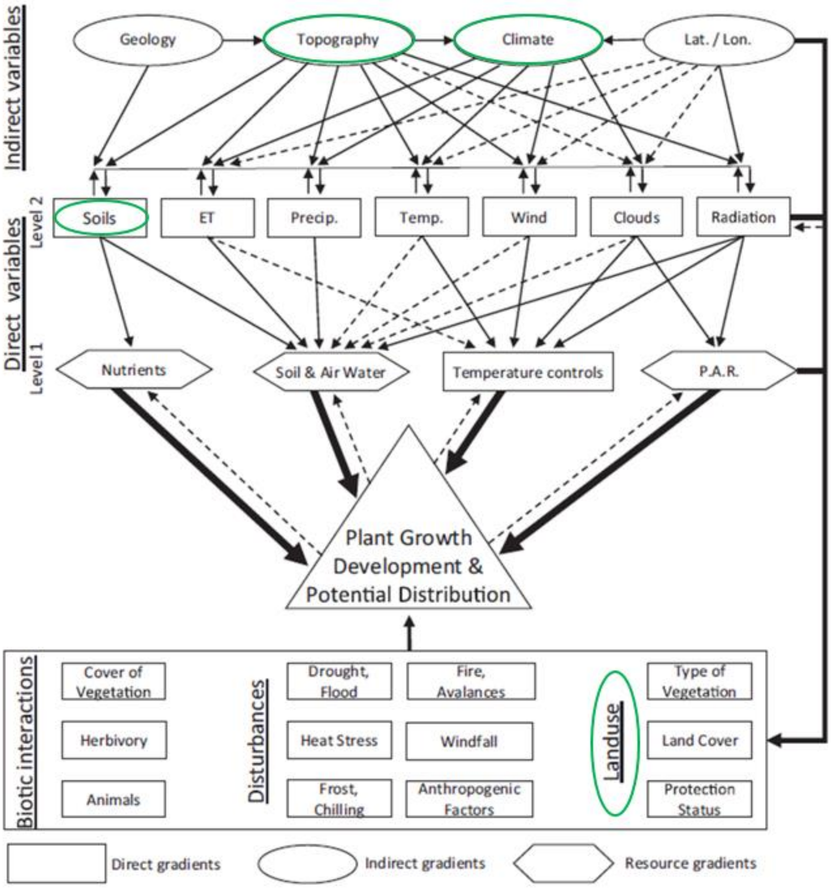


Figure 4: Conceptual framework for relationships between resources, direct and indirect environmental gradients and their influence on growth, performance and geographical distribution of vascular plants. Green circled are the categories of factors adopted in this study. (Mod et al., 2016 adapted from Guisan & Zimmermann, 2000

VARIABLE	DESCRIPTION [unit]	SOURCE
Height	[m ü.M]	Swisstopo (2001)
Slope	[%]	Swisstopo (2001)
Aspect	[°]	Swisstopo (2001)
Temp	Annual and seasonal Temperature [°C]	MeteoSchweiz (2016)
Prec	Annual and seasonal Precipitation [mm]	MeteoSchweiz (2016)
N_Load	Nitrogen load in soil [kg/year]	BAFU (2015)
P_Load	Phosphorus load in soil [kg/year]	BAFU (2015)
Soil_Suit	Soil Suitability for cultivation [1: very low – 4: very high]	BFS (2012)
Nutrient_Retention	[0: very high – 6: very low]	BFS (2012)
Waterlogging	[0: very high – 6:very low]	BFS (2012)
Permeability	[0: very high – 6:very low]	BFS (2012)
Dist_Water	Distance to water bodies [m]	BAFU (2013)
Dist_Building	Distance to buildings [m]	BAFU (2013)
Crop Shares	1) Different crop shares [%] of the arable land per grid cell 2) Share of extensive and intensive meadow (sum = 100%) per grid cell 3) Share of extensive and intensive pasture (sum = 100%) per grid cell	BLW (2015)
AS	Arealstatistik in area Classes and Groupings (m^2) (see Annex 2 for classes)	BFS (2016)

Table 1: List of environmental variables, given as raster data from different sources

The main set of variables in Table 1 includes some of the major driving forces for the distribution of the species. The digital elevation model (DEM) contains information about the elevation of each grid cell and provides the basis for the computation of *height, slope* and *aspect*. This are indirect predictors because they have no direct physiological relevance for the plants. Topography is strongly related to the climatic variables *temperature* and *precipitation*. Therefore, *height* can be used as approximation for these two climatic variables. In contrast to elevation, *Temperature* is a direct predictor, affecting directly the physiology of the plants (Mod et al., 2016). Information data about temperature (average) and precipitation (sum) is given in the form of seasonal and annual mean. The following predictors representing aspects of soil conditions, are variables that influence the natural resources of the plants which they need for growth (i.e. nutrients, water availability).

Figure 3 showed the heterogenous distribution of observation points, which were concentrated around cities and lakes. This is probably the effect of the observation bias, it means species are more probable to be recorded near places where people are likely to be. It is possible to account for this effect, by modelling presence data as function of known observer variables (Warton et al., 2013). Here, *distance to buildings* was integrated into the set of variables as observer bias variable.

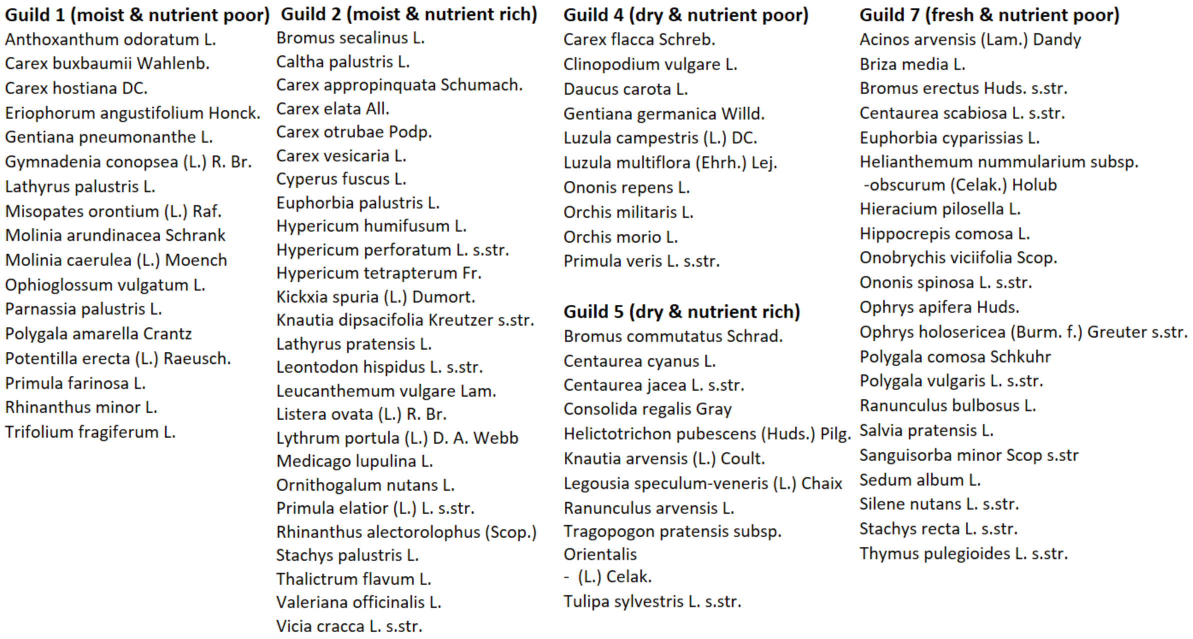
The different types of agricultural management are given in percent values. Important for this study is the proportion between *extensive* and *intensive meadows* or *pasture*. The two grassland management types differ mainly in terms of fertilization (extensive: none; intensive: mostly nitrogen as manure or compost) and cultivation regimes (extensive: 1-2 cuts per year; intensive: 4-6 cuts per year). The last category in the list of predictors consist of a classification of 72 land use types (see Annex 2) provided by the Swiss Areal Statistics (BFS, 2016).

3.4 Data Processing

After the selection of the raw data, multiple steps of data processing were required to ensure the applicability of the linear regression model. First, the relationships between the single species and the variables were analysed. A big portion of the species have been rarely observed. Moreover, some more frequent species did not show enough observations in order to model the distribution of the individual species. The correlations between single species observations and predictors were not satisfactory. This excluded the option to apply the cumulative approach which would have been also very time consuming for such a big data set. Therefore, modelling the species richness with the macroecological approach, was considered to be the best option.

To do so, the plants were grouped by similar biotic characteristics which increased the correlations.

As reference for the grouping we use the ecological indicator values from Landolt et al., (2010) consisting of a set of ecological and biological properties of plants. It resulted difficult to build coherent groups by including all the ecological indicators, therefore, a manual merging was conducted by dividing the species into 9 guilds (group of plants with similar ecological niche) only based on soil-related properties: humidity and nutrients availability. It was decided to not include the climatological factors for defining the guilds, because on average, these values were supposed to not vary significantly over the Broye region. The complete list of species divided in guilds can be seen in Annex 1. As the guilds 3, 6, 8 and 9 showed the lowest number of species observations, only the guilds 1, 2, 4, 5 and 7 were used for the analysis. At the same time, these guilds were the ones with the most contrasting humidity and nutrient values. The final guilds used for the modelling process are listed in Table 2.



Guild 1 (moist & nutrient poor)
Anthoxanthum odoratum L.
Carex buxbaumii Wahlenb.
Carex hostiana DC.
Eriophorum angustifolium Honck.
Gentiana pneumonanthe L.
Gymnadenia conopsea (L.) R. Br.
Lathyrus palustris L.
Misopates orontium (L.) Raf.
Molinia arundinacea Schrank
Molinia caerulea (L.) Moench
Ophioglossum vulgatum L.
Parnassia palustris L.
Polygala amarella Crantz
Potentilla erecta (L.) Raeusch.
Primula farinosa L.
Rhinanthus minor L.
Trifolium fragiferum L.

Guild 2 (moist & nutrient rich)
Bromus secalinus L.
Caltha palustris L.
Carex appropinquata Schumach.
Carex elata All.
Carex otrubae Podp.
Carex vesicaria L.
Cyperus fuscus L.
Euphorbia palustris L.
Hypericum humifusum L.
Hypericum perforatum L. s.str.
Hypericum tetrapterum Fr.
Kickxia spuria (L.) Dumort.
Knautia dipsacifolia Kreutzer s.str.
Lathyrus pratensis L.
Leontodon hispidus L. s.str.
Leucanthemum vulgare Lam.
Listera ovata (L.) R. Br.
Lythrum portula (L.) D. A. Webb
Medicago lupulina L.
Ornithogalum nutans L.
Primula elatior (L.) L. s.str.
Rhinanthus alectorolophus (Scop.)
Stachys palustris L.
Thalictrum flavum L.
Valeriana officinalis L.
Vicia cracca L. s.str.

Guild 4 (dry & nutrient poor)
Carex flacca Schreb.
Clinopodium vulgare L.
Daucus carota L.
Gentiana germanica Willd.
Luzula campestris (L.) DC.
Luzula multiflora (Ehrh.) Lej.
Ononis repens L.
Orchis militaris L.
Orchis morio L.
Primula veris L. s.str.

Guild 5 (dry & nutrient rich)
Bromus commutatus Schrad.
Centaurea cyanus L.
Centaurea jacea L. s.str.
Consolida regalis Gray
Helictotrichon pubescens (Huds.) Pilg.
Knautia arvensis (L.) Coult.
Legousia speculum-veneris (L.) Chaix
Ranunculus arvensis L.
Tragopogon pratensis subsp.
Orientalis
- (L.) Celak.
Tulipa sylvestris L. s.str.

Guild 7 (fresh & nutrient poor)
Acinos arvensis (Lam.) Dandy
Briza media L.
Bromus erectus Huds. s.str.
Centaurea scabiosa L. s.str.
Euphorbia cyparissias L.
Helianthemum nummularium subsp.
-obscurum (Celak.) Holub
Hieracium pilosella L.
Hippocrepis comosa L.
Onobrychis viciifolia Scop.
Ononis spinosa L. s.str.
Ophrys apifera Huds.
Ophrys holosericea (Burm. f.) Greuter s.str.
Polygala comosa Schkuhr
Polygala vulgaris L. s.str.
Ranunculus bulbosus L.
Salvia pratensis L.
Sanguisorba minor Scop s.str
Sedum album L.
Silene nutans L. s.str.
Stachys recta L. s.str.
Thymus pulegioides L. s.str.

Table 2: List of species grouped in the five guilds with different moisture and nutrient habitat conditions

The number of species within the guilds varies significantly. The “dry guilds” (4 and 5) consisted of less species than the moister ones, leading to less observations to be used for the model. The grouping of species into guilds did not supply enough count of species per 100x100m raster cell, to achieve robust correlation between the number of species and the predictors. Only a few cells counted more than one species per guild and therefore the correlation between the number of species and the climatic and land use variables was insignificant (low Pearson’s correlation). As the macroecological approach, required modelling the number of different species per area, higher counts per grid cell were needed. To increase the counts and to fill gaps within the spatial coverage of the plant distribution, simple methods of spatial interpolation are commonly used in the ecological model approaches. At the scale of our catchment, it was reasonable to adopt the interpolation technique of assign in plants records to larger grid cells (Ferrier, 2002). In a geographic information system ArcGIS (version 10.3.1), the tool *Fishnet,* allowed to create a matrix with 1x1km cell size, which was lied over the original floristic data and every variable was assigned to this new raster. The resulting count values for the cells were notably higher than at the original 100x100m spatial resolution. However, the correlation coefficients between guild counts and the predictor variables remained rather low. As further step, all the cells without any share of meadow or pasture were eliminated from the raster, what slightly increased the correlations. The resulting grid is illustrated in Figure 5.

