Wettelijke Onderzoekstaken Natuur & Milieu

BioScore 2 – Plants & Mammals

Background and pre-processing of distribution data

WOt-technical report 50

S.M. Hennekens, J.M. Hendriks, W.A. Ozinga, J.H.J. Schaminée & L. Santini

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Abstract
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This report highlights the background and pre-processing of the distribution of plant species, habitats and mammal species. For plants a selection of about 900 taxa has been made, based on 45 Annex I habitat types, which represent a substantial part of European natural and semi-natural vegetation. For animals all species existing in Europe have been taken into account. The data covers more or less all EU28 countries and is pre-processed in three steps to feed the BioScore 2 model. In the first step for each species or habitat type a climate/soil model has been created by using Boosted Regression Models (GBM). On the basis of these models presence/absence maps are derived to define the distribution range of the species/habitat types. In the second step additional knowledge was brought in to further specify the potential habitat within the distribution range, by laying an explicit mask over it, selecting only those land use types (land cover classes) suitable for the occurrence of the habitat type or species. In the third step the effect of human-induced pressures on habitat quality and species occurrence/abundance within the suitable habitats in the calculated distribution ranges was taken into account. The dose-effect relations were calculated on the basis of Generalized Linear Models (GLM). All outcomes of the three steps have been further used by the Netherlands Environmental Assessment Agency (PBL) to set up the BioScore 2 model.

Keywords: BioScore 2, Plants, Mammals, Species distribution, Multivariate regression models, Univariate regression models, TRIMMaps, European Vegetation Archive, Drivers, Pressures.

Referaat
Hennekens, S.M., J.M. Hendriks, W.A. Ozinga, J.H.J. Schaminée & L. Santini (2015). *BioScore 2 – Planten & Zoogdieren. Achtergronden en voorbewerking van verspreidingsgegevens*. Wettelijke Onderzoekstaken Natuur & Milieu. WOt-technical report 50. 221 blz.; div. figs.; div. tabs.; 14 refs.; 10 bijlagen.

Dit rapport belicht de achtergrond en voorbewerking van de verspreidingsgegevens van planten, habitats en zoogdieren. Voor planten is een selectie van ongeveer 900 taxa gemaakt op basis van 45 Annex I habitattypen, waarvoor de taxa min of meer typerend zijn. Voor de zoogdieren zijn alle in Europa voorkomende soorten in de analyse betrokken. De gegevens omvatten een groot deel van Europa en zijn in drie stappen bewerkt om uiteindelijk als basis te dienen voor het BioScore 2-model. In de eerste stap is voor iedere soort en habitattype een klimaat/bodem-model opgesteld met behulp van zogenaamde Boosted Regression Models (GBM). Op basis van deze modellen zijn presentie/absentie-kaarten opgesteld die de potentiële verspreiding van de soorten/habitattypen weergeeft. In de tweede stap is aanvullende kennis ingebracht om het potentiële habitat verder te preciseren. Dit is gedaan door een overlap te maken met de CLC-kaart (Corine Land Cover), nadat habitattypen en soorten aan specifieke landgebruiksklassen waren gekoppeld. Vervolgens zijn in de derde stap, binnen de potentiële verspreiding van de soorten en habitats, positieve en negatieve waarnemingen geselecteerd om dosis-effectrelaties op te stellen voor een aantal drukfactoren (o.a. stikstof- en zwaveldepositie, verdroging, fragmentatie). The dosis-effectrelaties zijn berekend op basis van zogenaamde Generalized Linear Models (GLM). De uitkomsten van alle drie de stappen zijn verder gebruikt door het Planbureau voor de Leefomgeving (PBL) om het BioScore 2-model op te stellen.

Trefwoorden: BioScore 2, Planten, Zoogdieren. Soortsverspreiding, Multivariate regressie modellen, Univariate regressie modellen, TRIMMaps, European Vegetation Archive, Drivers, Drukfacturen.

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Preface

In 2009 the BioScore biodiversity impact assessment tool was developed as part of a research project funded by EC DG Research and Technological Development FP6. The project was coordinated by the European Centre for Nature Conservation (ECNC) and implemented by a consortium of nine partners. The Netherlands Environmental Assessment Agency (PBL), together with Alterra Wageningen UR, was in charge of the technical development of the BioScore database and web tool. At the time of delivery it was recognized that BioScore was a first version and that there was much room for improvement.

Since then PBL has been actively using the BioScore tool for a number of Europe-wide scenario studies. Currently PBL is further developing BioScore 1.0 into BioScore 2.0 so that it can be used for the Netherlands Nature Assessment (Nature Outlook) 2016.

The Nature Outlook is produced every four years. It provides a perspective of nature and policy options for the next 30-40 years. Until now these assessments were restricted to the Netherlands. As national nature policy is increasingly decided at EU level, the Dutch government requested PBL to expand the study area to cover the whole EU28. However, PBL is politically independent as guaranteed by Dutch law. The Nature Outlook therefore offers an independent view, which may differ from Dutch national policy.

PBL initiated and financed BioScore 2.0, which it develops together with some old and new partners. This consortium enables PBL to deliver a new version of BioScore, which will be tested in 2015 and 2016 and applied in the Nature Outlook project. Information on species distribution and sensitivity to various environmental pressures was brought together and moulded into an improved model concept together with the following partners:

- European Bird Census Council / Henk Sierdsema, Sovon (NL);
- Butterfly Conservation Europe / Chris van Swaay, Vlinderstichting, (NL);
- European Vegetation Survey / Stephan Hennekens & Joop Schaminée, Alterra Wageningen UR, (NL);
- European Mammal Society / Carlo Rondinini, Sapienza University Rome, (It).

Stephan Hennekens, Marjon Hendriks, Wim Ozinga, Joop Schaminée & Luca Santini

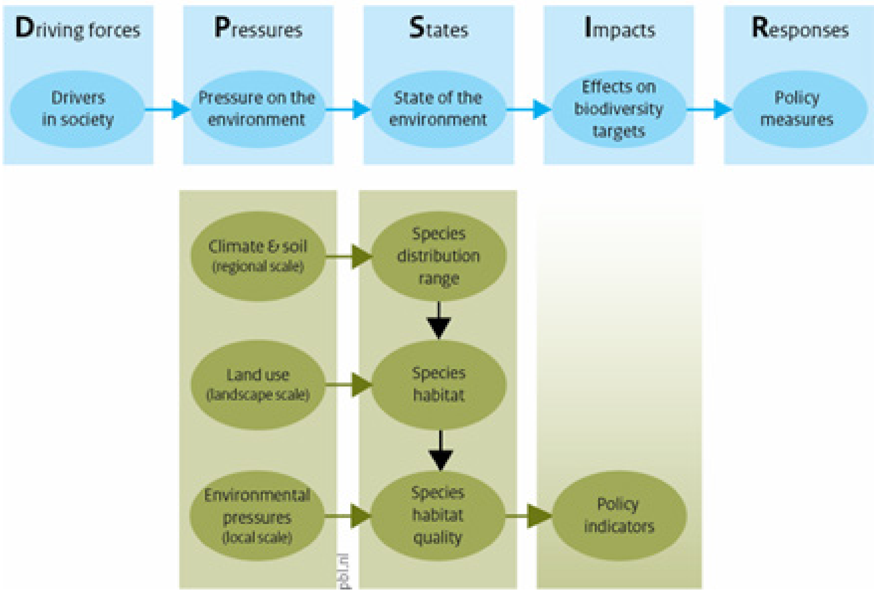
Contents

Summary

This report provides background information about the work on plant species and Natura 2000 habitats performed by Alterra Wageningen UR. The results of this work, dose-response functions for 45 Annex I habitat types and about 900 related plant species, serves as input for the new version of BioScore (2.0) to assess the impact of human-induced, and often policy driven pressures like desiccation, nitrogen and sulphur deposition and land use change. The report on mammals is also included in this report in Appendix 10, because the work on the distribution and dose-response functions of mammals was subcontracted by Alterra to Sapienza University of Rome.

General information on the conceptual framework of BioScore and a description of the relevant policy questions for BioScore 2.0 are explained in detail in the report 'BioScore 2.0. A tool to assess the impacts of European Community policies on Europe's biodiversity' (Van Hinsberg *et al.*, 2014). This report was written for the international review commission and provides background information about ongoing work. The meeting of consortium partners of the BioScore 2 project with the review commission took place on the 16th of October 2014.

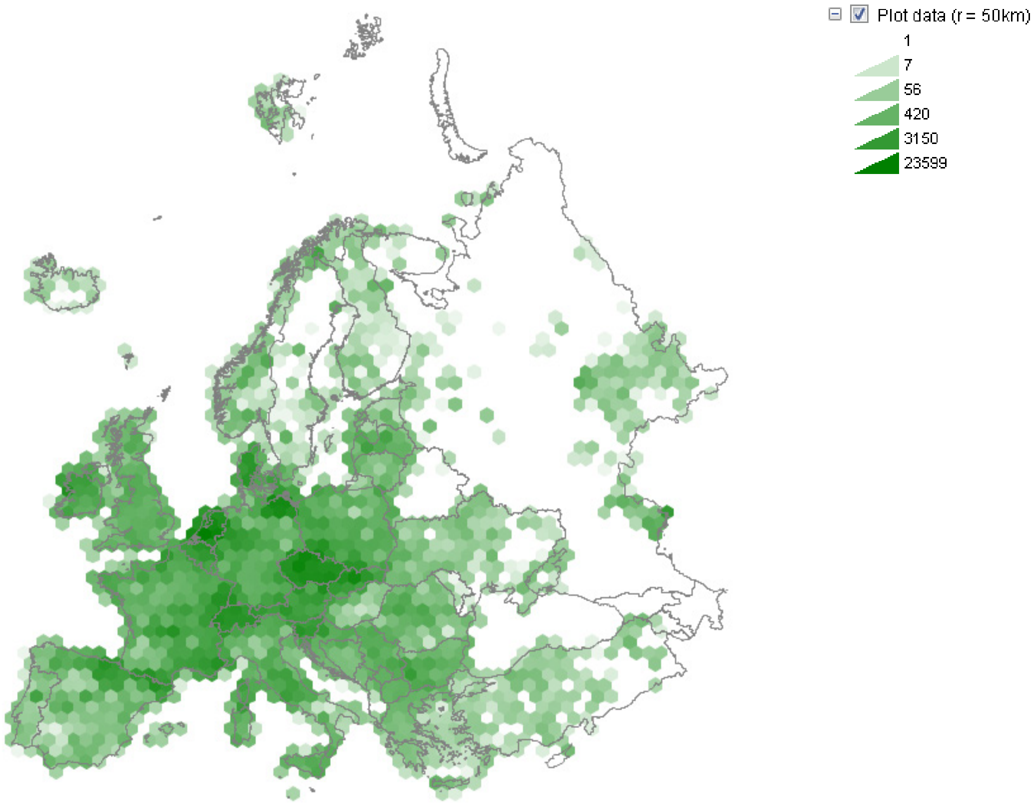
BioScore 1 introduced the sensitivity of individual species to a given environmental variable as the connector between a changing environmental pressure and an effect on species. By including this aspect in the DPSIR-chain we were able to derive a model which could help in revealing the links between drivers and changes in species occurrences. Transforming the sensitivity scores from BioScore 1.0 into quantitative dose-response functions relating species occurrences to pressures and threats, it is expected that BioScore 2.0 will become more suitable for assessing the effect of combinations of policy options.



Modelling the DPSIR-chain at different spatial scales. Source: PBL 2014.

In Chapter 2 it is explained how the 45 Annex I habitat types and the ca. 900 related species have been selected as indicators for the BioScore 2 model. The main sources for this selection were the 'Interpretation manual of European habitats' (European Commission DG Environment, 2013), unpublished synoptic tables of alliances from the 'EuroVegChecklist' and literature. Appendix 1 lists all the selected habitat types and for each the list of typical species.

The data collection is described in Chapter 3. For the plants two sources have been used, the European Vegetation Archive (EVA), a database with about 900.000 vegetation plots at the time of collection (comprising 23 million species records), and GBIF (www.gbif.org). The species data downloaded from GBIF are mainly used to fill the distribution gap in Scandinavia, an area which is relatively poor represented in EVA.



Density map of vegetation plots present in EVA.

Chapter 4 describes the revision of the selected species for each of the 45 Annex I habitat types. Also the optimal distribution of the habitats was determined by setting thresholds for the minimum number of typical species to be present in vegetation plots.

On the selection of drivers and pressures is reported in Chapter 5 with detailed background information in Appendix 4 and 5. As drivers the following environmental climate and soil variables have been selected:

Climate

- Precipitation seasonality (coefficient of variation)
- Precipitation of driest month
- Temperature Seasonality (standard deviation*100)
- Isothermality
- Mean temperature of driest quarter
- Precipitation of warmest quarter
- Minimum temperature of coldest month
- Annual mean moisture index
- Annual ratio of actual to potential evapotranspiration
- Temperature sum in growing season

Soil

- pH-H_2O in top soil
- Availability of salt
- Clay content in top soil
- Silt content in top soil

The selected pressures are the following variables:

- Acid deposition (total deposition of oxidized sulphur)
- Nitrogen deposition (total deposition of nitrogen)
- Agricultural intensity (nitrogen input by fertilizers, manure application and manure due to grazing in agricultural area)
- Forest management intensity (potential forest management approach)
- Desiccation (water exploitation index per sub-basins of rivers)
- Fragmentation (spatial cohesion of ecosystems)
- Land use (pan-European Land Cover Mosaics 2000)
- Roads (area impact by roads)
- Urbanisation (area impact by urban area)
- Hemeroby (proxy for management type)

In Chapter 6 a three step procedure describes the road to the univariate dose-response functions for the species and habitats. In step 1 the occurrences of the habitat types have served as input for the modelling based on bioclimatic and soil variables using Generalised Boosted Models (GBM). A subsequent action within step 1 is the transformation of the continues values generated by the models into binary maps () by defining habitat specific cut-offs. i.e. threshold values above which a given grid cell in the region is considered to be suitable for the habitat type.

In the second step additional knowledge is brought in to further specify the potential habitat within the distribution range (determined in step 1 by means of an absence/presence map) by laying an explicit mask over it, selecting only those specific land use types (Corine Land Cover classes) suitable for the occurrence of the habitat type or species. An overview of the 45 habitat types and their CLC preferences is given in Appendix 2.

The third step deals with the effect of human-induced pressures on habitat quality and species occurrence/abundance within the suitable habitats (step 2) in the calculated distribution ranges (step 1). Variables included in this step are nitrogen deposition, sulphur deposition, desiccation, agricultural intensity, forest management and fragmentation. For species and habitats the same selection procedure for positive and negative observations was followed. For the species this means that only those observations were selected which are located within the suitable geographical range of the corresponding habitat type and suitable land cover types. The resulting scores were then used as input for the GLM's (Generalized Linear Models), resulting in dose response functions. This univariate regression has the function to understand the relationship between the threats and the occurrence of species.

Chapter 7 presents an example of a multivariate approach for two habitat types. The results are presented in Chapter 7 and more in detail in Appendix 9. As part of a plausibility check for the third step a canonical correspondence analysis was performed to analyse the Natura 2000 habitat types H4010 and H6520 based on a detailed dataset. The analysis demonstrates that there is a moderate performance for nitrogen deposition and sulphur deposition and relatively poor performance for desiccation, N-application, forest management, and fragmentation. These variables have a large difference between their marginal and conditional effects (see "summary table with ordination results" in Appendix 9). This indicates a relatively high degree of multicollinearity requiring a more cautious interpretation of the dose-response curves.

In Chapter 8 a sensitivity analysis is described. A comparison between the method originally applied for selecting pseudo-absences for the univariate modelling (based on the total pool of vegetation plots), with a more stricter method was made. For a selected number of habitat types (10), a specific pool of vegetation plots was created, from which pseudo-absences were selected. It turned out that using the restricted habitat-specific pools less reliable univariate models are created, in comparison to the approach using the total pool of vegetation plots. It is therefore concluded that the original approach of selection pseudo-absences from the total pool, doesn't need to be replaced by the approach to select from habitat specific pools.

1 Introduction

This report provides background information about the work on plant species and Natura 2000 habitats performed by Alterra. The results of this work, dose-response functions for 45 Annex I habitat types and about 900 related plant species, will serve as input for the new version of BioScore (2.0) to assess the impact of human-induced pressures like desiccation, nitrogen deposition and land use change.

General information on the conceptual framework of BioScore and a description of the relevant policy questions for BioScore 2.0 are explained in detail in the report 'BioScore 2.0. A tool to assess the impacts of European Community policies on Europe's biodiversity' (Van Hinsberg *et al.*, 2014). This report was written for the international review commission and provides background information about ongoing work. The meeting of consortium partners of the BioScore 2 project with the review commission took place on the 16th of October 2014.

In this report we present information on how the plant species and habitats (indicators) were selected (Chapter 2), and how the data was collected and prepared for the analyses (Chapters 3 and 4). The selection of environmental variables and pressures is reported in Chapter 5. In Chapter 6 a three step procedure describes the road to the univariate dose-response functions for the species and habitats. As an example of a multivariate approach, two habitat types have been analysed. The results are presented in Chapter 7 and more in detail in Appendix 9.

The report on mammals is also included in this report in Appendix 10. The work on the distribution and dose-response functions of mammals was subcontracted by Alterra Wageningen UR to Sapienza University of Rome. The work was carried out by Luca Santini (Global Mammal Assessment program).

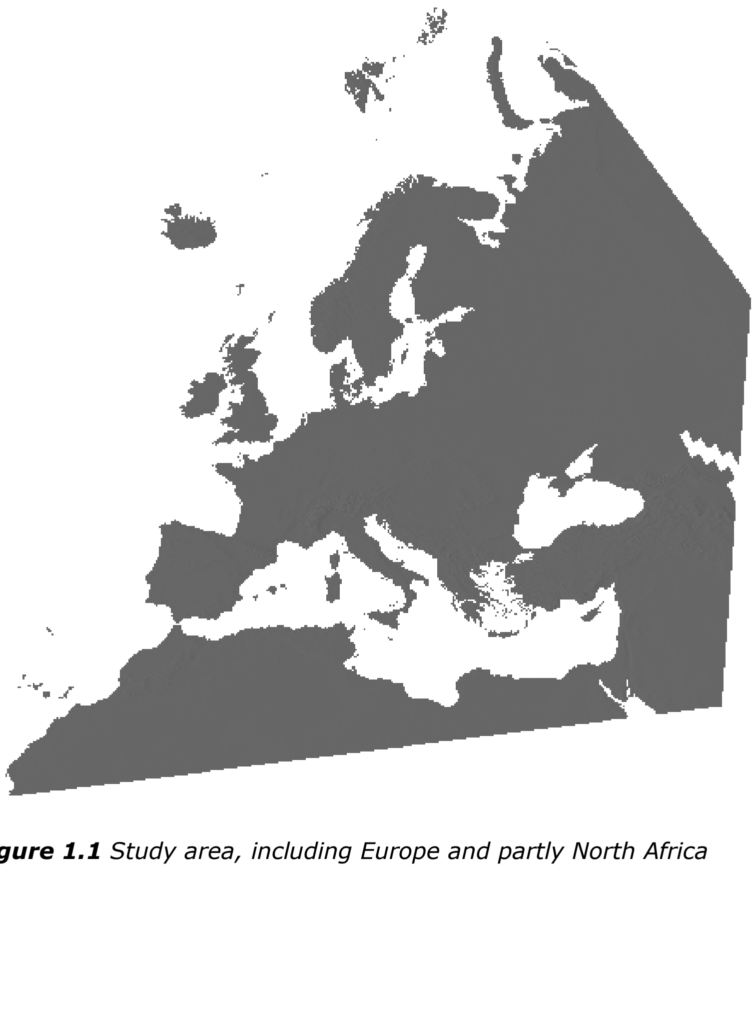


Figure 1.1 *Study area, including Europe and partly North Africa*

2 Selection of habitat types and species

Selection of habitat types
BioScore 2.0 aims at providing information on the effects of various environmental pressures on biodiversity indicators at the level of species and habitats. For vascular plants a two-step approach was used for the selection of species. First a set of 45 Natura 2000 habitats was selected (Appendix 1) using the following criteria:

- the habitat type is representative for the variation in main habitat types across Europe (e.g. including coastal habitats, grasslands, fens and forests);
- the habitat type has a broad distribution range across Europe, preferably covering multiple biogeographical regions, or the core of the distribution range is within Northwest Europe or the Mediterranean area;
- the habitat type is well characterized from a phytosociological point of view;
- the habitat type is representative for High Nature Value Farmland;
- the availability of data is good.

For the assessment of the distribution of Natura 2000 habitat types we used the database from the EU with information on Natura 2000 habitat types.

Selection of plant species per habitat type
In a second step for each habitat type a set of typical / characteristic species was selected based on the following data sources:

- the 'Interpretation manual of European habitats' (European Commission DG Environment 2013);
- unpublished synoptic tables of alliances from the 'EuroVegChecklist';
- literature.

For the selection of typical / characteristic species we used the 'Interpretation manual of European habitats' as a starting point (EC 2013). The 'Interpretation manual' however does not always provide sufficient and correct information on typical species of the habitats and therefore we did not always adopt this species lists. There were three reasons for not including typical species from the interpretation manual in our selection.

In the first place some species listed in the manual are more characteristic for other Annex-I habitat types. An example is Beta vulgaris which is considered in the manual as characteristic for H1330 'Atlantic salt meadows', but which actually occurs with an higher frequency in H1220 'Perennial vegetation of stony banks' and H1230 'Vegetated sea cliffs'.

The second exception are species for which the description in the manual is not unambiguous. An example is the listing of 'Elymus pycnanthus or Elymus repens' for the previously mentioned habitat type H1330 'Atlantic salt meadows'. From these two species Elymus pycnanthus is considered as characteristic species but Elymus repens not.

In the third place species with taxonomical difficulties are largely excluded. In H2130 'Fixed coastal dunes with herbaceous vegetation (grey dunes)' the variety dunense from Polygala vulgaris is listed as a characteristic species, but this taxon is often not acknowledged in European vegetation databases. The species Polygala vulgaris as a whole is too broad to be useful as a characteristic species. For species groups that are listed the genus level the group as a whole is often also too broad. In the case of 'Koeleria spp.' for example, only the species Koeleria macrantha is selected as a characteristic species for habitat type H2130.

A second data source for the selection of characteristic species are the synoptic tables for alliances in the EuroVegChecklist which are compiled in the Braun-Blanquet project (see http://euroveg.org/projects). In order to make these tables useful for our aims it was needed to link the alliances to the selected habitat types. For alliances that are not yet included in the EuroVegChecklist we used synoptic tables from the information system SynBioSys Europe (in which the information from EuroVegChecklist will be included in the near future). In principle, all species with a presence degree of >40% are included (with the exception of taxa with taxonomical problems), supplemented with characteristic species with a presence degree between 5-40%. A species like Arrhenatherum elatius occurs with a presence degree of 14% in the alliance Ammophilion which is linked to habitat type H2120 'Shifting dunes along the shoreline with Ammophila arenaria' (white dunes). This species is however not characteristic for this habitat type, while Calystegia soldanella in contrast, which occurs with a slightly lower presence degree (10%) is characteristic.

For habitat types that are not represented in the EuroVegChecklist or SynBioSys Europe and for which the species list in the 'Interpretation manual' was not sufficient, we made use of the international literature. For habitat type 2210 'Crucianellion maritimae fixed beach dunes', for example the interpretation manual lists only Crucianella maritima and Pancratium maritimum. Based on the literature this list is extended. For this we used, among others, the following studies: De Bolòs (1967) "Comunidades vegetales de las comarcas próximas al litoral situadas entre los ríos Llobregat y Segura", Llobera & Valladares (1989) "El litoral mediterráneo español. Introducción a la ecología de sus biocenosis terrestres", van Rivas-Martínez *et al.* (2002) "Vascular Plant Communities of Spain and Portugal", and Gómez-Serano & Sanjaume (2009) "2210. Dunas fijas del litoral del Crucianellion maritimae".

Appendix 1 presents a list of species for all 45 habitat types. In total about 900 species were selected.

3 Data collection

For the storage of vegetation data a prototype of the software package Turboveg 3 has been used (see Figure 3.1). This software package will be the successor of Turboveg 2 which is currently used for the storage of the majority of digital vegetation data across Europe. In Turboveg 3 several new functions are added to facilitate the selection of data for species distribution modelling.

The past two years part of the time was spend on the compilation and management of vegetation data across Europe as part of the European Vegetation Archive (EVA). This work is done in close cooperation with Masaryk University in Brno (Czech Republic), which was mainly responsible for the data collection. Alterra is mainly responsible for the harmonisation and integration of the data in a common data format. At present over 900.000 vegetation plots (relevés) are stored in the database, representing over 21 million species records. About 85% of the plot data is geo-referenced and this subset provides an important and high quality data source for species distribution models at the European scale.

The individual databases that need to be linked work with different national and regional species lists (with differences in nomenclature). Therefore it is crucial to synonymise the different species lists into a Europe wide species check list. Although a provisional species list was available, for some of the characteristic species for the 45 habitat types there were still some taxonomical or nomenclatorial issues to resolve last year.

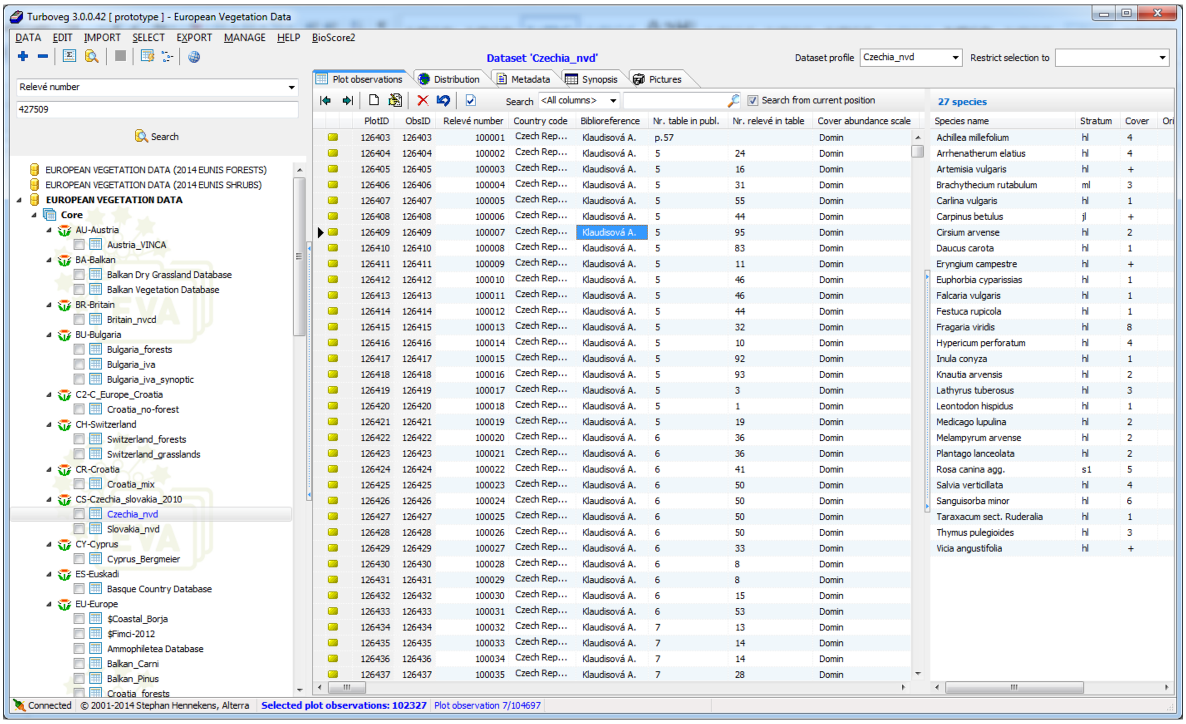
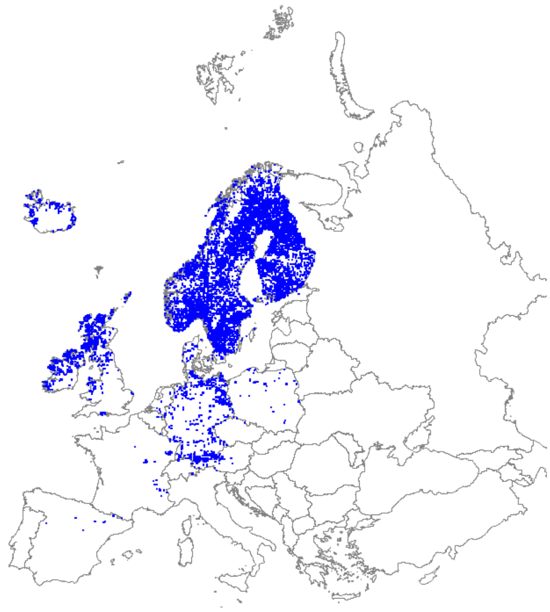


Figure 3.1 *Screenshot of the Turboveg 3 prototype, the software package used to manage the European Vegetation Archive.*

There are still several areas across Europe were the data-coverage in the European Vegetation Archive is very low. This is demonstrated by for example the distribution of *Carex limosa*. In Figure 3.2 the distribution as derived from plot information from the European Vegetation Archive (Fig. 3.2a) is compared with data from GBIF (Fig. 3.2b). This figure shows that the European Vegetation Archive still has important gaps that need to be filled in the coming years (e.g. Scandinavia).

For some regions with a strong underrepresentation in the European Vegetation Archive it is possible to use species information from GBIF (http://www.gbif.org/) such as Scandinavia. This is however not true for other regions were the coverage of GBIF is poor such as large parts of East Europe and the Mediterranean region. In total more than 20 million species records, covering the about 900 selected typical species, were downloaded via the GBIF web portal and stored in a separate database.

Figure 3.2a *Distribution of Carex limosa based on vegetation relevés extracted from EVA*



Figuur 3.2b *Distribution of Carex limosa based on species recordings extracted from GBIF*

4 Data review

After having selected the 45 Annex I habitat types and the associated typical species (Appendix 1) a review has been performed. On the basis of expert judgement each habitat type has been assessed by determining the optimal distribution by means of the how many typical species at least have to be present in a relevé. Concerning the GBIF species recordings we determined the minimum number of typical species to be present per 10x10 km. In this case we used the 10x10 km grid as a proxy for a relevé.

The assessment for the relevé data (EVA) and the GBIF data has been performed independently. In some cases a number of species were excluded to get a more optimal distribution pattern.

In Appendix 1 the threshold value for the minimum number of species to be present in a relevé (EVA) and a pseudo-relevé (10x10 km) is given for each of the 45 Annex I habitat types. Also the species that have been excluded from the original selection are listed.

In total the distribution of 834 species have been used for the modelling, with 987 combinations within the 45 habitat types (some species are assigned to more than one habitat type).

5 Selection of drivers and pressures

In BioScore 2.0 the drivers and pressures are categorized into three main groups. First of all a group of climate and soil variables is identified which determine the biogeographical distribution of species. These variables are also known as the state factors (drivers). The next group is land use, which impacts the amount of species habitat. The third group are the human-induced pressures operating in different land use classes, like agricultural intensity, nitrogen deposition and forest management type, which impact the quality of the habitat. With each group a set of most important variables is selected.

Drivers
In order to derive climate envelops a set of climate and soil variables is selected, which is based on the following criteria:

- ecologically relevant for at least one of the species groups.
- not correlated with other selected variables.
- available at low resolution for EU28 (preferably 1*1 km) and computable with models (with respect to climate change).

With respect to soil conditions focus was on the variables mostly used in soil classification systems; i.e. humidity (pH-H_2O in top soil), organic carbon content in top soil, clay content in top soil, silt content in top soil and availability of salt. These soil factors are likely to be most important for the distribution of plants and habitats. Elevation was added to this list. With respect to the climate conditions a set of the biological meaningful climatic variables was selected. These variables were derived from the BioClim database (http://worldclim.org/bioclim), a database often used in ecological niche modelling (e.g., Beaumont *et al*., 2005). From this set of 19 BioClim variables the following were selected:

- Precipitation seasonality (coefficient of variation).
- Precipitation of driest month.
- Temperature Seasonality (standard deviation*100).
- Isothermality.
- Mean temperature of driest quarter.
- Precipitation of warmest quarter.
- Minimum temperature of coldest month.
- Annual mean moisture index.
- Annual ratio of actual to potential evapotranspiration.
- Temperature sum in growing season.

This selection is based on climate variables that proved to be important for the climatic modelling of breeding birds, butterflies and plants (e.g. Settele *et al.*, 2008; Huntley *et al.*, 2007; Bakkenes *et al*., 2002).

Pressures
The selection of pressures was based on the following criteria (see also Table 5.1):

- a pressure is known to effect species occurrence or quality of habitat and;
- a pressure is relevant in European policies and goals and;
- variation of a pressure can be described with high spatial resolution information in the EU28 and;
- information can be modelled or based on scenario choices.

Detailed information on all the selected drivers and pressures is given in Appendix 4 and 5 respectively.

Table 5.1
List of selected pressures

Pressure	Variable
Acid deposition	Total deposition of oxidized sulphur
Nitrogen deposition	Total deposition of nitrogen
Agricultural intensity	Nitrogen input by fertilizers, manure application and manure due to grazing in agricultural area
Forest management intensity	Potential forest management approach
Desiccation	Water exploitation index per sub-basins of rivers
Fragmentation	Spatial cohesion of ecosystems
Land use	Pan-European Land Cover Mosaics 2000*
Roads	Area impact by roads
Urbanisation	Area impact by urban area
Hemeroby	Proxy for management type**

* The PLCM2000 (Hazeu *et al*., Alterra Wageningen UR, unpublished) is a pan-European map of land cover in which the Corine Land Cover 2000 has been integrated. The land use classes in the PLCM map are in accordance with land use classes in the CLC2000 map.