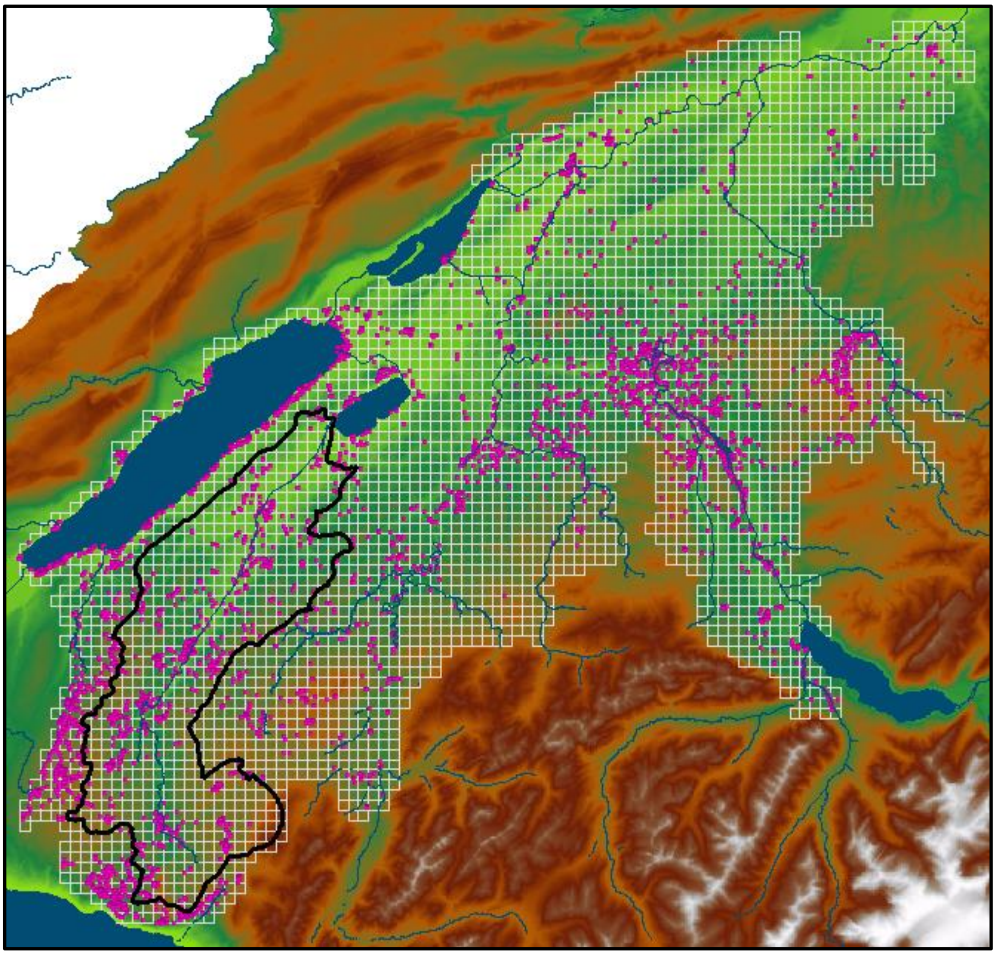


Figure 5: Raster with 1x1km cells, floristic observation data (pink points) and Broye catchment (black line). (InfoFlora, 2017; Swisstopo, 2001)

Since this initial set of predictors still consisted of too many variables to include them all in the model, a selection process had to be conducted. For each of the five guilds, the selection of predictors was based on the following criteria:

1. Variables with the highest Pearson's correlation coefficients concerning the species count and significant p-value (<0.05)
2. Check for multicollinearity: Remove collinear predictors with low correlations regarding the guild counts
3. Keep only guild-specific meaningful variables – exclude clear noise variables

This results of the selection process described above were five matrices, one for every guild, with the species presence count and the interpolated predictor variables for every matrix cell. These data sets were ready to be integrated into a model and the selection process for the most suitable model could be undertaken.

3.5 Model Specification

The model specification defines how the selected variables are related to another by choosing the most appropriate functional form (Potts & Elith, 2006). The first step in the model selection process consisted of checking the characteristics of the response variable (number of species per cell) and its associated probability distribution (density function). As mentioned above, the response variable is composed of count data, with no negative data. This type of data follows a Poisson or a negative binomial distribution (Guisan & Zimmermann, 2000), for which the best suitable statistical model had to be chosen (see chapter 2.2).

The choice of the best model should be based on the knowledge of the species and characteristics of the available data (Pott & Elith, 2006). First, we looked at the distribution of the response variables. Figure 6 shows the histogram of the abundances of species per raster cell for all guilds. The most striking feature is the very high number of cells with no species observations. The exact amount of zero cells is 2355, from a total of 3623 cells. 1268 guild cells count at least one observation of the species of the five different guilds, which is equal to almost half of the zeros. This is a clear evidence for zero-inflation in the dataset. Due to this trait of the data, the focus was put on zero-inflated models. The next step was to choose between a mixture model or a two-part model.

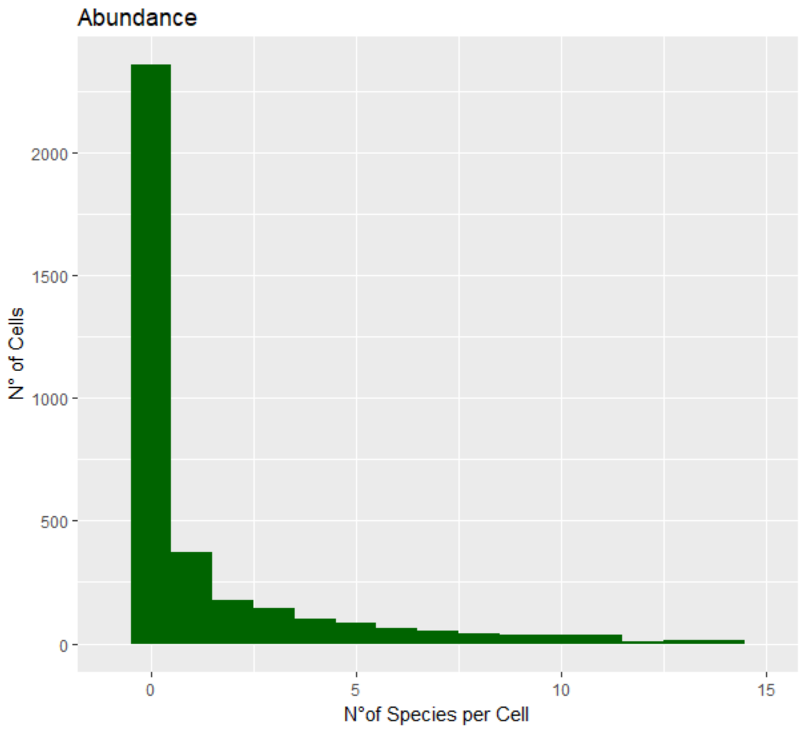


Figure 6: Histogram of species abundance: with n° of species per cell on the x-axis and n° of cells on the y-axis

The given floristic data consisted of presence information only and many regions of the study area were probably not surveyed. These facts suggest insufficient knowledge about true negatives (areas where in reality the habitat is not suitable for the species to grow). Since we do not need to differentiate between true and false negatives but rather focus on the higher species counts and the correlation with predictors, the use of a two-part model was decided to be most appropriate. The output of hurdle models facilitates the interpretation of the predictors, defining the absence or presence of species and affecting the richness (Pott & Elith, 2006). Moreover, the interpretation is more straightforward when the effects on all zero counts are directly modelled (Cameron & Trivedi, 1999).

In a next step, we had to choose the type of distribution to be used for the zero part and which one for the count part of the hurdle model. The zero part modelling presence or absence, was ordinary fitted with a binomial distribution. However, the distribution for the count part of the hurdle model had to be defined, by choosing between a Poisson or a negative binomial. Therefore, the single guilds have been tested for both distribution types. One criteria for the selection of the correct distribution was based on the overdisperson of the count data. Another selection criteria was the Akaike Information Criterion (AIC). This relative measure helps to compare the models and corresponds to an estimation for model quality by evaluating the trade-off between goodness of fit and the complexity of the model (Zuur et al., 2009). Other evaluation criteria for the model performance are the Pearson's correlation coefficient *r*, which provides an indication of similitude between observed and predicted values (perfect correlation = ±1); and the Root Mean Square Error (RMSE), which measures the difference between observed and predicted values (Pott & Elith, 2006). For each guild, the AIC value was lower for the hurdle model with a NB distribution than with a Poisson distribution. However, the other evaluation parameters (Pearson's correlation and RMSE) showed better results for the Poisson distributed count model. By comparing the coefficients of the model, the significance of the predictors did not change substantially between the two models. Since there were no clear indicators for a overdispersion in the count data and as the Pearson's coefficients for guilds 1 and 2 showed considerably better correlations between observed and predicted values, the hurdle model with Poisson distribution was used for the count part. Once the best model was specified, a validation process had to be conducted to measure the quality of the fit and evaluate its performance.

3.6 Model Validation

The high number of grid cells (3623) in the dataset allowed to apply a cross-validation. This validation method fits the model using only a part of the data set. The dataset on which the model is run is called *training data* and the subset of removed data is called *testing data*. Afterwards, the model fitted with the training data was used to predict the responses for the observations in the testing data. The comparison of the results is used as estimation goodness (Korner-Nievergelt et al., 2015). Here, a repeated random sub-sampling validation, also referred to as Monte-Carlo cross-validation, was applied. With this method, the separation between training and testing data is done randomly and repeated several times. The fraction between training and testing data is defined manually, such as for the number of repetitions (Xu, 2004).

In our case, the fraction of training data was set at 75% and at 25% for testing data. The random separation process was repeated 20 times. These decisions were based on the analysis of the evaluation statistics (Pearson's correlation and RMSE) of the predictions for the training and validation data for different number of repetitions. For the case of less than 20 repetitions, the average of the evaluation parameters varied strongly. From more than 20 repetitions, the mean of the parameters remained stable (see Table 3). Afterward, the models for each guild were reiterated 20 times with different randomly chosen training data and the average of the model's coefficients was used to fit the predictive models.

After the first run of cross-validation only the predictors that were still significant ($p < 0.05$) for the respective parts of the hurdle model of each guild were retained for a second run. The final set of predictors for every guild is displayed in Table 4. In order to ensure comparable scales between the predictors a standardisation of the remaining variables was conducted before the last model run (*scale{base}*, R-3.2.5). The resulting coefficients of the models (Annex 3) allow a relative comparison between the predictors and an evaluation of the weight of each predictor within the linear regression model (Vittinghoff et al., 2012). The values of the coefficients vary between -1 (negative correlation) and + 1 (positive correlation). A detailed comparison of the different predictors is described in chapter 4.2.1.

3.7 Future Scenarios

To assess possible shifts in grassland plants richness under changing climatic and land use conditions, the values in the input dataset of relevant predictors have been modified. After running and validating the models (chapter 4.1) the predictors *mean winter temperature* and *pasture intensive* were the only significant variables still present in all guilds' models (see Table 4). By altering the values of this predictor future scenarios could be produced (chapter 4.2.2.1).

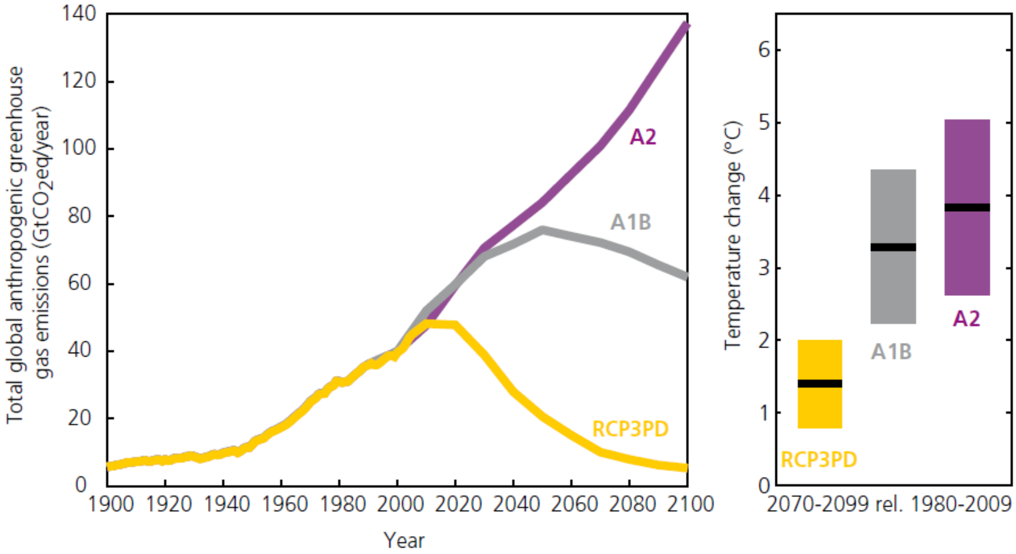


Figure 7: Left: Three scenarios for total global anthropogenic greenhouse gas emissions. Right: related potential temperature increase for the 30-year average centred at 2085 (aggregated from the four seasons and three representative regions). (CH2011, 2011)

The two future climate scenarios were represented by a mean winter temperature increase of 2 °C and 4 °C. According to the Swiss Climate Change Report (CH2011, 2011) an increase of only 2° C in the next 70 years would only be possible if greenhouse gases emissions were decreasing by now, while an increase of 4° C until 2085 is probable to occur if the emissions were to continue with the current trend.

The four land use scenarios were divided into two moderate and two extreme scenarios. For the first two, intensive pasture was reduced by 20% and 40%. The thresholds were arbitrarily set, but took into account feasible targets within an agropolicy context that strives for less intensive agriculture. Two additional extreme forms of land use scenarios have been applied in the Broye catchment: land sharing and land sparing, which are currently under discussion as potential trade-off strategies to balance food production and biodiversity (Grau et al. 2013, Fischer et al. 2014). The first one refers to a broad extensification of agriculture and to an improvement of agroecosystems by expanding nature conservation into agricultural areas. The second, land sparing, seeks to stimulate production to achieve nationwide self-sufficiency regarding food production. Whereas intensive agriculture is concentrated in areas with fertile soils, mild climate and sufficient water supply. Less suitable areas are supposed to become fully protected natural hotspots.

Land use management strategies to address trade-offs between food production and biodiversity conservation must be imbedded in a local socioeconomic context (Grau et al. 2013). In order to not only address the theoretical aspect of these extreme conservation strategies, stakeholders in the TALE project were actively included in the production of the scenarios and allowed to take into account the management implications. The stakeholders presented concrete actions for a hypothetical land sharing or sparing scenario in the Broye region, which were implemented in the modelling process. The land sharing scenario implies an extensification of all pastures and meadows, which means that all pasture intensive present in a cell is changed to pasture extensive use (chapter 4.2.2.2). In order to ensure high productivity (with unlimited irrigation in the flat and suitable region) the land sparing scenario was defined as follows: all actual meadow and pastures were intensified, the crop regions with a slope bigger than 7.5 % and with a good soil suitability were converted to intensive meadow and the ones with bad soil suitability were converted to forest. This leads to a general intensification of grassland and increase in natural woods (chapter 4.2.2.2). Reflecting potential future warming in the next decades (Figure 7) and current course of agropolicies towards less intense managing, it was decided to combine the +2° C increase in winter and the 20% extensification to produce a species richness prediction map for a plausible future scenario (chapter 4.2.2.3).

4 Results

After fitting the hurdle model for each guild, the models were run by using the open-source integrated development environment for R-3.2.5, RStudio (hurdle{pscl}). This chapter shows and describes the results from the model outputs. In section 4.1, the results from the cross-validation process are listed in order to give an estimate for the model performances. Furthermore, the types of correlation (negative vs. positive) between the predictors and response variables are described. Section 4.2 consists of an illustration and description of all relevant prediction maps.

4.1 Model Performance

The average of all the regression coefficients from 20x model outputs was used to produce the final model for each guild. To validate these models, two commonly used statistical performance coefficients have been applied: The Pearson's correlation coefficient *r* and the Root Mean Square Error (RMSE) (see chapter 3.6). Table 3 shows the averaged validation coefficients for the 20 randomised Monte-Carlo cross-validations for each guild.

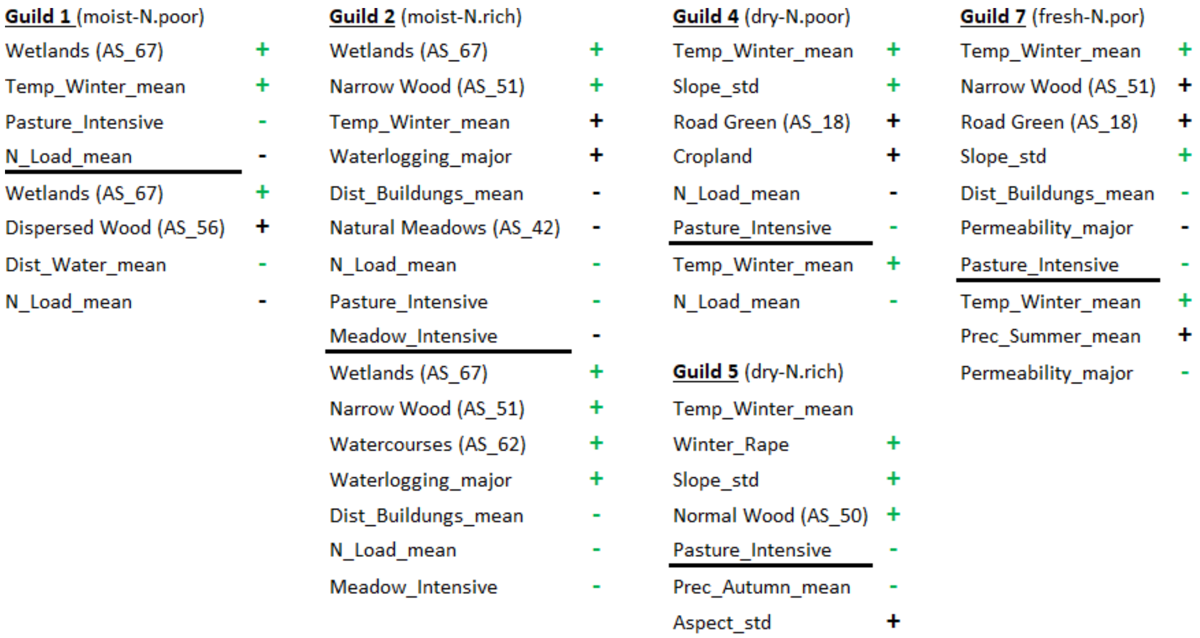
	Testing Data	
	r	RMSE
Guild 1	0.519	1.025
Guild 2	0.480	2.040
Guild 4	0.229	1.081
Guild 5	0.274	0.810
Guild 7	0.317	1.117

Table 3: Model evaluation coefficients *r* and RMSE for the testing data of the five guilds after a 20x Monte-Carlo cross-validation.

It is noticeable that the goodness of model performance varies between the different guilds. The models for guild 1 (moist and nutrient poor) and 2 (moist and nutrient rich) show the highest correlation coefficients, meaning that the predicted counts of species are in better agreement with the observed counts compared to the other guilds. The dry guilds (4 and 5) show the lowest coefficients with 0.229 and 0.274 respectively. Concerning the RMSE, guild 2 shows the highest value with 2.04. This suggests a rather large discrepancy between predictions and observations. On the other hand, guild 5 shows the best results in terms of the

RMSE (0.81). The causes for the differences in performance between the guilds can be explained with help of the regression coefficients estimated by the models (see Annex 3), which are described in the next sections.

Table 4 shows the types of correlations between the response variable (number of species of the guild) and the selected predictors (environmental variables). The plus (+) stands for positive correlations and minus (-) for negative correlations. A green symbol indicates that the predictor is highly significant with a p-value lower than 0.001, whereas the black coloured symbols stands for significance with a p-value lower than 0.05. The predictors above the line account for the zero-part, whereas the ones below the line stand for the count-part of the hurdle model.



Guild 1 (moist-N.poor)	
Wetlands (AS_67)	+
Temp_Winter_mean	+
Pasture_Intensive	-
N_Load_mean	-
Wetlands (AS_67)	+
Dispersed Wood (AS_56)	+
Dist_Water_mean	-
N_Load_mean	-

Guild 2 (moist-N.rich)	
Wetlands (AS_67)	+
Narrow Wood (AS_51)	+
Temp_Winter_mean	+
Waterlogging_major	+
Dist_Buildungs_mean	-
Natural Meadows (AS_42)	-
N_Load_mean	-
Pasture_Intensive	-
Meadow_Intensive	-
Wetlands (AS_67)	+
Narrow Wood (AS_51)	+
Watercourses (AS_62)	+
Waterlogging_major	+
Dist_Buildungs_mean	-
N_Load_mean	-
Meadow_Intensive	-

Guild 4 (dry-N.poor)	
Temp_Winter_mean	+
Slope_std	+
Road Green (AS_18)	+
Cropland	+
N_Load_mean	-
Pasture_Intensive	-
Temp_Winter_mean	+
N_Load_mean	-

Guild 5 (dry-N.rich)	
Temp_Winter_mean	
Winter_Rape	+
Slope_std	+
Normal Wood (AS_50)	+
Pasture_Intensive	-
Prec_Autumn_mean	-
Aspect_std	+

Guild 7 (fresh-N.por)	
Temp_Winter_mean	+
Narrow Wood (AS_51)	+
Road Green (AS_18)	+
Slope_std	+
Dist_Buildungs_mean	-
Permeability_major	-
Pasture_Intensive	-
Temp_Winter_mean	+
Prec_Summer_mean	+
Permeability_major	-

Table 4: Significant predictors for the zero (above line) and count part (below line) of the hurdle model for all five guilds. Green plus: p-value < 0.001; black plus: p-value 0.05

It may be noticed that each guild has a different amount of predictors. However, the comparison with the model validation results in Table 3 reveals that the number of predictors has no effect on the goodness of the model. Most of the variables are highly significant with p-values smaller 0.001. *Mean winter temperature* and *pasture intensive* management are the only predictors present in all guilds. During the predictors selection process, mean winter temperature showed higher correlation with the guilds, than the other seasonal temperature means. Same for pasture intensive, which had always the highest correlation in comparison to the other pasture or meadow shares. Mean winter temperature is present in the zero part of every model and shows a throughout positive correlation with the presence of the guilds' species. In guilds 4 and 7, mean winter temperature is also significantly present in the count-part, which indicates that higher winter temperatures would lead to higher counts (or abundances) in these guilds. Intense pasture management is only present in the zero-parts, resulting in a negative effect on the presence of the species.

The variable accounting for the observational bias (*distance to buildings*) is only significantly present in two of the five guilds. Whereas it is slightly negatively correlated with the zero-part (absence of species) in both guilds, only guild 2 reveals a similar correlation with the count-part (presence of species). Once the model performance could not be enhanced, the corresponding significant predictors and their coefficients were used to form the linear regression models for each guild allowing for the calculation of the prediction maps.

4.2 Model Predictions

The resulting maps are divided in two categories according to their time horizon: Maps of predicted present distributions (chapter 4.2.1) and prediction maps for future climate and land management scenarios (chapter 4.2.2).

4.2.1 Present Distribution

The maps with the potential present distribution throughout the study area and its surroundings enable the identification of areas that would be potentially suitable habitats for the corresponding species. In the following sections, the maps for every guild are described and the visible patterns of species richness are being related to the different predictors (model outputs in Annex 3).

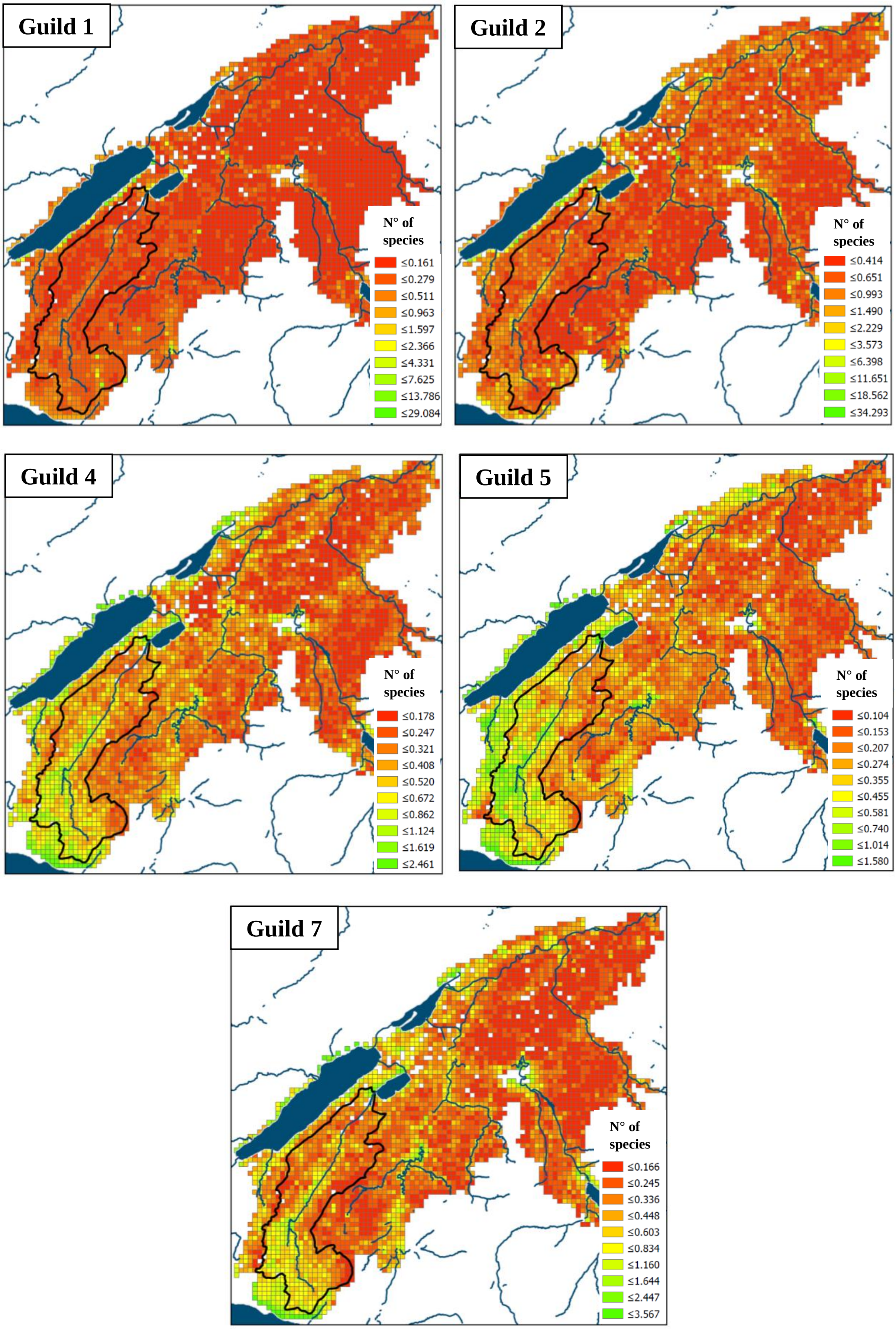


Figure 8: Species richness predictions for the single guilds (1, 2, 4, 5, 7)

4.2.1.1 Guild 1 - Moist and Nutrients Poor

Overall, the prediction map for the species of guild 1 shows only a few scattered patches reaching higher values than two species per grid cell. Nevertheless, a distinctive pattern of high biodiversity is present at the southern shore of lake Neuchatel, where the number of predicted species reaches almost 30. These values are much higher than the in the rest of the prediction area. Such high values only exist for the same grid cells of guild 2 (max. 34.293). Within the Broye catchment, only a few cells in the highlands show an elevated number of species, whereas the rest of the catchment the species richness for this guild is low. Around the city of Bern, the values are slightly increasing, which is probably due to higher density of observations (observational bias). The model of guild 1 predicts a total of 174.75 (± 0.338) species for the Broye region, 34.247 (or 16.38 %) less than to the total summed species observations. The presence of the species of guild 1 (zero part) is strongly dependent on the predictor *wetlands* due the high correlation coefficient of 0.6412 (see Annex 4 – Guild 1). Furthermore, the removal of the predictor *wetlands* from the model led to significantly lower correlations between predicted and observed values. The negative correlation with *pasture intensive* is highly significant, meaning that the higher the share of intense pasture management gets, the less probable is the presence of the species from guild 1. In the count part, the negative correlation with *distance to water* shows the highest correlation coefficients, what is comprehensible since moist plant habitats are usually close to water bodies.

4.2.1.2 Guild 2 – Moist and Nutrients Rich

The pattern of the moist and nutrient rich guild 2 is very similar to guild 1, although the maximum number of predicted species is higher with values of up to 34 species per grid cell. Nevertheless, the highest values are also located at the southern shore of Lake Neuchatel. Within the Broye catchment, a zone of higher diversity spreads on both sides of the river. Some grasslands in the highland also seem to provide suitable habitats for the species of this guild. For the Broye region, the model of guild 2 predicts 16.56 % less total species, than have been observed on the field (equivalent to – 100.68 ±0.51 species). Overall, guild 2 has the largest number of predictors, nine for the zero part and seven for the count part (Table 4). Again, the predictor *wetland* shows the strongest correlation with the presence of species with a value of 0.846, what could explain the similarities between the patterns of guild 1 and 2. Surprisingly, *natural meadows* are negatively correlated with the presence of species. This might be due to the fact that natural meadows are mostly found within a rather steep and hilly topography, while wet soil conditions are mostly found in flat lowlands. Since meadows and pastures are less presents in the lowland than in the highland, this negative correlation is reasonable. Although the species of this guild are supposed to prefer nutrient rich habitats, the predictor *meadow intensive* shows a negative correlation with the zero part, and *pasture intensive* is negatively correlated the count part. This could point towards an indirect effect due to divergent locations of the predictor and response variable. The predictor for observational bias *distance to buildings* shows a significant negative correlation with the count part of the model, which means that closely to densely populated areas the presence of more than one species from this guild is more likely. For the zero part of the model the observer bias variable does not shows very significant correlation, nevertheless it was included in the model, because the model outputs did not vary in performance.

4.2.1.3 Guild 4 – Dry and Nutrients Poor

Diversity predictions for species preferring dry and nutrients poor habitats show different patterns compared to the moist guilds. This model predicts for the the Broye catchment, the most alike total number of species in comparison to the observations with an underestimation of 5.45 %. Overall, the highest values are found closely to water bodies as well as generally on south-orientated slopes (i.e. along the Jura and just north of the Lake of Geneva). The latter pattern may be explained by the negative correlation between temperature and soil moisture. Further evidence evolves from the fact that the predictor *winter mean temperature* is significantly correlated with the zero and also the count part of the model. The surprisingly larger area with greenish colours (compared to guild 1 and 2) indicating high species abundances needs to be interpreted carefully. This effect is mostly due to a change of the scale, which only varies between 0.2 and 2.5 species per grid cell. As guild 4 only includes 10 species, the number of species could be too low for the usually very diverse dry and nutrient poor grasslands. Therefore, the low predictions may reflect the scarce representation of this guild. The higher species richness around lakes and rivers is most probably due to different reasons than for the moist guilds 1 and 2, since *wetland* and *distance to water* are not present in the set of correlated predictors. *Slope* correlates positively with the zero part, because in steeper meadows and pastures water may drain and wash out the nutrients. Hence, highly diverse dry meadows (*Trockenwiesen*) are often found on steep terrain, where cultivation is not profitable. *Nitrogen load* is the second predictor affecting species abundance by a strong negative correlation. Therefore, the greenish areas in the map are supposed to be the ones with lower nitrogen inputs.