** Management measures are only partly included in the selected pressures for BioScore. Forest management approach and nitrogen application include the intensity of management on forests and agriculture. However, measures as grazing and mowing at low agricultural intensity in herbaceous vegetation are not included in the pressures. Therefore hemeroby-levels are used as a proxy for the stopping of management on agricultural fields or in herbaceous vegetation. The appearance of species or the expansion of species due to the stopping of management could not be included.

A 5-level scale of hemeroby is used. The highest three levels include a degree of active management. Per species information is available with which hemeroby-levels it may occur. Species are selected which are only occurring with hemeroby levels 3, 4 or 5. It is assumed that it depends on a certain management intensity for its occurrence. When this management stops, the habitat is not suitable anymore, as a result the species will disappear.

This is implemented in the BioScore model in the land use scenarios. When in a scenario agriculture is recently abandoned, or management on herbaceous vegetation is recently stopped, these cells are excluded from the habitat for the selected, management dependent, species. When management is stopped longer than 5 years ago, the land use type is changed due to succession and not excluded anymore for the species dependent on management.

6 Distribution and univariate modelling

To eventually obtain dose-effect responses for all habitat types and species a three step approach has been followed.

6.1 Step 1: Defining distribution range

In the **first step** the positive (presence) and negative (absence) occurrences of the habitat types has served as input for the modelling based on bioclimatic and soil variables in TRIMmaps (Hallman *et al.*, 2014) using Generalised Boosted Models (GBM) at a resolution of 5x5 km. 10.000 absences, or better to say pseudo-absences, were randomly taken from the pool of vegetation data (i.e. EVA-plots and GBIF-grid cells) in which the habitat type does not occur. Because the vegetation databases do not cover the whole study area we also let TRIMmaps generate an additional 10.000 pseudo-absences using MaxEnt (Phillips *et al.*, 2006). Figure 6.1 shows the distribution of presences and pseu-absences of habitat type H4010. The full R-code to run the GBM, including the addition of additional pseudo-absences, under TRIMmaps is listed in Appendix 6. The result of the GBM is the predicted distribution of the habitat type (Figure 6.2). The predicted presence (or better to say habitat suitability) values range from 0 to 1.

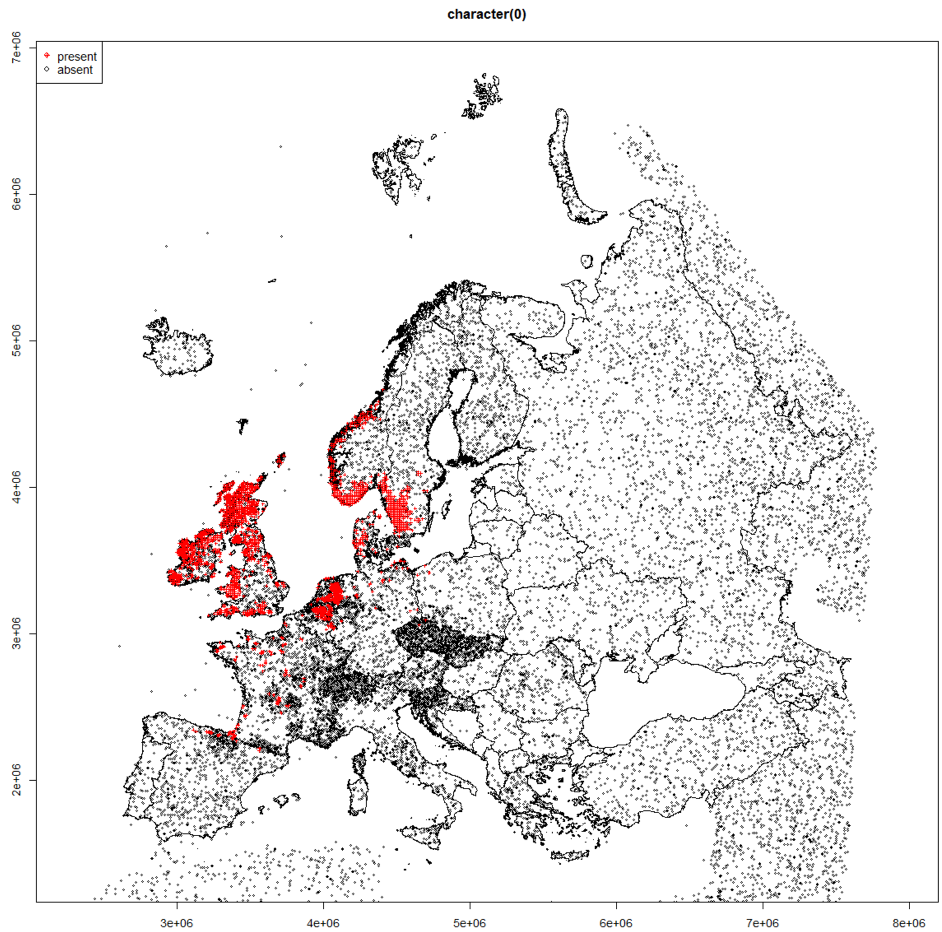


***Figure 6.1** Presences (red) and pseudo-absences (black) of habitat type H4010*

Figure 6.2 *Predicted presence of H4010. Colours vary from grey (lowest predicted values) to red (highest predicted values).*

A subsequent action within step 1 was to transform the continues values generated by the models into binary maps, with Boolean suitable/non-suitable values, by defining habitat specific cut-offs. i.e. threshold values above which a given grid cell in the region is considered to be suitable for the habitat type. Cut-off values are calculated to maximise the relationship between model sensitivity (ability to classify presences of the habitat type) and specificity (ability to classify absences of the habitat type). The R-script to calculate the cut-off values is listed in Appendix 7. Figure 6.3 shows the presence/ absence map of habitat type H4010 (Northern Atlantic wet heaths with Erica tetralix) applying a cut-off value of 0.29, obtained by equally weighting model specificity and sensitivity. The resulting map indicates the distribution range of the habitat type.

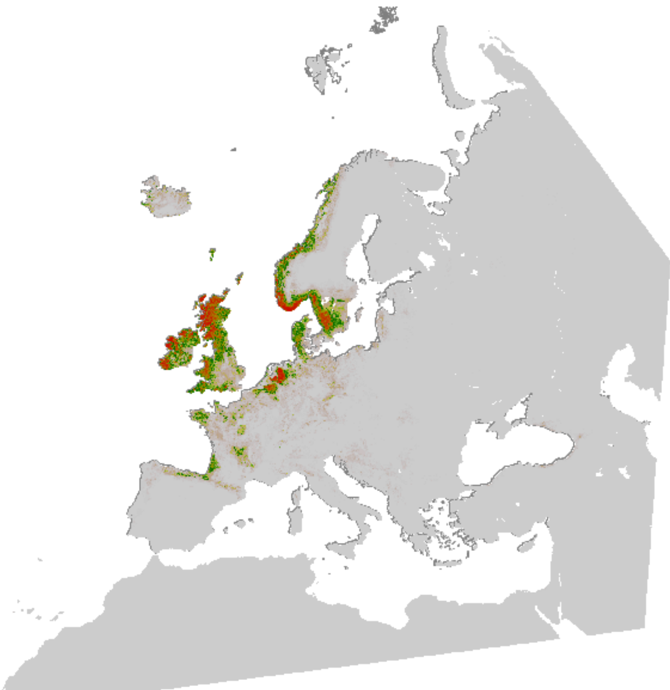


Figure 6.3 *Presence/absence map of habitat type H4010*

6.2 Step 2: Specifying potential habitat

In the **second step** additional knowledge was brought in to further specify the potential habitat within the distribution range (determined in step 1) by laying an explicit mask over it, selecting only those specific land use types (land cover classes) suitable for the occurrence of the habitat type or species. Land use is explicitly incorporated as a separate step, because the distribution of land use types depends on climate and soil characteristics.

In order to determine the suitable land cover classes in the PLCM map, for each of the 45 habitat types an overlay was made with the observations and PLCM map. From these the proportion of observations in each land cover-class was determined. Classes with more than 5% of the observations were considered to be (major) habitats for the habitat type. This automated classification was then edited by an expert to exclude or include certain habitats. The mask prepared for a specific habitat type (range map plus preferential CLC classes) was then applied for all typical species in the further analysis.

An overview of the 45 habitat types and their CLC preferences is given in Appendix 2 (Table 6.1 an example is given of H4010).

Table 6.1
Example of H4010, with most frequent CLC classes matching the type. Taken only frequency values greater or equal 5% into account, it can be concluded that in this case H4010 matches best with peat bogs, moors and heathlands, pastures, coniferous forest and natural grasslands. When interpreting these figures we have to take into account that small patches of the habitat will not appear on the PCLM map. Small patches therefore 'disappears' in larger landcover units, like in this case, coniferous forest.

Habitat	CLC	Class	Freq. (%)
H4010	36	peat bogs	22
H4010	27	moors and heath lands	17
H4010	18	pastures	14
H4010	24	coniferous forest	11
H4010	26	natural grasslands	5

6.3 Step 3: Determining effect of pressures

The **third step** deals with the effect of human-induced pressures on habitat quality and species occurrence/abundance within the suitable habitats in the calculated distribution ranges. Variables included in this step are nitrogen deposition, sulphur deposition, desiccation, agricultural intensity, forest management and fragmentation (see Appendix 5 for an extensive description of the variables). From literature it is known that the effects of these drivers vary across ecosystem types. For example, sensitivity for nitrogen deposition, expressed in terms of critical nitrogen deposition levels, differs between land use classes (Bobbink and Hettelingh, 2011) and effects of land use intensity, in terms of agricultural intensity and forest management, are by definition nested within the land use classes of forests and grasslands. Therefore, the dose response functions have to be derived within the suitable ecosystems within the calculated distribution range (second step).

Overlaying the occurrence data defined in the first step, and the mask based on distribution range (step 1) and suitable CLC classes (step 2) a number of positive occurrences was extracted. These occurrences were then supplemented with a more or less equal number of randomly selected pseudo-absences from the total pool of vegetation plots, and also selected within the geographical range of the mask.

For species and habitats the same selection procedure was followed. For the species this means that their dose-effect response is only valid within the area in which the corresponding habitat type is likely to be present. Next the positive and negative occurrences were overlayed with the variables expressing the human treats (nitrogen deposition etc.). The resulting scores were then used as input for the GLM's (Generalized Linear Models), resulting in dose response functions (see Figure 6.4). This univariate regression has the function to understand the relationship between the threats and the occurrence of species. In Appendix 8 the full R-code is given to run the GLM's on all species and habitats. The script also provides in a summary of the model outcomes listed in the file 'Univariate_models_plants.csv'. Models with AUC values for the full model above 0.6 can be considered to be meaningful. Whereas models can be discarded when minimum cross-validation values are below 0.55.

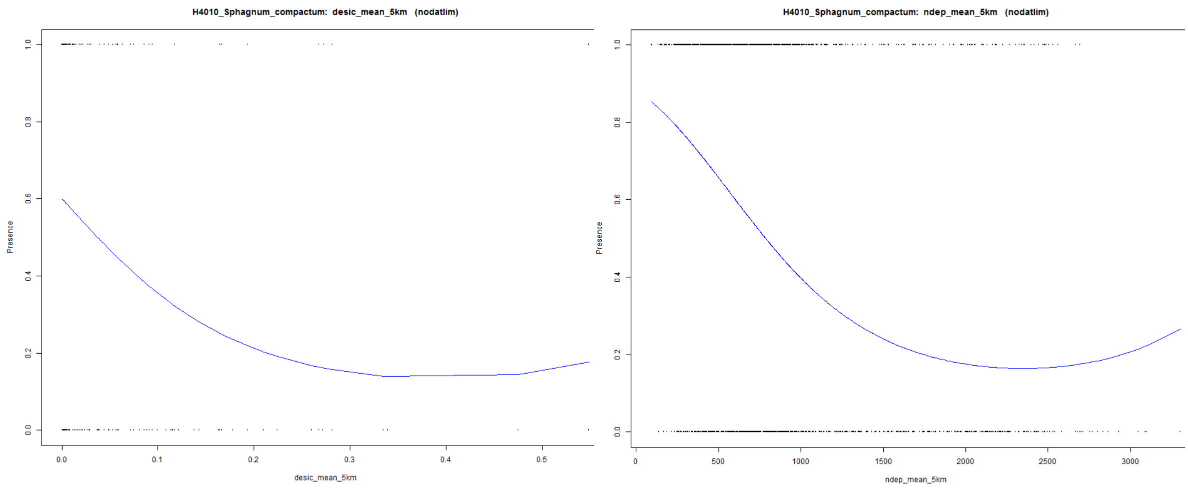


Figure 6.4 *Dose-response curve of Sphagnum compactium to desiccation (AUC 0.65) and nitrogen deposition (AUC 0.73).*

Note that for fragmentation different classes have been set up based on CLC level 2. In Appendix 3 it is indicated which fragmentation class should be taken into account for a certain habitat type and the it's associated typical species. This for example means that for dose response functions for H1330 (Atlantic salt meadows (Glauco-Puccinellietalia maritimae)) only fragmentation class 4.2 may be taken into account.

The same applies for the FMA's (Forest Management Approaches). Here only dose response functions for forest types (H9xxx) and their associated typical species may be taken into account.

7 Multivariate analysis of vascular plants in two habitat types

Background
In the third step of the BioScore approach, the effects of human-induced pressures on habitat quality and species occurrence/abundance within the suitable habitats are assessed with dose-response functions. This is done with univariate regression within the distribution range (as derived in step 1). The relationships between species occurrences and the environmental parameters are determined by means of logistic regression (assuming a Gaussian response curve). In a next step the dose-response functions for environmental drivers are multiplied in order to calculate the overall change of habitat suitability for a given species. This multiplication however assumes independence between the various explanatory variables, i.e. it assumes negligibly effects of multicollinearity (multicollinearity is a statistical phenomenon in which predictor variables in a multiple regression model are highly correlated). It is therefore important to have more insight in the degree of multicollinearity between the various variables based on multivariate statistics.

By selecting or weighting the most important variables (based on ecological knowledge and the results of multivariate analyses) it should subsequently be possible to increase the ecological relevance of the BioScore tool.

As part of a plausibility check for the third step we used ordination models (Canonical Correspondence Analysis) to analyse two Natura 2000 habitat types (H4010 and H6520) based on a more detailed dataset. The approach and conclusions are briefly described in this paragraph and for the results we refer to Appendix 9. The approach differs in two ways from the method used in BioScore: 1) the analysis is based on high-resolution co-occurrence data from the European Vegetation Archive (instead of presence-only data) and 2) the relative effect of the environmental variables on species composition is assessed with a multivariate approach (instead of univariate regression) allowing the assessment of marginal and conditional effects of each environmental variable.

Use of high-resolution co-occurrence data
The use of vegetation plots with co-occurrence data has at least two advantages. In the first place the high-resolution co-occurrence data include reliable information on absences (in contrast to BioScore were presence-only data and inferred absences are used). In the second place several environmental drivers act mainly indirectly on plant occurrences through changes in the competitive abilities among the co-occurring species. With co-occurrence data it is possible to account for such context dependent effects. High resolution co-occurrence data are therefore more suitable for niche modelling than data derived from atlases. The spatial coverage of this dataset is however smaller as compared to the BioScore approach (which also uses atlas data from GBIF and includes areas that are less well covered by the European Vegetation Archive).

Selection of plots
The selection of plots for the two habitat types was based on the co-occurrence of several characteristic species for the habitat type with a habitat-specific threshold value (see step 1).

Selection of species
For the selection of species we used the following criteria:
- occurrence in ≥ 25 plots;
- no lichens and mosses, with the exception of a few well known and characteristic species;
- no trees (for these two habitat types);
- no subspecies (were aggregated at the species level);
- no species groups with difficult / cryptic taxa that are represented in the dataset with multiple taxa (e.g. *Alchemilla, Festuca, Hieracium, Taraxacum*).

Assessment of relative effect of the environmental variables on species composition
Analyses with ordination techniques (Canonical Correspondence Analysis) allow an assessment of the

relative effect of various explanatory variables on species composition. Using Monte-Carlo permutation tests it is possible to give estimates of the explanatory power of each environmental variable based on:

- its *marginal effect* on species composition (i.e. the simple effect without considering other explanatory variables);
- its *conditional effect* on species composition (i.e. the unique effects after accounting for the effects of other environmental variables).

Large differences between the marginal effect and the conditional effect of a given variable are indicative of strong correlations with one or more other explanatory variables. Any two explanatory variables that are correlated share part of their effect exercised upon the species data (in the statistical, not necessarily the causal sense). Variables with a large difference in effect size between marginal and conditional effects in the ordination model (indicating a high degree of multicollinearity) require a more cautious interpretation of the dose-response curves.

Data analyses

As response data we use log-transformed co-occurrence data. As explanatory data we used: a) the environmental variables used in BioScore step 3: nitrogen deposition, sulphur deposition, desiccation, N-application (agricultural intensity), forest management and fragmentation; b) the environmental variables used in step 1, and c) mean Ellenberg indicator values. For each explanatory variables the conditional and marginal effect were tested with a Monte-Carlo permutation test.

For a subset of environmental variables and species response curves are quantified. Second order polynomial and linear models in GLM are strict specifications for the shape of the response curve. Since the response often takes more complicated, asymmetric shapes we used GAM. In order to make the models not too complex we used a maximum of three degrees of freedom (allowing asymmetric unimodal shapes) with a stepwise selection of the best model based on AIC. The results are given in Appendix 9.

General conclusions

The relative performance of the environmental drivers in the two habitat types is roughly comparable although the performance of Nitrogen deposition is lower in H6520.

The following environmental drivers have a moderate performance based on the size of their conditional effect: Nitrogen deposition and Sulphur deposition. For Nitrogen deposition there is a moderate correlation with several BioClim variables (e.g. Bio4, Bio14, Bio28: r>0.5-0.7) which is reflected in a relatively large decline in its conditional effect relative to its marginal effect. On the other hand the correlation between Nitrogen deposition and Ellenberg Nitrogen is low (<.010).

The following environmental drivers have a *relatively* poor performance (based on the size of their conditional effect): desiccation, N-application, forest management, (fragmentation). These variables have a large difference between their marginal and conditional effects (see "summary table with ordination results" in Appendix 9). This indicates a relatively high degree of multicollinearity requiring a more cautious interpretation of the dose-response curves. In future version of BioScore the performance of these drivers might be improved by using GIS data with a higher spatial resolution.

In comparison to the GIS-based environmental drivers, Ellenberg indicator values have a relatively large conditional effect for Nitrogen (N), Soil acidity (R), Moisture (M) and Light (L). This is probably at least partly related to the higher spatial resolution of the Ellenberg indicator values.

For the response curves of individual species (see Appendix 9) it appears that for GAM-models with a high R^2 (>0.50) the shape of the response curves shows a reasonable similarity to the curve shapes as produced in step 3 in Bioscore. Deviations mainly occur in data-ranges with a low data-coverage (for example at very high levels of Sulphur deposition), therefore requiring a more cautious interpretation of these data-ranges.

The performance of the ordination models themselves (as used for the multivariate analyses in this chapter) can probably be improved by using stricter filters for the selection of plots for a given habitat type and by excluding additional species (e.g. very rare species and species with a very broad niche).

8 Sensitivity analysis

To supply the univariate modelling in step 3 with pseudo-absences (see Chapter 6, step 3) random selections have been performed on the total pool of vegetation plots. This way of selecting data can be criticised, because the pseudo-absences are in most cases not related to the positive observations, meaning that they quite likely represent completely different habitat types. To analyse the sensitivity of the model results in the way the pseudo-absences are generated, we compared this approach with an alternative approach in which pseudo-absences are derived from a more restricted set of plots. We therefore created, for a selection of habitat types (see Table 8.1), a specific pool of vegetation plots, from which pseudo-absences were selected. This pool was created by decreasing the threshold value for the number of typical species of a habitat type to be present in a vegetation plot. Next the selection of plots based on the initial threshold were removed from the pool. What is left is a number of plots which still may represent the habitat type concerned, but comprises less well-developed vegetation stands. The assumption is that these plots occur in areas where the environmental conditions are less suitable for the occurrence of well-developed vegetation stands and/or the human-induced pressures are more intense than in areas where the positive observations are located.

In total for 222 species and 10 habitat types univariate models have been recreated, based on the habitat-specific pool of vegetation plots. The results have been compared with the previously performed analyses based on the pool with the total number of vegetation plots.

Table 8.1
Selection of habitat types and there thresholds used for building the pools.

Selected Annex I habitat type		Threshold (original threshold)
1330	Atlantic salt meadows (Glauco-Puccinellietalia maritimae)	4 (6)
3130	Oligotrophic to mesotrophic standing waters with vegetation of the Littorelletea uniflorae and/or of the Isoëto-Nanojuncetea	3 (4)
4010	Northern Atlantic wet heaths with Erica tetralix	3 (4)
4030	European dry heaths	3 (4)
4060	Alpine and Boreal heaths	4 (5)
6210	Semi-natural dry grasslands and scrubland facies on calcareous substrates (Festuco-Brometalia) (* important orchid sites)	5 (6)
6410	Molinia meadows on calcareous, peaty or clayey-silt-laden soils (Molinion caeruleae)	5 (6)
6520	Mountain hay meadows	3 (4)
9150	Medio-European limestone beech forests of the Cephalanthero-Fagion	4 (5)
9190	Old acidophilous oak woods with Quercus robur on sandy plains	6 (8)

To extract the reliable univariate models from the results two different sets of criteria have been applied of which the first one is much more strict than the second one:

- Criterion 1 (proposed by SOVON):
  - explained deviance >=4;
  - AUC mean >= 0.6;
  - AUC min >= 0.55;
  - one habitat type specifiek fragmentation class (see Appendix 3);
  - dispersal distance with highest AUC.

- Criterion 2 (proposed by PBL):
  - $p < 0.05$ or $p2 < 0.05$ (p = significance of linear parameter; p2 = significance value of quadratic parameter);
  - one habitat specific fragmentation class (see Appendix 3);
  - dispersal distance with highest AUC.

Even though the two criteria result in very different numbers of reliable models, the netto result – i.e. the ratio between Improved/Worsened models - is more or less the same. The overview below shows that by using the restricted habitat-specific pools of vegetation plots less reliable models are created, in comparision to the approach using the total pool of vegetation plots. We therefore conclude that the pool with the total number of vegetation plots as the basis for the selection of pseudo-absences, doesn't need to be replaced by habitat specific pools.

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Justification

The research is part of the development op the Bioscore 2.0 model. In this report the main focus is on plant species and their habitats. The analysis of the mammal species was solely carried out by Sapienza University Rome (Luca Santini), a work which was subcontracted by Alterra Wageningen UR, and therefore included in this report (Annex 10).

The project was supervised by Arjen van Hinsberg (later on by Marjon Hendriks), both working at PBL, and Rogier Pouwels (Alterra Wageningen UR) and the results of the project were used by PBL to develop the Bioscore model itself. As this was done in cooperation, the report contains some of the work of others.

The procedures which were followed for the 3 steps approach (multivariate modelling, masking, and univariate modelling) were mainly determined by PBL, in cooperation with Henk Sierdsema (SOVON) , who also wrote most of the R-scripts (together with his colleague Christian Kampichler) that were used for the modelling.

As one the authors of this report Marjon Hendriks of the PBL wrote Chapter 5 on drivers and pressures, with an addition on hemeroby by Wim Ozinga. Extensive information on all drivers and pressures is included in respectively Annex 4 and 5.

A multivariate analysis of vascular plants in two habitat types (Chapter 7) was carried out by Wim Ozinga.

A special thanks to all the custodians of the various vegetation databases across Europe who gave permission to use their data, as included in EVA (European Vegetation Archive) for this project.

Due to the deadline of the publication of this report the results of the comparison of the FMM (Full Model Multivariate Modelling) and the first outcomes of the BioScore model are unfortunately not taken into account. We expect to include this assessment in a future version of this report.

Annex 1 Selected Natura 2000 habitat types

For each of the 45 selected Natura 2000 habitat types the following is presented:

- a list of typical species;
- which species have been excluded after evaluation;
- which thresholds have to be set for EVA atabase and GBIF database to get an optimal distribution;
- a distribution map based on occurrences of vegetation plots and combinations of single species observations;
- a presence/absence map based on a distribution model presenting the the areas with highest probability of occurrence.

Selected Natura 2000 habitat types

1330	Atlantic salt meadows (Glauco-Puccinellietalia maritimae)
1340	Inland salt meadows
2120	Shifting dunes along the shoreline with Ammophila arenaria ("white dunes")
2130	Fixed coastal dunes with herbaceous vegetation ("grey dunes")
2160	Dunes with Hippophaë rhamnoides
2210	Crucianellion maritimae fixed beach dunes
3110	Oligotrophic waters containing very few minerals of sandy plains (Littorelletalia uniflorae)
3130	Oligotrophic to mesotrophic standing waters with vegetation of the Littorelletea uniflorae and/or of the Isoëto-Nanojuncetea
3150	Natural eutrophic lakes with Magnopotamion or Hydrocharition - type vegetation
3260	Water courses of plain to montane levels with the Ranunculion fluitantis and Callitricho-Batrachion vegetation
4010	Northern Atlantic wet heaths with Erica tetralix
4030	European dry heaths
4060	Alpine and Boreal heaths
4070	Bushes with Pinus mugo and Rhododendron hirsutum (Mugo-Rhododendretum hirsuti)
5110	Stable xerothermophilous formations with Buxus
5130	Juniperus communis formations on heaths or calcareous grasslands
5210	Arborescent matorral with Juniperus spp.
5420	Sarcopoterium spinosum phryganas
6110	Rupicolous calcareous or basophilic grasslands of the Alysso-Sedion albi
6120	Xeric sand calcareous grasslands
6150	Siliceous alpine and boreal grasslands
6170	Alpine and subalpine calcareous grasslands
6210	Semi-natural dry grasslands and scrubland facies on calcareous substrates (Festuco-Brometalia) (* important orchid sites)
6220	Pseudo-steppe with grasses and annuals of the Thero-Brachypodietea

6230	Species-rich Nardus grasslands, on silicious substrates in mountain areas (and submountain areas in Continental Europe)
6240	Sub-Pannonic steppic grasslands
6410	Molinia meadows on calcareous, peaty or clayey-silt-laden soils (Molinion caeruleae)
6430	Hydrophilous tall herb fringe communities of plains and of the montane to alpine levels
6510	Lowland hay meadows (Alopecurus pratensis, Sanguisorba officinalis)
6520	Mountain hay meadows
7110	Active raised bogs
7130	Blanket bogs (if active bog)
7140	Transition mires and quaking bogs
7150	Depressions on peat substrates of the Rhynchosporion
7210	Calcareous fens with Cladium mariscus and species of the Caricion davallianae
7230	Alkaline fens
8210	Calcareous rocky slopes with chasmophytic vegetation
8220	Siliceous rocky slopes with chasmophytic vegetation
9110	Luzulo-Fagetum beech forests
9150	Medio-European limestone beech forests of the Cephalanthero-Fagion
9160	Sub-Atlantic and medio-European oak or oak-hornbeam forests of the Carpinion betuli
9190	Old acidophilous oak woods with Quercus robur on sandy plains
91E0	Alluvial forests with Alnus glutinosa and Fraxinus excelsior (Alno-Padion, Alnion incanae, Salicion albae)
91H0	Pannonian woods with Quercus pubescens
9410	Acidophilous Picea forests of the montane to alpine levels (Vaccinio-Piceetea)

Habitat type 1330
Atlantic salt meadows (Glauco-Puccinellietalia maritimae)

Initial species selection

Agrostis stolonifera	Armeria maritima
Artemisia maritima	Aster tripolium
Blysmus rufus	Carex distans
Carex extensa	Festuca rubra
Frankenia laevis	Glaux maritima
Halimione pedunculata	Halimione portulacoides
Juncus gerardi	Juncus maritimus
Limonium vulgare	Plantago maritima
Puccinellia distans	Puccinellia distans s. borealis
Puccinellia distans s. distans	Puccinellia fasciculata
Puccinellia maritima	Salicornia europaea
Spergularia marina	Spergularia media
Suaeda maritima	Triglochin maritima

Species evaluation

Selected species: (1) Deleted from the original selection are Agrostis stolonifera (too broad, taxonomic difficulties, Festuca rubra (too broad, taxonomic difficulties), Frankenia laevis (more in other types), and Salicornia europaea (taxonomic difficulties, more in other habitat types).

Thresholds EVA: 6

Threshold GBIF: 6

Additional selection criteria: Restrict to coastal habitats, exclude mediterranean.

Comments: GBIF is needed not only for NW Europe but also for Atlantic coast Spain.
Quality A-E: A, but Baltic States not represented.

Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type H1340
Inland salt meadows

Initial species selection

Artemisia santonicum
Aster tripolium
Bupleurum tenuissimum
Carex distans
Festuca pseudovina
Halimione pedunculata
Hordeum marinum
Juncus gerardii
Lotus tenuis
Plantago coronopus
Plantago maritima
Puccinellia distans
Puccinellia fasciculata
Salicornia europaea
Scorzonera cana
Spergularia media
Spergularia salina
Suaeda maritima
Triglochin maritima

Species evaluation

Selected species:

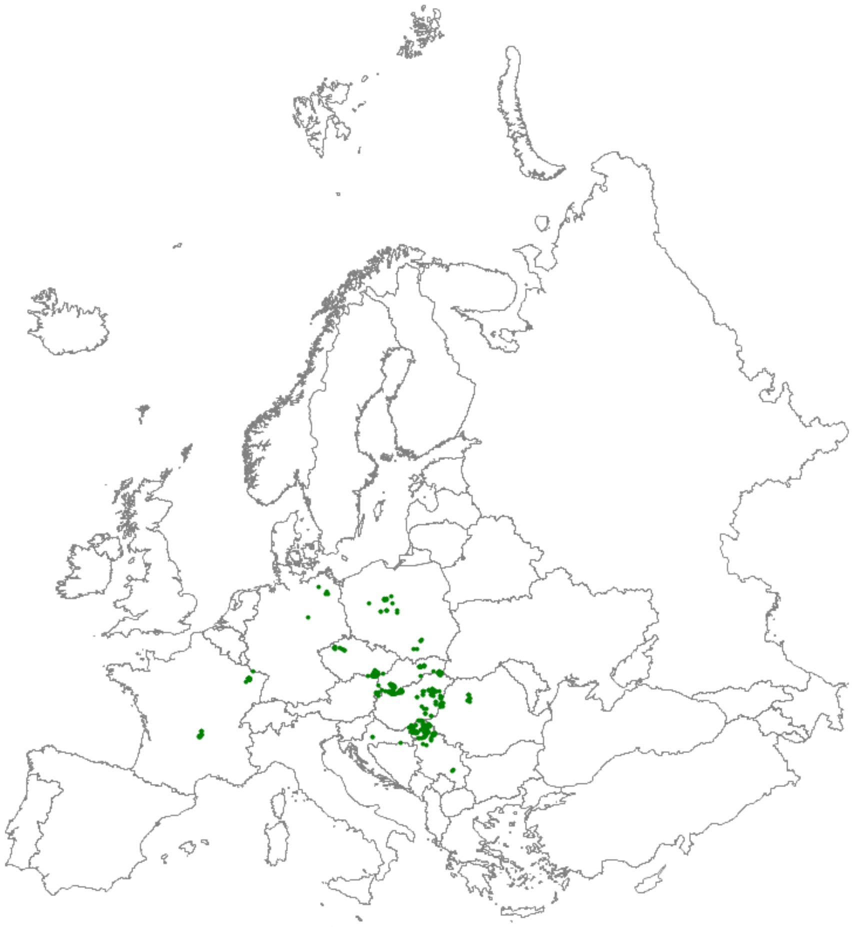
Thresholds EVA: 3

Threshold GBIF: -

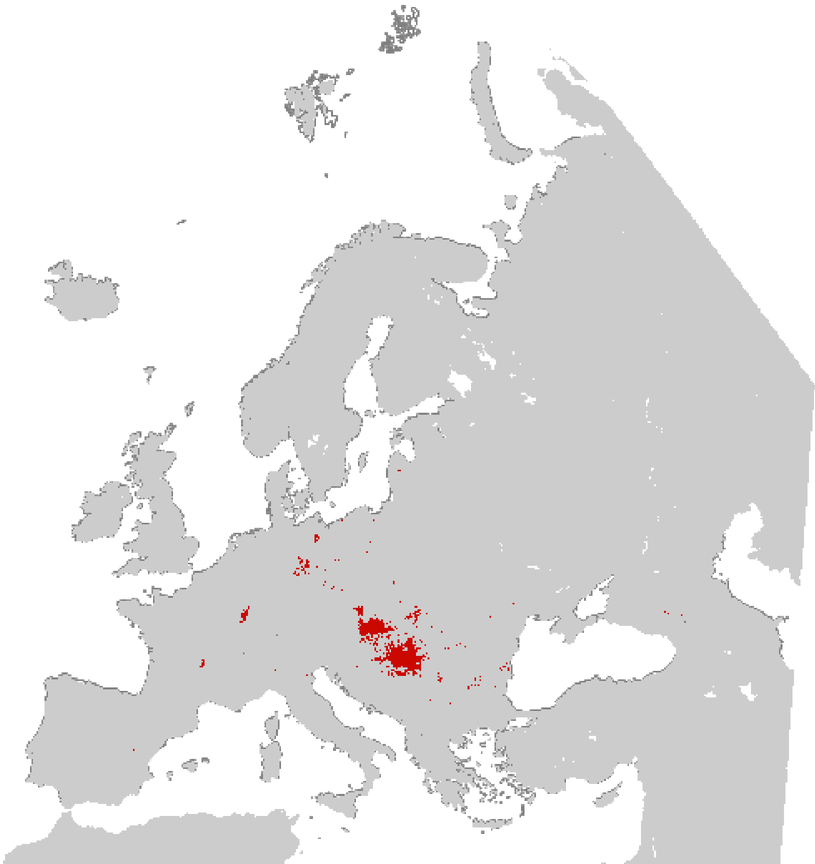
Additional selection criteria: Coastal areas excluded.