4.2.1.4 Guild 5 – Dry and Nutrients Rich

The distribution pattern of guild 5 does not substantially differ from guild 4, although a different set of predictors is used for the models (Table 4). In comparison to guild 4, the predicted values are even lower, with a maximum of 1.58 and Figure 8 (Guild 5) shows overall more greenish and less reddish cells. Since the range of predicted values is smaller, it is also more probable that a cell plot takes a rather greenish colour. For the Broye region, the model predicts relatively high values over a big portion of the area with a maximum in the western central part (around Moudon). The underestimation of predictions in comparison to observations is 14.52%. Although *slope* shows the highest correlation coefficients in the zero part, increased levels of nutrients cannot be explained by drainage processes.

4.2.1.5 Guild 7 – Fresh and Nutrients Poor

Guild 7 is composed by species that have no preference for either dry or moist conditions (“fresh”), but that grow on nutrient poor soils. Nevertheless, the patterns of species richness distribution are more similar to the dry guilds. The more diverse regions are generally located around lakes, rivers, and cities but also on the slopes just north of Lake Geneva. The model predicted for the Broye catchment 58.08 ±0.3 less species than the total observed amount. Guild 7 includes predictors previously seen in the regression models of the moist (*narrow wood*, *distance to buildings*) and of the dry (*slope* and *road green*) guilds or in both (*winter temperature*, *pasture intensive*). Additionally, *permeability* (the capacity of the soil allowing for water to pass through) is negatively correlated to the zero and count part of the model. Therefore, the species from guild 7 seem to prefer less permeable soil textures like loam or clay.

4.2.1.6 Absolute Sum

In order to make inferences about the total species richness of the study area, the predictions of the five guilds were merged into a new map by summing up the absolute number of predicted species of every grid cell. The resulting map (Figure 9) includes the predictions of all five guilds species as well as all the observation points of the plants survey (black dots).

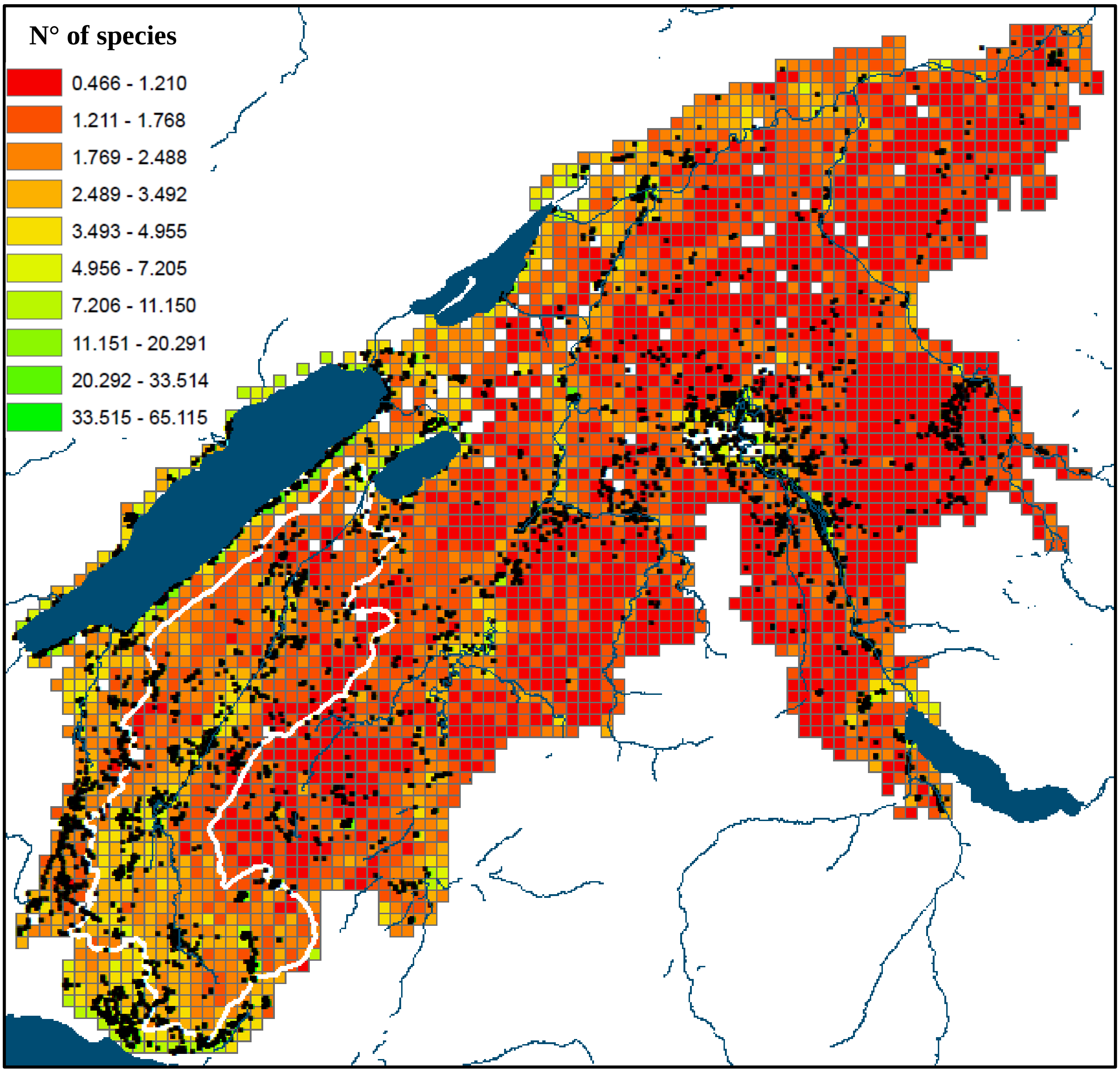


Figure 9: Absolute map: Sum of current species richness predictions of all guilds and observation points (black). (InfoFlora, 2017)

The number of predicted species per grid cell varies between 0.466 and 65.115. The regions with highest values are again situated along the southern shore of Lake Neuchatel. Moreover, the distinct pattern of enhanced species richness around populated areas and waterbodies points towards a dominating effect of the observational bias despite the removal attempts during the modelling process. A second explanation originates from the higher weight in the total sum of the two moist guilds (overrepresentation), since they account for more species and show higher correlations than the other models. Within the Broye region, the intensively managed lowland in the northern part with less grasslands shows rather low species numbers. Along the river itself and towards the southern part, the number of species increases. In the highland, the same patches with high counts as in guild 1 and 2 appear. This map of absolute numbers may help to give an impression about the species richness, but is not very representative for the ecological value of the patterns because it does not allow making inferences about the detailed species composition of each grid cell. Furthermore, the guilds with higher maximum numbers of projected species are overrepresented.

4.2.1.7 Standardized model predictions

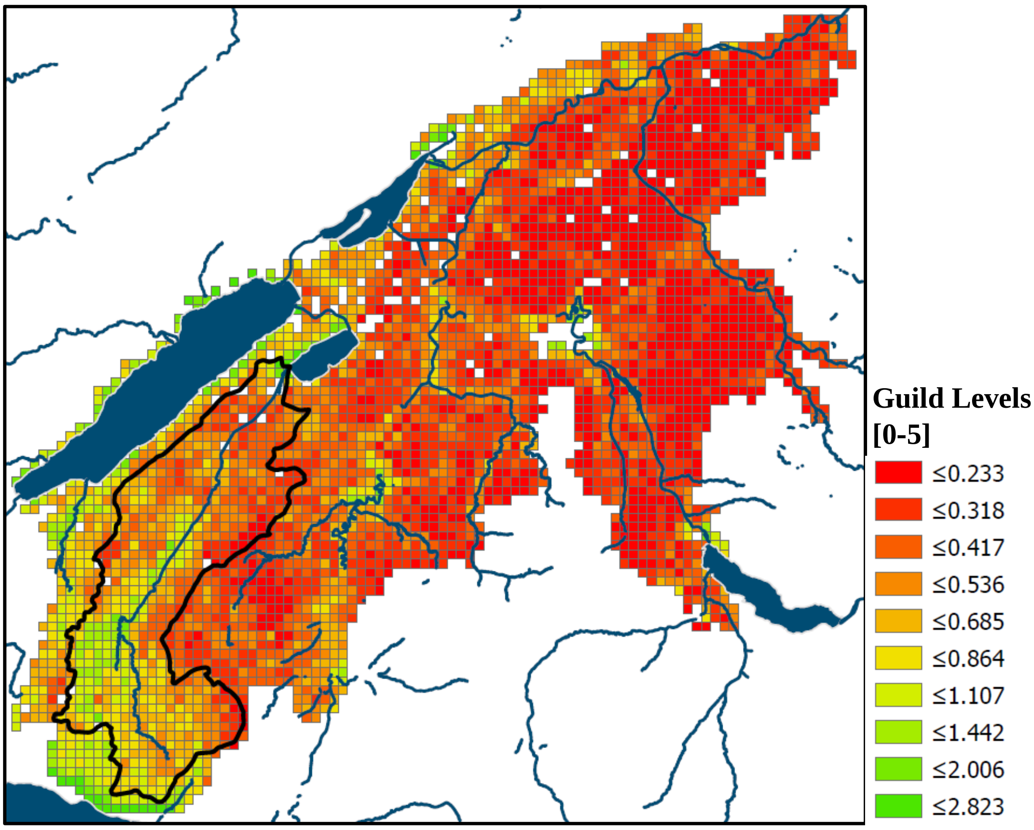


Figure 10: Standardized map of summed current species richness predictions.

In order to face the above-mentioned bias probably originating from the overrepresentation of the moist guilds, the predictions were standardized. Therefore, the predicted average value of each grid cell was divided by the maximum of predicted values of each guild. The resulting scale of each guild ranged from 0 to 1, which allows for a direct comparison of the different guilds. For example, the value 0.5 means that half of the potential number of predicted species of a specific guild is present in that cell. These values are referred to as “Guild Levels”. Figure 10 illustrates the sum of the standardized values from each grid with a potential scale ranging from 0 to 5.

One may still recognize distinct patterns around rivers and lakes, although weaker than in the absolute map. Therefore, the effect of the observational bias seems to be present in all guilds. The regions with the highest guilds levels (1.5 - 2.5) are found along the northern shore of Lake Neuchatel with some cells also on the southern shore. Other hotspot-regions are located at the northern shore of Lake Morat and around the northern top of Lake Biel. High guild levels are also present at the very bottom of the modelled area, namely on the northern slopes of Lake Geneva. By comparing this map with the ones of the single guilds, is possible to attribute the high values on the southern shore of Lake Neuchatel mostly to the moist guilds, whereas the high numbers of species on the northern shores of the lakes (south-facing) may mostly linked to the impact of dry guilds. For the Broye region, regions of higher values are located around the city of Moudon to the west and a buffer zone along the river bend to the north. However, the comparison with the observations points (Figure 10 above) indicates a possible effect of the observational bias.

4.2.1.8 Comparison between model prediction and observation

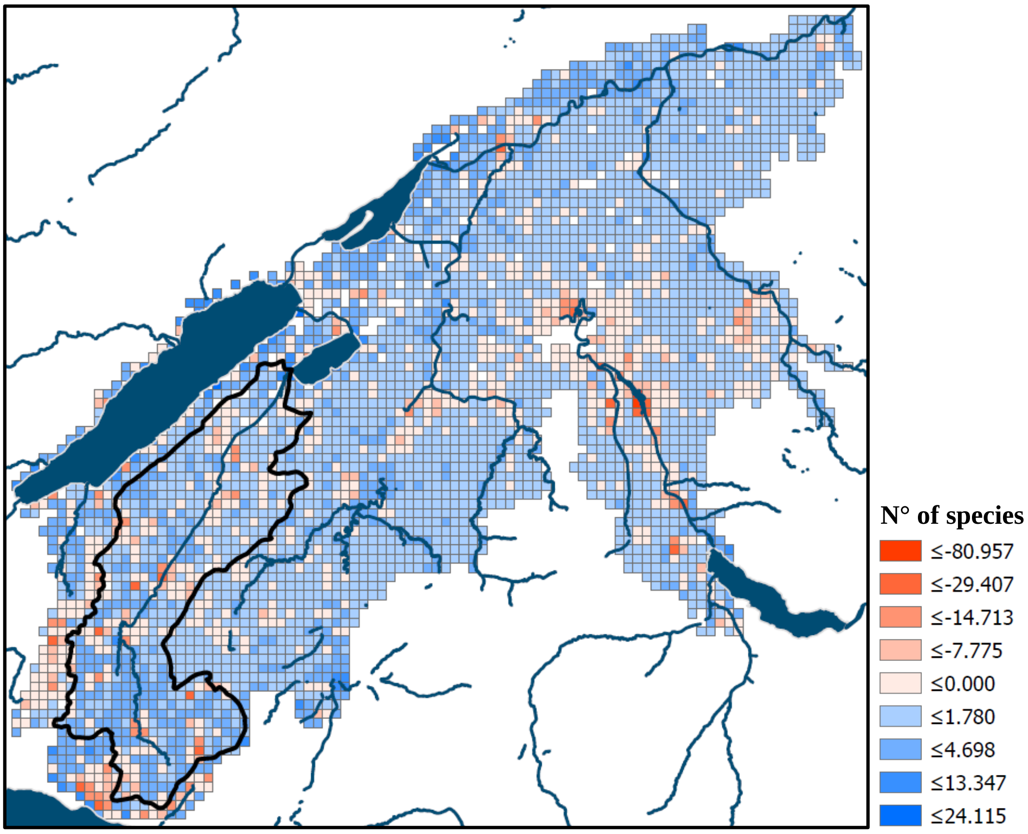


Figure 11: Difference between absolute map of current species richness predictions and observed count of species per cell

Figure 11 illustrates the difference between the predicted species richness (chapter 4.2.1.6) and the observed number of species for each grid cell. The cells with positive values are predominating the negative ones. Most of the blue cells are just slightly positive, this is due to many cells having no observations at all (compare with Figure 5 or 9). This could erroneously lead to the conclusion, that the hurdle model overestimates the number of species over most of the modelled region, but per definition the hurdle model, does not predict zeros, but the probability of them (formula 5 in chapter 2.2.2.2). The cells with a probability for positive counts that outreaches the hurdle threshold will produce higher values. The darker blue cells are regions of overestimation and the areas with darker red cells is where the model underestimated the number of species present in comparison to the observations. The underestimated areas, have considerably bigger margin of error, than in the overestimated (see legend). These are some singles cells, where the model was not able to predict the high amount of species. If we compare these results with the distribution of the observation points (Figure 5 or 9), we can recognise that areas with more observations tend to be underestimated. The brightest cells, are regions where predictions and observations agree the most. The highest number of species predicted in a cell is 65.115, whereas the highest number of surveyed species per cell is 99. Regarding the Broye region, the models, predict in total about 260 less species (-13.78 %) than observed in the region.

4.2.2 Future Predictions

In order to evaluate the impact of future climatic changes and potential land management strategies on the species richness of grasslands within the study area, six different scenarios were applied to the five guilds ‘models. The sum of the predictions (as for the absolute map in chapter 4.2.1.6) are displayed in the next sub-chapters.

4.2.2.1 Climate Scenarios

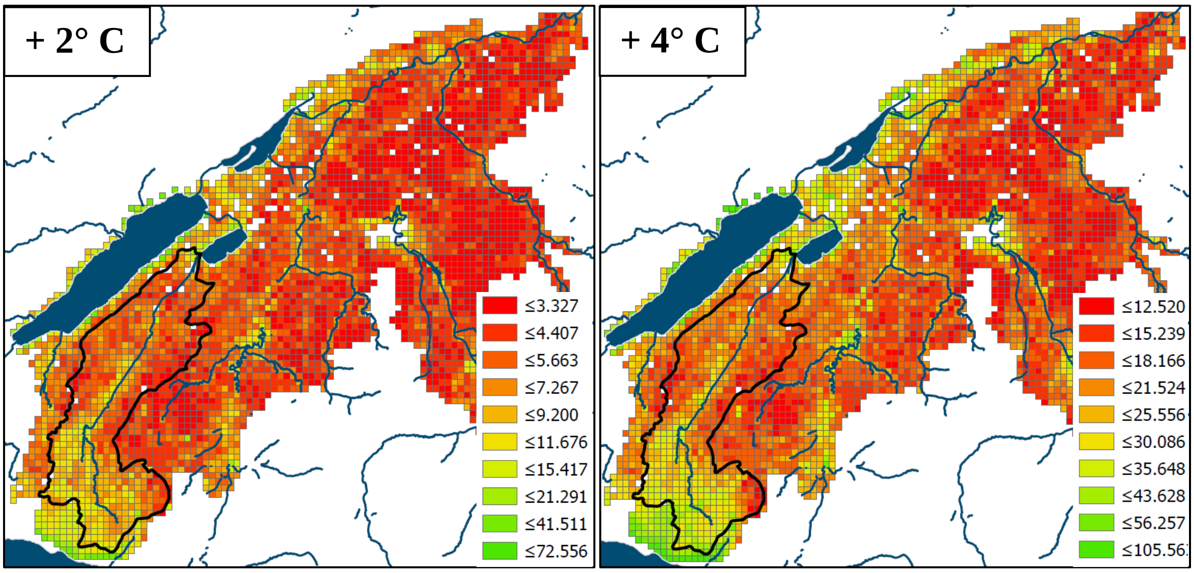


Figure 12: Species richness predictions for potential future mean winter temperature increase of 2° C (left) and 4° C (right). [n° of species]

As illustrated in Figure 12, an increase in mean winter temperatures would generally lead to an increase in the absolute number of predicted species (max number of species respectively 72.556 and 105.561). In contrast to these substantial increases concerning the absolute number of species, the spatial distribution patterns remain more or less stable. Compared to the model predictions for the present situation (Figure 9), the total number of species increases by 65.73% for the +2° C scenario and by 89.86% for the +4° C scenario. However, an increase in mean winter temperatures by 4° C would have a clearly stronger effect on grassland species than on the + 2° C scenario, which reflects the linear relationship in the model of this predictor with the species richness. Given that *temperature winter mean* is only significantly present in the count part of the model for guild 4 and 7 (Table 4), species growing on rather dry soils with low nutrient concentrations would probably profit the most from an increase in winter temperatures.

4.2.2.2 Land Use Scenarios

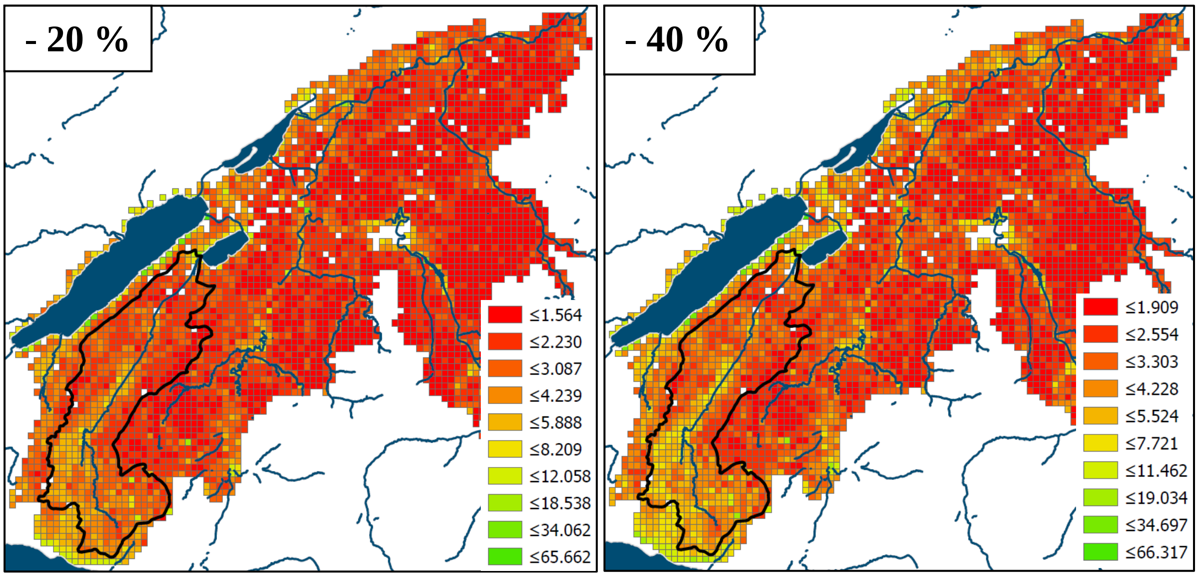


Figure 13: Species richness predictions for 20% (left) and 40% (right) extensification of pastures [n° of species]

The first two land use scenarios describe a moderate conversion of intensively managed pasture to a form of extensive management. For the scenarios of 20% and 40% extensification, the absolute sums of predicted species do not increase as significantly as for the climate scenarios. In the Broye catchment, an extensification by 20% would lead to an average increase of 21.35%. For the scenario of a stronger extensification (-40%), the number of species increases by 36.94%. The small differences regarding the two scenarios may be explained by the absence of the predictor *pasture intensive* in the count part of the models of all guilds. Therefore, this variable accounts only for the presence or absence and not for the amount of species.

The "extreme" version of the previous scenarios, would be to change all pastures from intensive to extensive management (100% extensification), this is represented here by the *land sharing* scenario (Figure 14). The species richness is predicted to increase in some specific patches along some northern parts of the Broye river. In the highland, the number of species is generally much higher, which is probably due to the higher share of grasslands compared to the lowland. Therefore, the highland, some parts of the river surroundings, and the area around the river estuary seem to profit the most from a rigorous reduction of intensive grassland management. According to this model, an overall extensification of meadows and pasture in the Broye, would lead to an increase of 60.88% in total species.

In accordance with its definition, the predictions for the land sparing scenario show a less homogeneous picture compared to the land sharing scenario. There are no large areas with high species richness, but rather single scattered patches or pixels. The maximum values are lower than for the land sharing scenario and areas of poor diversity are much more pronounced. An intensification of the grasslands in the Broye region as defined by the land sparing scenario (chapter 3.7) would lead to a 14.57% decrease in total species. The focus of the conservation efforts is set on forests, which do not directly promote a higher diversity of grasslands plants. An interesting feature evolves from the several green patches along the river within the intensively cultivated region in the north, suggesting that in the context of a land sparing scenario it might be profitable to create protected areas close to the Broye river.

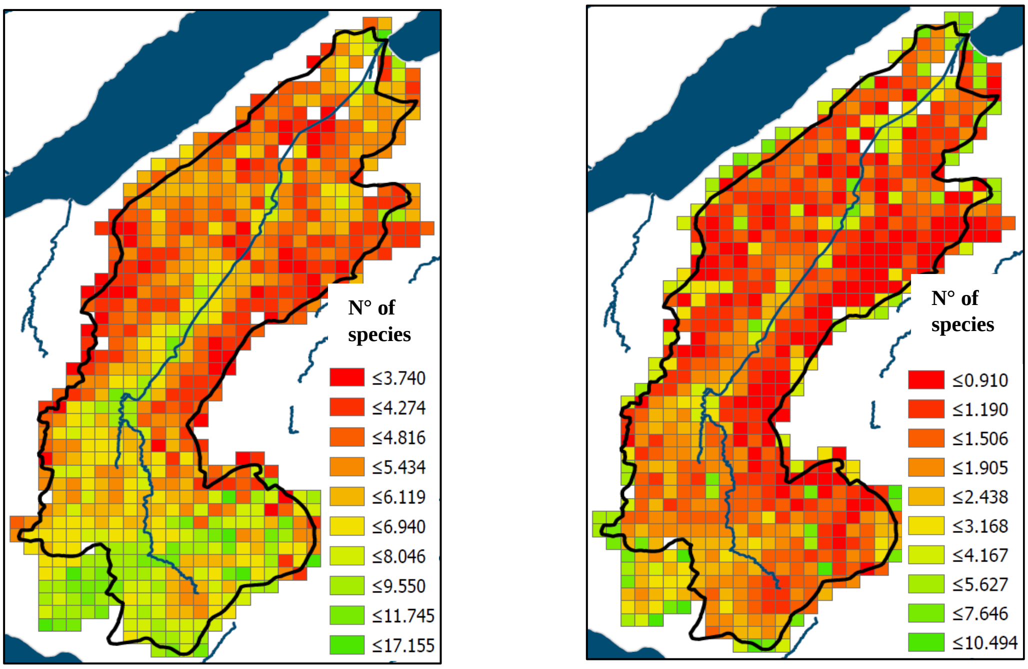


Figure 14: Species richness predictions for a land sharing (left) and land sparing (right) scenario (Broye).

4.2.2.3 Combined Scenario

In order to evaluate a plausible combination of rather moderate climate and land use scenarios within the next decades (i.e. until 2050), the effects of an increase in mean winter temperature by 2° C as well as an extensification by 20% on the species richness of grasslands were combined. The general increase in species richness is 70.96%. This result was expected due to the combination of linear effects of the positive correlation with *winter temperature* and the negative correlation with *intensive pasture*.

For the assessment of specific regions that would profit the most from a less intense pasture management combined with a warmer winter temperatures, the differences between the combined future scenario and the present predictions (absolute sum in chapter 4.2.1.6) were calculated and illustrated in Figure 15. The zones that would increase the most in species richness, are mostly regions with already high diversity (compare with figure 9), like at the northern shore of lake Morat, near the lake Geneva, some cells around lake Neuchatel and the upland in the Broye. These are regions mostly occupied by the dry guilds. It could be interpreted, that a warmer climate and less intensive pastures, would increase significantly the number of dry-loving species in regions where they are already have suitable habitat. These regions, provide already a hotspot for biodiversity and will probably remain diverse if no additional land use activities. Thereby and are therefore worthy to conserve. The greener areas in the southern part of the Broye region and the pre-alpine zones, are the areas where species richness in pastures and meadows would profit the most and therefore a less intense land management could be profitable.

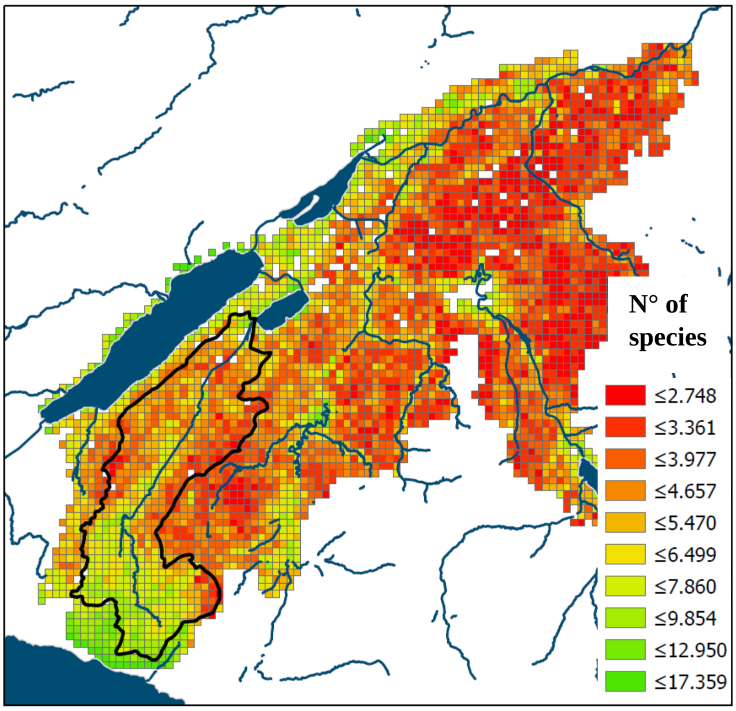


Figure 15: Difference between species richness predictions for plausible future scenario, as combination of +2° C mean winter temperature and -20% intensive pasture, and the current predictions.

5 Discussion

The following chapter consists of an interpretation and discussion of the methodological aspects of the study as well as the resulting findings. Following the research questions posed in the introduction, outcomes, strengths, and limitations of the study are being critically discussed and set into context with available literature.

Which climatic and land use factors affect current biodiversity patterns of grasslands within the Broye catchment, and is it possible to predict them with a statistical modelling approach?

Using a simple statistical model like the two-part hurdle model (Pott & Elith, 2006; Zeileis et al. 2008; Zuur et al. 2009;), it was possible to assess different climatic and land use factors affecting current species richness of grasslands at catchment scale. The current distribution of different guilds consisting of sets of species with similar preferences in terms of nutrient and water supply, was modelled to identify spatial patterns of species richness. The hurdle model allowed distinguishing between predictors accounting for the presence as well as for the count of species. The number and composition of predictors varied among the different guilds (see chapter 4.1). The results indicate that the models for the moist guilds performed better and the predictions showed overall higher counts than the ones for the dry guilds (see chapter 4.1 and 4.2.1). While the models for the dry guilds produced lower abundances of species, the potential habitats covered a larger area (see chapter 4.2.1.3, 4.2.1.4 & 4.2.1.5). By merging the predictions for all guilds, it was possible to identify regions within the Broye catchment offering potential habitats for the selected grassland species (chapter 4.2.1.6 / figure 9). Although the estimated species richness was generally lower in the lowland compared to the highland, some areas along the river also showed exceptionally high numbers of species within the intensively cultivated areas. These results on one hand highlight the potential of the presented approach regarding the analysis of relationships between selected environmental factors and species richness. On the other hand, the predictive capacities of the models were not fully satisfactory, and therefore the modelling approach as well as the data selection and processing steps need to be revised for further improvement.