Comments:

Quality A-E: B.



Distribution: green dots represent vegetation plot data



Map with modelled distribution

Habitat type 2120
Shifting dunes along the shoreline with Ammophila arenaria (‘white dunes’)

Initial species selection

Ammophila arenaria
Anthemis maritima
Calystegia soldanella
Cerastium diffusum
Cutandia maritima
Echinophora spinosa
Eryngium maritimum
Festuca rubra
Leymus arenarius
Ononis natrix
Polycarpaea nivea
Zygophyllum fontanesii
Androcymbium psamophyllum
Cakile maritima
Carex arenaria
Convolvulus caput-medusae
Cyperus capitatus
Elymus pycnanthus
Euphorbia paralias
Honkenya peploides
Medicago marina
Otanthus maritimus
Polygonum maritimum

Species evaluation

Selected species: (1) Deleted from the original selection are Cakile maritima (more in other types) and Carex arenaria (too broad, more in other types), and replace Festuca rubra by Festuca rubra subsp. arenaria. (2) Ammophila arenaria required (add children).

Thresholds EVA: 3

Threshold GBIF: 3

Additional selection criteria: Restrict to coastal habitats.

Comments: GBIF has limited additional value.

Quality A-E: B (France poorly represented).

Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type 2130
Fixed coastal dunes with herbaceous vegetation (‘grey dunes’)

Initial species selection

Aira praecox	Anacamptis pyramidalis
Artemisia campestris s. maritima	Calamagrostis epigejos
Carex arenaria	Cerastium semidecandrum
Ceratodon purpureus	Cladonia foliacea
Cladonia furcata	Cladonia rangiformis
Coelocaulon aculeatum	Corynephorus canescens
Erodium cicutarium s. dunense	Erodium lebelii
Festuca rubra s. rubra	Galium verum
Gentiana cruciata	Gentianella campestris
Hypnum cupressiforme	Koeleria macrantha
Milium scabrum	Myosotis ramosissima
Ononis repens	Phleum arenarium
Sedum acre	Senecio jacobaea
Silene conica	Silene otites
Tortula ruraliformis	Trifolium scabrum
Tuberaria guttata	Viola tricolor s. curtisii

Species evaluation

Selected species: Exclude Aira praecox, Ceratodon purpureus, Cladonia furcata, Festuca rubra subsp. rubra, Hypnum cupressiforme and Senecio jacobaea... Include Helichrysum stoechas, Ephedra distachya, Galium arenarium and Medicago littoralis, and also Crucianella maritima, Calystegia soldanella and Eryngium maritimum (for the Iberian coast).

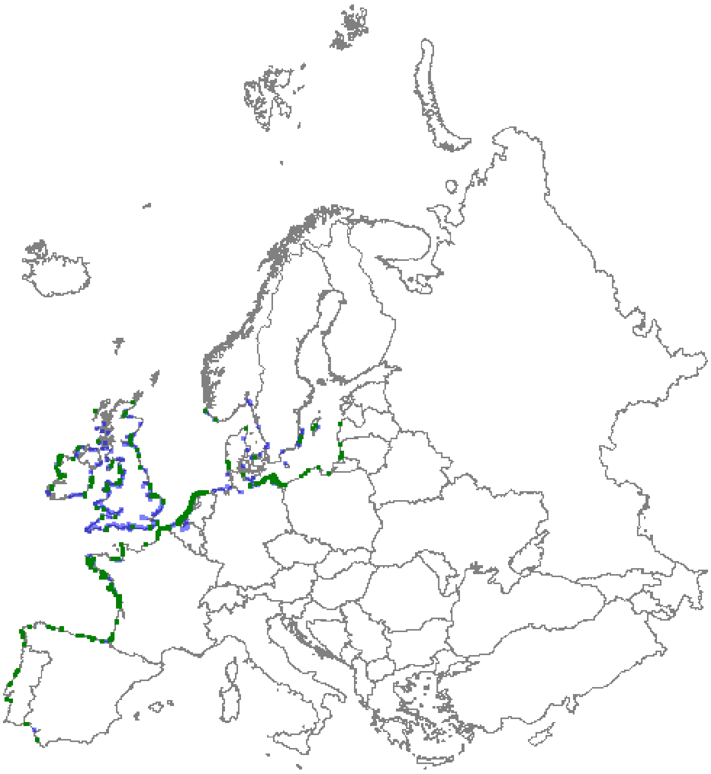
Thresholds EVA: 4

Threshold GBIF: 9 (Senecio jacobaea = Jacobaea vulgaris, Tortula ruraliformis = Tortula ruralis)

Additional selection criteria: Restrict to coastal habitats, exclude mediterranean coasts westwards to Gibraltar.

Comments:

Quality A-E: A (but Baltic states poorly represented).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 2160
Dunes with Hippophaë rhamnoides

Initial species selection

Anthriscus caucalis
Berberis vulgaris
Bryonia cretica
Bryonia cretica s. dioica
Calamagrostis epigejos
Carex arenaria
Crataegus monogyna
Cynoglossum officinale
Euonymus europaeus
Hippophae rhamnoides
Ligustrum vulgare
Moehringia trinervia
Polygonatum odoratum
Rhamnus catharticus
Rosa canina
Rosa rubiginosa
Rubus caesius
Salix repens
Salix repens s. arenaria
Sambucus nigra
Urtica dioica

Species evaluation

Selected species: Hippophae rhamnoides required.

Thresholds EVA: 3

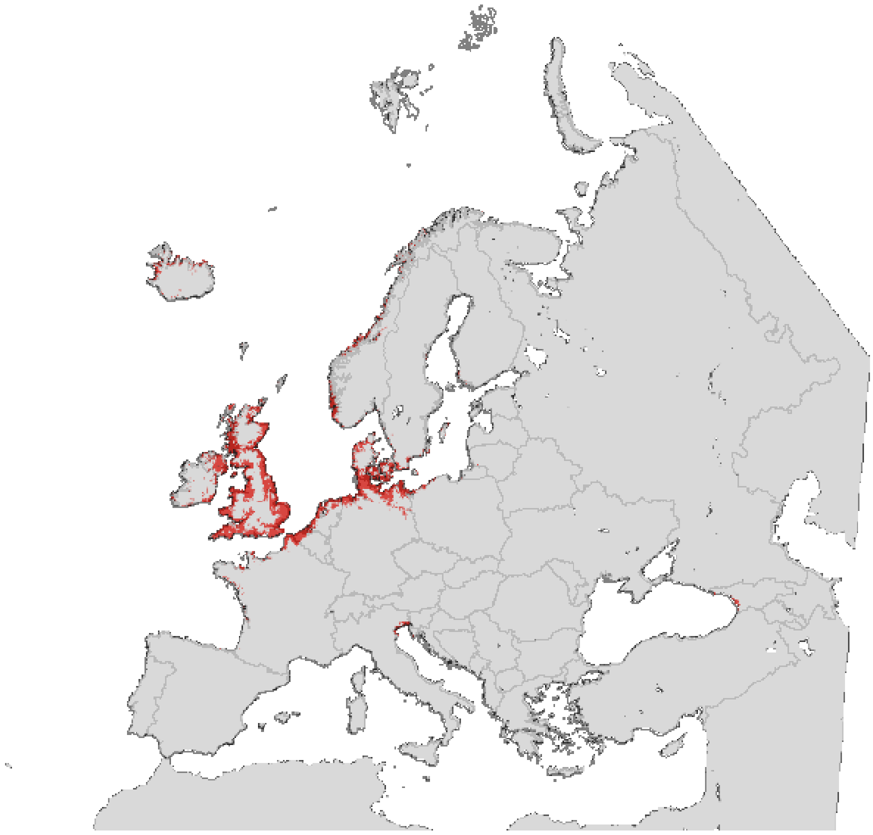
Threshold GBIF: 3

Additional selection criteria: Restrict to coastal habitats.

Comments:

Quality A-E: B

Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 2210
Crucianellion maritimae fixed beach dunes

Initial species selection

Aetheorhiza bulbosa
Ambrosia maritima
Calystegia soldanella
Crucianella maritima
Desmazeria rigida s. hemipoa
Echium sabulicola
Eryngium maritimum
Euphorbia terracina
Helichrysum stoechas
Launaea resedifolia
Lotus creticus
Malcolmia littorea
Maresia nana
Matthiola sinuata
Ononis crispa
Ononis natrix s. ramosissima
Pancratium maritimum
Scabiosa atropurpurea
Scrophularia frutescens
Scrophularia ramosissima
Silene nicaeensis
Teucrium dunense
Teucrium polium

Species evaluation

Selected species: Crucianella maritima required.

Thresholds EVA: 3

Threshold GBIF: - (no additional information)

Additional selection criteria: Restrict to coastal habitats, exclude thermo-atlantic coast (= eastwards u to Gibraltar, so exclude Portugal and southwestern part of Spain)

Comments:

Quality A-E: A

Distribution: green dots represent vegetation plot data.

Map with modelled distribution

Habitat type 3110
Oligotrophic waters containing very few minerals of sandy plains (Littorelletalia uniflorae)

Initial species selection

Deschampsia setacea	Eleocharis acicularis
Eleocharis multicaulis	Eriocaulon aquaticum
Isoetes echinospora	Isoetes lacustris
Juncus bulbosus	Littorella uniflora
Lobelia dortmanna	Myriophyllum alterniflorum
Pilularia globulifera	Potamogeton polygonifolius
Subularia aquatica	

Species evaluation

Selected species: Exclude Juncus bulbosus (too broad) and Pilularia globulifera (too broad, also with regard to distribution).

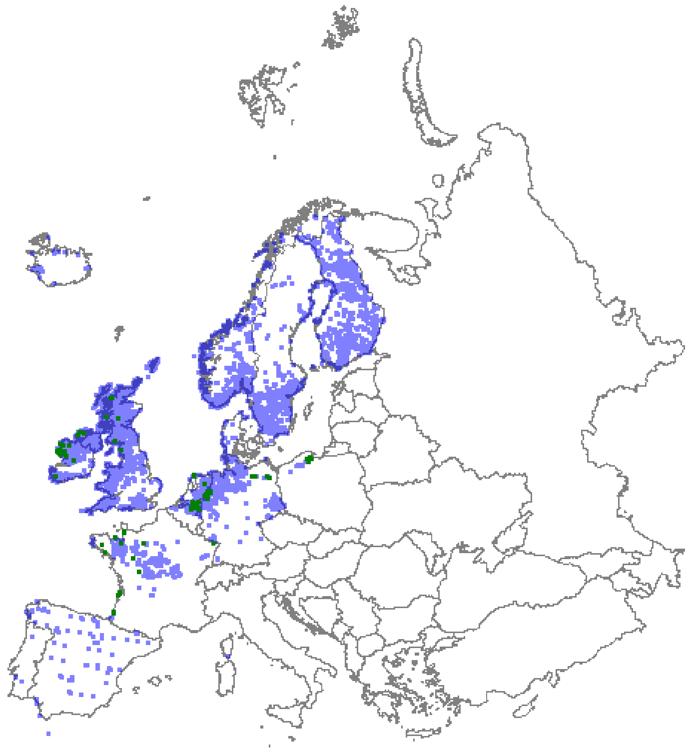
Thresholds EVA: 3

Threshold GBIF: 3

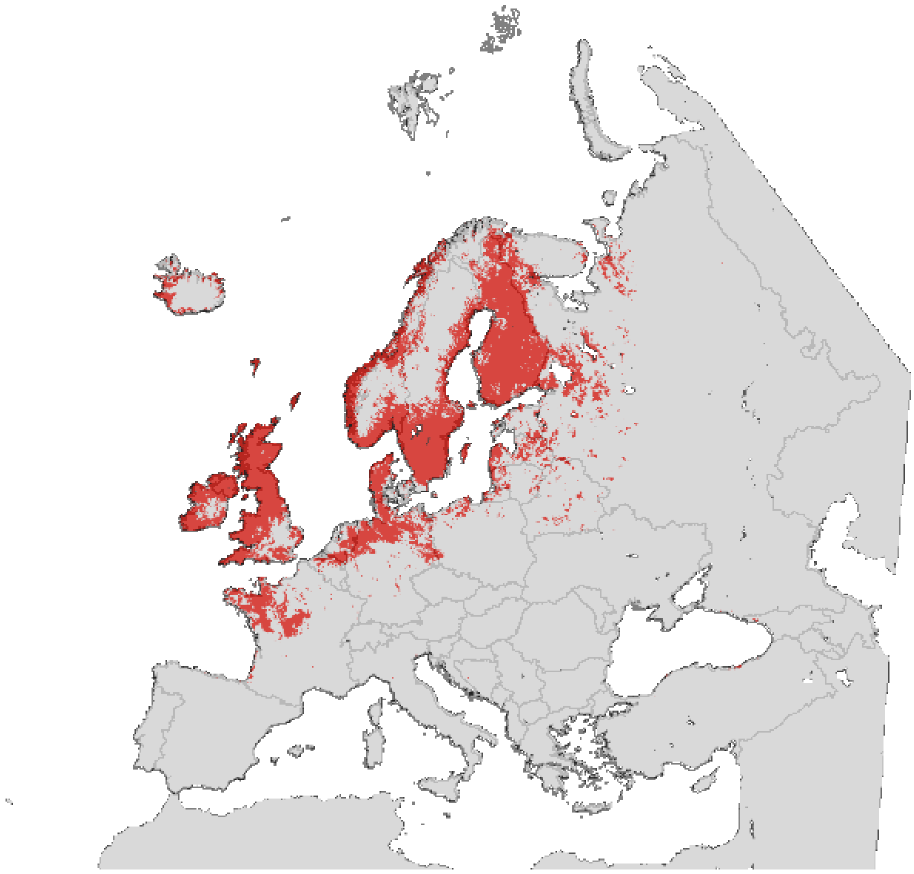
Additional selection criteria:

Comments: Poland and Spain are missing, but the question is if this habitat type is really occurring there (could be 3130).

Quality A-E: B (see comments).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 3130

Oligotrophic to mesotrophic standing waters with vegetation of the Littorelletea uniflorae and/or of the Isoëto-Nanojuncetea

Initial species selection

Anagallis minima
Baldellia ranunculoides
Centaurium pulchellum
Cicendia filiformis
Cyperus flavescens
Cyperus fuscus
Cyperus michelianus
Deschampsia setacea
Elatine hexandra
Elatine hydropiper
Eleocharis acicularis
Eleocharis multicaulis
Eleocharis ovata
Hypericum elodes
Juncus bufonius
Juncus bulbosus
Juncus capitatus
Juncus pygmaeus
Juncus tenageia
Limosella aquatica
Lindernia procumbens
Littorella uniflora
Luronium natans
Pilularia globulifera
Potamogeton gramineus
Potamogeton polygonifolius
Radiola linoides
Scirpus fluitans
Scirpus setaceus
Scirpus supinus
Sparganium minimum

Species evaluation

Selected species: Excluded Centaurium pulchellum (too broad) and Juncus bufonius (too broad). Include Ranunculus reptans.

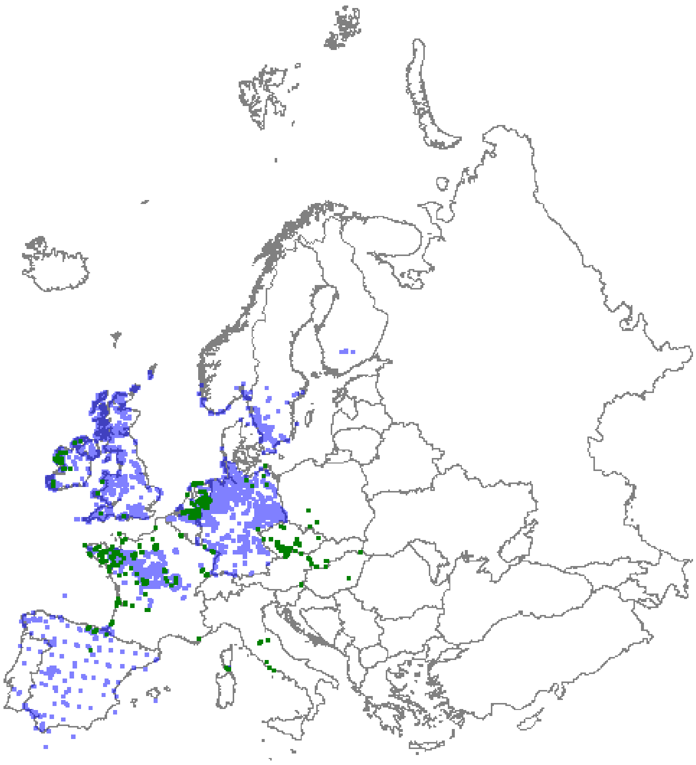
Thresholds EVA: 4

Threshold GBIF: 6

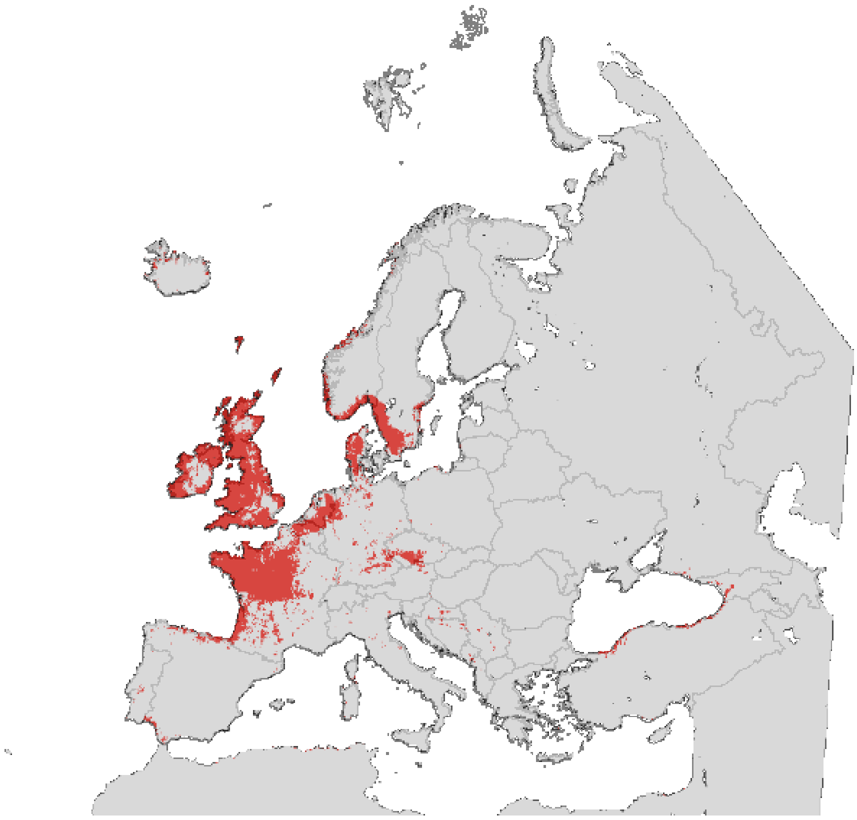
Additional selection criteria: Exclude coasts because those sites would be habitat type 2190.

Comments: There are some doubts with regard to assignment of sites in Eastern Europe.

Quality A-E: C (two different ecosystems are brought together in one habitat type, which gives difficulties with selection; Spain, France and maybe also Eastern European countries are poorly represented). Option: produce different for both maps and then merge these into one map.



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 3150

Natural eutrophic lakes with Magnopotamion or Hydrocharition - type vegetation

Initial species selection

Aldrovanda vesiculosa	Ceratophyllum demersum
Hydrocharis morsus-ranae	Lemna trisulca
Myriophyllum spicatum	Myriophyllum verticillatum
Nuphar lutea	Nuphar pumila
Nymphaea alba	Nymphaea candida
Nymphoides peltata	Polygonum amphibium
Potamogeton lucens	Potamogeton natans
Potamogeton pectinatus	Potamogeton perfoliatus
Potamogeton praelongus	Potamogeton x zizii
Spirodela polyrhiza	Stratiotes aloides
Trapa natans	Utricularia australis
Utricularia vulgaris	Wolffia arrhiza

Species evaluation

Selected species: Exclude Polygonum amphibium (because of land forms), Utricularia australis (more in less eutrophic waters), Potamogeton x zizii (hybrid). Include Salvinia natans.

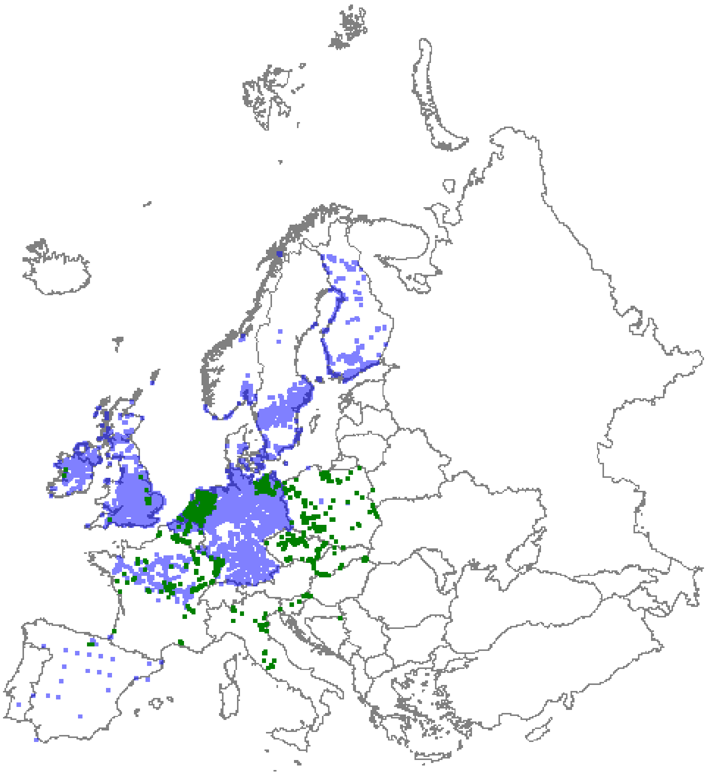
Thresholds EVA: 4

Threshold GBIF: 7

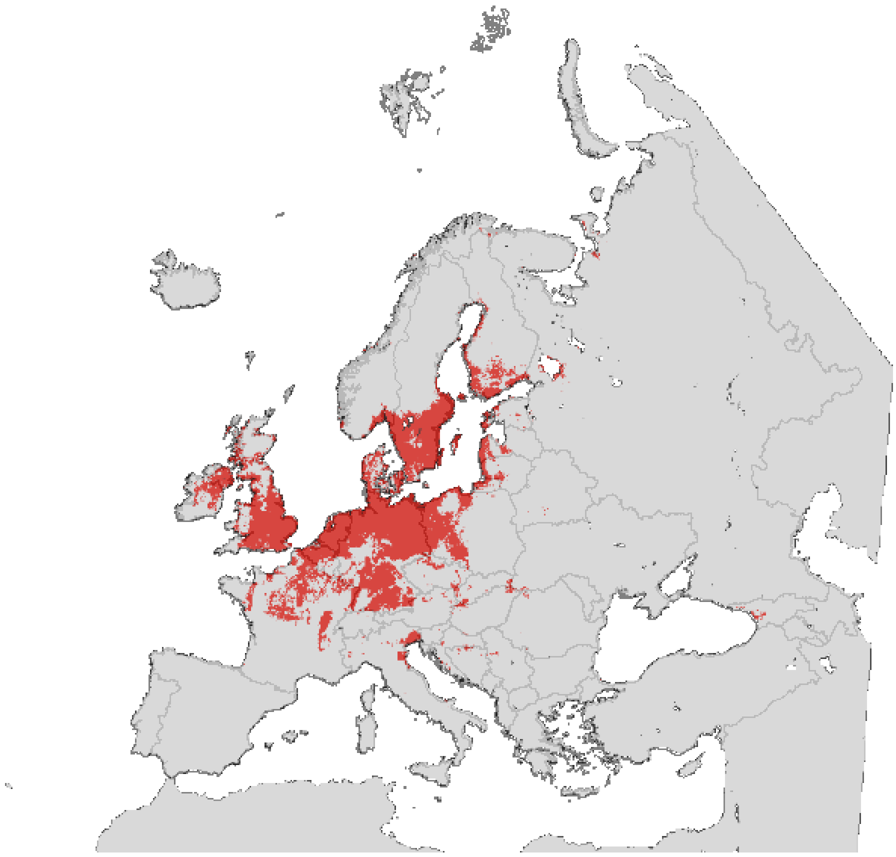
Additional selection criteria:

Comments: Difficult type, because of naturalness, difficult to exclude form artificial water bodies, like ditches and ponds (bearing the same vegetation).

Quality A-E: D (e.g. Germany hardly presented)



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 3260

Water courses of plain to montane levels with the Ranunculion fluitantis and Callitricho-Batrachion vegetation

Initial species selection

Calendula suffruticosa s. lusitanica
Callitriche hamulata
Fontinalis antipyretica
Groenlandia densa
Myriophyllum spicatum
Potamogeton nodosus
Potamogeton perfoliatus
Ranunculus fluitans
Ranunculus peltatus s. fucoides
Ranunculus penicillatus s. penicillatus
Ranunculus trichophyllus
Veronica beccabunga
Callitriche brutia
Callitriche stagnalis
Glyceria declinata
Myriophyllum alterniflorum
Potamogeton alpinus
Potamogeton pectinatus
Ranunculus aquatilis
Ranunculus peltatus
Ranunculus penicillatus
Ranunculus penicillatus s. pseudofluitans
Sparganium emersum
Zannichellia palustris

Species evaluation

Selected species: Restrict to just four species, all of running water and somehow complementary: Potamogeton alpinus, Potamogeton nodosus, Ranunculus fluitans and Ranunculus penicillatus.

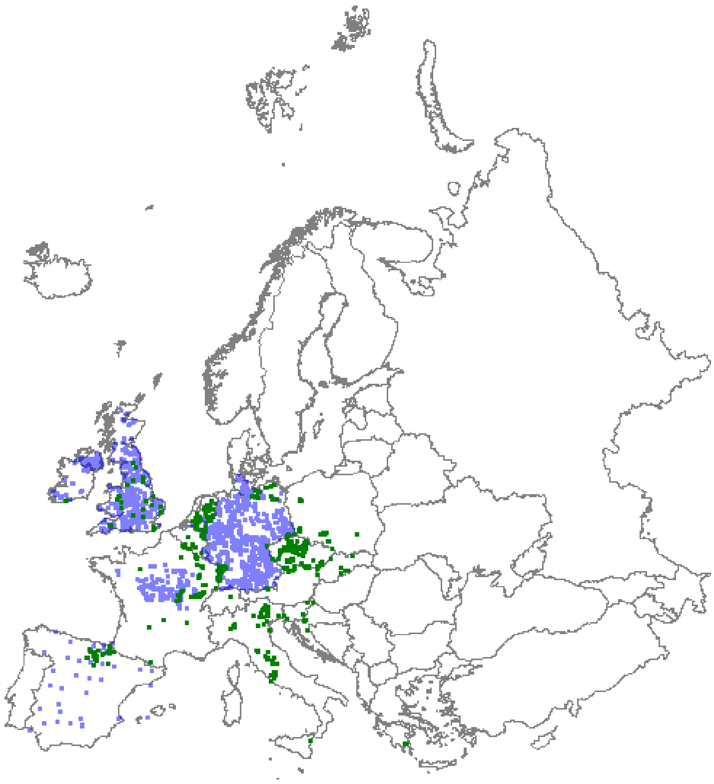
Thresholds EVA: 1

Threshold GBIF: 2

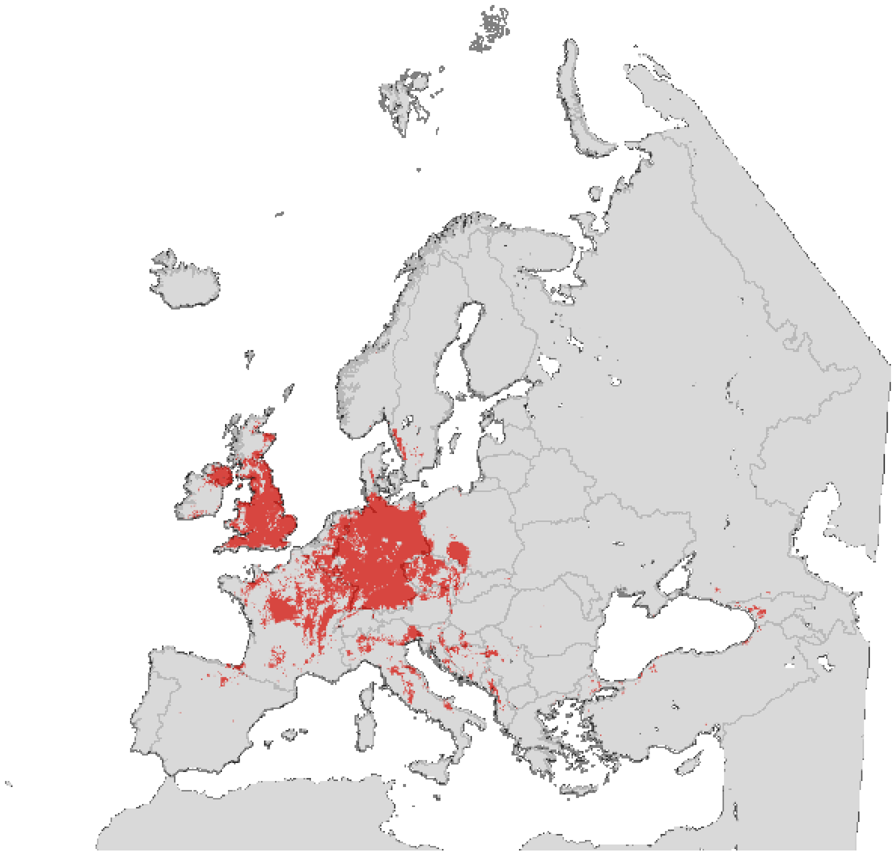
Additional selection criteria:

Comments:

Quality A-E: D (Lack of data, limited number of relevés, both from Eastern Europe and for instance Germany and Spain).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 4010
Northern Atlantic wet heaths with Erica tetralix

Initial species selection

Calluna vulgaris	Carex panicea
Dactylorhiza maculata	Drosera intermedia
Drosera rotundifolia	Erica tetralix
Eriophorum angustifolium	Gentiana pneumonanthe
Juncus squarrosus	Molinia caerulea
Narthecium ossifragum	Potentilla erecta
Rhynchospora alba	Rhynchospora fusca
Scirpus cespitosus	Sphagnum compactum
Sphagnum tenellum	Trichophorum cespitosum ag.

Species evaluation

Selected species: Erica tetralix required. Exclude Calluna vulgaris, Molinia caerulea and Potentilla erecta. Include: Trichophorum cespitosum and children.

Thresholds EVA: 4

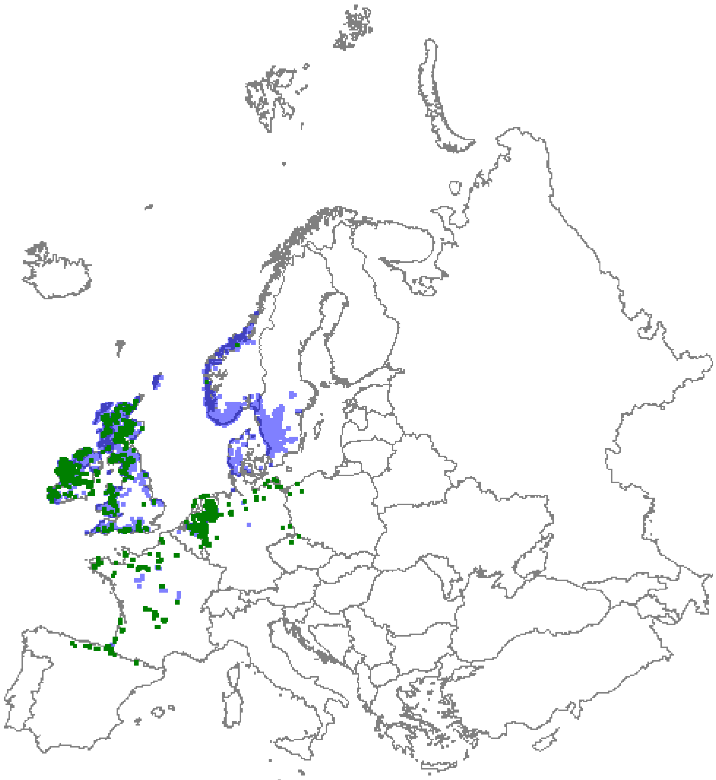
Threshold GBIF: 9

Additional selection criteria:

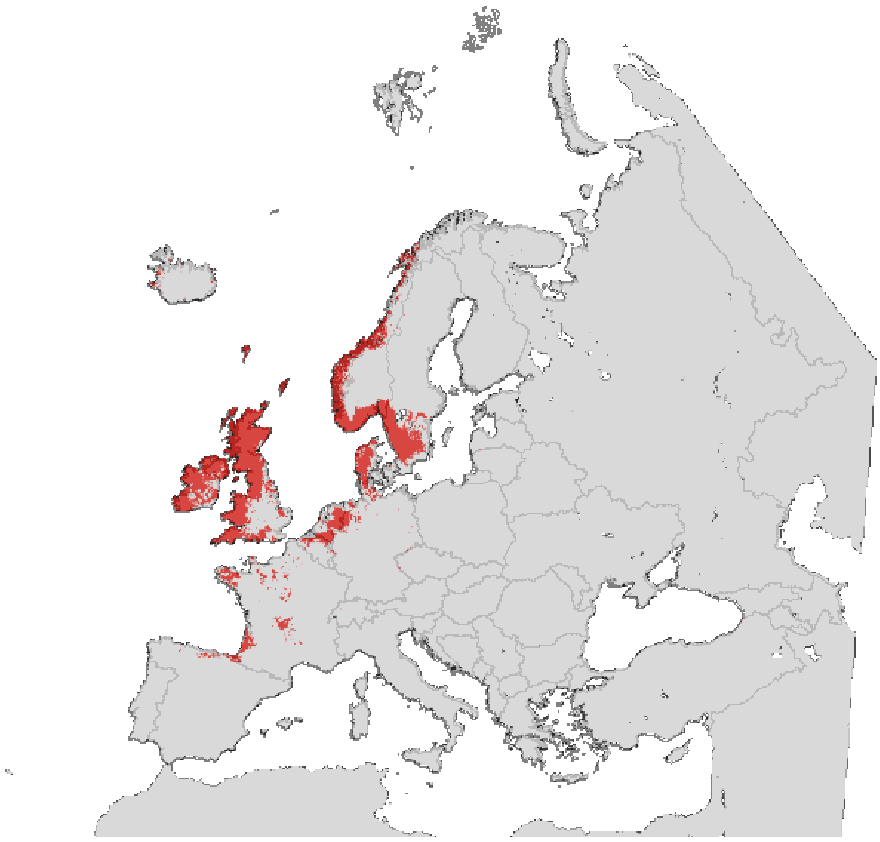
Comments:

Quality A-E: B (some gaps in Germany and some doubtful assignments in France and Scandinavian coast).