Among the three different aspects of biodiversity (see figure 1), the focus of this study was set on species richness. Considerable problems regarding the assessment of the overall species richness in agricultural landscapes can be avoided by using particular taxa as indicators for general biodiversity (Billeter et al., 2008; Herzog et al., 2012). The richness in vascular plants was identified to be a good general indicator for biodiversity (Duelli et al., 1999; Peters et al., 2016), and grasslands offer suitable ecological traits to assess simultaneously the effect of climate and land use changes on biodiversity (Pearson et al., 2004; Shoyama & Yamagata, 2014; Schirpke et al., 2017).

Using a selection of species as indicator for biodiversity requires the existence of empirically collected data with sufficient spatial coverage (Ferrier, 2002). Such species surveys are getting more precise and cover larger areas thanks to digitally based platforms like InfoFlora, where everyone may contribute to the sampling. However, a considerable part of the information is still unknown for most regions (Peters et al., 2016). In case of the Broye region, the available species distribution data revealed some limitations: The accumulation of observations around densely populated areas was attempted to be taken into account by introducing the variable *distance to building*. However, the removal of this observational bias was not fully possible and was visible in the prediction maps (chapter 4.2). This source of error is a common problem for ecological modelling approaches using survey data recorded by volunteers (Morrison, 2016). Different solutions to overcome sampling biases have already been proposed: Stolar & Nielsen (2015) suggest a sample weighting term estimated as the inverse of probability of sampling, and Bird et al. (2014) introduced alternative modelling approaches (i.e. mixed-effect and hierarchical models). A second limitation regarding the raw data is the missing information about true negatives. Presence-only data is a very common characteristic of directly surveyed biological data sets. In this study, a zero-inflated model was applied, but other approaches, i.e. pseudo-absences, could have been implemented for the type of data used in this study. This method, in case a species has not being observed at a certain location, where others are, the not surveyed species is treated as absent, true negative (Ferrier & Guisan, 2006; Pearce & Boyce, 2006). A third, possible constrain of the raw data is the autocorrelation between the observation points. If this effect of similarity in characteristics of two elements been located near to each other, is reproduced in the residuals of the model, it can affect the modelling results, in general causing overestimation (Dormann et al., 2007). In this study, the presence of this bias was not tested.

In the presented modelling approach, guilds of similar species were formed to enhance the correlations between the species and environmental variables. Moreover, this allowed producing species counts that were not given by the raw presence-only data. The resulting guilds were created manually based on only two ecological indicator values (moisture and nutrients). However, the ecological niche of a specific plant includes many other variables than just the availability of moisture and nutrients. This might be the reason why the spatial patterns of the guilds did not fully correspond to the topographical distribution of their traits. In regions with high concentrations of observations, species of multiple guilds were present. This suggests that grouping the indicator species with respect to only these two variables was not sufficient to allow for a distinction between the different habitats. Alternative approaches for the grouping of species (i.e. in community types) could have provided better results than in functional groups (guilds) (Guisan & Rahbek, 2011; D'Amen et al., 2017).

The unique characteristic of this study was the attempt of modelling directly the number (abundance) of species by relating it to available environmental predictors. The floristic data was processed without reaching satisfactory amount of species counts per grid cell. Given the characteristics and quality of the raw data, which not allowed to build sufficient abundance data, a binary model, where the probability of presence of species is modelled instead of the abundance, may be more suitable (Ferrier & Guisan, 2006; Bird et al., 2014; Stolar & Nielsen; 2015). This could have been implemented in a macroecological approach without losing its benefits: The potential presence or absence of the guilds is modelled by using a GLM or GAM in order to generate distribution maps of the guilds consisting of the probability of occurrence for each grid-cell (Guisan & Zimmermann, 2000; Zuur et al. 2009). By merging the different distribution maps into one, it would be then possible to identify the cells with highest probability of occurrence for all the guilds. In case the ecological value of each guild would have to be investigated, grid cells could be assigned to the guild with the highest predicted probability of occurrence (Ferrier et al., 2002). A second commonly used type of modelling within the macroecological approach is to fit a single model to all guilds simultaneously by using a classification by regression trees (e.g. random forest or BIOCLIM). By the use of a recursive portioning technique generating discrete environmental rules, the grid cells are then assigned to the different communities (Ferrier & Guisan, 2006).

The models' outputs were than used to produce distribution maps of species richness for every guild. Due to the guilds' model quality (Table 3), the different spatial distribution and diverging maximal number of predicted species per cell (chapter 4.2), it could be distinguished between two groups: moist and dry guilds (including guild 7). Moist guilds showed better model performance and higher maximal predicted values in comparison to the dryer ones. The high number of total predicted moist species could be attributed to the fact that these guilds were originally composed by higher number of species (Table 2). However, guild 7 is composed by more species than guild 1 and the maximal predicted value is merely 3.567. This could let deduce that in the models of the moist guilds a correlation with some predictor is causing high predictions Indeed, by analysing the models' coefficients (see Annex 3), it emerged that wetlands have the strongest correlation of all guilds models' coefficients. This is in accordance with Steinmann *et al.* 2009, where they compared two modelling approaches and for both it resulted, that perennial plants richness in wetlands of Switzerland where the best predicted and resulted in high local abundance. The moist species require specific habitat conditions to grow, which are found in floodplains and moors. In Switzerland, these habitats are relatively well protected and inventoried (BAFU & BLW 2013). This would explain the observation pattern on the southern shore of lake Neuchatel (see Figure 5). Wetlands account mainly for the zero part of the moist guilds' model; other variables show higher correlations for the prediction of counts. For guild 1, *distance to water* is apparently a driver for higher counts, while in guild 2 (nutrient rich), intensive agriculture (*intensive pasture* and *nitrogen load*) leads to higher number of species. The variable *narrow wood* has a significant positive correlation with presence and count of guild 2. What is leading to this relationship is unclear. Marchand & Houle (2006) and Bailey *et al.* (2014) analysed the variation in species richness as a function of distance to forest edge in temperate southern Quebec, Canada. They found, that soil moisture and organic matter were higher at the edge than in the forest interior. These conditions would promote growth of guild 2. They also detected that plant species richness decreased with distance to the forest edge. These finding are possible explanations for the detected correlation of species richness with *narrow wood* in our model.

The models of the dry guilds have more predictors representing the absence/presence process than the count. *Road green*, *cropland* (guild 4) and *winter rape* (guild 5) have a positive correlation in the zero part. These predictors could be an effect of observation bias, explained above. Observations of plants are more probable to occur near roads and farmers must survey species, if they seek direct payments. Low number of predicted species in guild 4 and 5 are probably caused by insufficient predictors for the count part of the hurdle model (Table 4) ans/or by the low number of species representing them (Table 2). The inclusion of additional variables, could have improved the performance of these models. For example, the presence and intensity of herbivories could be worthy to integrate, since it has a strong impact on the habitat of dry grassland species (Zulka et al. 2014; Moore et al. 2015).

The sum of all guilds' predictions, was used to display the total species richness in the study area (Figure 9). Generally, regions with more observations points coincide with the cells with higher predicted species richness. This indicates that the observation bias could not successfully be removed during the model processing and it is affecting all guilds predictions. Hence, it is difficult to identify present valuable biodiversity hotspots. An attempt to highlight more valuable regions was done by standardising the predictions and trying to identify potential areas of occurrence for multiple guilds simultaneously, also described as functional diverse regions. Functionally diverse communities have more stable ecosystem functioning, and are resilient against stress or shock and are less likely to change their behaviour (Allan et al. 2011; Laurila-Pant et al. 2015). In the Broye region, these ecological valuable areas, where identified on the western part of Moudon and direction north along the river shore (Figure 10).

What is the effect of future changes regarding climatic drivers and land use practices on patterns of species richness?

The models of every guild, where run with modified datasets to produce species richness distribution maps for two future climate scenarios and four land use scenarios. The result of these models showed that warmer winter temperatures strongly increased the number of species in the region. Extensification of pastures had a clear positive effect on the number of species but only if implemented wide-ranging on all grasslands (land-sharing). The land-sparing scenario applied in this study, caused fragmentation of species richness and a significant decrease in total species amount.

The climate scenarios applied in this study (i.e. increasing the mean winter temperature by 2°C and 4°C) are a very simplified form. They do not take into account other aspects of climate change which also affect species richness, such as changes in precipitation patterns or extreme events (Theurillat & Guisan, 2001; de Chazal, 2009; CH2011, 2011; Bellard et al. 2012, Oijen et al. 2017). Only winter temperature increase is not a full representation of complex future climate in Switzerland and possible side-effects caused by an increase in temperature in winter, cannot be observed in these results. During the last 50 years the average temperatures in Switzerland increased while winter and spring precipitation decreased. This led to shifts in species distribution and composition, e.g. short-living and drought resistant species increased significantly (BAFU, 2017). Near the alpine region, warm-loving species tend to expand into higher altitudes (CH2011, 2011; Bellard et al. 2012). This may partly explain the higher increase rate of species richness in the upland of the Broye catchment in comparison to the lowland (Figure 12). However, through the predicted number of species, it is not possible to analyse the future composition of the species and the functional diversity, but only analyse the estimated total number of species. Bühler & Roth (2011) assessed the current trend in grassland vascular plants richness and dissimilarity (difference in composition between two sites) in Switzerland for the time periods 2001-2004 and 2006-2009. They found an increase in species richness but a decrease in dissimilarity which suggests a local-scale homogenization of grassland due to the spread of the more common species adapted to high nutrients and moderate temperature levels.

Cumulative and macroecological approaches assume that species are in a state of equilibrium (static) with the factors that determine their distribution, but group of specie (guilds or communities) are not moving as an entity under changing climatic conditions (D’Amen et al. 2017). With the macroecological approach it is not possible to simulate the individualistic behaviour of species, e.g. migration, seed dispersal, migration and adaptation (Guisan & Zimmermann, 2000; Latimier et al. 2006). By including these properties, as well as between-species interactions in the modelling process should improve the prediction in community shifts. Under this aspect, the cumulative approach is more suitable, because it is capable of taking into account responses as well as migration rates of different species (Ferrier & Guisan, 2006).

Of the four land use scenarios applied, three were different shares of extensive vs. intensive pasture. Under the moderate scenarios, with 20% and 40% extensification the species richness increased overall in the study area, but not as strong as for the temperature increase scenarios. The spatial pattern remained almost the same, as for the total current prediction map (Figure 9). In the land sharing scenario, all intensive pastures were converted into extensive ones (Figure 14 – land sharing). Here, a much clearer spatial pattern could be observed, with high number of species in the upland, probably due to more grasslands, and less species in the lowland. In contrary, the land sparing scenarios led to overall fewer species then the sharing scenario and no spatial subdivision could be observed. The scenarios proposed by the stakeholders were simplified into few criteria, in order to easily shape the dataset. Some other more precise aspects of the scenarios, could be integrated in the model (e.g. buffer zone around river, hedges, etc.) to produce more detailed prediction maps. Especially for the land sparing scenario, the results would probably show higher number of species.

In the research field of conservation biology, it is still highly debated, which strategy should provide the best results (Fischer et al. 2014, Barral et al. 2015). Land sharing would probably imply lower food production and only an extensification of grasslands could be insufficient to protect species, because conservation should achieve a network of high-quality grassland patches (Zulka et al. 2014). Land sparing would maintain constant food supply, but not provide fundamental interconnections between biodiversity hotspots. In addition, a community with low species richness, but composed by rare species is as important to protect as hotspots with a high number of species (Marchese, 2015).

Is it possible to identify potential regions for conservation or agricultural extensification?

The results produced by this study, do not allow to define clear and reliable present and future hotspot biodiversity regions. The different causes, where discussed in the previous sections. To predict such an output would require additional information about the species distribution in the region and maybe adopt another modelling approach. Spatial differences in species richness could be observed within the Broye region, mainly between the intensively managed lowland, which in average had lower species richness through all scenarios and the upland in the south. Based on what emerged from the stakeholders' scenario and the local management strategies, the land management strategy in the Broye region would be a combination of the two extreme scenarios presented in this study. However, the current trend is more toward a land sharing strategy, dictated by new measures (e.g. direct payments) promoting less intensive agriculture, while areas of intensive cropland (e.g. in the fertile lowland) and natural reservoirs (e.g. along river, forests) would be maintained or extended. Extensification of agricultural management would mainly take place in the upland and this would be supported by the results of this master's thesis.

6 Conclusions and Outlook

6.1 Summary and Conclusion

This study aimed at predicting future biodiversity hotspots, under climatic and land use changes within the Broye region. Loss of biodiversity is mainly caused by anthropogenically driven environmental changes. Among the major sources of pressure are climate change and intensification of agriculture (Secretariat of the Convention on Biological Diversity, 2014). To stem the persisting decrease in species richness it is important to understand the reaction of biodiversity to such changes. As shown in this study, statistical modelling represents a helpful tool to investigate these interactions. Biodiversity has been modelled for an agroecosystem at regional scale, with integration of both climate and land use predictors.

For the Broye catchment, the application of a statistical hurdle model technique allowed to recognize significant interactions between the species richness in grasslands and a selection of environmental factors. Common and rare grassland species of the region were selected and used as biodiversity indicators. These were merged into five guilds according to their preferences in moisture and nutrients availability. The combination of predictors and the strength of interactions varied between the five different guilds. For the two moist guilds the model performance was better than for the dryer groups. By merging the predicted distribution maps of all guilds it allowed to recognize spatial patterns of potential grassland species richness. However, the results could not be efficiently uncoupled from the observation bias, which influenced the distribution maps of all guilds. Therefore, the spatial patterns did not vary substantially in the single guilds and in the summed maps. Nevertheless, future changes in grassland plant species richness could be modelled by changing significantly correlated predictors. Mean winter temperature was increased to predict species richness under two scenarios of warmer climate. Furthermore, four land use scenarios (two levels of pastures extensification, a land sharing and a land sparing scenario) were implemented to assess the impacts of different agriculture management on grassland plants richness. An increase in winter temperature considerably increased the number of species. On the other hand moderate extensification of pastures did not show a high increase in species abundance. For the extreme land use scenarios, land sharing and land sparing, the first one demonstrated higher count values over an extended area; while for the second one the number of predicted species decreased, with exception for a few patches. To identify potential biodiversity hotspot regions that could be particularly worthy to be protected or extensified in the next 30 years, a combined scenario, with a 2° C increase in winter temperature and a 20% extensification of pastures was applied. The results suggested that the actual spatial pattern of regions with high species richness would remain more or less stable. For this future scenario, the upland of the Broye catchment would profit the most in terms of total amount of grassland species.