Multi-variate analysis: Erica tetralix not required



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 4030
European dry heaths

Initial species selection

Calluna vulgaris
Carex pilulifera
Chamaespartium tridentatum
Cistus ladanifer
Cistus salvifolius
Daboecia cantabrica
Deschampsia flexuosa
Dicranum scoparium
Erica australis
Erica cinerea
Erica mackaiana
Erica umbellata
Galium saxatile
Genista anglica
Genista germanica
Genista pilosa
Hylocomium splendens
Hypnum jutlandicum
Nardus stricta
Pleurozium schreberi
Potentilla erecta
Ulex gallii
Ulex minor
Vaccinium myrtillus
Vaccinium vitis-idaea

Species evaluation

Selected species: Exclude Carex pilulifera, Deschampsia flexuosa, Dicranum scoparium, Hylocomium splendens, Hypnum jutlandicum, Nardus stricta, Pleurozium schreberi (bryophytes also in acid forests) and Potentilla erecta. Include Erica tetralix for a better Atlantic representation.

Thresholds EVA: 4

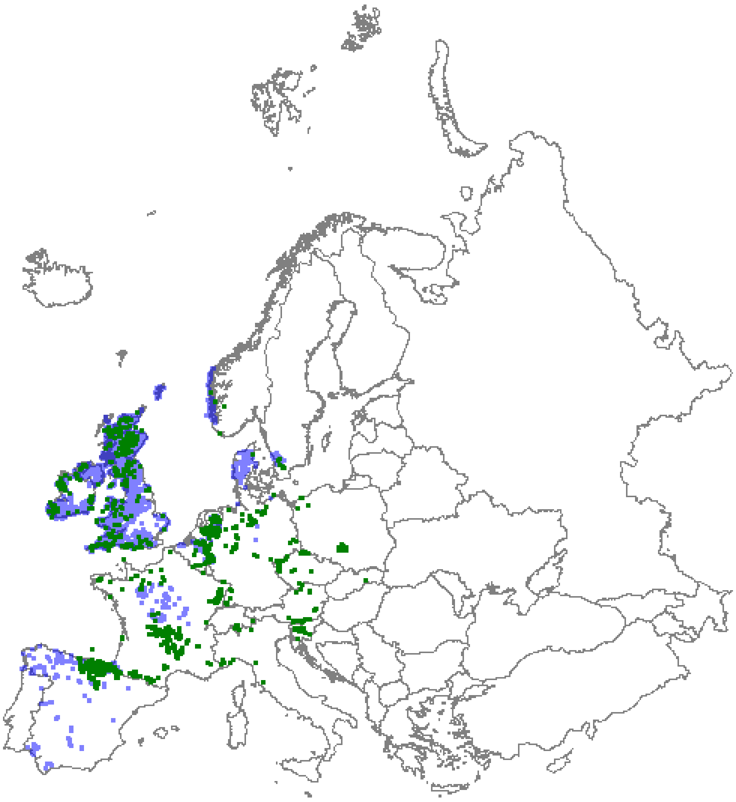
Threshold GBIF: 6

Additional selection criteria:

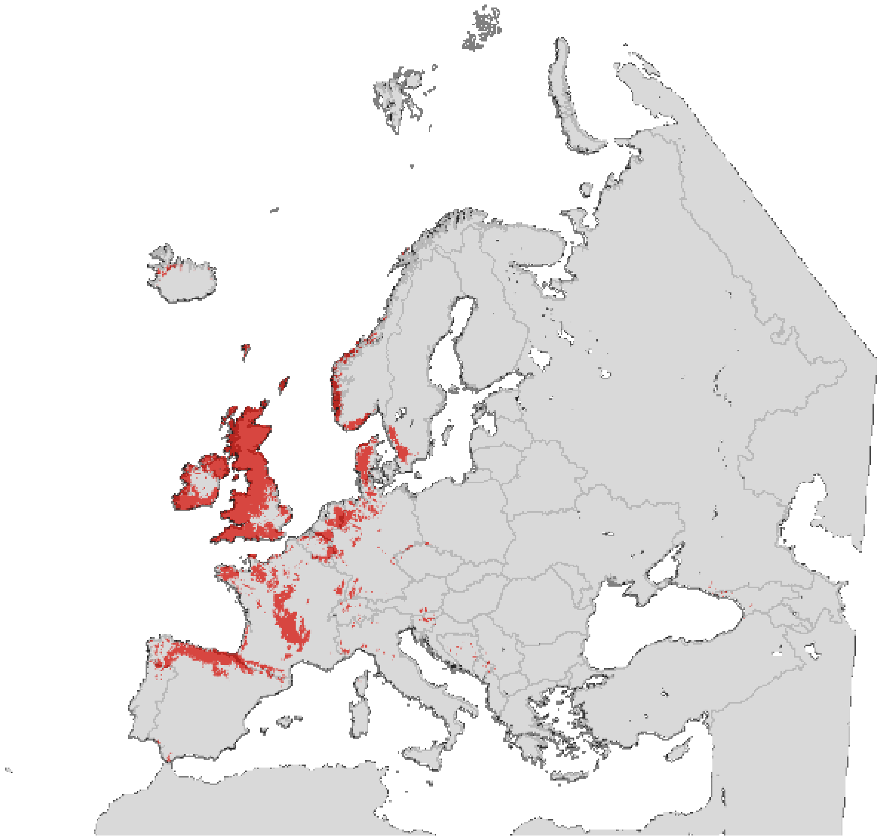
Comments:

Quality A-E: B (e.g. gaps in Franc en Germany)

Multi-variate analysis: EVA threshold: 3



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 4060
Alpine and Boreal heaths

Initial species selection

Arctostaphylos alpinus
Arctostaphylos uva-ursi
Betula nana
Bruckenthalia spiculifolia
Calluna vulgaris
Carex bigelowii
Cassiope tetragona
Cetraria islandica
Cetraria nivalis
Cladonia arbuscula
Cladonia rangiferina
Cladonia uncialis
Cornus suecica
Deschampsia flexuosa
Dryas octopetala
Empetrum nigrum s. hermaphroditum
Erica herbacea
Galium saxatile
Geum montanum
Homogyne alpina
Huperzia selago
Hylocomium splendens
Juncus trifidus
Juniperus communis s. alpina
Ligusticum mutellina
Loiseleuria procumbens
Nardus stricta
Phyllodoce caerulea
Pleurozium schreberi
Potentilla aurea
Racomitrium lanuginosum
Rhododendron ferrugineum
Rhododendron hirsutum
Rhodothamnus chamaecistus
Vaccinium myrtillus
Vaccinium uliginosum
Vaccinium vitis-idaea s. vitis-idaea

Species evaluation

Selected species: Exclude Cladonia arbuscula, Cladonia rangiferina, Cladonia uncialis, Deschampsia flexuosa, Galium saxatile, Hylocomium splendens, Juncus trifidus and Nardus stricta.

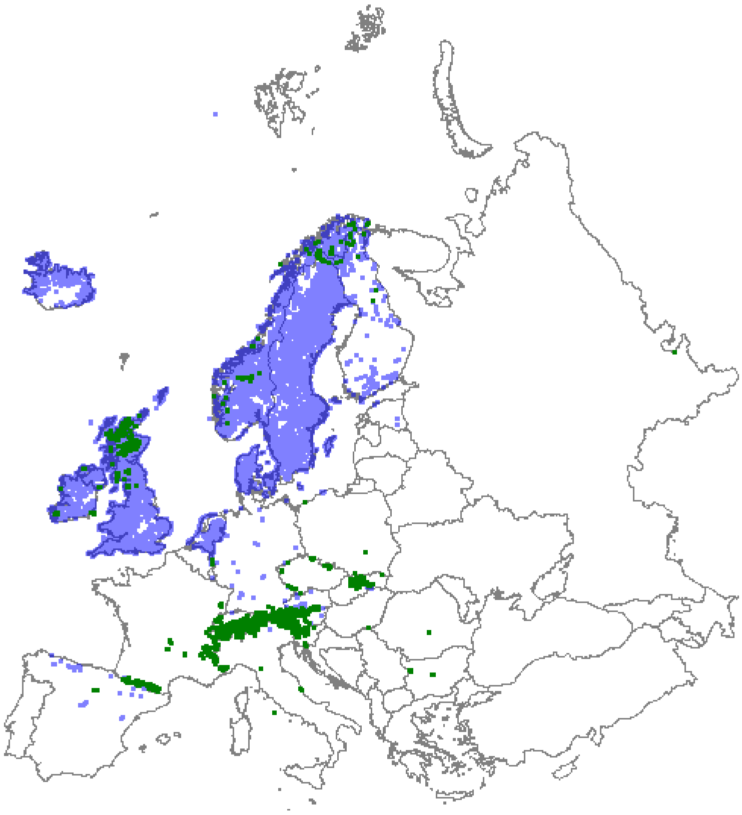
Thresholds EVA: 5

Threshold GBIF: 8

Additional selection criteria:

Comments:

Quality A-E: B (lack of data for Spain, Balkan and Apennines)



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 4070

Bushes with Pinus mugo and Rhododendron hirsutum (Mugo-Rhododendretum hirsuti)

Initial species selection

Calamagrostis varia	Calamagrostis villosa
Clematis alpina	Daphne mezereum
Erica herbacea	Homogyne alpina
Larix decidua	Luzula sylvatica
Picea abies	Pinus mugo
Rhododendron ferrugineum	Rhododendron hirsutum
Rhododendron myrtifolium	Rhodothamnus chamaecistus
Vaccinium myrtillus	Vaccinium vitis-idaea
Valeriana tripteris	Viola biflora

Species evaluation

Selected species: Pinus mugo required. Exclude Picea abies and Larix decidua.

Thresholds EVA: 4

Threshold GBIF: - (no additional information)

Additional selection criteria:

Comments:

Quality A-E: B (Bulgaria and Italy are missing)

Distribution: green dots represent vegetation plot data

Map with modelled distribution

Habitat type: 5110

Stable xerothermophilous formations with Buxus

Initial species selection

Amelanchier ovalis
Berberis vulgaris
Buxus sempervirens
Cornus mas
Cornus sanguinea
Crataegus monogyna
Cytisys sessilifolium
Daphne laureola
Dictamnus albus
Euphorbia amygdaloides
Geranium sanguineum
Ligustrum vulgare
Lonicera xylosteum
Prunus mahaleb
Prunus spinosa
Rosa rubiginosa
Rubia peregrina
Ruscus aculeatus
Sorbus aria
Viburnum lantana
Vincetoxicum hirundinaria

Species evaluation

Selected species:

Thresholds EVA: 3

Threshold GBIF: -

Additional selection criteria:

Comments:

Quality A-E: B.

Distribution: green dots represent vegetation plot data

Map with modelled distribution

Habitat type: 5130

Juniperus communis formations on heaths or calcareous grasslands

Initial species selection

Berberis vulgaris	Calluna vulgaris
Carex flacca	Crataegus monogyna
Deschampsia flexuosa	Dicranum scoparium
Empetrum nigrum	Hypnum jutlandicum
Juniperus communis	Nardus stricta
Pinus sylvestris	Pleurozium schreberi
Potentilla fruticosa	Prunus spinosa
Rosa canina	Rosa rubiginosa
Sesleria caerulea	Sorbus aucuparia
Sorbus intermedia	Vaccinium myrtillus

Species evaluation

Selected species: Juniperus communis required. Exclude Dicranum scoparium, Hypnum jutlandicum, Nardus stricta, Pinus sylvestris and Pleurozium schreberi.

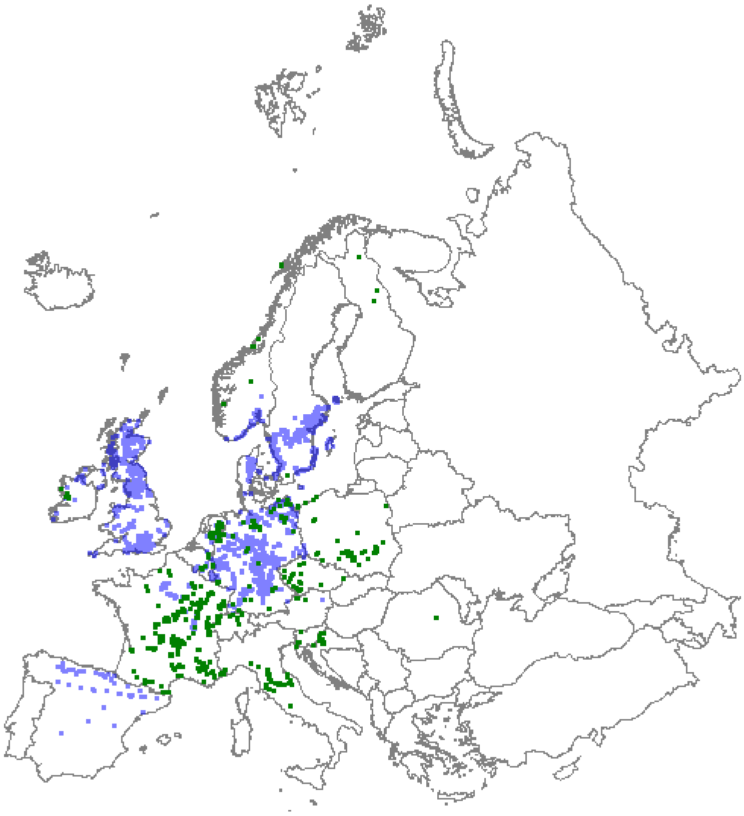
Thresholds EVA: 5

Threshold GBIF: 11 (How to deal with coastal area in GBIF data, e.g. two occurrences at the Dutch coast?)

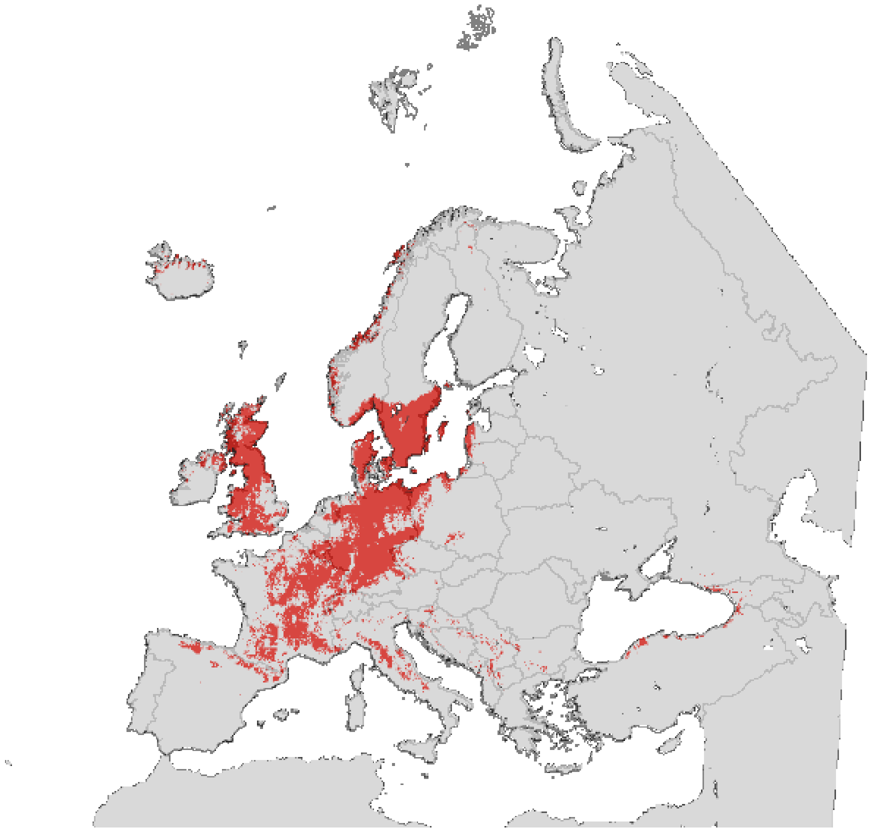
Additional selection criteria: Restrict to altitudes below 1500 m in alpine regions (so not in arctic Northern-Europe).

Comments:

Quality A-E: B (e.g. Bulgaria and Baltic countries missing.



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 5210

Arborescent matorral with Juniperus spp.

Initial species selection

Berteroa obliqua
Clematis flammula
Genista scorpius
Juniperus communis
Juniperus excelsa
Juniperus oxycedrus
Juniperus phoenicea
Olea europaea
Pistacia lentiscus
Quercus coccifera
Quercus pubescens
Rosmarinus officinalis
Teucrium chamaedrys
Thymus sibthorpii
Brachypodium retusum
Galium album
Jasminum fruticans
Juniperus drupacea
Juniperus foetidissima
Juniperus oxycedrus s. macrocarpa
Juniperus thurifera
Phillyrea angustifolia
Prasium majus
Quercus ilex
Rhamnus myrtifolius
Stipa bromoides
Teucrium polium
Thymus vulgaris

Species evaluation

Selected species: Exclude Quercus ilex and Quercus pubescens.

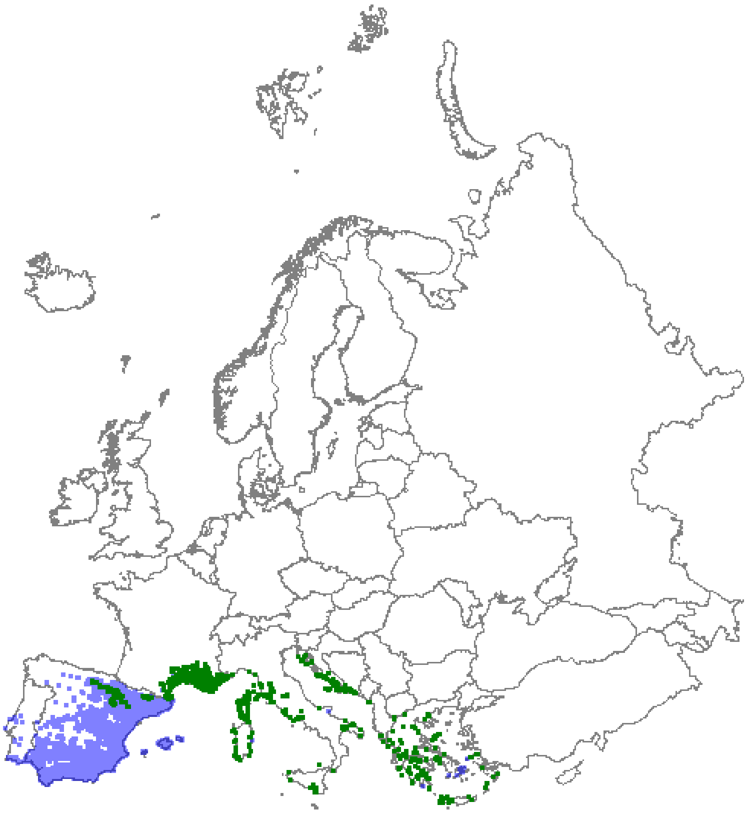
Thresholds EVA: 4

Threshold GBIF: 5

Additional selection criteria: Restrict to Mediterranean region.

Comments:

Quality A-E: C (lack of data in Portugal, Bulgaria and large parts of Spain and Italy.



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 5420
Sarcopoterium spinosum phryganas

Initial species selection

Anthyllis hermanniae	Asparagus acutifolius
Ballota pseudodictamnus	Calicotome villosa
Centaurea spinosa	Cistus incanus s. creticus
Cistus monspeliensis	Cistus parviflorus
Cistus salvifolius	Erica manipuliflora
Euphorbia acanthothamnos	Fumana arabica
Fumana thymifolia	Genista acanthoclada
Helichrysum italicum s. italicum	Helichrysum italicum s. microphyllum
Lithodora hispidula	Lonicera implexa
Micromeria graeca	Micromeria juliana
Micromeria nervosa	Ononis spinosa
Osyris alba	Phagnalon graecum
Phillyrea angustifolia	Pistacia lentiscus
Rhamnus lycioides s. oleoides	Salvia triloba
Sarcopoterium spinosum	Satureja thymbra
Smilax aspera	Stachys spinosa
Teucrium brevifolium	Teucrium divaricatum
Teucrium polium	Thymus capitatus

Species evaluation

Selected species: Sarcopoterium spinosum required. Exclude Cistus monspeliensis, Fumana thymifolia, Helichrysum italicum subsp. italicum, Helichrysum italicum subsp. microphyllum, Lonicera implexa, Ononis spinosa, Osyris alba, Phillyrea angustifolia, Salvia triloba and Teucrium polium.

Thresholds EVA: 3

Threshold GBIF: - (no additional information)

Additional selection criteria: Restrict to Mediterranean region and exclude one dot on Sicily.

Comments:

Quality A-E: A

Distribution: green dots represent vegetation plot data

Map with modelled distribution

Habitat type: 6110
Rupicolous calcareous or basophilic grasslands of the Alysso-Sedion albi

Initial species selection

Acinos arvensis
Allium senescens s. montanum
Alyssum alyssoides
Arabis hirsuta
Arabis recta
Arenaria serpyllifolia
Arenaria serpyllifolia ag.
Asperula cynanchica
Cardaminopsis arenosa
Cerastium pumilum
Echium vulgare
Hornungia petraea
Jovibarba globifera s. globifera
Jovibarba globifera s. hirta
Koeleria macrantha
Poa badensis
Poa compressa
Potentilla cinerea
Potentilla tabernaemontani
Sanguisorba minor
Saxifraga tridactylites
Sedum album
Sedum sexangulare
Teucrium botrys
Thymus pulegioides
Tortella tortuosa

Species evaluation

Selected species: Exclude Sanguisorba minor.

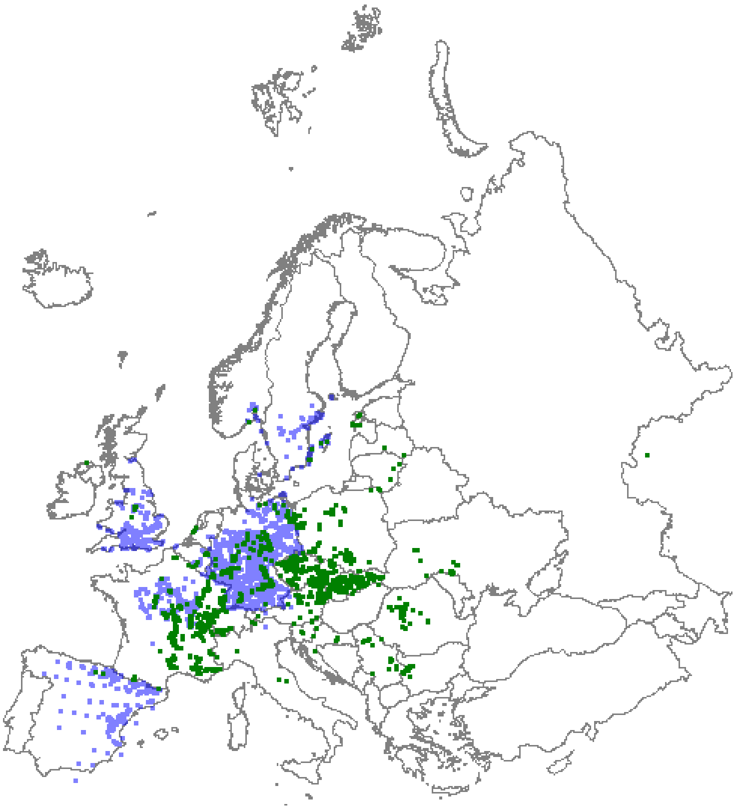
Thresholds EVA: 5

Threshold GBIF: 10 (will add e.g. Öland, as long as no Scandinavian relevé data are available)

Additional selection criteria:

Comments:

Quality A-E: B (some gaps due of limited data, Bulgaria missing as well as Italy largely).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 6120
Xeric sand calcareous grasslands

Initial species selection

Allium schoenoprasum
Alyssum montanum s. gmelinii
Artemisia campestris
Astragalus arenarius
Cardaminopsis arenosa
Carex arenaria
Carex ligerica
Carex praecox
Cerastium semidecandrum
Corynephorus canescens
Dianthus arenarius
Dianthus deltoides
Euphorbia seguierana
Festuca psammophila
Galium verum
Gypsophila fastigiata
Helichrysum arenarium
Herniaria glabra
Jasione montana
Koeleria glauca
Koeleria macrantha
Petrorhagia prolifera
Phleum arenarium
Sedum acre
Sedum rupestre
Silene chlorantha
Silene conica
Thymus serpyllum
Tortula ruralis s. ruraliformis

Species evaluation

Selected species: Exclude Carex arenaria, Cerastium semidecandrum, Corynephorus canescens, Jasione montana, Phleum arenarium and Tortula ruralis subsp. ruraliformis.

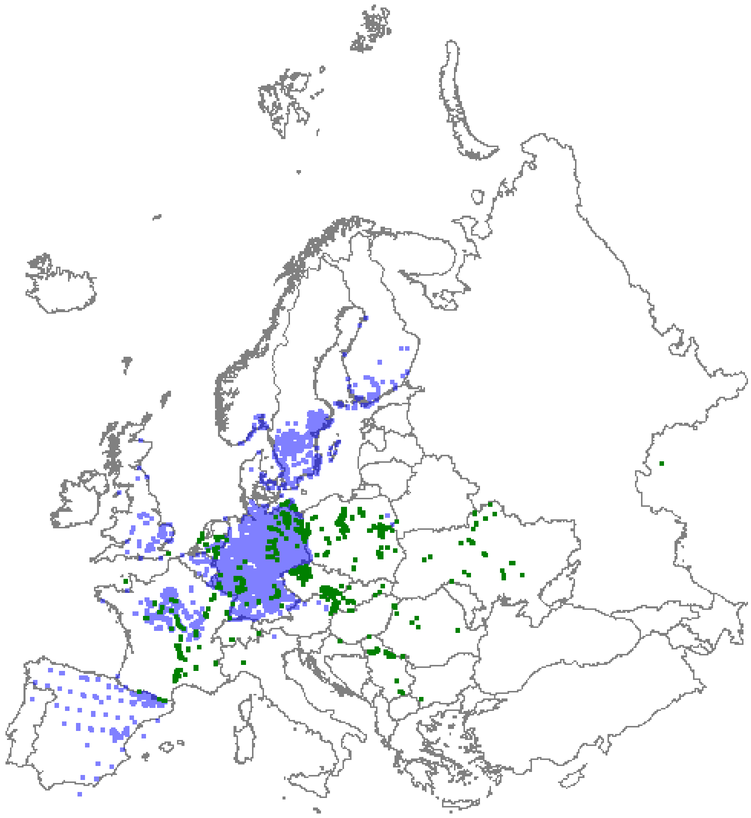
Thresholds EVA: 4

Threshold GBIF: 6 (South Sweden!)

Additional selection criteria: Exclude coastal belt.

Comments: Assignments to this habitat type seem to be not balanced between countries (e.g. no assignments in Czech Republic).

Quality A-E: B (Baltic countries more or less missing, as well as Rumania).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 6150
Siliceous alpine and boreal grasslands

Initial species selection

Agrostis rupestris
Avenula versicolor
Campanula alpina
Carex bigelowii
Carex sempervirens
Cassiope tetragona
Cetraria islandica
Festuca airoides
Hieracium alpinum
Homogyne alpina
Juncus trifidus
Ligusticum mutellina
Luzula alpinopilosa
Oreochloa disticha
Potentilla aurea
Primula minima
Pulsatilla alpina
Racomitrium lanuginosum
Soldanella carpatica

Species evaluation

Selected species: Exclude Cetraria islandica and Racomitrium lanuginosum.

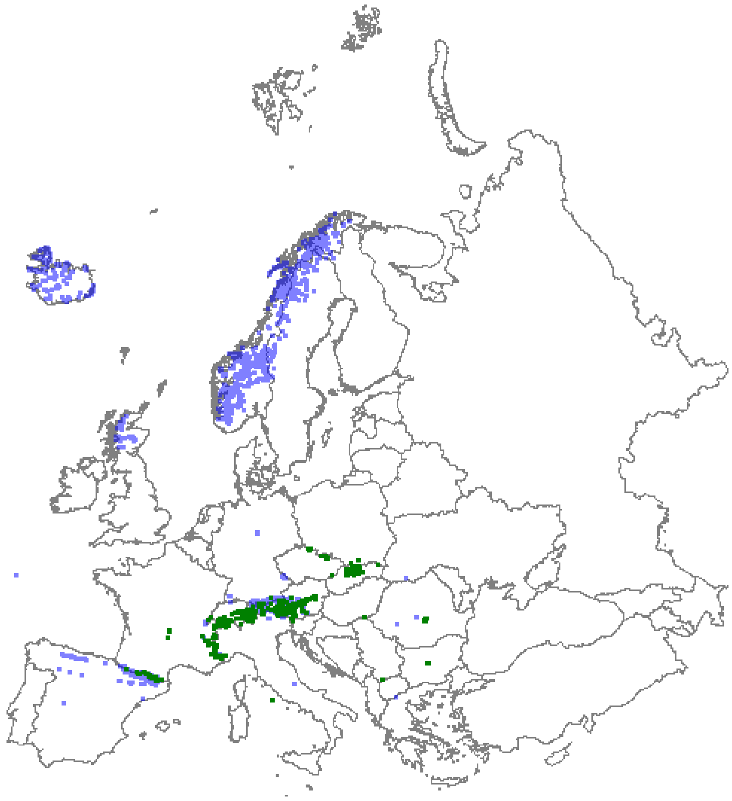
Thresholds EVA: 4

Threshold GBIF: 3

Additional selection criteria:

Comments:

Quality A-E: B (Carpathians maybe underrepresented, Rumania and Bulgaria).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 6170
Alpine and subalpine calcareous grasslands

Initial species selection

Achillea clavennae	Alchemilla conjuncta
Alchemilla flabellata	Alchemilla hoppeana
Antennaria carpatica	Anthyllis vulneraria s. alpestris
Armeria multiceps	Aster alpinus
Astragalus alpinus	Astrantia major
Bellardiochloa violacea	Campanula scheuchzeri
Carex atrata	Carex brevicollis
Carex capillaris	Carex ferruginea
Carex firma	Carex foetida
Carex rupestris	Carex sempervirens
Daphne striata	Dianthus glacialis
Draba aizoides	Dryas octopetala
Galium anisophyllon	Gentiana nivalis
Gentianella campestris	Geum montanum
Globularia nudicaulis	Helianthemum nummularium s. grandiflorum
Helianthemum oelandicum s. alpestre	Hieracium villosum
Minuartia sedoides	Oxytropis jacquinii
Paronychia polygonifolia	Phyteuma orbiculare
Plantago subulata s. insularis	Polygala alpestris
Potentilla nivea	Primula auricula
Pulsatilla alpina s. alpina	Sagina pilifera
Saussurea alpina	Scabiosa lucida
Sesleria albicans	Sibbaldia procumbens
Stachys alopecuros	Thymus pulcherrimus
Trifolium thalii	Veronica alpina

Species evaluation

Selected species: Exclude Astrantia major, Gentianella campestris and Sesleria albicans.

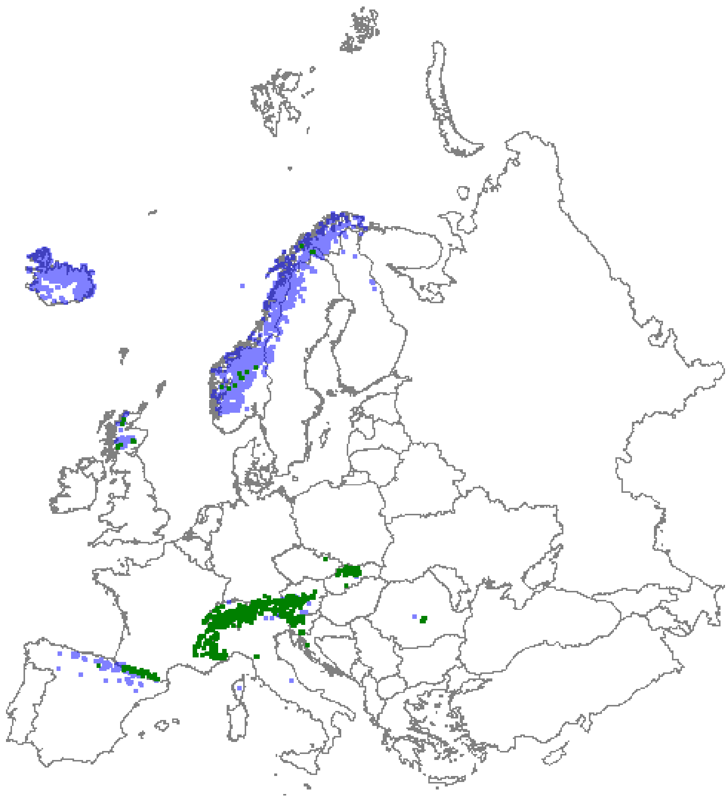
Thresholds EVA: 4

Threshold GBIF: 5

Additional selection criteria: Restrict to altitudes below 1500 m in alpine regions (so not in arctic Northern-Europe).

Comments:

Quality A-E: B (Carpathians are missing, as well alpine zones of Corsica and Apennines).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 6210

Semi-natural dry grasslands and scrubland facies on calcareous substrates (Festuco-Brometalia) (* important orchid sites)

Initial species selection

Adonis vernalis
Anthyllis vulneraria ag.
Asperula cynanchica
Brachypodium pinnatum
Bromus erectus
Carex caryophyllea
Carlina vulgaris
Cirsium acaule
Dianthus sylvestris
Euphorbia cyparissias
Fumana procumbens
Hippocrepis comosa
Leontodon hispidus
Ophrys apifera
Orchis militaris
Petrorhagia saxifraga
Plantago media
Potentilla cinerea
Potentilla tabernaemontani
Sanguisorba minor
Scabiosa ochroleuca
Stipa joannis
Teucrium montanum
Anthyllis vulneraria
Arabis hirsuta
Avenula pratensis
Briza media
Campanula glomerata
Carex flacca
Centaurea scabiosa
Dianthus carthusianorum
Eryngium campestre
Festuca valesiaca
Globularia punctata
Koeleria pyramidata
Medicago sativa s. falcata
Ophrys insectifera
Orchis ustulata
Phleum phleoides
Polygala comosa
Potentilla pusilla
Primula veris
Scabiosa columbaria
Stipa capillata
Teucrium chamaedrys

Species evaluation

Selected species: Exclude Anthyllis vulneraria ag. Briza media, Leontodon hispidus, Plantago media en Petrorhagia saxifraga.

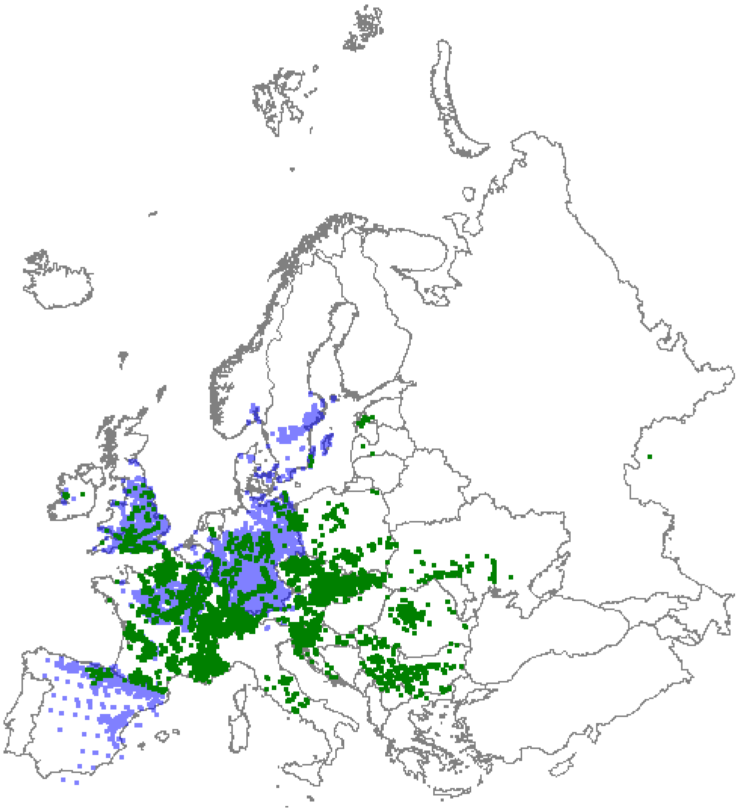
Thresholds EVA: 6

Threshold GBIF: 10

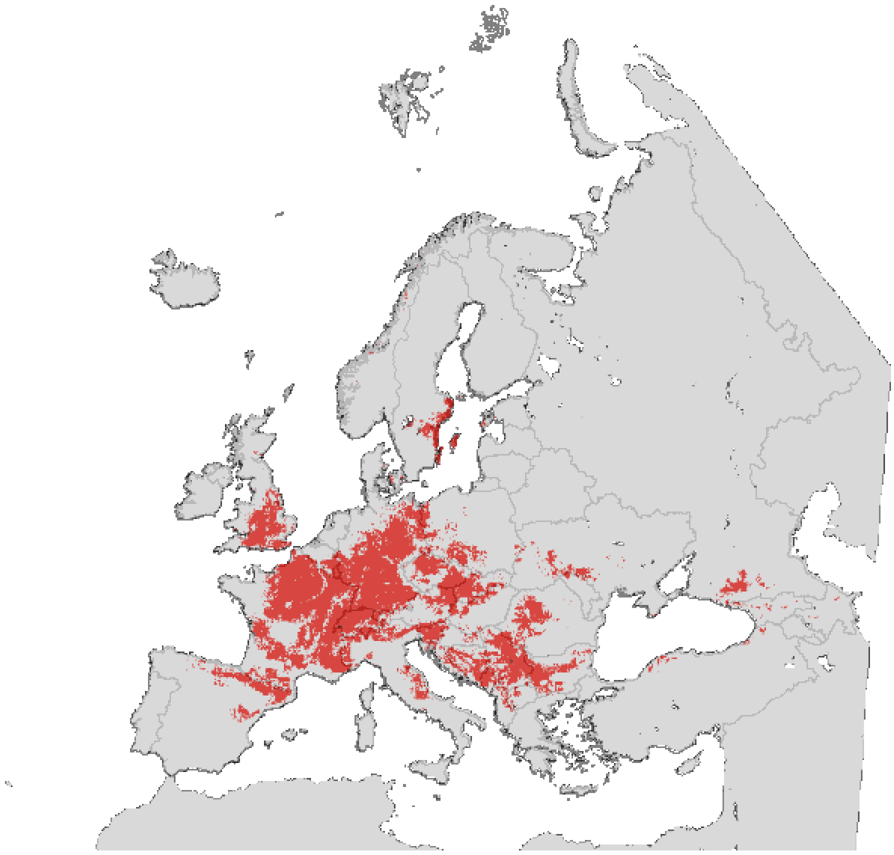
Additional selection criteria: Exclude Russia.

Comments:

Quality A-E: B (Northern Italy incomplete possible in gaps in Balkan).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 6220
Pseudo-steppe with grasses and annuals of the Thero-Brachypodietea

Initial species selection

Aira cupaniana	Anthyllis lotoides
Arenaria modesta	Arenaria retusa
Asterolinon linum-stellatum	Avenula bromoides
Brachypodium distachyon	Brachypodium retusum
Bromus rubens	Campanula fastigiata
Chaenorhinum rubrifolium	Convolvulus althaeoides
Desmazeria rigida	Eryngium campestre
Euphorbia exigua	Filago pyramidata
Hippocrepis ciliata	Jasione penicillata
Linaria saturejoides	Linum strictum
Logfia gallica	Medicago minima
Micropyrum tenellum	Narduroides salzmannii
Ornithopus compressus	Phlomis lychnitis
Plantago lagopus	Reseda stricta
Sedum gypsicola	Sedum sediforme
Teesdalia coronopifolia	Thymus vulgaris
Trifolium scabrum	Tuberaria guttata
Valantia hispida	Vulpia myuros

Species evaluation

Selected species: Exclude: Eryngium campestre. Include Dactylis glomerata subsp. hispanica, Hyparrhenia hirta, Plantago albicans, Poa bulbosa, Trifolium subterraneum and Trisetum velutinum.

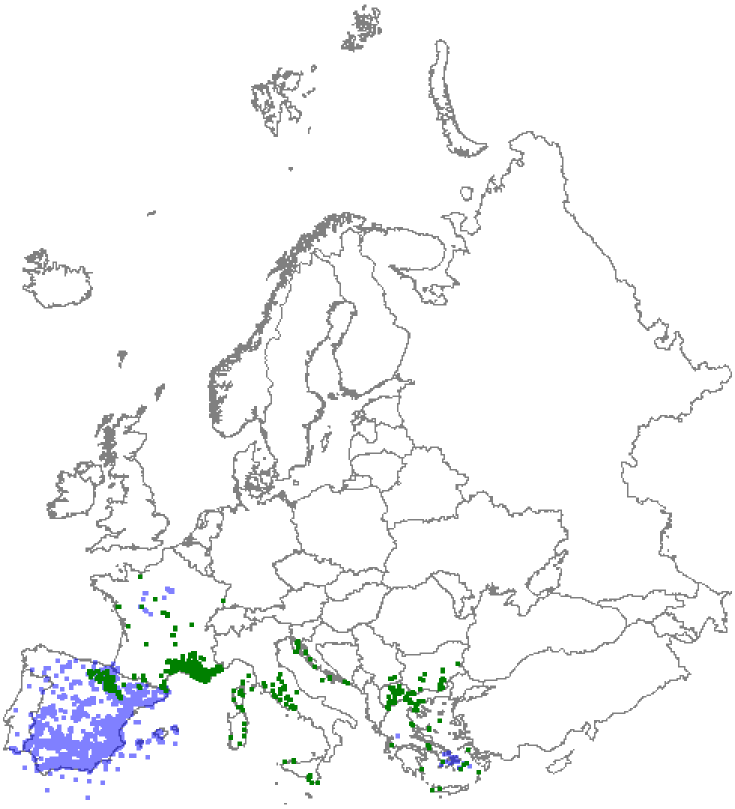
Thresholds EVA: 4

Threshold GBIF: 8

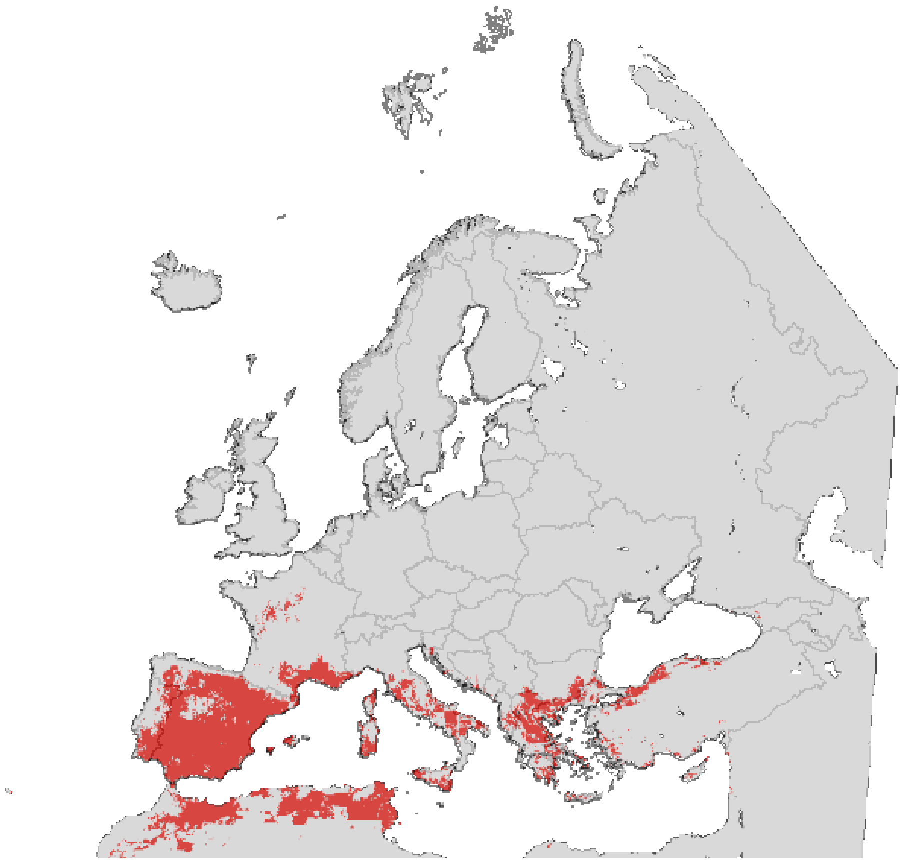
Additional selection criteria: Exclude coastal belt/

Comments:

Quality A-E: D (lack of data in e.g. Portugal, Cyprus (general remark: NOT ON MAP AT ALL), Bulgaria and in large part of Spain and Italy; lack of relevés of these vegetation types in general).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 6230
Species-rich Nardus grasslands, on silicious substrates in mountain areas (and submountain areas in Continental Europe)

Initial species selection

Antennaria dioica	Arnica montana
Campanula barbata	Campanula scheuchzeri
Carex ericetorum	Carex pallescens
Carex panicea	Deschampsia flexuosa
Festuca ovina	Galium saxatile
Gentiana pneumonanthe	Geum montanum
Homogyne alpina	Hypericum maculatum
Hypochoeris maculata	Lathyrus montanus
Leontodon pyrenaicus s. helveticus	Ligusticum mutellina
Meum athamanticum	Nardus stricta
Pedicularis sylvatica	Plantago alpina
Platanthera bifolia	Poa alpina
Polygala vulgaris	Potentilla aurea
Potentilla erecta	Pseudorchis albida
Selinum pyrenaeum	Soldanella alpina
Trifolium alpinum	Vaccinium myrtillus
Veronica officinalis	Viola canina

Species evaluation

Selected species: Nardus stricta required.

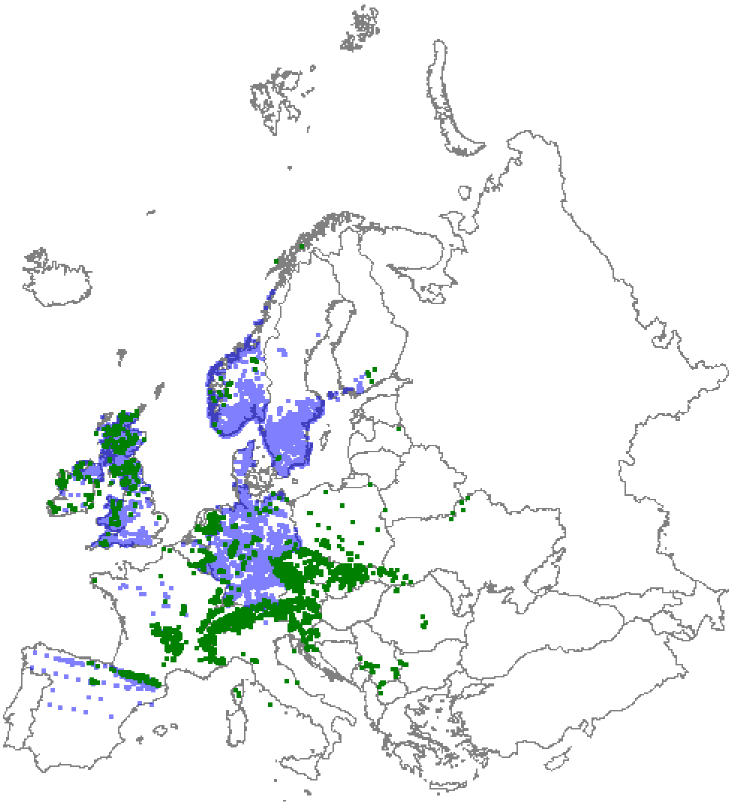
Thresholds EVA: 5 (11750 plots)

Threshold GBIF: 14 (9872 locations)

Additional selection criteria:

Comments:

Quality A-E: B (some countries need better representation, like France, Spain and Germany, and this also counts for Carpathians and Balkan Mountains of Bulgaria).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 6240
Sub-Pannonic steppic grasslands

Initial species selection

Allium flavum	Alyssum alyssoides
Artemisia austriaca	Astragalus austriacus
Astragalus exscapus	Carex humilis
Chrysopogon gryllus	Daphne cneorum
Dichanthium ischaemum	Eryngium campestre
Euphorbia cyparissias	Festuca rupicola
Festuca valesiaca	Gagea pusilla
Globularia cordifolia	Helianthemum canum
Hesperis tristis	Iris humilis
Iris pumila	Medicago minima
Oxytropis pilosa	Poa badensis
Potentilla cinerea	Ranunculus illyricus
Scorzonera austriaca	Stipa capillata
Stipa joannis	Teucrium chamaedrys

Species evaluation

Selected species: Buxus sempervirens required

Thresholds EVA: 4

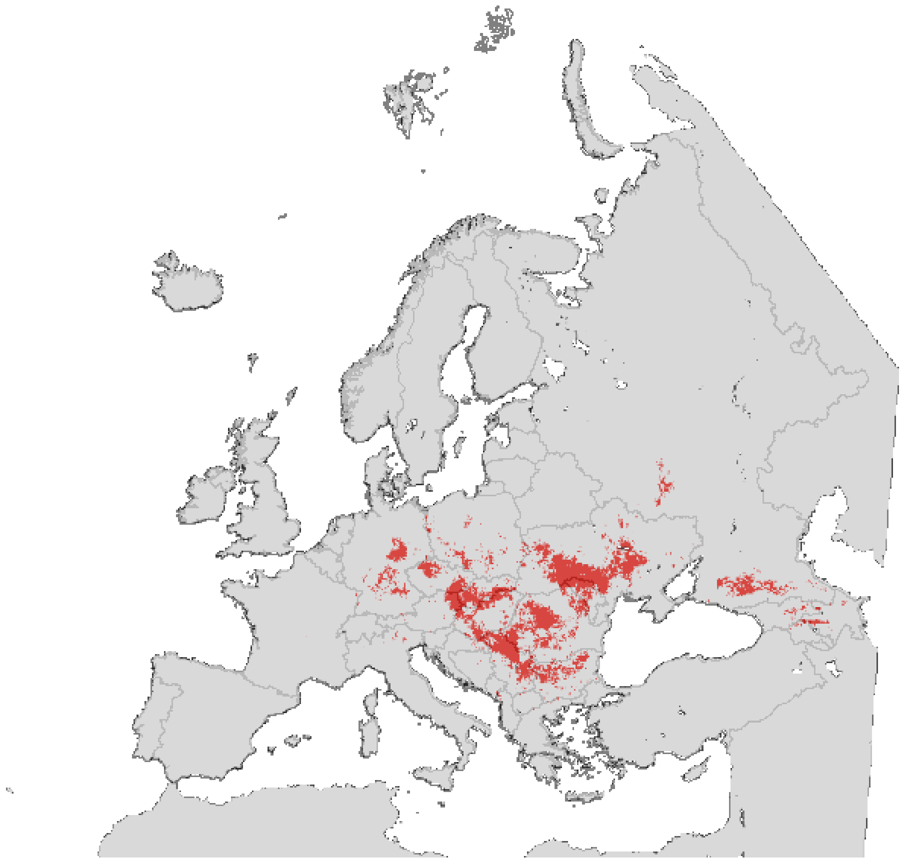
Threshold GBIF: - (no additional information)

Additional selection criteria:

Comments:

Quality A-E: C (Crucial countries like Hungary and Bulgaria are missing because of lack of data).

Distribution: green dots represent vegetation plot data



Map with modelled distribution

Habitat type: 6410

Molinia meadows on calcareous, peaty or clayey-silt-laden soils (Molinion caeruleae)

Initial species selection

Carex pallescens	Cirsium dissectum
Cirsium tuberosum	Colchicum autumnale
Crepis paludosa	Dianthus superbus
Galium uliginosum	Inula salicina
Juncus conglomeratus	Lotus pedunculatus
Luzula multiflora	Molinia caerulea
Ophioglossum vulgatum	Potentilla anglica
Potentilla erecta	Sanguisorba officinalis
Selinum carvifolia	Serratula tinctoria
Silaum silaus	Succisa pratensis
Viola palustris	Viola persicifolia

Species evaluation

Selected species: Exclude Potentilla erecta.

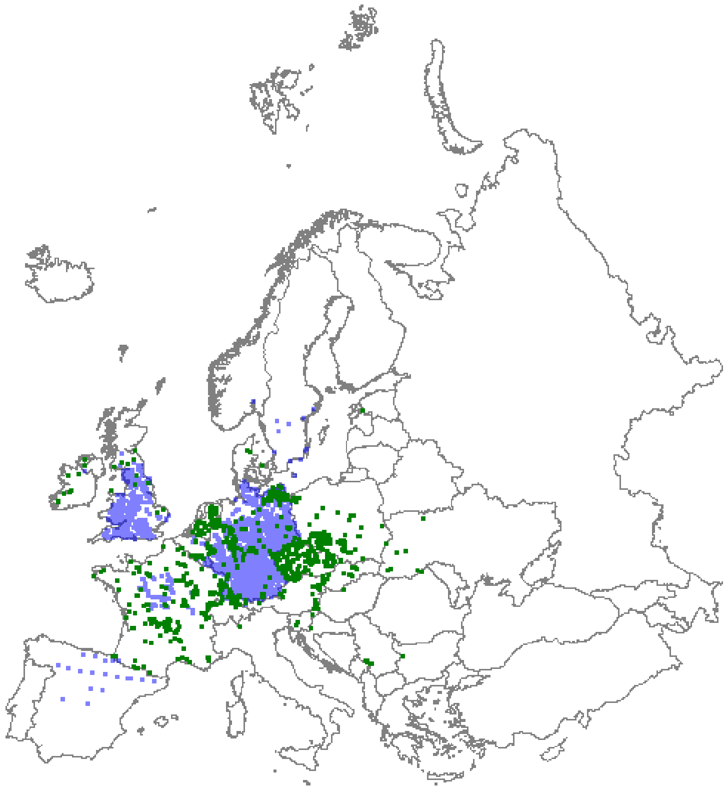
Thresholds EVA: 6 (2019 plots)

Threshold GBIF: 13 (rather strict to have Britain not overrepresented; 1684 locations)

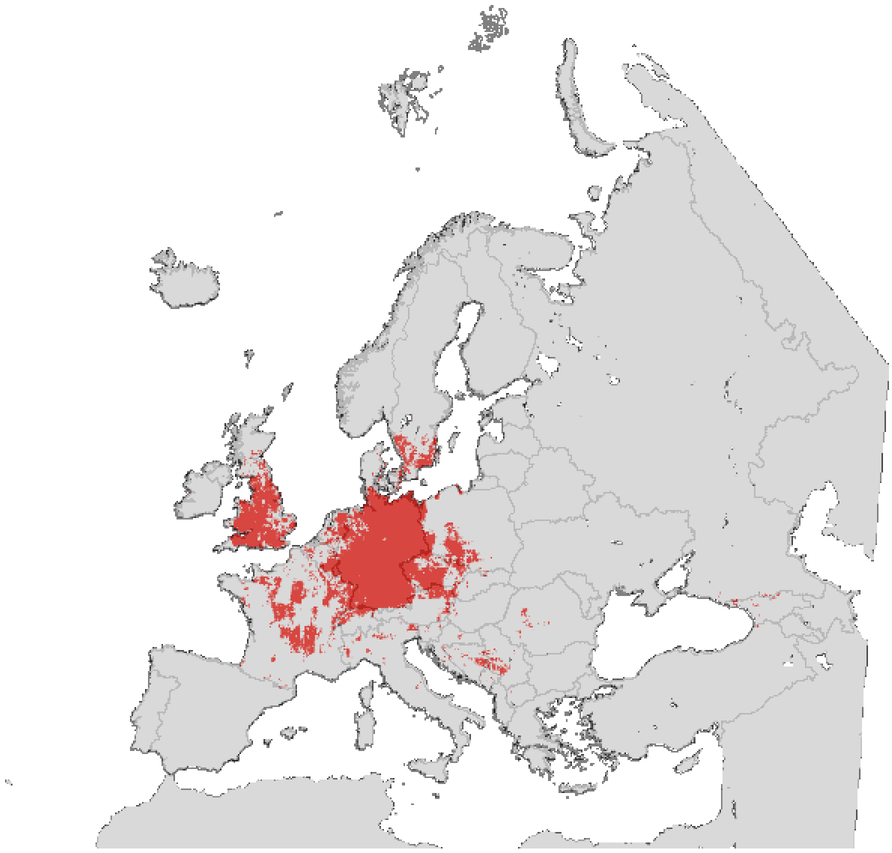
Additional selection criteria:

Comments:

Quality A-E: B (lack of data in e.g. France and Germany).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 6430

Hydrophilous tall herb fringe communities of plains and of the montane to alpine levels

Initial species selection

Aconitum lycoctonum	Aconitum napellus
Adenostyles alliariae	Aegopodium podagraria
Alliaria petiolata	Angelica archangelica
Angelica sylvestris	Athyrium distentifolium
Calamagrostis arundinacea	Calystegia sepium
Campanula serrata	Chaerophyllum hirsutum
Cicerbita alpina	Cicerbita plumieri
Cirsium helenioides	Cirsium oleraceum
Crepis paludosa	Digitalis grandiflora
Epilobium hirsutum	Filipendula ulmaria
Gentiana asclepiadea	Geranium robertianum
Geranium sylvaticum	Glechoma hederacea
Hypericum maculatum	Lamium album
Lilium martagon	Lysimachia vulgaris
Lythrum salicaria	Petasites hybridus
Peucedanum ostruthium	Ranunculus platanifolius
Rumex alpestris	Senecio fluviatilis
Silene dioica	Trollius europaeus
Valeriana officinalis	Veratrum album

Species evaluation

Selected species: Exclude Aegopodium podagraria, Alliaria petiolata, Angelica sylvestris, Calystegia sepium, Crepis paludosa, Glechoma hederacea, Hypericum maculatum, Lamium album and Silene dioica.

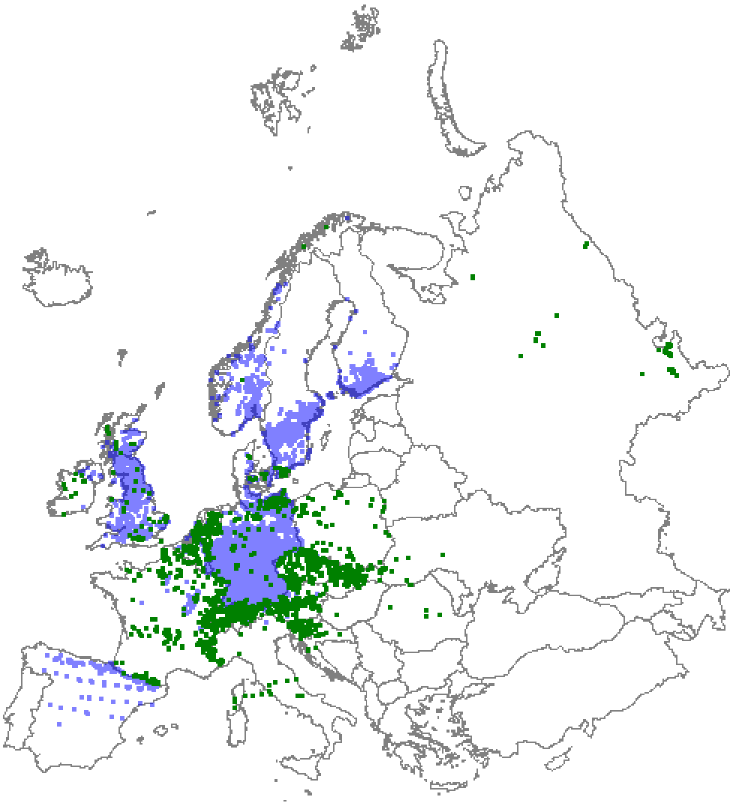
Thresholds EVA: 5 (5211 plots)

Threshold GBIF: 9 (1678 plots)

Additional selection criteria:

Comments: Many of the species mentioned in the EU Manual are much too broad (see above) and therefore have not been selected. Habitat type consists of two quite diverse types, one from the lowlands and one from the mountains with hardly any species in common.

Quality A-E: C (lack of data in a large part of the lowland distribution area, e.g. Spain, France, Germany and Eastern Europe).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 6510

Lowland hay meadows (Alopecurus pratensis, Sanguisorba officinalis)

Initial species selection

Alopecurus pratensis	Arrhenatherum elatius
Campanula patula	Centaurea jacea
Centaurea jacea subsp. Jacea	Crepis biennis
Daucus carota	Galium mollugo
Knautia arvensis	Lathyrus pratensis
Leontodon autumnalis	Leontodon hispidus
Leucanthemum vulgare	Malva moschata
Oenanthe pimpinelloides	Pastinaca sativa
Pimpinella major	Ranunculus acris
Rhinanthus minor	Rumex acetosa
Sanguisorba officinalis	Tragopogon pratensis
Tragopogon pratensis ag. L.	Trisetum flavescens

Species evaluation

Selected species: Exclude Daucus carota, Leontodon autumnalis (= Scorzoneroides autumnalis in GBIF) and Rhinanthus minor.

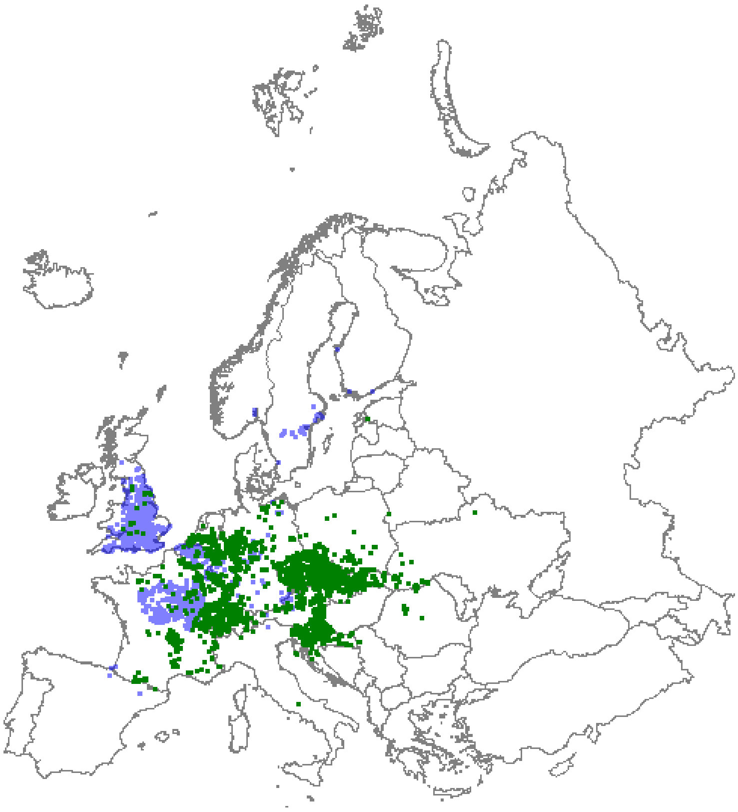
Thresholds EVA: 7 (12013 plots)

Threshold GBIF: 15 (1150 plots)

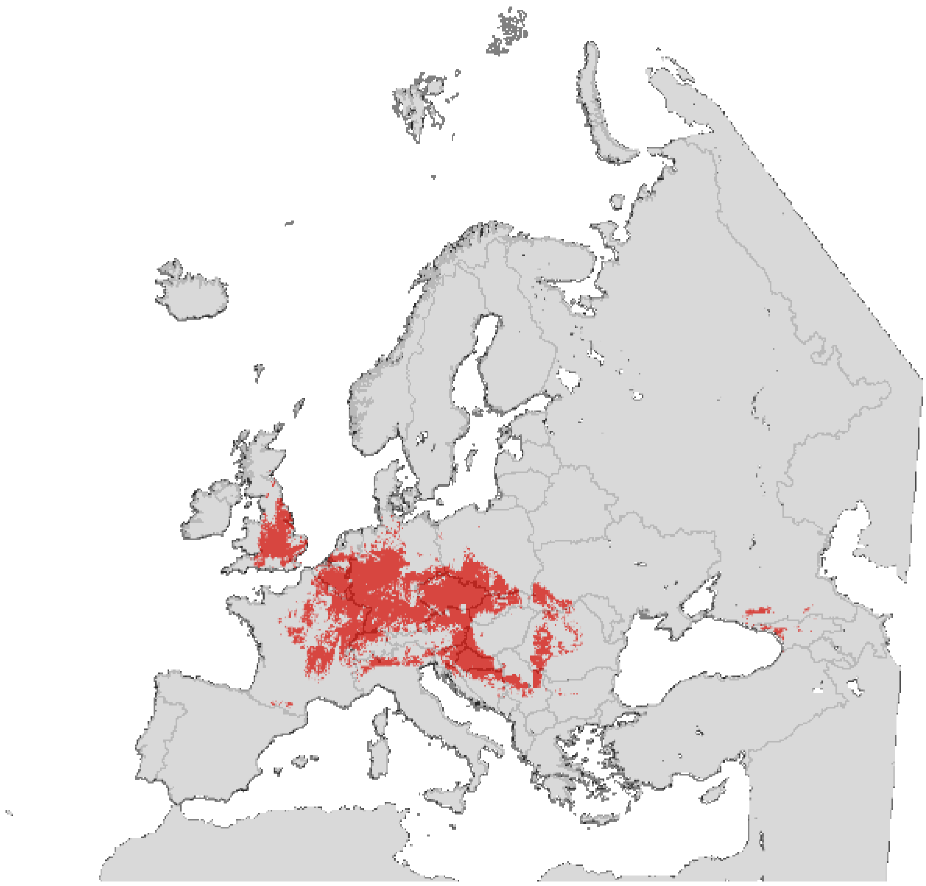
Additional selection criteria:

Comments:

Quality A-E: C (lack of data from countries like Spain, Northern Italy Romania, Bulgaria and Baltic States).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 6520
Mountain hay meadows

Initial species selection

Astrantia major	Campanula glomerata
Carum carvi	Centaurea debeauxii s. nemoralis
Chaerophyllum hirsutum	Cirsium helenioides
Conopodium majus	Crepis mollis
Crepis pyrenaica	Crocus albiflorus
Geranium phaeum	Geranium sylvaticum
Meum athamanticum	Muscari botryoides
Narcissus poeticus	Phyteuma orbiculare
Phyteuma ovatum	Phyteuma spicatum
Pimpinella major	Poa chaixii
Polygonum bistorta	Salvia pratensis
Sanguisorba officinalis	Silene vulgaris
Thlaspi caerulescens	Trisetum flavescens
Trollius europaeus	Valeriana repens
Viola cornuta	Viola tricolor s. subalpina

Species evaluation

Selected species: Exclude Campanula glomerata, Carum carvi, Meum athamanticum, Muscari botryoides, Pimpinella major, Silene vulgaris and Thlaspi caerulescens (= Noccaea caerulescens in GBIF).