Although biodiversity is too complex to be modelled as a single entity, this study showed that some aspects of it, with regard to specific species in particular habitats can be analysed by simple statistical approaches like a general linear regression model. However, this depends on the existence of reliable observation data which is not always available. The combination of bioclimatic, edaphic and land use variables can improve the model performance compared to a pure bioclimatic model (Pompe et al. 2008). The correlations between environmental factors and species richness can be analysed with a linear regression model, while understanding the complex interactions which cause actual and future shifts in grassland biodiversity of agroecosystems requires more precise data and may a different methodical approach. Biodiversity conservation strategies are imbedded in local socioeconomic contexts. Modelling at a regional scale can help to better understand the relevant environmental processes. To predict and identify potential future biodiversity conservation areas, involving local stakeholders in the definition of future land use scenarios, can improve the applicability of the results.

6.2 Outlook

Biodiversity is the basis of many ecosystem services. Biodiversity-ecosystem functioning relationships are affected by the number and identities of species, with species rich communities tending to perform better than species poor systems (Allan et al., 2011; Laurila-Pant et al., 2015; Oijen et al. 2017). Predicting spatial patterns of species richness remains challenging (D’Amen et al., 2017). Coarse and unsystematically surveyed biological data do not provide a reliable assessment of species distribution and of conservation areas across a landscape (Mossman et al., 2015). More collection data from all types of habitats will be required in the future to enhance the predictive capacity of biodiversity models. Improvements have been achieved with regard to integrating collection data from the field with remote-sensed data (Ferrier et al. 2017). To achieve more efficient regional conservation strategies in agroecosystems, more efforts should be put on improving biodiversity modelling at a landscape scale (Billeter et al., 2008). New methods that consider multiple aspects of biodiversity could help to provide new insights into the mechanisms that determine the current patterns of biological diversity (Marchese 2015). Modelling interactions between climate change, biodiversity and agricultural productivity could benefit from integrating different modelling approaches across different spatial scales (Oijen et al.; 2017). There is still a huge margin of improvement and very high potential available for biodiversity modelling in the years to come.

References

Adler, P.B., Leiker, J. & Levine, J.M., 2009. Direct and indirect effects of climate change on a prairie plant community. *PLoS ONE*, 4(9), pp.1–6.

Allan, E. et al., 2011. More diverse plant communities have higher functioning over time due to turnover in complementary dominant species. *Proceedings of the National Academy of Sciences*, 108(41), pp.17034–17039.

Altieri, M.A., 1999. The ecological role of biodiversity in agroecosystems. *Agriculture, Ecosystems and Environment*, 74(1–3), pp.19–31.

BAFU, 2013. Fliessgewässertypisierung der Schweiz. Eine Grundlage für Gewässerbeurteilung und -entwicklung, Bundesamt für Umwelt, Umwelt-Wissen Nr. 1329, p.63.Altieri, M.A., 1999. The ecological role of biodiversity in agroecosystems. *Agriculture, Ecosystems and Environment*, 74(1–3), pp.19–31.

BAFU, 2015. Abschätzung diffuser Stickstoff- und Phosphoreinträge in die Gewässer der Schweiz MODIFFUS 3.0, Bundesamt für Umwelt, p.117.

BAFU, 2017a. Biodiversität in der Schweiz : Zustand und Entwicklung. Ergebnisse des Überwachungssystems im Bereich Biodiversität, Stand 2016. Bundesamt für Umwelt, Bern. *Umwelt-Zustand* Nr. 1630, p.60.

BAFU, 2017b. Bundesrat beschliesst den Aktionsplan zur Erhaltung und Förderung der Biodiversität. Bundesamt für Umwelt, Bern, [accessed on 7.09.2017] https://www.bafu.admin.ch/bafu/de/home/themen/biodiversitaet/mitteilungen.msg-id-68017.html.

BAFU & BLW, 2008. Umweltziele Landwirtschaft: Hergeleitet aus bestehenden rechtlichen Grundlagen. Bundesamt für Umwelt und Bundesamt für Landwirtschaft, *Umwelt-Wissen* Nr. 0820, p.221.

BAFU & BLW, 2013. Operationalisierung der Umweltziele Landwirtschaft. Bundesamt für Umwelt und Bundesamt für Landwirtschaft, *ART-Schriftenreihe*, 18, p.136.

Bailey, S. et al., 2014. Distance from forest edge affects bee pollinators in oilseed rape fields. *Ecology and Evolution*, 4(4), pp.370–380.

Barral, M.P. et al., 2015. Quantifying the impacts of ecological restoration on biodiversity and ecosystem services in agroecosystems: A global meta-analysis. *Agriculture, Ecosystems and Environment*, 202, pp.223–231.

Bellard, C., Bastawrous, M. & Hennig, B., 2012. Impacts of Climate Change on the Future of Biodiversity. *Ecology Letters*, 15(4), pp.365–377.

BFS, 2012. Soil suitability map of Switzerland. Bundesamt für Statistik, Neuchatel.

BFS, 2016. Arealstatistik der Schweiz. Bundesamt für Statistik, Neuchatel.

Billeter, R. et al., 2008. Indicators for biodiversity in agricultural landscapes: a pan-European study. *Journal of Applied Ecology*, 45, pp.141–150.

Bird, T.J. et al., 2014. Statistical solutions for error and bias in global citizen science datasets. *Biological Conservation*, 173, pp.144–154.

BLW, 2014. Weisungen nach Artikel 59 und Anhang 4 der Verordnung über die Direktzahlungen an die Landwirtschaft (Direktzahlungsverordnung, DVZ) – Extensiv genutzte Weiden und Wiesen der Qualitätsstufe II. Bundesamt für Landwirtschaft.

BLW, 2015. Agrarpolitische Informationssystem AGIS 2014. Bundesamt für Landwirtschaft.

Bühler, C. & Roth, T., 2011. Spread of common species results in local-scale floristic homogenization in grassland of Switzerland. *Diversity and Distributions*, 17(6), pp.1089–1098.

Büchs, W., 2003. Biotic indicators for biodiversity and sustainable agriculture - Introduction and background. *Agriculture, Ecosystems and Environment*, 98(1–3), pp.1–16.

Cameron, A.C. & Trivedi, P.K., 1999. Essentials of Count Data Regression. *A Companion to Theoretical Econometrics*, pp.331–348.

CH2011, 2011. Swiss Climate Change Scenarios CH2011, published by C2SM, MeteoSwiss, ETH, NCCR Climate, and OcCC, p. 88.

D’Amen, M. et al., 2017. Spatial predictions at the community level: from current approaches to future frameworks. *Biological Reviews*, 92(1), pp.169–187.

de Chazal, J. & Rounsevell, M.D.A., 2009. Land-use and climate change within assessments of biodiversity change: A review. *Global Environmental Change*, 19(2), pp.306–315.

Dormann, C. F. et al., 2007. Methods to account for spatial autocorrelation in the analysis of species distributional data: A review. *Ecography*, 30(5), pp.609–628.

Duelli, P., Obrist, M.K. & Schmatz, D.R., 1999. Biodiversity evaluation in agricultural landscapes: Above-ground insects. *Agriculture, Ecosystems and Environment*, 74(1–3), pp.33–64.

Duelli, P. & Obrist, M.K., 2003. Biodiversity indicators: The choice of values and measures. *Agriculture, Ecosystems and Environment*, 98(1–3), pp.87–98.

Ferrier, S., 2002. Mapping Spatial Pattern in Biodiversity for Regional Conservation Planning: Where to from Here? *Systematic Biology*, 51(2), pp.331–363.

Ferrier, S. et al., 2002. Extended statistical approaches to modelling spatial pattern in biodiversity in northeast New South Wales. II. *Biodiversity and Conservation*, 11(12), pp.2309–2338.

Ferrier, S. & Guisan, A., 2006. Spatial modelling of biodiversity at the community level. *Journal of Applied Ecology*, 43(3), pp.393–404.

Ferrier, S., Jetz, W. & Scharlemann, J., 2017. Chapter 10: Biodiversity Modelling as Part of an Observation System. In *The GEO Handbook on Biodiversity Observation Networks*. pp. 239–257.

Fischer, J. et al., 2014. Land sparing versus land sharing: Moving forward. *Conservation Letters*, 7(3), pp.149–157.

Fuhrer et al., 2013. Water demand in Swiss agriculture - sustainable adaptive options for land and water management to mitigate impacts of climate change. *ART-Schriftenreihe*, (19), p.56 pp.

Grau, R., Kuemmerle, T. & Macchi, L., 2013. Beyond “land sparing versus land sharing”: Environmental heterogeneity, globalization and the balance between agricultural production and nature conservation. *Current Opinion in Environmental Sustainability*, 5(5), pp.477–483.

Guisan, A. & Rahbek, C., 2011. SESAM - a new framework integrating macroecological and species distribution models for predicting spatio-temporal patterns of species assemblages. *Journal of Biogeography*, 38(8), pp.1433–1444.

Guisan, A. & Zimmermann, N.E., 2000. Predictive habitat distribution models in ecology. *Ecological Modelling*, 135, pp.147–186.

Hammond, A. et al., 1995. Environmental Indicators : A Systematic Approach to Measuring Sustainable Development, World Resources Institute, p.58.

Herzog, E.F. et al., 2012. Biodiversity Indicators for European Farming Systems - A Guidebook. *ART-Schriftenreihe*, p.105.

InfoFlora, 2017. Raw data: maximal available accuracy (presence data per 100x100m), Das Nationale Daten- und Informationszentrum der Schweizer Flora, Bern, [Received on 25.01.2017].

Korner-Nievergelt, F. et al., 2015. Model Selection and Multimodel Inference. In *Bayesian Data Analysis in Ecology Using Linear Models with R, BUGS, and STAN*. pp. 175–196.

Landolt, E. et al., 2010. *Flora indicativa - Ökologische Zeigerwerte und biologische Kennzeichen zur Flora der Schweiz und der Alpen*, 2. Auflage, p.325.

Latimer, A.M. et al., 2010. Building Statistical Moels To Analyze Species Distributions. *Ecological Applications*, 16(1), pp.33–50.

Laurila-Pant, M. et al., 2015. How to value biodiversity in environmental management? *Ecological Indicators*, 55, pp.1–11.

Lehmann, A., Overton, J.M. & Austin, M.P., 2002. Regression models for spatial prediction: Their role for biodiversity and conservation. *Biodiversity and Conservation*, 11(12), pp.2085–2092.

Marchand, P. & Houle, G., 2006. Spatial patterns of plant species richness along a forest edge: What are their determinants? *Forest Ecology and Management*, 223(1–3), pp.113–124.

Marchese, C., 2015. Biodiversity hotspots: A shortcut for a more complicated concept. *Global Ecology and Conservation*, 3, pp.297–309.

Martin, T.G. et al., 2005. Zero tolerance ecology: Improving ecological inference by modelling the source of zero observations. *Ecology Letters*, 8(11), pp.1235–1246.

Mclaughlin, A. & Mineau, P., 1995. The impact of agricultural practices on biodiversity. *Agriculture, Ecosystems and Environment*, 55, pp.201–212.

MeteoSchweiz, 2016. Monthly and Yearly Mean Temperature: TabsM and TabsY. Swiss Federal Office of Meteorology and Climatology.

Mod, H.K. et al., 2016. What we use is not what we know: environmental predictors in plant distribution models. *Journal of Vegetation Science*, 27(6), pp.1308–1322.

Moore, E.K. et al., 2015. Landscape-scale vegetation patterns influence small-scale grazing impacts. *Biological Conservation*, 192, pp.218–225.

Morrison, L.W., 2016. Observer error in vegetation surveys: A review. *Journal of Plant Ecology*, 9(4), pp.367–379.

Mossman, H.L., Panter, C.J. & Dolman, P.M., 2015. Modelling biodiversity distribution in agricultural landscapes to support ecological network planning. *Landscape and Urban Planning*, 141, pp.59–67.

OECD, 1996. Environmental indicators for agriculture - Vol. 3 Methods and Results. Organisation for Economic Co-Operation and Development, p.400.

Oijen, M. Van & Bellocchi, G., 2017. Effects of Climate Change on Grassland Biodiversity and Productivity : The Need for a Diversity of Models. *Preprints*, (December).

Pearce, J.L. & Boyce, M.S., 2006. Modelling distribution and abundance with presence-only data. *Journal of Applied Ecology*, 43(3), pp.405–412.

Pearson, R.G., Dawson, T.P. & Liu, C., 2004. Modelling species distributions in Britain: A hierarchical integration of climate and land-cover data. *Ecography*, 27(3), pp.285–298.

Peters, V.E. et al., 2016. Ants and plants as indicators of biodiversity, ecosystem services, and conservation value in constructed grasslands. *Biodiversity and Conservation*, 25(8), pp.1481–1501.

Pfestorf, H. et al., 2013. Community mean traits as additional indicators to monitor effects of land-use intensity on grassland plant diversity. *Perspectives in Plant Ecology, Evolution and Systematics*, 15(1), pp.1–11.

Plantureux, S., Peeters, a & McCracken, D., 2005. Biodiversity in intensive grasslands : Effect of management , improvement and challenges. *Agronomy Research*, 3(2), pp.153–164.

Pompe, S. et al., 2008. Climate and land use change impacts on plant distributions in Germany. *Biology Letters*, 4(5), pp.564–567.

Potts, J.M. & Elith, J., 2006. Comparing species abundance models. *Ecological Modelling*, 9, pp.153–163.

Reidsma, P. et al., 2006. Impacts of land-use change on biodiversity: An assessment of agricultural biodiversity in the European Union. *Agriculture, Ecosystems and Environment*, 114(1), pp.86–102.

Root, T. et al., 2003. Fingerprints of global warming on wild animals and plants. *Nature*, 421(6918), pp.57–60.

Schirpke, U. et al., 2017. Future impacts of changing land-use and climate on ecosystem services of mountain grassland and their resilience. *Ecosystem Services*, 26, pp.79–94.

Secretariat of the Convention on Biological Diversity, 2014. *Global Biodiversity Outlook 4*. Montréal, p.115.

Shoyama, K. & Yamagata, Y., 2014. Predicting land-use change for biodiversity conservation and climate-change mitigation and its effect on ecosystem services in a watershed in Japan. *Ecosystem Services*, 8, pp.25–34.

Steinmann, K., Linder, H.P. & Zimmermann, N.E., 2009. Modelling plant species richness using functional groups. *Ecological Modelling*, 220(7), pp.962–967.

Stolar, J. & Nielsen, S.E., 2015. Accounting for spatially biased sampling effort in presence-only species distribution modelling. *Diversity and Distributions*, 21(5), pp.595–608.

Swisstopo, 2001, DHM25: Das Digitale Höhenmodell der Schweiz. Bundesamt für Landestopographie.

Theurillat, J. & Guisan, A., 2001. Potential Impact of Climate Change on Vegetation in the European Alps : A Review. *Climate Change*, 50, pp.77–109.

UFZ, 2015. Towards multifunctional agricultural landscapes in Europe: Assessing and governing synergies between food production, biodiversity, and ecosystem services – TALE, [accessed on 15.11.2016], http://www.ufz.de/tale/

Ver, J.M., Boveng, P.L. & Jay, M., 2015. Quasi-Poisson vs. Negative Binomial Regression: How Should We Model Overdispersed Count Data?. *Ecology*, 88(11), pp.2766–2772.