Thresholds EVA: 4 (4496 plots)

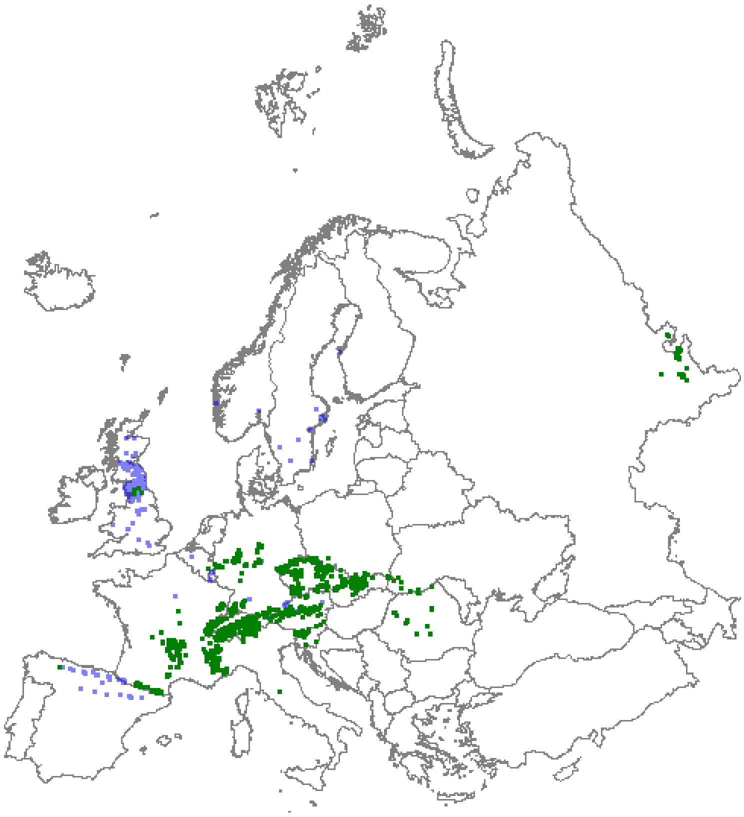
Threshold GBIF: 8 (182 plots)

Additional selection criteria: see under comments.

Comments: Restriction of altitude not needed because of restricted (mountainous) distribution of selected species. Habitat type occurs mostly above 600 metres but at lower altitude in British Isles. GBIF gives a few extra dots in Great Britain and Sweden, delete Spain from GBIF map.

Quality: B (lack of data from Carpathians).

Multi-variate analysis: EVA: 3



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 7110
Active raised bogs

Initial species selection

Beta nana	Calluna vulgaris
Carex limosa	Carex pauciflora
Chamaedaphne calyculata	Cladonia arbuscula
Cladonia uncialis	Drosera anglica
Drosera intermedia	Drosera rotundifolia
Erica tetralix	Eriophorum angustifolium
Eriophorum gracile	Eriophorum vaginatum
Ledum palustre	Narthecium ossifragum
Odontoschisma sphagni	Rhynchospora alba
Rhynchospora fusca	Scheuchzeria palustris
Scirpus cespitosus	Sphagnum angustifolium
Sphagnum balticum	Sphagnum capillifolium
Sphagnum fallax	Sphagnum fuscum
Sphagnum imbricatum	Sphagnum magellanicum
Sphagnum majus	Sphagnum papillosum
Utricularia intermedia	Utricularia minor
Utricularia ochroleuca	Vaccinium oxycoccos

Species evaluation

Selected species: Add Andromeda polifolia. Exclude Betula nana, Calluna vulgaris, Cladonia arbuscula, Cladonia uncialis, Drosera intermedia, Drosera rotundifolia, Erica tetralix, Eriophorum angustifolium, Eriophorum gracile, Rhynchospora alba, Rhynchospora fusca, Scirpus cespitosus, Sphagnum fallax, Sphagnum majus, Utricularia intermedia, Utricularia minor and Utricularia ochroleuca.

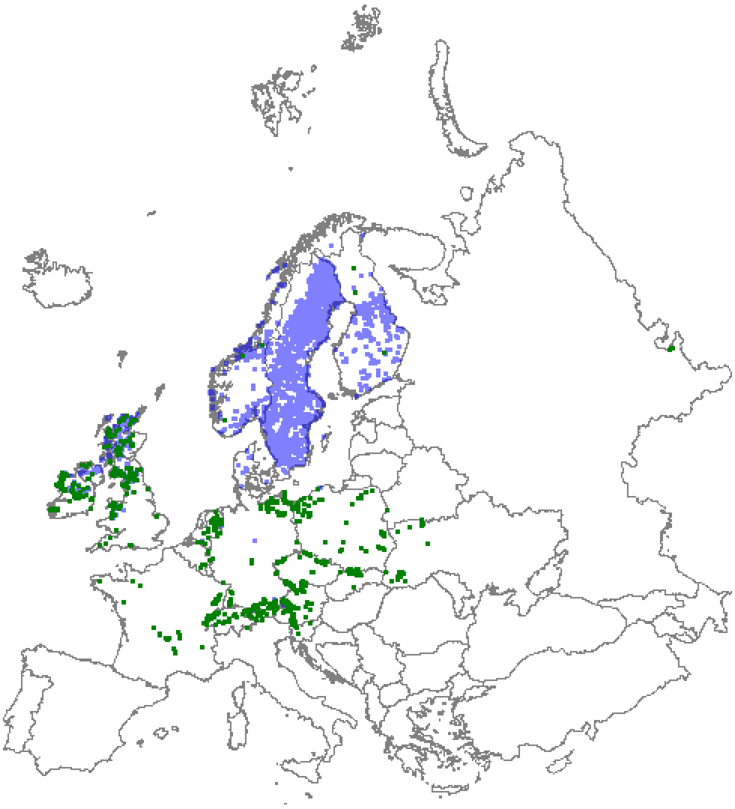
Thresholds EVA: 4 (3807 plots)

Threshold GBIF: 9 (2966 plots). Andromeda polifolia added to the GBIF species selection. (Rhododendron tomentosum = Ledum palustre).

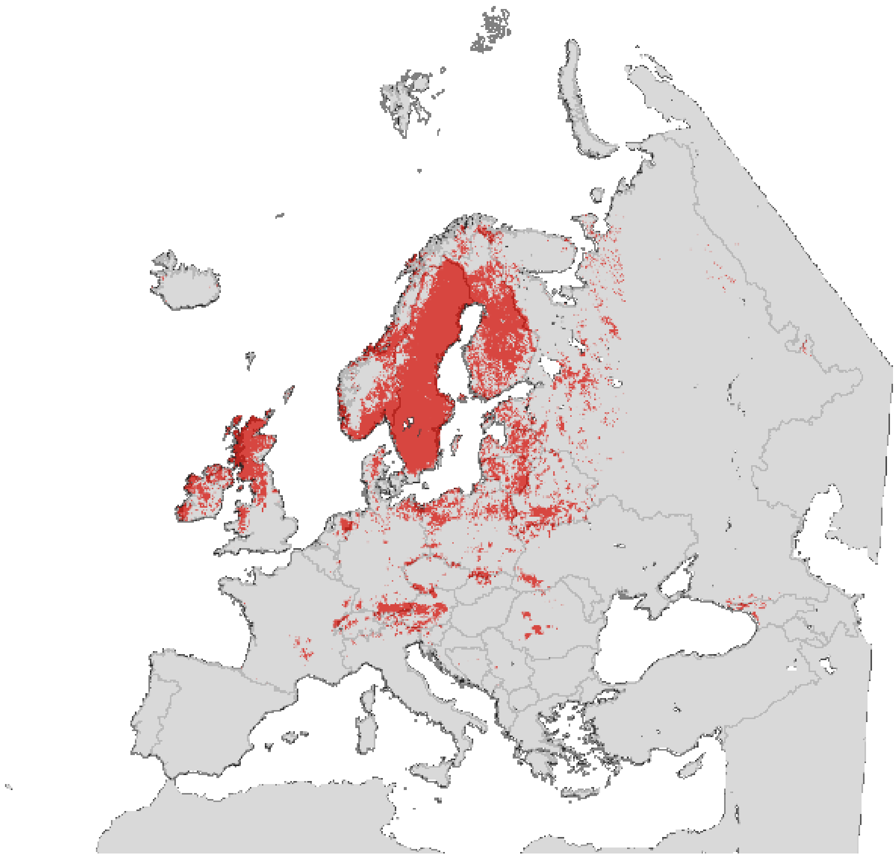
Additional selection criteria:

Comments: Criteria rather small-defined because of overlap with other peat habitats. GBIF needed for Scandinavia but extra difficult to define because of grid approach and (subsequent) overlap with other peat types, especially in the northern parts of Scandinavia.

Quality: C (lack of data from countries like Spain, Northern Italy, Romania and Baltic States).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 7130
Blanket bogs (if active bog)

Initial species selection

Calluna vulgaris
Carex panicea
Drosera rotundifolia
Erica tetralix
Molinia caerulea
Narthecium ossifragum
Pinguicula lusitanica
Potentilla erecta
Rhynchospora alba
Schoenus nigricans
Sphagnum auriculatum
Sphagnum magellanicum
Sphagnum pulchrum
Sphagnum strictum
Sphagnum tenellum
Campylopus atrovirens
Diplophyllum albicans
Empetrum nigrum
Eriophorum vaginatum
Mylia taylorii
Pedicularis sylvatica
Pleurozia purpurea
Racomitrium lanuginosum
Rubus chamaemorus
Scirpus cespitosus
Sphagnum compactum
Sphagnum papillosum
Sphagnum rubellum
Sphagnum subnitens

Species evaluation

Selected species: Exclude Calluna vulgaris, Carex panicea, Drosera rotundifolia, Empetrum nigrum, Molinia caerulea, Pedicularis sylvatica, Potentilla erecta, Racomitrium lanuginosum, Rhynchospora alba, Rubus chamaemorus, Sphagnum auriculatum, Sphagnum magellanicum, Sphagnum papillosum, Sphagnum pulchrum, Sphagnum rubellum and Sphagnum subnitens.

Thresholds EVA: 6

Threshold GBIF: - (no additional information)

Additional selection criteria: Habitat type restricted to Ireland, Great Britain and Norway, which could be used as an extra selection criterion; not applied in this analysis).

Comments: Criteria rather small-defined because of overlap with other peat habitats.

Quality: A (missing Norwegian coast, but habitat type here rather marginal and only occurring scattered at few locations).

Distribution: green dots represent vegetation plot data

Map with modelled distribution

Habitat type: 7140
Transition mires and quaking bogs

Initial species selection

Bryum pseudotriquetrum	Hammarbya paludosa
Calliergon giganteum	Liparis loeselii
Campylium stellatum	Menyanthes trifoliata
Carex chordorrhiza	Pedicularis palustris
Carex diandra	Potentilla palustris
Carex lasiocarpa	Rhynchospora alba
Carex limosa	Rhynchospora fusca
Carex rostrata	Scheuchzeria palustris
Epilobium palustre	Scorpidium revolvens
Equisetum fluviatile	Scorpidium scorpioides
Eriophorum gracile	

Species evaluation

Selected species: -

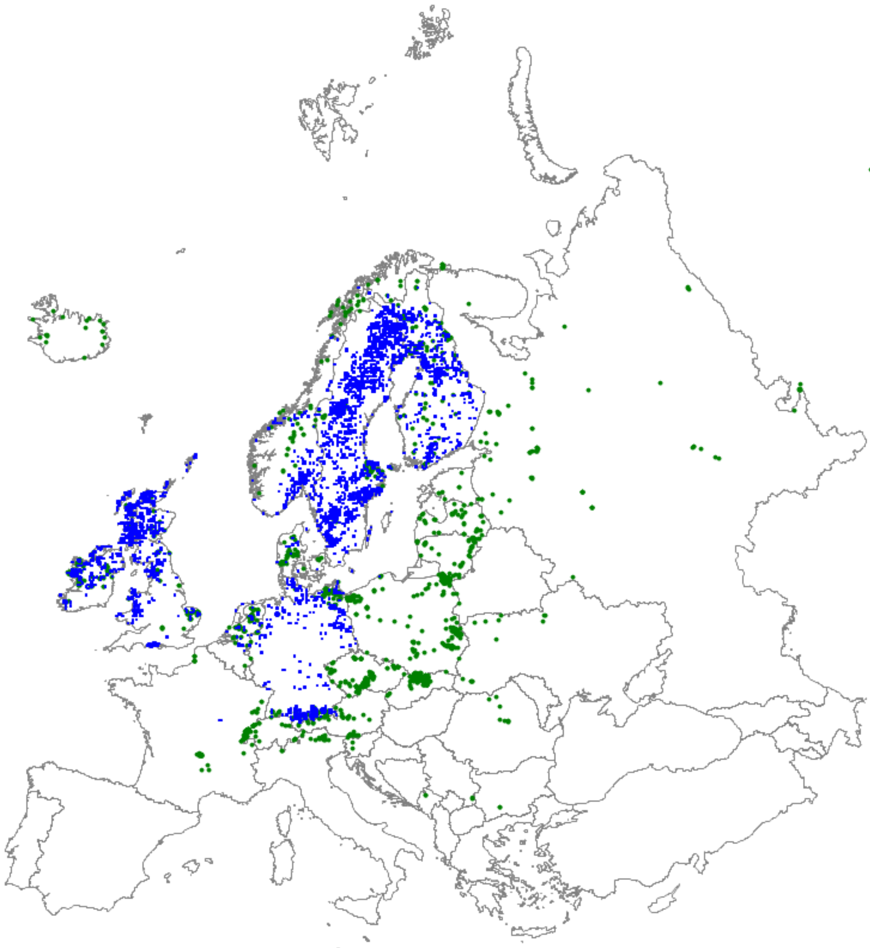
Thresholds EVA: 6

Threshold GBIF: 11

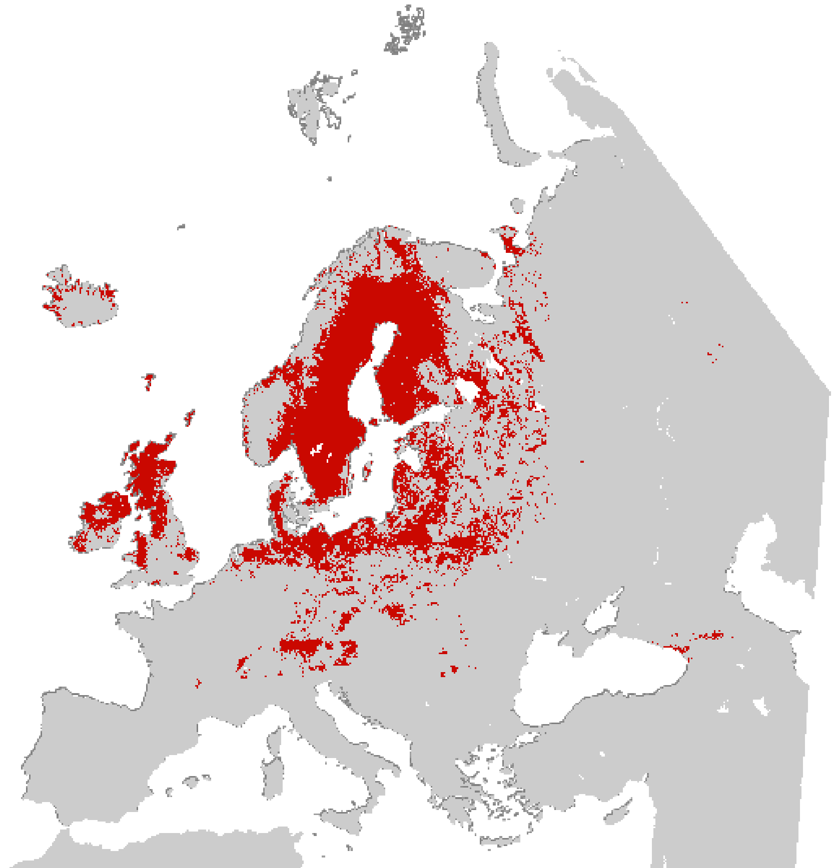
Additional selection criteria: -

Comments: -

Quality: A



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 7150
Depressions on peat substrates of the Rhynchosporion

Initial species selection

Carex limosa	Carex rostrata
Drepanocladus fluitans	Drosera intermedia
Drosera rotundifolia	Eriophorum angustifolium
Lycopodiella inundata	Molinia caerulea
Rhynchospora alba	Rhynchospora fusca
Scheuchzeria palustris	Sphagnum cuspidatum
Sphagnum denticulatum	Sphagnum fallax
Sphagnum recurvum	Vaccinium oxycoccos

Species evaluation

Selected species: Exclude Carex limosa, Carex rostrata, Drepanocladus fluitans, Eriophorum angustifolium, Molinia caerulea, Scheuchzeria palustris, Sphagnum cuspidatum, Sphagnum denticulatum, Sphagnum fallax, Sphagnum recurvum and Vaccinium oxycoccos.

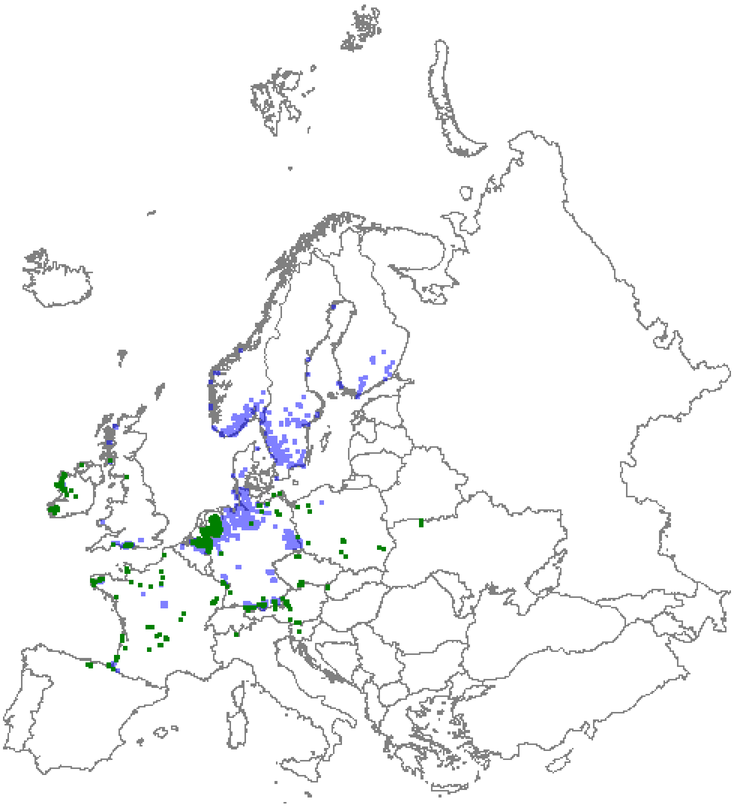
Thresholds EVA: 3 (1355 plots)

Threshold GBIF: 5 (388); will add parts of Southern Scandinavia, although no sites have been assigned there).

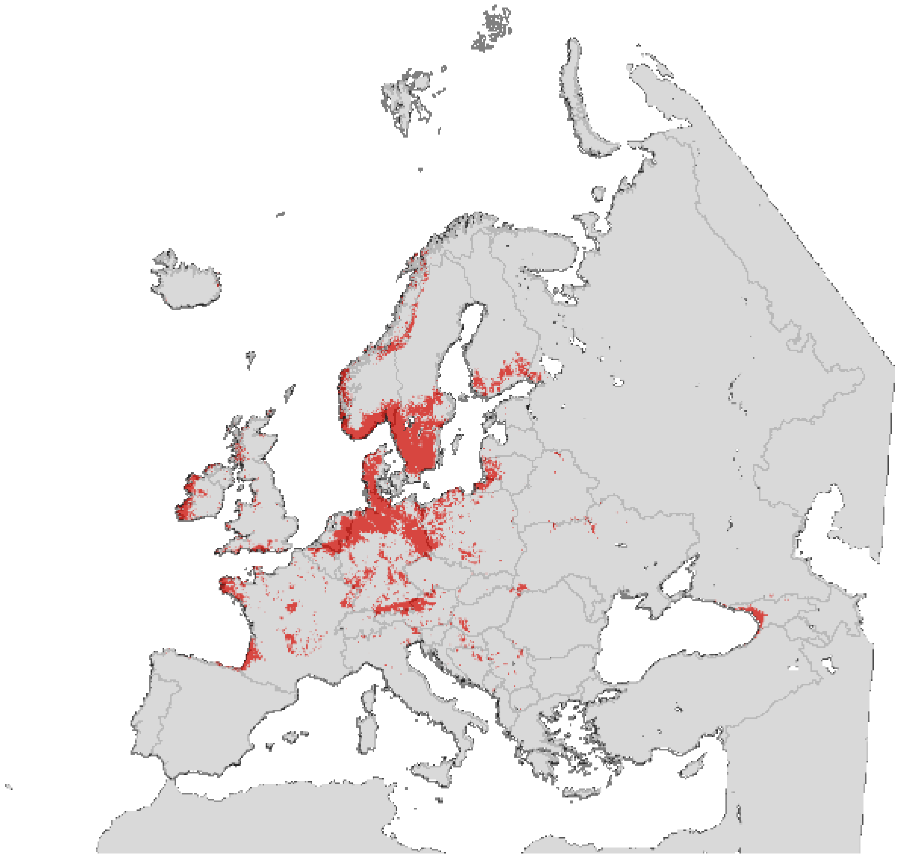
Additional selection criteria:

Comments: Criteria defined according to species listed in the Manual (to excluded terrestrialisation part of Rhynchosporion).

Quality: B (Baltic States, Spain and parts of Denmark, Poland and Italy missing, but core area good represented).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 7210
Calcareous fens with Cladium mariscus and species of the Caricion davallianae

Initial species selection

Cladium mariscus	Galium palustre
Iris pseudacorus	Kosteletzkya pentacarpos
Lycopus europaeus	Lysimachia vulgaris
Lythrum salicaria	Phragmites australis

Species evaluation

Selected species: Cladium mariscus required with minimal cover of 5%. Exclude Galium palustre, Iris pseudacorus, Kosteletzkya pentacarpos, Lycopus europaeus, Lysimachia vulgaris, Lythrum salicaria and Phragmites australis.

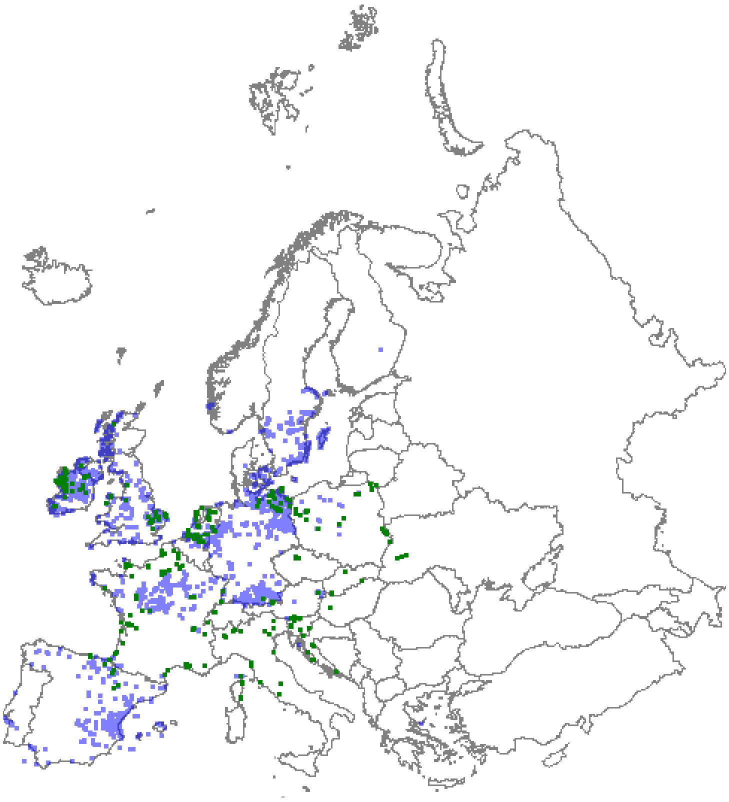
Thresholds EVA: 1 (1661 plots)

Threshold GBIF: 1 (981 plots)

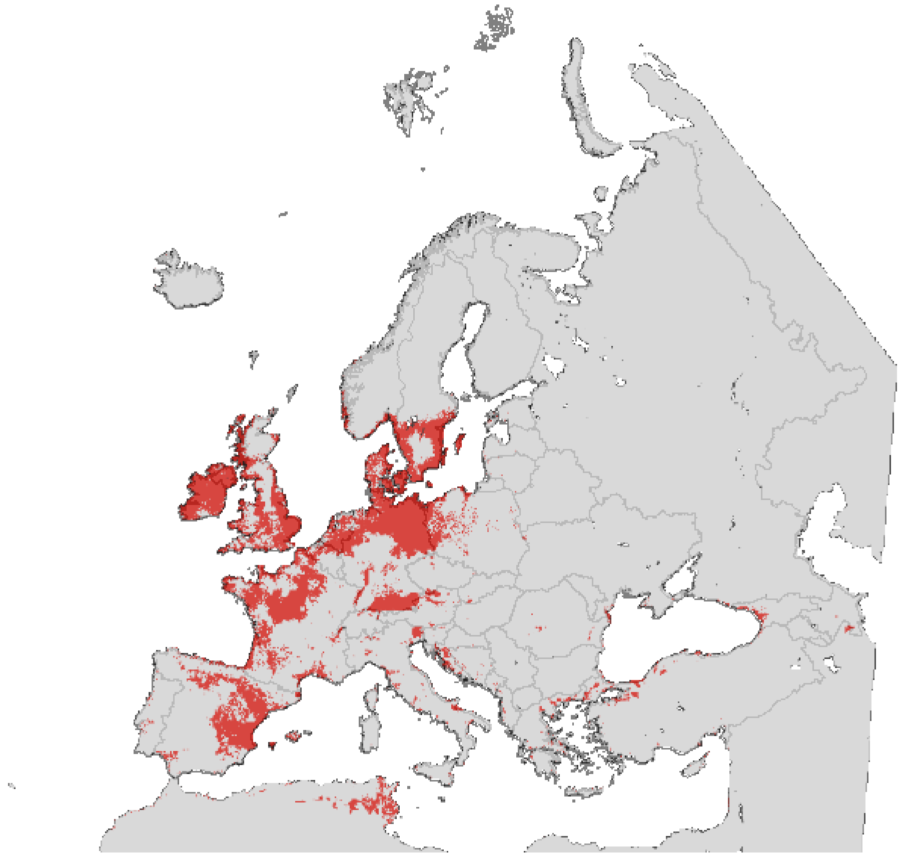
Additional selection criteria:

Comments:

Quality: A (Baltic states missing; some parts slightly over-represented because of GBIF, but selection by GBIF data required for geographic reasons (e.g. Spain).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 7230
Alkaline fens

Initial species selection

Aneura pinguis	Aster bellidiastrum
Bartsia alpina	Bryum pseudotriquetrum
Calliergon cuspidatum	Campylium stellatum
Carex davalliana	Carex dioica
Carex flava	Carex hostiana
Carex lepidocarpa	Carex pulicaris
Cinclidium stygium	Ctenidium molluscum
Dactylorhiza incarnata	Dactylorhiza incarnata s. cruenta
Dactylorhiza russowii	Dactylorhiza traunsteineri
Drepanocladus revolvens	Eleocharis quinqueflora
Epipactis palustris	Equisetum variegatum
Eriophorum latifolium	Fissidens adianthoides
Herminium monorchis	Juncus subnodulosus
Liparis loeselii	Parnassia palustris
Pedicularis sceptrum-carolinum	Pinguicula vulgaris
Primula farinosa	Schoenus ferrugineus
Schoenus nigricans	Selaginella selaginoides
Swertia alpestris	Tofieldia calyculata
Tomentypnum nitens	Valeriana dioica

Species evaluation

Selected species: Exclude Calliergon cuspidatum, Drepanocladus revolvens (=Limprichtia revolvens), Fissidens adianthoides, Herminium monorchis, Juncus subnodulosus.

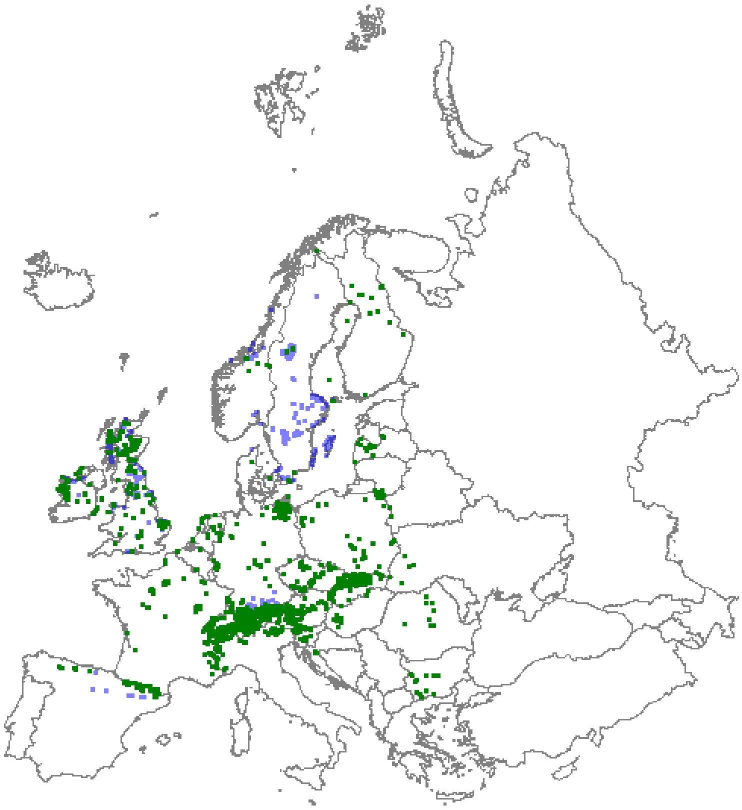
Thresholds EVA: 6 (6457 plots)

Threshold GBIF: 16 (249 plots)

Additional selection criteria:

Comments:

Quality: A (some parts of Spain, Italy, Greece and Baltic States are missing).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 8210
Calcareous rocky slopes with chasmophytic vegetation

Initial species selection

Achillea oxyloba s. schurii
Alyssum pyrenaicum
Androsace cylindrica
Androsace helvetica
Antirrhinum siculum
Artemisia eriantha
Asperula hirta
Asplenium ceterach
Asplenium jahandiezii
Asplenium petrarchae
Asplenium ruta-muraria
Asplenium seelosii s. glabrum
Asplenium trichomanes
Asplenium trichomanes s. pachyrachis
Asplenium trichomanes-ramosum
Ballota frutescens
Biscutella laevigata
Campanula carpatica
Campanula cochlearifolia
Campanula rupestris
Campanula tanfanii
Campanula versicolor
Carex firma
Carex mucronata
Chaenorhinum origanifolium
Cheilanthes acrostica
Cymbalaria muralis s. pubescens
Cystopteris fragilis
Dianthus rupicola
Draba aizoides
Draba kotschyi
Draba tomentosa
Erinus alpinus
Erodium petraeum
Globularia repens
Gypsophila petraea
Hieracium stelligerum
Inula verbascifolia s. methanea
Kernera saxatilis
Melica minuta
Minuartia rupestris
Phyteuma charmelii
Phyteuma cordatum
Potentilla alchimilloides
Potentilla caulescens
Potentilla nivalis
Potentilla saxifraga
Primula allionii
Primula auricula
Primula marginata
Pteris cretica
Ramonda myconi
Saxifraga aretioides
Saxifraga canaliculata
Saxifraga cuneifolia
Saxifraga longifolia
Saxifraga marginata
Saxifraga media
Saxifraga mutata s. demissa
Scabiosa limonifolia
Sedum dasyphyllum
Silene campanula
Thymus pulcherrimus
Trisetum bertolonii
Valeriana globulariifolia
Valeriana officinalis s. sambucifolia
Woodsia glabella

Species evaluation

Selected species: Add Asplenium viride. Exclude Carex firma

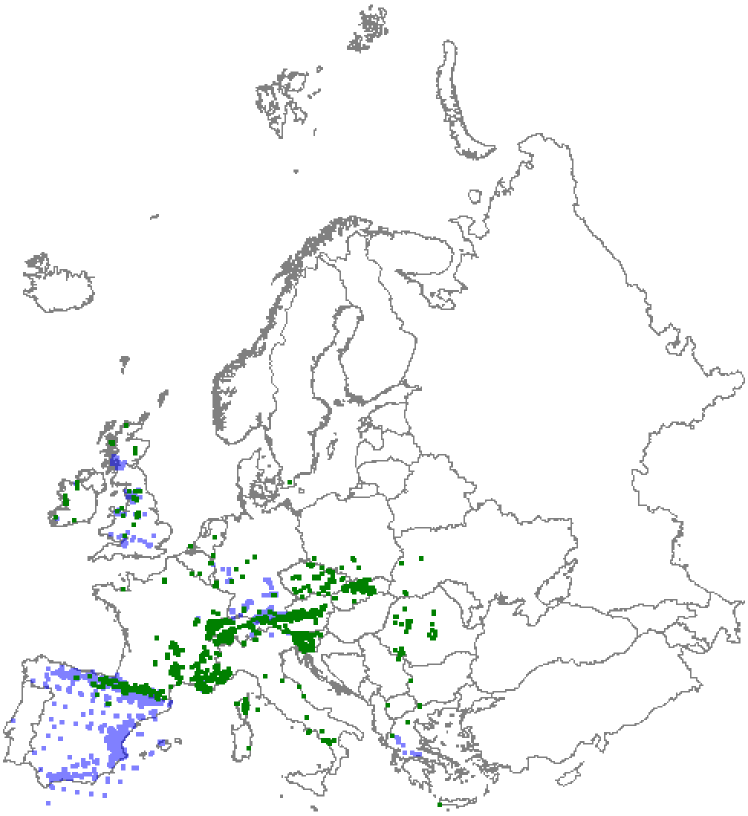
Thresholds EVA: 3 (4190 plots)

Threshold GBIF: 6 (299 plots)

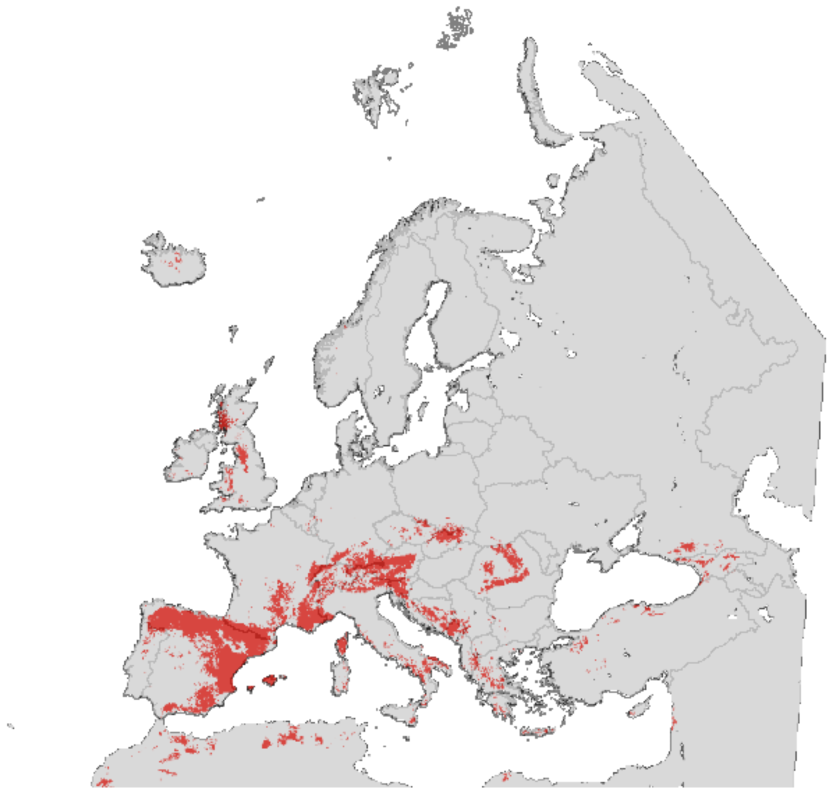
Additional selection criteria:

Comments:

Quality: B (Mediterranean region underrepresented, as well as Sweden and Baltic states; at lower regions habitat type impoverished with only few characteristic species of the type).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 8220
Siliceous rocky slopes with chasmophytic vegetation

Initial species selection

Anarrhinum bellidifolium
Androsace pyrenaica
Androsace vandellii
Anogramma leptophylla
Armeria leucocephala
Asarina procumbens
Asplenium adiantum-nigrum
Asplenium adulterinum
Asplenium balearicum
Asplenium cuneifolium
Asplenium foreziense
Asplenium obovatum s. lanceolatum
Asplenium onopteris
Asplenium septentrionale
Carex kitaibeliana
Cheilanthes hispanica
Cheilanthes maderensis
Cheilanthes tinaei
Cosentinia vellea
Dianthus graniticus
Dianthus henteri
Eritrichium nanum
Galium tendae
Haberlea rhodopensis
Jovibarba globifera s. allionii
Jovibarba heuffelii
Minuartia bulgarica
Murbeckiella boryi
Notholaena marantae
Phyteuma hemisphaericum
Phyteuma scheuchzeri
Potentilla crassinervia
Potentilla haynaldiana
Primula hirsuta
Rhodiola rosea
Saxifraga aspera
Saxifraga continentalis
Saxifraga florulenta
Saxifraga juniperifolia
Saxifraga nevadensis
Saxifraga pedemontana
Saxifraga pedemontana s. cervicornis
Saxifraga pedemontana s. cymosa
Saxifraga retusa s. retusa
Sempervivum montanum s. burnatii
Senecio glaberrimus
Silene dinarica
Silene lerchenfeldiana
Silene requienii
Symphyandra wanneri
Umbilicus rupestris
Veronica bachofenii

Species evaluation

Selected species: Add Polypodium vulgare and Polypodium vulgare agg.

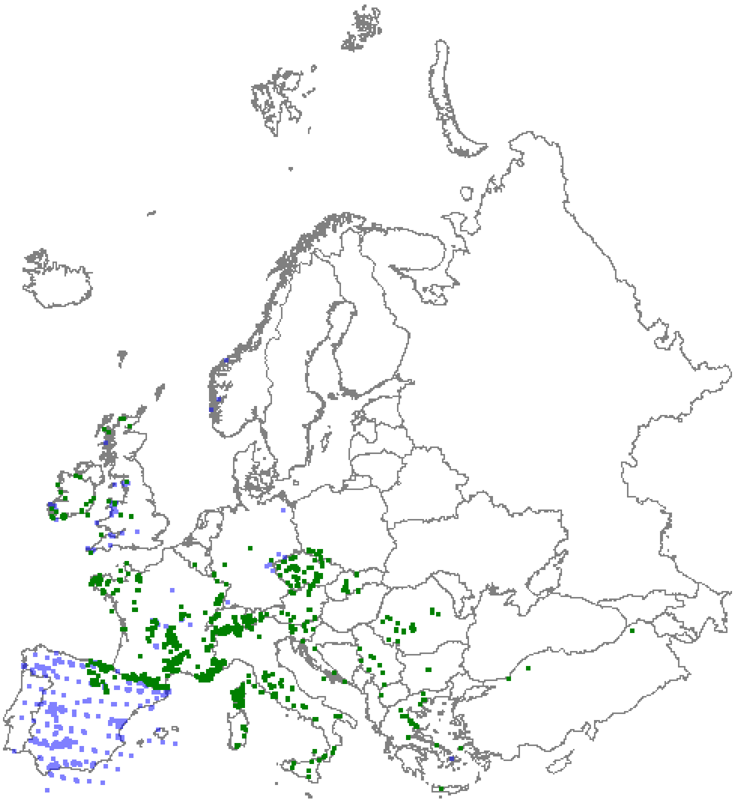
Thresholds EVA: 2 (2625 plots)

Threshold GBIF: 5 (195 grids). Polypodium vulgare added to the GBIF species selection.

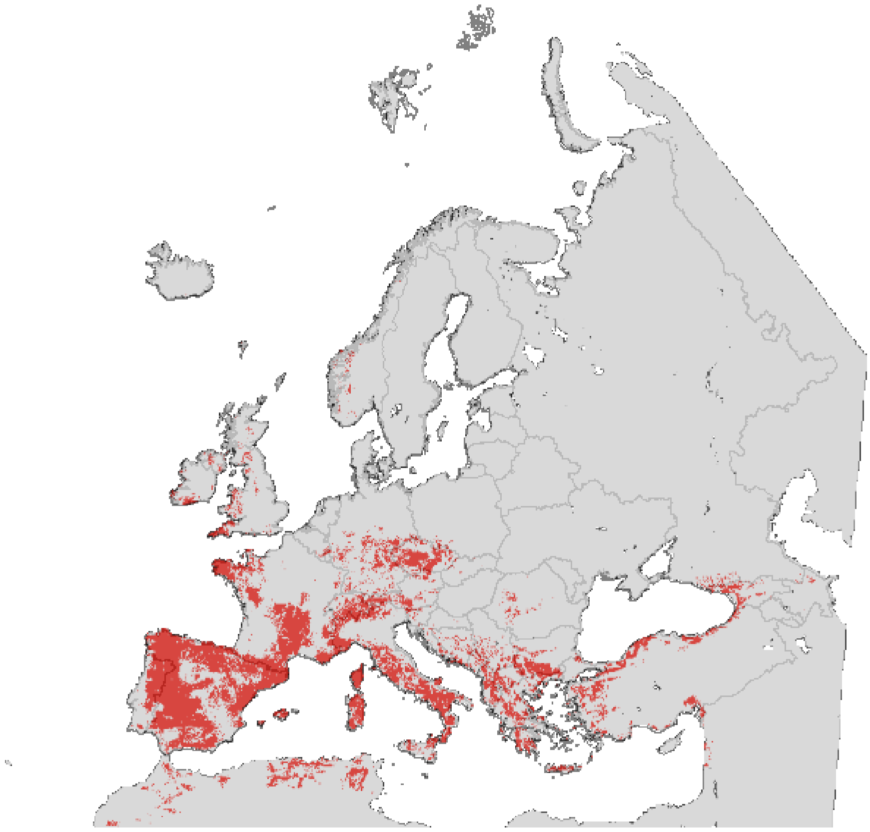
Additional selection criteria:

Comments:

Quality: C (Scandinavia and Baltic states missing and some areas in Southern and eastern Europe poorly represented).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 9110
Luzulo-Fagetum beech forests

Initial species selection

Abies alba
Calamagrostis arundinacea
Calamagrostis villosa
Fagus sylvatica
Gymnocarpium dryopteris
Ilex aquifolium
Leucobryum glaucum
Luzula luzuloides
Luzula sylvatica
Oxalis montana
Picea abies
Polygonatum verticillatum
Polytrichastrum formosum
Prenanthes purpurea
Pteridium aquilinum
Sambucus racemosa
Vaccinium myrtillus

Species evaluation

Selected species: -

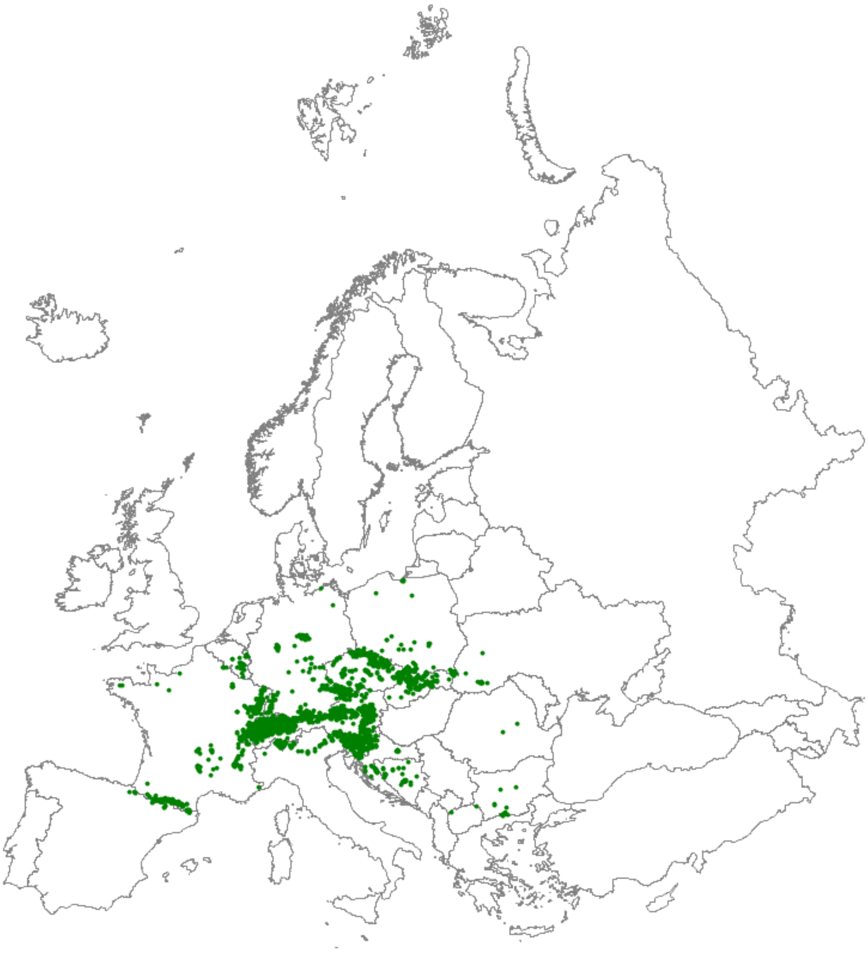
Thresholds EVA: 8

Threshold GBIF: -

Additional selection criteria: -

Comments: -

Quality: A



Distribution: green dots represent vegetation plot data

Map with modelled distribution

Habitat type: 9150
Medio-European limestone beech forests of the Cephalanthero-Fagion

Initial species selection

Acer campestre	Berberis vulgaris
Buxus sempervirens	Carex alba
Carex digitata	Carex flacca
Carex montana	Cephalanthera damasonium
Cephalanthera rubra	Epipactis leptochila
Epipactis microphylla	Fagus sylvatica
Hieracium murorum	Lathyrus vernus
Lonicera xylosteum	Mycelis muralis
Neottia nidus-avis	Sesleria albicans
Solidago virgaurea	Sorbus aria

Species evaluation

Selected species: Fagus sylvatica required with cover > 5%. Exclude Carex flacca, Hieracium murorum, Mycelis muralis and Sesleria albicans.

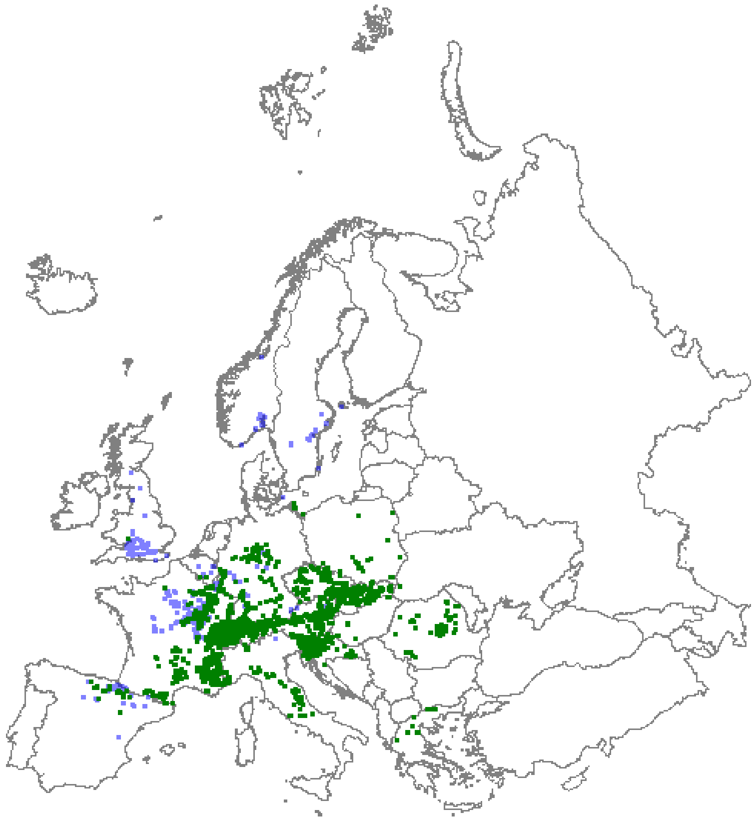
Thresholds EVA: 4 (3630 plots)

Threshold GBIF: - (no additional information)

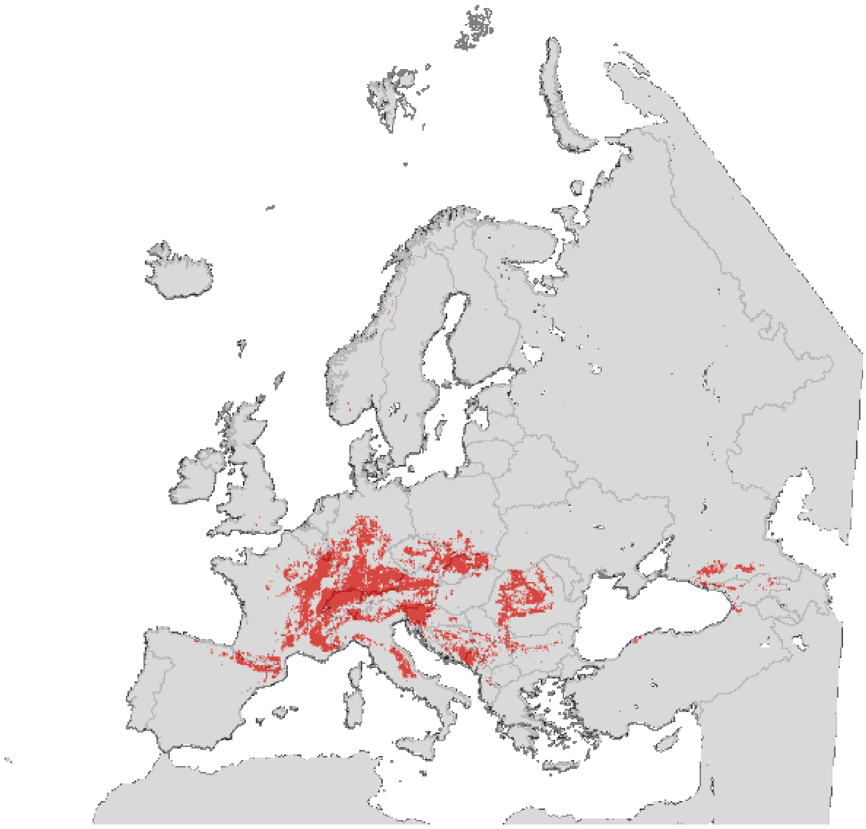
Additional selection criteria:

Comments:

Quality: B (Bulgaria, Denmark missing).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 9160
Sub-Atlantic and medio-European oak or oak-hornbeam forests of the Carpinion betuli

Initial species selection

Acer campestre
Brachypodium sylvaticum
Carpinus betulus
Dactylis glomerata s. aschersoniana
Fraxinus excelsior
Galium sylvaticum
Melica nutans
Poa chaixii
Prunus avium
Ranunculus serpens
Tilia cordata
Anemone nemorosa
Carex brizoides
Corylus avellana
Fragaria vesca
Galium odoratum
Hedera helix
Mercurialis perennis
Potentilla sterilis
Quercus robur
Stellaria holostea
Viola reichenbachiana

Species evaluation

Selected species: Exclude Dactylis glomerata subsp. aschersoniana, Fraxinus excelsior, Quercus robur and Ranunculus serpens, Carex brizoides, Hedera helix.

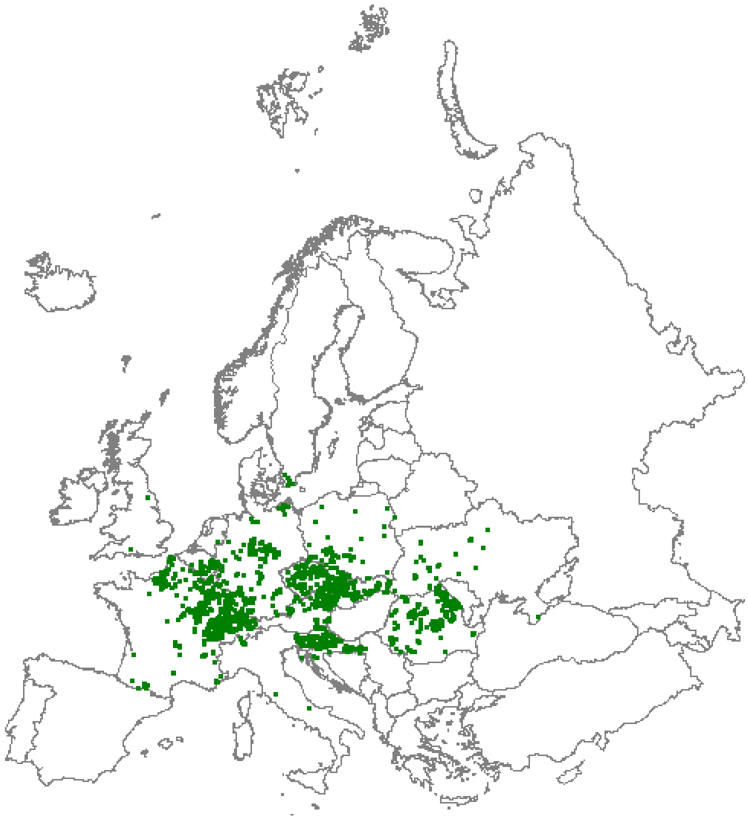
Thresholds EVA: 8 (5174 plots)

Threshold GBIF: - (no additional information)

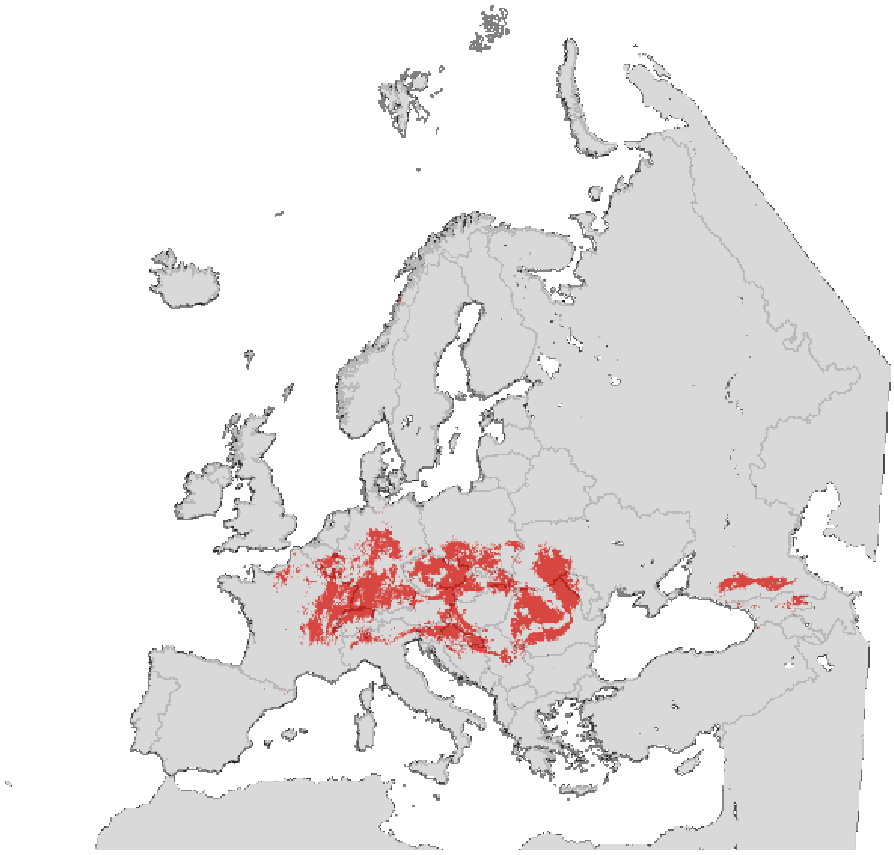
Additional selection criteria:

Comments: The alliance *Carpinion ebuli* has a clear distribution in Eastern Europe, but in Romania for instance no sites have been assigned.

Quality: A (see comment).



Distribution: green dots represent vegetation plot data



Map with modelled distribution

Habitat type: 9190
Old acidophilous oak woods with Quercus robur on sandy plains

Initial species selection

Amelanchier lamarckii	Betula pendula
Betula pubescens	Ceratocapnos claviculata
Deschampsia flexuosa	Frangula alnus
Holcus mollis	Lonicera periclymenum
Maianthemum bifolium	Melampyrum pratense
Molinia caerulea	Peucedanum gallicum
Populus tremula	Pteridium aquilinum
Quercus petraea	Quercus robur
Sorbus aucuparia	Vaccinium myrtillus

Species evaluation

Selected species: Add Trientalis europaeus. Exclude Betula pubescens, Molinia caerulea, Peucedanum gallicum and Vaccinium myrtillus.

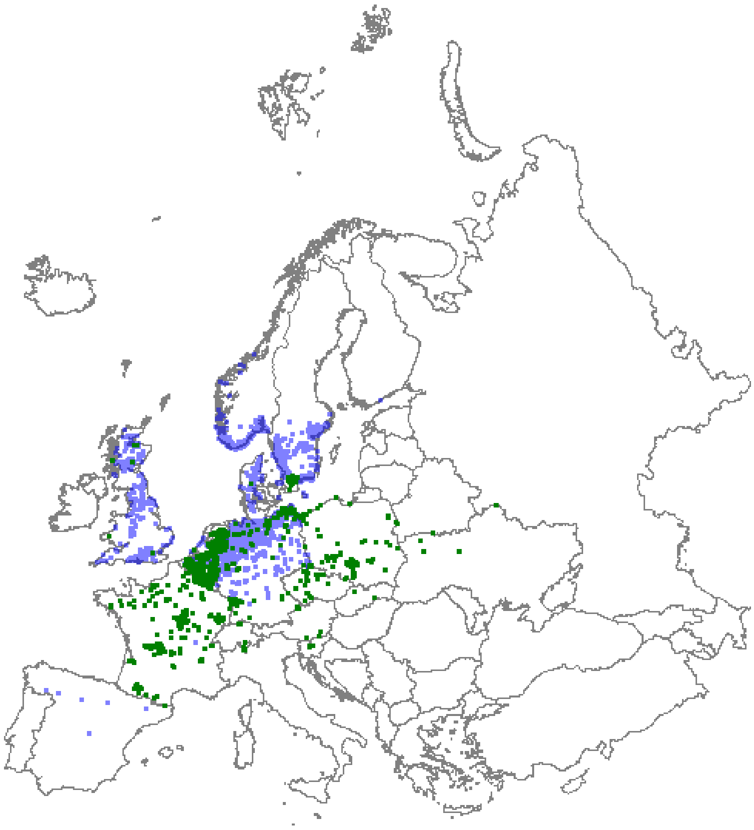
Thresholds EVA: 8 (3167 plots).

Threshold GBIF: 11 (1175 plots). Trientalis europaeus added to the GBIF species selection.

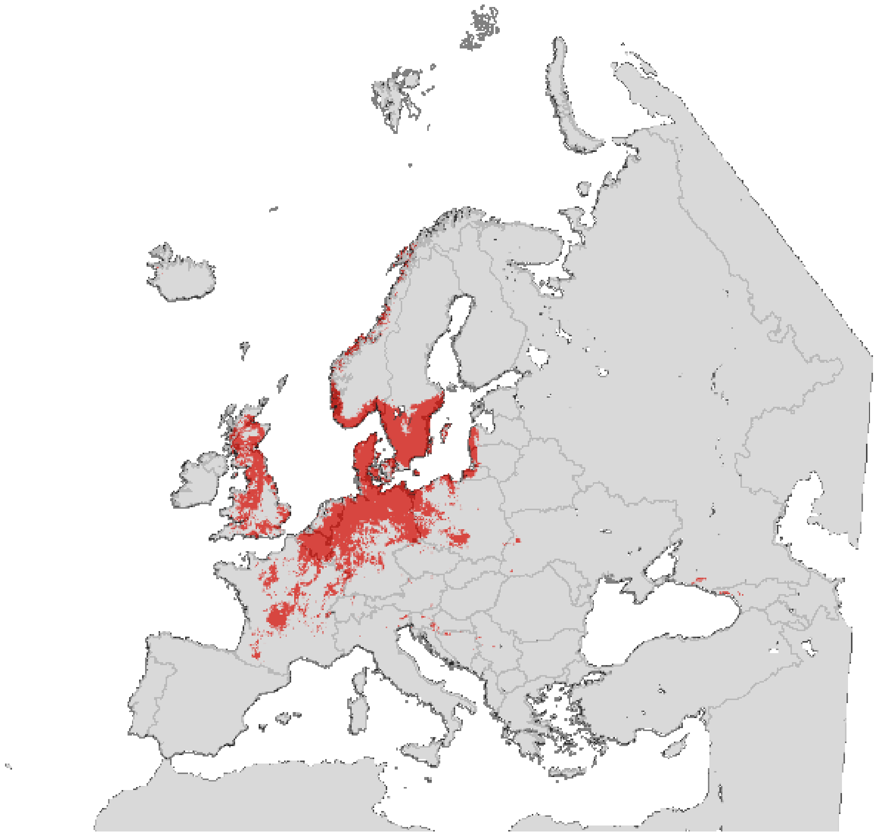
Additional selection criteria:

Comments:

Quality: B (type should be somewhat more restricted to the Nordwest European sandy planes, with more emphasis on Northern Germany and Western Poland).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data



Map with modelled distribution

Habitat type: 91E0

Alluvial forests with Alnus glutinosa and Fraxinus excelsior (Alno-Padion, Alnion incanae, Salicion albae)

Initial species selection

Alnus glutinosa	Alnus incana
Angelica sylvestris	Betula pubescens
Cardamine amara	Carex acutiformis
Carex pendula	Carex remota
Carex strigosa	Cirsium oleraceum
Equisetum hyemale	Equisetum telmateia
Festuca gigantea	Filipendula ulmaria
Fraxinus excelsior	Galium aparine
Geranium robertianum	Geum rivale
Geum urbanum	Glechoma hederacea
Humulus lupulus	Impatiens noli-tangere
Lysimachia nemorum	Lysimachia nummularia
Populus nigra	Ranunculus ficaria
Rumex sanguineus	Salix fragilis
Salix alba	Salix purpurea
Salix triandra	Salix viminalis
Silene dioica	Stellaria nemorum
Ulmus glabra	Urtica dioica

Species evaluation

Selected species: Exclude Betula pubescens, Carex acutiformis, Equisetum hyemale, Filipendula ulmaria, Galium aparine, Lysimachia nummularia and Urtica dioica.

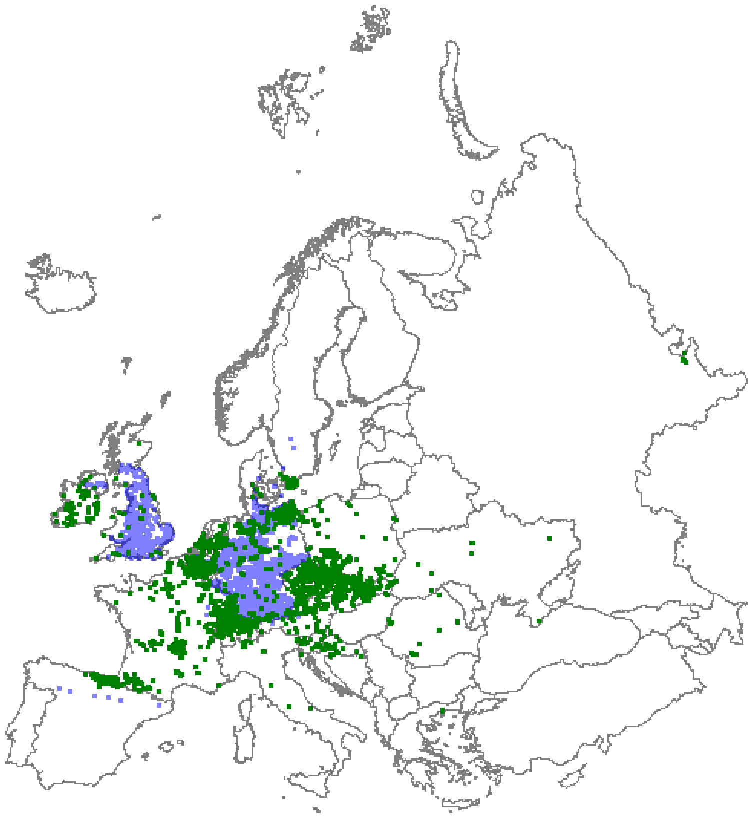
Thresholds EVA: 7 (6637 plots)

Threshold GBIF: 23 (5148 observations; these woodlands are mainly characterized by common species, which makes it difficult the make specific selections)

Additional selection criteria:

Comments: GBIF only gives extra spots for Central Germany and a few spots in Southern Scandinavia (see remark above).