Vittinghoff, E. et al., 2012. *Regression Methods in Biostatistics – Linear, Logistic, Survival and Repeated Measures Models*, second edition. P.501

Warton, D.I., Renner, I.W. & Ramp, D., 2013. Model-based control of observer bias for the analysis of presence-only data in ecology. *PLoS ONE*, 8(11).

Xu, Q.S., Liang, Y.Z. & Du, Y.P., 2004. Monte Carlo cross-validation for selecting a model and estimating the prediction error in multivariate calibration. *Journal of Chemometrics*, 18(2), pp.112–120.

Zeileis, A., Kleiber, C. & Jackman, S., 2008. Regression models for count data in R. *Journal of Statistical Software*, 27(8), pp.1–25.

Zulka, K.P. et al., 2014. Species richness in dry grassland patches of eastern Austria: A multi-taxon study on the role of local, landscape and habitat quality variables. *Agriculture, Ecosystems and Environment*, 182, pp.25–36.

Zuur, A.F. et al., 2009. Chapter 11: Zero-Truncated and Zero-Inflated Models for Count Data. In *Mixed effects models and extensions in ecology with R*. pp. 261–293.

Appendix

Annex 1

Guild 1: moist & nutrient poor
Anthoxanthum odoratum L.
Carex buxbaumii Wahlenb.
Carex hostiana DC.
Eriophorum angustifolium Honck.
Gentiana pneumonanthe L.
Gymnadenia conopsea (L.) R. Br.
Lathyrus palustris L.
Misopates orontium (L.) Raf.
Molinia arundinacea Schrank
Molinia caerulea (L.) Moench
Ophioglossum vulgatum L.
Parnassia palustris L.
Polygala amarella Crantz
Potentilla erecta (L.) Raeusch.
Primula farinosa L.
Rhinanthus minor L.
Trifolium fragiferum L.

Guild 2: moist & nutrient rich
Bromus secalinus L.
Caltha palustris L.
Carex appropinquata Schumach.
Carex elata All.
Carex otrubae Podp.
Carex vesicaria L.
Cyperus fuscus L.
Euphorbia palustris L.
Hypericum humifusum L.
Hypericum perforatum L. s.str.
Hypericum tetrapterum Fr.
Kickxia spuria (L.) Dumort.
Knautia dipsacifolia Kreutzer s.str.
Lathyrus pratensis L.
Leontodon hispidus L. s.str.
Leucanthemum vulgare Lam.
Listera ovata (L.) R. Br.
Lythrum portula (L.) D. A. Webb
Medicago lupulina L.
Ornithogalum nutans L.
Primula elatior (L.) L. s.str.
Rhinanthus alectorolophus (Scop.) Pollich
Stachys palustris L.
Thalictrum flavum L.
Valeriana officinalis L.
Vicia cracca L. s.str.

Guild 3: moist & nutrient neutral
Anthriscus cerefolium (L.) Hoffm.
Aristolochia clematitis L.
Cirsium oleraceum (L.) Scop.
Conium maculatum L.
Dipsacus pilosus L.
Filipendula ulmaria (L.) Maxim.
Picris echioides L.
Sanguisorba officinalis L.
Spergula arvensis L.

Guild 4: dry & nutrient poor
Carex flacca Schreb.
Clinopodium vulgare L.
Daucus carota L.
Gentiana germanica Willd.
Luzula campestris (L.) DC.
Luzula multiflora (Ehrh.) Lej.
Ononis repens L.
Orchis militaris L.
Orchis morio L.
Primula veris L. s.str.

Guild 5: moist & nutrient rich
Bromus commutatus Schrad.
Centaurea cyanus L.
Centaurea jacea L. s.str.
Consolida regalis Gray
Helictotrichon pubescens (Huds.) Pilg.
Knautia arvensis (L.) Coult.
Legousia speculum-veneris (L.) Chaix
Ranunculus arvensis L.
Tragopogon pratensis subsp. orientalis (L.) Celak.
Tulipa sylvestris L. s.str.

Guild 6: dry & nutrient neutral
Hyoscyamus niger L.
Leonurus cardiaca L.
Verbascum blattaria L.

Guild 7: fresh & nutrient poor
Acinos arvensis (Lam.) Dandy
Briza media L.
Bromus erectus Huds. s.str.
Centaurea scabiosa L. s.str.
Euphorbia cyparissias L.
Helianthemum nummularium subsp. obscurum (Celak.) Holub
Hieracium pilosella L.
Hippocrepis comosa L.
Onobrychis viciifolia Scop.
Ononis spinosa L. s.str.
Ophrys apifera Huds.
Ophrys holosericea (Burm. f.) Greuter s.str.
Polygala comosa Schkuhr
Polygala vulgaris L. s.str.
Ranunculus bulbosus L.
Salvia pratensis L.
Sanguisorba minor Scop s.str
Sedum album L.
Silene nutans L. s.str.
Stachys recta L. s.str.
Thymus pulegioides L. s.str.

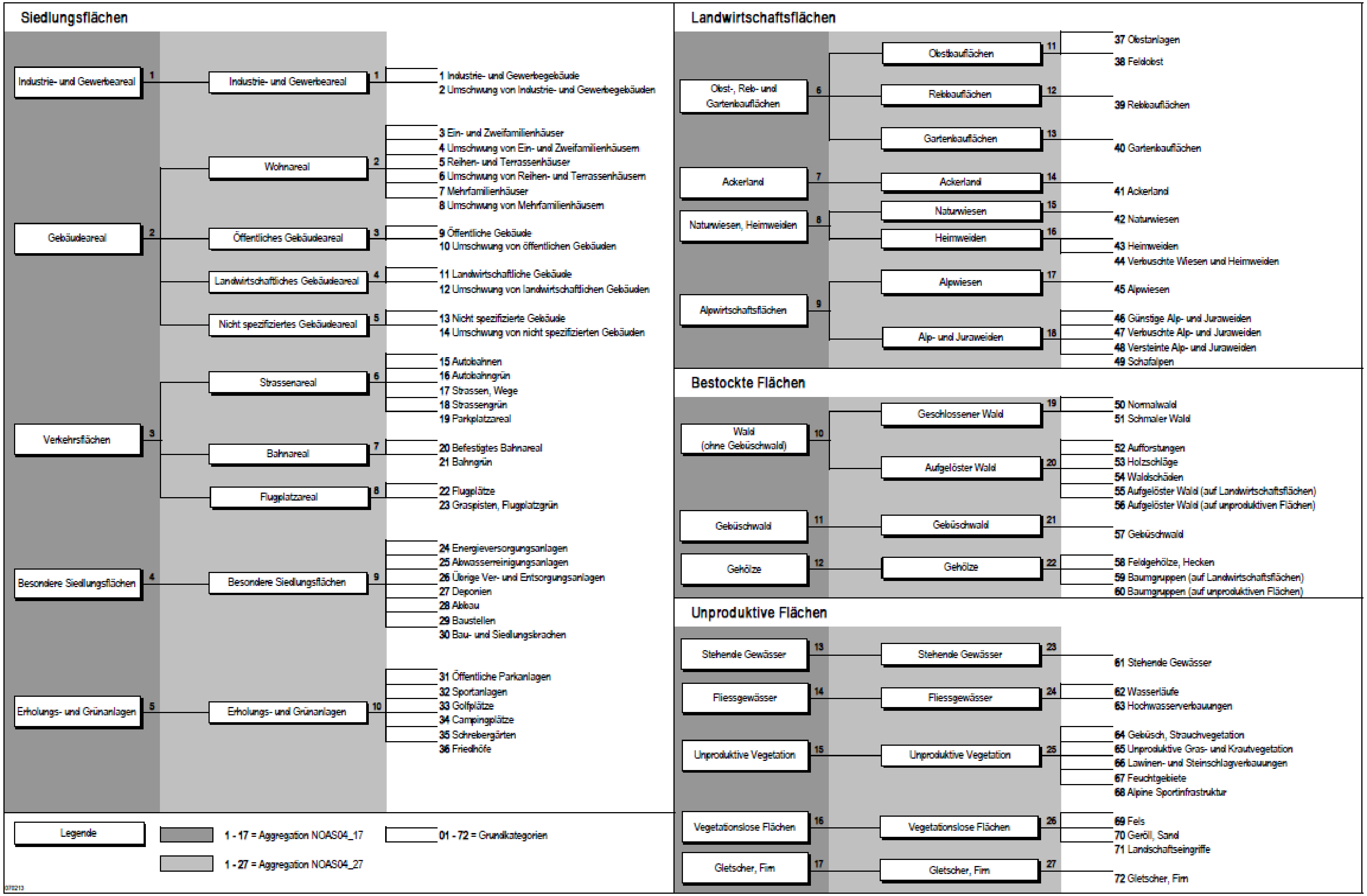
Guild 8: fresh & nutrient rich
Agrimonia eupatoria L.
Campanula rapunculoides L.
Campanula rapunculus L.
Lathyrus tuberosus L.
Origanum vulgare L.
Plantago media L.
Sedum sexangulare L.
Sedum telephium L. s.str.
Tragopogon pratensis subsp. minor (Mill.) Hartm.
Veronica triphyllos L.

Guild 9: fresh & nutrient neutral
Onopordum acanthium L.
Tragopogon dubius Scop.
Verbascum phlomoides L.

Annex 2

Arealstatistik Schweiz — Standardnomenklatur NOAS04: Grundkategorien und Aggregationen

BFS, Arealstatistik 2006



Annex 3

Guild 1 - zero			
	estimate_mean	std_mean	p_mean
(Intercept)	-2.1998	0.0675	2.00E-228
scale(AS_67)	0.6412	0.0942	4.59E-09
scale(Temp_Winter_mean)	0.2749	0.0677	0.000571879
scale(Pasture_Intensive)	-0.2721	0.0578	3.85E-05
scale(N_Load_mean)	-0.2375	0.0724	0.002587678
Guild 1 - count			
(Intercept)	0.1455	0.0718	0.108421382
scale(AS_67)	0.0988	0.0081	5.75E-22
scale(AS_56)	0.0744	0.0149	0.002096383
scale(Dist_Water_mean)	-0.3422	0.0706	0.000423223
scale(N_Load_mean)	-0.1875	0.0661	0.018545666

p < 0.05
p < 0.01
p < 0.001

Guild 2 - zero			
	estimate_mean	std_mean	p_mean
(Intercept)	-1.0864	0.0480	1.07E-106
scale(AS_67)	0.8459	0.1260	6.12E-11
scale(AS_51)	0.1662	0.0453	0.000830332
scale(Temp_Winter_mean)	0.1650	0.0553	0.009731697
scale(Waterlogging_major)	0.1272	0.0466	0.012623898
scale(Dist_Buildungs_mean)	-0.0867	0.0475	0.109465315
scale(AS_42)	-0.2441	0.0677	0.001005215
scale(N_Load_mean)	-0.3227	0.0558	2.12E-07
scale(Pasture_Intensive)	-0.2522	0.0467	2.83E-07
scale(Meadow_Intensive)	-0.2056	0.0649	0.004448759
Guild 2 - count			
(Intercept)	0.6931	0.0325	2.24E-83
scale(AS_67)	0.1157	0.0070	1.12E-47
scale(AS_51)	0.1090	0.0213	0.000138499
scale(AS_62)	0.1157	0.0189	0.000341848
scale(Waterlogging_major)	0.2250	0.0213	9.37E-20
scale(Dist_Buildungs_mean)	-0.1257	0.0261	0.000784145
scale(N_Load_mean)	-0.1713	0.0335	0.000147212
scale(Meadow_Intensive)	-0.1648	0.0305	8.37E-05

Guild 4 - zero			
	estimate_mean	std_mean	p_mean
(Intercept)	-1.6258	0.0541	6.45E-195
scale(Temp_Winter_mean)	0.3788	0.0568	1.81E-09
scale(Slope_std)	0.2796	0.0558	3.99E-06
scale(AS_18)	0.1478	0.0467	0.004033822
scale(CropLand)	0.3093	0.1372	0.038869479
scale(N_Load_mean)	-0.3695	0.1459	0.01784855
scale(Pasture_Intensive)	-0.2632	0.0495	8.84E-07
Guild 4 - count			
(Intercept)	0.3179	0.0506	4.17E-07
scale(Temp_Winter_mean)	0.1954	0.0384	3.94E-05
scale(N_Load_mean)	-0.3903	0.0522	3.05E-11

Guild 5 - zero			
	estimate_mean	std_mean	p_mean
(Intercept)	-2.0122	0.0640	1.74E-215
scale(Temp_Winter_mean)	0.2415	0.0642	0.000411384
scale(Winter_Rape)	0.3084	0.0546	3.48E-07
scale(Slope_std)	0.3898	0.0640	1.14E-08
scale(AS_50)	-0.3833	0.0768	2.13E-06
scale(Pasture_Intensive)	-0.3335	0.0527	3.21E-08
Guild 5 - count			
(Intercept)	0.2162	0.0584	0.001318245
scale(Prec_Autumn_mean)	0.1424	0.0407	0.011333543
scale(Aspect_std)	-0.2369	0.0550	0.000200831

Guild 7 - zero			
	estimate_mean	std_mean	p_mean
(Intercept)	-1.7883	0.0586	4.17E-202
scale(Temp_Winter_mean)	0.3925	0.0576	4.67E-10
scale(AS_51)	0.1309	0.0499	0.016931105
scale(AS_18)	0.1836	0.0481	0.002628109
scale(Slope_std)	0.3719	0.0549	1.73E-10
scale(Dist_Buildungs_mean)	-0.2311	0.0629	0.000945804
scale(Permeability_major)	-0.1296	0.0495	0.018578901
scale(Pasture_Intensive)	-0.3021	0.0507	1.79E-08
Guild 7 - count			
(Intercept)	0.4297	0.0488	4.85E-11
scale(Temp_Winter_mean)	0.3224	0.0420	5.57E-10
scale(Prec_Summer_mean)	0.1962	0.0503	0.002782373
scale(Permeability_major)	-0.1556	0.0294	2.99E-05

Declaration

under Art. 28 Para. 2 RSL 05

Last, first name:	Bussani, Luca		
Matriculation number:	11-744-117		
Programme:	Master in Climate Science		
	Bachelor ☐	Master ☐	Dissertation ☐
Thesis title:	Grassland biodiversity indicators in the Western Swiss Plateau – Modelling possible impacts of climate vs. management changes		
Thesis supervisor:	Prof. Dr. Annelie Holzkämper		

I hereby declare that this submission is my own work and that, to the best of my knowledge and belief, it contains no material previously published or written by another person, except where due acknowledgement has been made in the text. In accordance with academic rules and ethical conduct, I have fully cited and referenced all material and results that are not original to this work. I am well aware of the fact that, on the basis of Article 36 Paragraph 1 Letter o of the University Law of 5 September 1996, the Senate is entitled to deny the title awarded on the basis of this work if proven otherwise. I grant inspection of my thesis.

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Place, date

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Signature