Quality: C (Southern and eastern Europe are poorly represented; the same applies to Scandinavia, where this vegetation types also occurs).



Distribution: green dots represent vegetation plot data; blue dots represent GBIF data

Map with modelled distribution

Habitat type: 91H0

Pannonian woods with Quercus pubescens

Initial species selection

Amygdalus nana
Arabis brassica
Arabis turrita
Astragalus austriacus
Astragalus monspessulanus
Buglossoides purpurocaerulea
Campanula bononiensis
Carex humilis
Carex michelii
Colutea arborescens
Cornus mas
Cotinus coggygria
Dictamnus albus
Euphorbia angulata
Fraxinus ornus
Geranium sanguineum
Lactuca quercina
Limodorum abortivum
Melittis melissophyllum
Orchis purpurea
Potentilla alba
Potentilla micrantha
Pyrus pyraster
Quercus cerris
Quercus pubescens
Sorbus domestica
Sorbus torminalis
Tanacetum corymbosum
Viola suavis

Species evaluation

Selected species: -

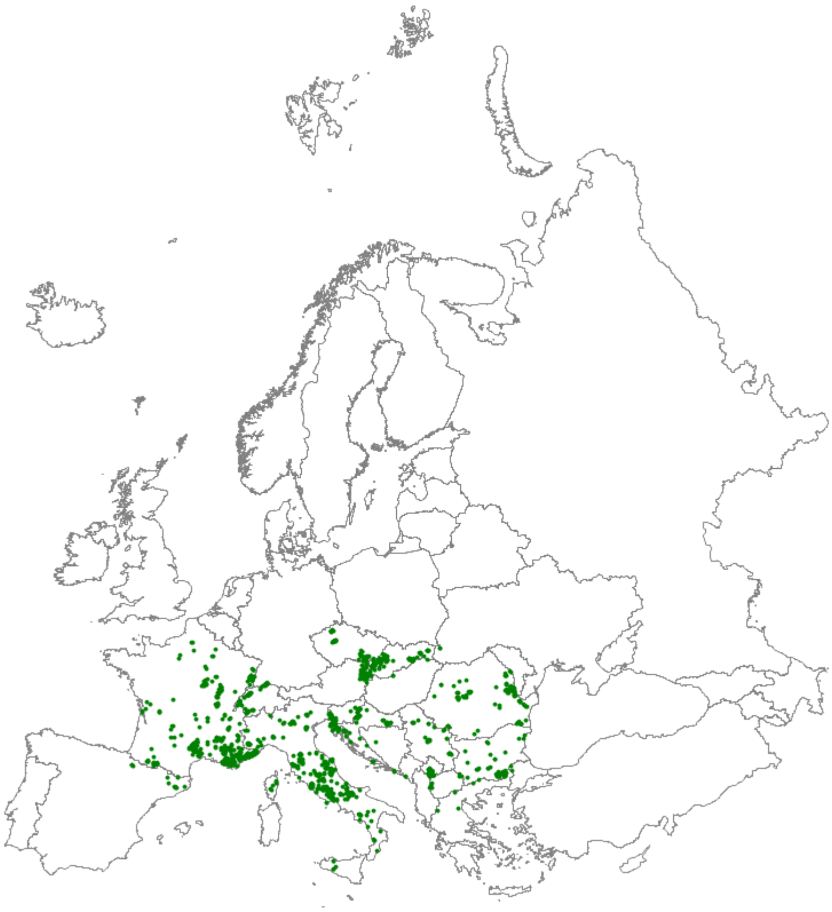
Thresholds EVA: 4

Threshold GBIF:

Additional selection criteria:

Comments:

Quality:



Distribution: green dots represent vegetation plot data

Map with modelled distribution

Habitat type: 9410
Acidophilous Picea forests of the montane to alpine levels (Vaccinio-Piceetea)

Initial species selection

Abies alba	Athyrium filix-femina
Calamagrostis varia	Fragaria vesca
Gymnocarpium dryopteris	Hieracium murorum
Luzula luzuloides	Luzula sylvatica
Maianthemum bifolium	Melampyrum sylvaticum
Mycelis muralis	Oxalis acetosella
Petasites albus	Picea abies
Picea orientalis	Polygonatum verticillatum
Prenanthes purpurea	Rubus idaeus
Senecio nemorensis s. fuchsii	Solidago virgaurea
Sorbus aucuparia	Vaccinium myrtillus

Species evaluation

Selected species: Exclude Athyrium filix-femina, Fragaria vesca, Hieracium murorum, Maianthemum bifolium, Mycelis muralis, Oxalis acetosella, Rubus idaeus, Solidago virgaurea, Sorbus aucuparia and Vaccinium myrtillus.

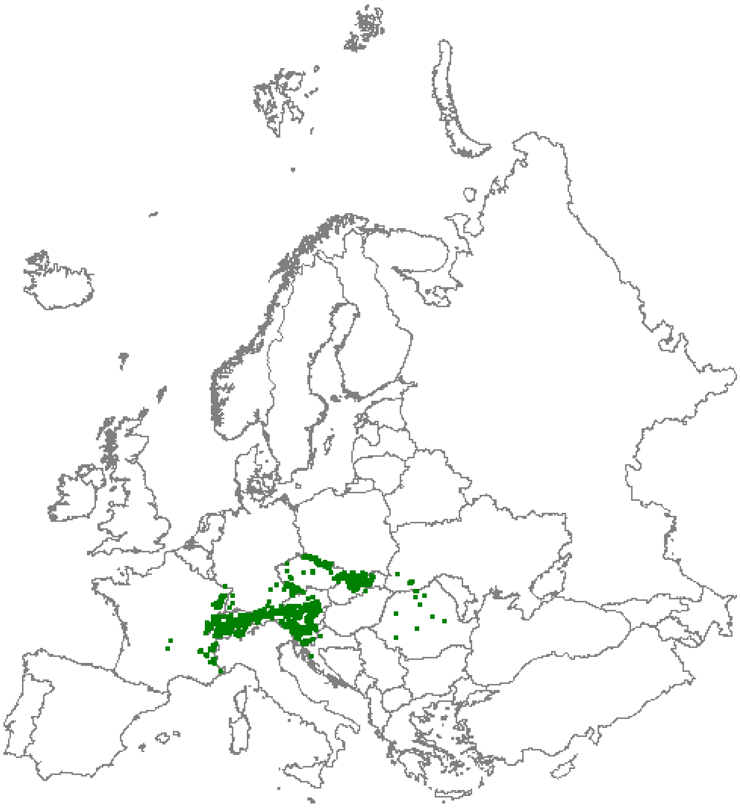
Thresholds EVA: 6 (4717 plots)

Threshold GBIF: - (no additional information)

Additional selection criteria:

Comments:

Quality: B (Bulgaria, Romania and Northern Italy are missing).



Distribution: green dots represent vegetation plot data

Map with modelled distribution

Annex 2 Relation between Natura 2000 habitats and CLC classes

Only frequencies greater then 5% have been taken into account.

Habitat type	CLC class		Freq. (%)
H1330	37	salt marshes	19
H1330	39	intertidal flats	18
H1330	12	non-irrigated arable land	15
H1330	26	natural grasslands	11
H1330	18	pastures	9
H1330	30	beaches, sand, dunes	9
H2120	44	sea and ocean	30
H2120	30	beaches, sand, dunes	12
H2130	26	natural grasslands	50
H2130	44	sea and ocean	8
H2130	30	beaches, sand, dunes	8
H2160	26	natural grasslands	52
H2160	30	beaches, sand, dunes	8
H2210	44	sea and ocean	37
H2210	30	beaches, sand, dunes	8
H2210	28	sclerophyllous vegetation	7
H3110	24	coniferous forest	14
H3110	36	peat bogs	14
H3110	18	pastures	14
H3110	20	complex cultivation patterns	12
H3130	18	pastures	14
H3130	24	coniferous forest	13
H3130	20	complex cultivation patterns	11
H3130	12	non-irrigated arable land	11
H3130	23	broad-leaved forest	9
H3130	21	land principally occupied by agriculture with significant natural vegetation	7
H3130	41	water bodies	7
H3150	18	pastures	53
H3150	12	non-irrigated arable land	13
H3150	23	broad-leaved forest	6
H3260	12	non-irrigated arable land	23
H3260	23	broad-leaved forest	15
H3260	18	pastures	12
H3260	21	land principally occupied by agriculture with significant natural vegetation	8
H3260	24	coniferous forest	8
H4010	36	peat bogs	22
H4010	27	moors and heath lands	17

Habitat type	CLC class		Freq. (%)
H4010	18	pastures	14
H4010	24	coniferous forest	11
H4010	26	natural grasslands	5
H4030	24	coniferous forest	20
H4030	27	moors and heath lands	19
H4030	23	broad-leaved forest	11
H4030	26	natural grasslands	10
H4030	18	pastures	8
H4030	25	mixed forest	7
H4030	36	peat bogs	6
H4060	26	natural grasslands	27
H4060	27	moors and heath lands	18
H4060	32	sparsely vegetated areas	17
H4060	24	coniferous forest	13
H4060	31	bare rocks	10
H4070	27	moors and heath lands	26
H4070	24	coniferous forest	22
H4070	26	natural grasslands	18
H4070	32	sparsely vegetated areas	8
H4070	25	mixed forest	8
H4070	31	bare rocks	7
H5130	23	broad-leaved forest	24
H5130	24	coniferous forest	18
H5130	12	non-irrigated arable land	11
H5130	25	mixed forest	11
H5130	18	pastures	8
H5210	28	sclerophyllous vegetation	16
H5210	24	coniferous forest	11
H5210	29	transitional woodland-scrub	10
H5210	25	mixed forest	9
H5210	23	broad-leaved forest	8
H5210	44	sea and ocean	7
H5210	26	natural grasslands	6
H5420	28	sclerophyllous vegetation	30
H5420	26	natural grasslands	14
H5420	21	land principally occupied by agriculture with significant natural vegetation	12
H5420	24	coniferous forest	10
H5420	29	transitional woodland-scrub	10
H5420	44	sea and ocean	10
H6110	12	non-irrigated arable land	21
H6110	23	broad-leaved forest	20
H6110	25	mixed forest	11
H6110	21	land principally occupied by agriculture with significant natural vegetation	8
H6110	18	pastures	8
H6110	20	complex cultivation patterns	5

Habitat type	CLC class		Freq. (%)
H6120	12	non-irrigated arable land	31
H6120	18	pastures	9
H6120	24	coniferous forest	8
H6120	23	broad-leaved forest	8
H6120	21	land principally occupied by agriculture with significant natural vegetation	8
H6120	20	complex cultivation patterns	7
H6120	25	mixed forest	6
H6150	26	natural grasslands	43
H6150	31	bare rocks	18
H6150	32	sparsely vegetated areas	18
H6150	27	moors and heath lands	12
H6150	24	coniferous forest	6
H6170	26	natural grasslands	30
H6170	31	bare rocks	14
H6170	32	sparsely vegetated areas	14
H6170	24	coniferous forest	14
H6170	27	moors and heath lands	12
H6170	25	mixed forest	7
H6170	18	pastures	6
H6210	12	non-irrigated arable land	18
H6210	18	pastures	15
H6210	23	broad-leaved forest	15
H6210	24	coniferous forest	11
H6210	25	mixed forest	11
H6210	26	natural grasslands	6
H6210	21	land principally occupied by agriculture with significant natural vegetation	5
H6210	20	complex cultivation patterns	5
H6220	28	sclerophyllous vegetation	14
H6220	23	broad-leaved forest	12
H6220	26	natural grasslands	9
H6220	29	transitional woodland-scrub	8
H6220	12	non-irrigated arable land	7
H6220	20	complex cultivation patterns	6
H6220	21	land principally occupied by agriculture with significant natural vegetation	5
H6230	26	natural grasslands	25
H6230	24	coniferous forest	20
H6230	18	pastures	11
H6230	27	moors and heath lands	9
H6230	23	broad-leaved forest	6
H6230	25	mixed forest	6
H6230	32	sparsely vegetated areas	6
H6240	12	non-irrigated arable land	30
H6240	23	broad-leaved forest	18
H6240	21	land principally occupied by agriculture with significant natural vegetation	10
H6240	25	mixed forest	6

Habitat type	CLC class		Freq. (%)
H6240	20	complex cultivation patterns	6
H6410	18	pastures	22
H6410	12	non-irrigated arable land	21
H6410	24	coniferous forest	12
H6410	23	broad-leaved forest	10
H6410	25	mixed forest	7
H6410	21	land principally occupied by agriculture with significant natural vegetation	6
H6410	20	complex cultivation patterns	6
H6430	24	coniferous forest	23
H6430	26	natural grasslands	12
H6430	18	pastures	12
H6430	25	mixed forest	10
H6430	23	broad-leaved forest	10
H6430	12	non-irrigated arable land	7
H6430	27	moors and heath lands	5
H6510	12	non-irrigated arable land	20
H6510	18	pastures	19
H6510	23	broad-leaved forest	13
H6510	25	mixed forest	10
H6510	20	complex cultivation patterns	10
H6510	21	land principally occupied by agriculture with significant natural vegetation	9
H6510	24	coniferous forest	7
H6520	24	coniferous forest	25
H6520	26	natural grasslands	22
H6520	18	pastures	15
H6520	25	mixed forest	9
H6520	23	broad-leaved forest	7
H7110	24	coniferous forest	29
H7110	36	peat bogs	17
H7110	18	pastures	10
H7110	29	transitional woodland-scrub	8
H7110	27	moors and heath lands	6
H7110	25	mixed forest	6
H7110	26	natural grasslands	5
H7110	12	non-irrigated arable land	5
H7130	36	peat bogs	54
H7130	27	moors and heath lands	19
H7130	26	natural grasslands	8
H7130	24	coniferous forest	5
H7150	24	coniferous forest	18
H7150	18	pastures	18
H7150	27	moors and heath lands	13
H7150	36	peat bogs	9
H7150	25	mixed forest	9
H7150	21	land principally occupied by agriculture with significant natural vegetation	8

Habitat type	CLC class		Freq. (%)
H7150	20	complex cultivation patterns	8
H7210	12	non-irrigated arable land	17
H7210	18	pastures	12
H7210	35	inland marshes	11
H7210	23	broad-leaved forest	11
H7210	36	peat bogs	7
H7230	24	coniferous forest	19
H7230	18	pastures	16
H7230	26	natural grasslands	12
H7230	12	non-irrigated arable land	10
H7230	25	mixed forest	9
H7230	21	land principally occupied by agriculture with significant natural vegetation	5
H8210	25	mixed forest	17
H8210	24	coniferous forest	17
H8210	23	broad-leaved forest	16
H8210	26	natural grasslands	10
H8210	31	bare rocks	8
H8210	32	sparsely vegetated areas	8
H8210	27	moors and heath lands	7
H8220	23	broad-leaved forest	24
H8220	24	coniferous forest	10
H8220	25	mixed forest	10
H8220	26	natural grasslands	9
H8220	31	bare rocks	8
H8220	32	sparsely vegetated areas	6
H8220	18	pastures	5
H8220	29	transitional woodland-scrub	5
H9150	23	broad-leaved forest	29
H9150	25	mixed forest	27
H9150	24	coniferous forest	13
H9160	23	broad-leaved forest	39
H9160	12	non-irrigated arable land	17
H9160	25	mixed forest	17
H9190	18	pastures	20
H9190	20	complex cultivation patterns	17
H9190	21	land principally occupied by agriculture with significant natural vegetation	13
H9190	23	broad-leaved forest	12
H9190	25	mixed forest	10
H91E0	23	broad-leaved forest	23
H91E0	12	non-irrigated arable land	17
H91E0	18	pastures	13
H91E0	25	mixed forest	12
H91E0	24	coniferous forest	10
H9410	24	coniferous forest	47
H9410	25	mixed forest	24

Annex 3 Relation between habitats and fragmentation classes/FMA

Habitat type		Fragmentation class(es)	FMA
1330	Atlantic salt meadows (Glauco-Puccinellietalia maritimae)	4.2	
2120	Shifting dunes along the shoreline with Ammophila arenaria ("white dunes")	3.2	
2130	Fixed coastal dunes with herbaceous vegetation ("grey dunes")	3.2	
2160	Dunes with Hippophaë rhamnoides	3.2	
2210	Crucianellion maritimae fixed beach dunes	3.2	
3110	Oligotrophic waters containing very few minerals of sandy plains (Littorelletalia uniflorae)	5.1	
3130	Oligotrophic to mesotrophic standing waters with vegetation of the Littorelletea uniflorae and/or of the Isoëto-Nanojuncetea	5.1	
3150	Natural eutrophic lakes with Magnopotamion or Hydrocharition - type vegetation	5.1	
3260	Water courses of plain to montane levels with the Ranunculion fluitantis and Callitricho-Batrachion vegetation	5.1	
4010	Northern Atlantic wet heaths with Erica tetralix	4.1	
4030	European dry heaths	3.2	
4060	Alpine and Boreal heaths	3.2	
4070	Bushes with Pinus mugo and Rhododendron hirsutum (Mugo-Rhododendretum hirsuti)	3.2	
5130	Juniperus communis formations on heaths or calcareous grasslands	3.2	
5210	Arborescent matorral with Juniperus spp.	3.2	
5420	Sarcopoterium spinosum phryganas	3.2	
6110	Rupicolous calcareous or basophilic grasslands of the Alysso-Sedion albi	3.2	
6120	Xeric sand calcareous grasslands	3.2	
6150	Siliceous alpine and boreal grasslands	3.2	
6170	Alpine and subalpine calcareous grasslands	3.2	
6210	Semi-natural dry grasslands and scrubland facies on calcareous substrates (Festuco-Brometalia) (* important orchid sites)	3.2	
6220	Pseudo-steppe with grasses and annuals of the Thero-Brachypodietea	3.2	
6230	Species-rich Nardus grasslands, on silicious substrates in mountain areas (and submountain areas in Continental Europe)	3.2	
6240	Sub-Pannonic steppic grasslands	3.2	
6410	Molinia meadows on calcareous, peaty or clayey-silt-laden soils (Molinion caeruleae)	3.2	
6430	Hydrophilous tall herb fringe communities of plains and of the montane to alpine levels	3.2	
6510	Lowland hay meadows (Alopecurus pratensis, Sanguisorba officinalis)	3.2	
6520	Mountain hay meadows	3.2	
7110	Active raised bogs	4.1	
7130	Blanket bogs (* if active bog)	4.1	

Habitat type		Fragmentation class(es)		FMA
7150	Depressions on peat substrates of the Rhynchosporion	4.1		
7210	Calcareous fens with Cladium mariscus and species of the Caricion davallianae	4.1		
7230	Alkaline fens	4.1		
8210	Calcareous rocky slopes with chasmophytic vegetation	3.1	3.3	
8220	Siliceous rocky slopes with chasmophytic vegetation	3.1	3.3	
9150	Medio-European limestone beech forests of the Cephalanthero-Fagion	3.1		x
9160	Sub-Atlantic and medio-European oak or oak-hornbeam forests of the Carpinion betuli	3.1		x
9190	Old acidophilous oak woods with Quercus robur on sandy plains	3.1		x
91E0	Alluvial forests with Alnus glutinosa and Fraxinus excelsior (Alno-Padion, Alnion incanae, Salicion albae)	3.1		x
9410	Acidophilous Picea forests of the montane to alpine levels (Vaccinio-Piceetea)	3.1		x

Annex 4 Description of environmental data used to create distribution models

Study area

Selected climate and soil parameters to calculate the current species range

Variable	Source	Spatial resolution	Time	Source location	Projection
Precipitation seasonality (coefficient of variation)	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984
Precipitation of driest month	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984
Temperature Seasonality (standard deviation*100)	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984
Isothermality	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984
Mean temperature of driest quarter	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984
Precipitation of warmest quarter	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984
Min temperature of coldest month	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984
Elevation	BioClim[1]	30 arc seconds	~1950-2000	http://www.worldclim.org/current	GCS_WGS_1984

Annual mean moisture index	BioClim[2]	10 arc minutes	~1950-2000	https://www.climond.org/Download.aspx	GCS_WGS_1984
annual ratio of actual to potential evatranspiration	Image[3]	0.5 arc degrees		http://themasites.pbl.nl/tridion/en/themasites/image/index.html	GCS_WGS_1984
Temperature sum in growing season	Image[3]	0.5 arc degrees		http://themasites.pbl.nl/tridion/en/themasites/image/index.html	GCS_WGS_1984
pH-H_2O in top soil	HWSD [4]	5*5km		http://worldgrids.org/doku.php?id=wiki:tphhws	GCS_WGS_1984
Availability of salt	Sworld-soil map[5]	1*1 km?		Not yet published.	GCS_WGS_1984
Organic carbon content in top soil	ESDB[5]	1*1 km		http://eusoils.jrc.ec.europa.eu/ESDB_Archive/ESDB_Data_Distribution/derived_data.html	ETRS_1989_LAEA
Clay content in top soil	ESDB[5]	1*1 km		http://eusoils.jrc.ec.europa.eu/ESDB_Archive/ESDB_Data_Distribution/derived_data.html	ETRS_1989_LAEA
Silt content in top soil	ESDB[5]	1*1 km		http://eusoils.jrc.ec.europa.eu/ESDB_Archive/ESDB_Data_Distribution/derived_data.html	ETRS_1989_LAEA

1) Hijmans, R.J., S.E. Cameron, J.L. Parra, P.G. Jones and A. Jarvis (2005). Very high resolution interpolated climate surfaces for global land areas. International Journal of Climatology 25: 1965-1978.

2) Kriticos, D.J., Webber, B.L., Leriche, A., Ota, N., Macadam, I., Bathols, J. & Scott, J.K. (2012) CliMond: global high resolution historical and future scenario climate surfaces for bioclimatic modelling. *Methods in Ecology and Evolution* 3: 53-64. DOI: 10.1111/j.2041-210X.2011.00134.x

3) MNP (2006) (Edited by A.F. Bouwman, T. Kram and K. Klein Goldewijk), Integrated modelling of global environmental change. An overview of IMAGE 2.4. Netherlands Environmental Assessment Agency (MNP), Bilthoven, The Netherlands.

4) FAO/IIASA/ISRIC/ISSCAS/JRC (2012). *Harmonized World Soil Database (version 1.2)*. FAO, Rome, Italy and IIASA, Laxenburg, Austria.

5) Hiederer, R. (2013). Mapping Soil Properties for Europe - Spatial Representation of Soil Database Attributes. Luxembourg: Publications Office of the European Union – 2013 – 47pp. – EUR26082EN Scientific and Technical Research series, ISSN 1831-9424, doi:10.2788/94128

Selection criteria

The selection of the climate and soil variables is based on the following selection criteria.

1. Low resolution (preferably 1*1 km)
2. Availability of climate scenario's
3. Ecologically relevant for at least one of the species groups[6,7]
4. As much as possible same data source
5. Extent including Europe, North Africa and West Russia
6. Preferably scale variables

6) Josef Settele, O Kudrna, Alexander Harpke, Ingolf Kühn, Chris van Swaay, Rudi Verovnik, Martin Warren, Martin Wiemers, Jan Hanspach, Thomas Hickler, Elisabeth Kühn, Inge van Halder, Kars Veling, Albert Vliegenthart, Irma Wynhoff, Oliver Schweiger (2008). Climatic risk atlas of European Butterflies. Pensoft Publishers, Bulgaria.

7) Huntley B, Green R.E, Collingham YC, & Willis S.G. (2007) A climatic atlas of European breeding birds. Barcelona: Lynx Edicions.

Preparation of data

Data preparation applicable to all data:

1. Projection of all data is changed into ETRS_1989_LAEA.
2. Only the part of the data within the study area is selected.
3. Spatial resolution is changed to 1x1 km
4. Data is saved in an ascii grid.

The soil parameters, pH, organic carbon content, silt content and clay content, did not cover the full study area. So extra steps had to be taken.

pH:

The HWSD has across the study area missing values. These missing values within Europe are filled with the "map of soil pH in Europe" from the JRC[8]. Acidity in this map is given as pH-$CaCl_2$. The following calculation is used to derive pH-H_2O[9].

$$pHwater = (0.427 + pHCaCl2)/0.9761$$

The islands north of the European continent, which are permanently covered with ice, still had missing values. These areas were given a value of 7, like fresh water.

But we also see large areas in northern Africa that have no pH. These turn out to be dune shiftsands, where no soil formation has taken place yet. These areas are rather large and we want to incorporate them in our scope as they provide routes along which plants, butterflies (and maybe even mammals?) can migrate in northern direction. So we need to fill in an pH value for these very young soils. I consulted Jetse Stoorvogel, one of the authors of the WHSD. His advice was to use a value of pH-H20 of 6.0. This matches best with very young soil types.
The last area of missing values were large lakes. These areas were left with no data and are therefore not part of the study area.

8) Böhner, J., Blaschke, T., Montanarella, L. [Eds.] (2008): SAGA – Seconds Out. Hamburger Beiträge zur Physischen Geographie und Landschaftsökologie, Vol.19, 113pp

9) Reuter,H.I, Rodriguez Lado,L., Hengl, T., Montanarella,L. (2008) Continental Scale Digital Soil Mapping using European Soil Profile Data: soil pH. - in Eds: Böhner,J. ,Blaschke,T. and Montanarella,L. SAGA – Seconds Out,&xnbsp; Hamburger Beiträge zur Physischen Geographie und Landschaftsökologie, Heft 19, Universität Hamburg, Institut für Geographie, ISSN: 1866-170X"

Salt in soil

Availability of salt in the top soil is derived from the Sworld soil map[5]. The European soil types in this map are classified in four categories of salinity; saline, moderately saline, locally saline and non-saline.

Saline: Soils with high content of salts. These are bare soils or soils covered with saline vegetation. They include salty tidal and coastal flats, salt pans, and inland salt plains

Moderately saline: Soils which locally vary in salt content from saline tot non-saline in the rootzone. In semiarid zones the soils are mostly saline. In temperate zone the salinity is slight or absent in the root zone and even agricultural land use is possible.

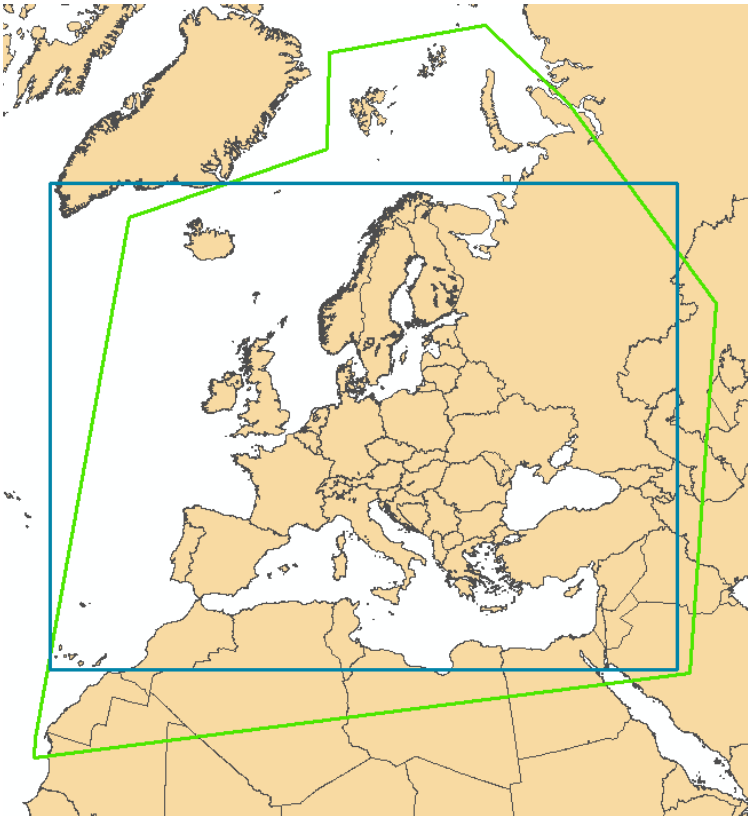
Locally saline: Only locally the circumstances are salty or brackish in the root zone. This is caused by association with saline soils as an impurity of the map unit (for example salty calcisols) or human influence (badly managed irrigated soils).

Non-Saline: Soils are not salty or brackish.

Symbol	Description	Salinity	Comments
DS	Dunes & Shift.sands	Non-saline	
Anthrosols			
AT	Anthrosols	Non-saline	
ATc	Cumulic Anthrosols	Locally saline	Cumulic Anthrosols in West-Europe are non-saline
ATu	Urbic Anthrosols	Non-saline	
Calcisols			
CL	Calcisols	Locally saline	
FLs	Salic Fluvisols	Saline	

Symbol	Description	Salinity	Comments
Solonchaks			
SC	Solonchaks	Saline	
SCg	Gleyic Solonchaks	Saline	
SCh	Haplic Solonchaks	Saline	
Sci	Gelic Solochaks	Saline	
SCk	Calcic Solonchaks	Saline	
SCm	Mollic Solonchaks	Saline	
SCn	Sodic Solonchaks	Saline	
Scy	Gypsic Solonchaks	Saline	
Solonetz			
SN	Solonetz	Moderately saline	
SNg	Gleyic Solonetz	Moderately saline	
SNh	Haplic Solonetz	Moderately saline	
SNj	Stagnic Solonetz	Moderately saline	
SNk	Calcic Solonetz	Moderately saline	
SNm	Mollic Solonetz	Moderately saline	
SNy	Gypsic Solonetz	Moderately saline	

<u>Organic carbon, clay and silt content in top soil</u>
Organic carbon content, clay content and silt content in the top soil (0-30 cm) come from the European Soil Database. The extent of this database does not cover the entire study area (blue line in figure). Missing data was filled with data from the HWSD. As was the case with the pH-data, the HWSD does not cover the ice covered islands north of Europe nor the dunes and shifting sands in the Sahara. These areas were given the value of 0 for all three soil parameters, because there is no soil in ice and there is only sand shifting sands, where no soil formation has started.



Scenario data from Image

For the temperature Sum in growing season and the annual ratio of actual to potential evatranspiration we have used a baseline scenario that was been calculated using the IMAGE model. This is a global scenario and it was taken from the Global Biodiversity Outlook 4 project.

This scenario has also been used in the Roads to Rio project (2012 in the biodiversity chapter of the EOCD Global Environmental Outlook. (2012) In the latter publication it is well described.

We have made a slight extension to the IMAGE model to derive the variable Temperature sum in the growing season. The algorithm is like this:

For each cell (0,5*0,5 degree) and for every day

- Check whether temperature > 5 degree and humidity >0
- If yes, consider this is a growing season day and add the temperature value.
- The range of the temperature sum On Global scale was 0 to 10,655.2 degrees.
- After we clipped part of the map for the European situation the range was 0 to 5,970.44 degrees. Apparently we see the effect of the hottest regions round the equator having been cut off.

Annex 5 Description of environmental data used to derive dose-response curves

Land use
(used as mask before deriving and applying dose response curves)

Content: Pan European Landcover Mozaiek

Description: The PLCM2000 (Hazeu *et al.*, unpubl.) is a pan-European map of land cover in which the Corine Land Cover 2000 has been integrated. The land use classes in the PLCM map are in accordance with land use classes in the CLC2000 map. The map is a thematic refinement of the CORINE land cover map, which is a visual interpretation from satellite images.

Unit: percentage cover per CLC level 3 class

Source: Corine land cover (EEA), PELCOM (Alterra) and GLC2000 (JRC)

Spatial resolution: original: 100x100m, processed: 1x1 km, 5x5 km, 10x10 km

Year: 2000

Coverage: See figure 1

Website: No website

Prepocessing/data adjustments: Percentage cover per gridcell is calculated.

Pan-European Landcover

Code	Level 3 CORINE land cover class	Grid code
1.1.1	continuous urban fabric	1
1.1.2	discontinuous urban fabric	2
1.2.1	industrial and commercial units	3
1.2.2	road and rail networks and associated land	4
1.2.3	port areas	5
1.2.4	airports	6
1.3.1	mineral extraction sites	7
1.3.2	dump sites	8
1.3.3	construction sites	9
1.4.1	green urban areas	10
1.4.2	port and leisure facilities	11
2.1.1	non-irrigated arable land	12
2.1.2	permanently irrigated land	13
2.1.3	rice fields	14
2.2.1	vineyards	15
2.2.2	fruit trees and berry plantation	16
2.2.3	olive groves	17
2.3.1	pastures	18
2.4.1	annual cops associated with permanent crops	19
2.4.2	complex cultivation patterns	20
2.4.3	land principally occupied by agriculture with significant natural vegetation	21
2.4.4	agro-forestry areas	22
3.1.1	broad-leaved forest	23
3.1.2	coniferous forest	24
3.1.3	mixed forest	25
3.2.1	natural grasslands	26
3.2.2	moors and heath lands	27
3.2.3	sclerophyllous vegetation	28
3.2.4	transitional woodland-scrub	29
3.3.1	beaches, sand, dunes	30
3.3.2	bare rocks	31
3.3.3	sparsely vegetated areas	32
3.3.4	burnt areas	33
3.3.5	glaciers and perpetual snow	34
4.1.1	inland marshes	35
4.1.2	peat bogs	36
4.2.1	salt marshes	37
4.2.2	salines	38
4.2.3	intertidal flats	39
5.1.1	water courses	40
5.1.2	water bodies	41
5.2.1	coastal lagoons	42
5.2.2	estuaries	43
5.2.3	sea and ocean	44

Sulphur deposition

Content: Total deposition of oxidized sulpher

Description: Total deposition of oxidized sulpher

Unit: mg S/m^2

Source: TNO; LOTOS-EUROS model

Spatial resolution: original: 1/16 degree, processed: 1x1 km, 5x5 km, 10x10 km

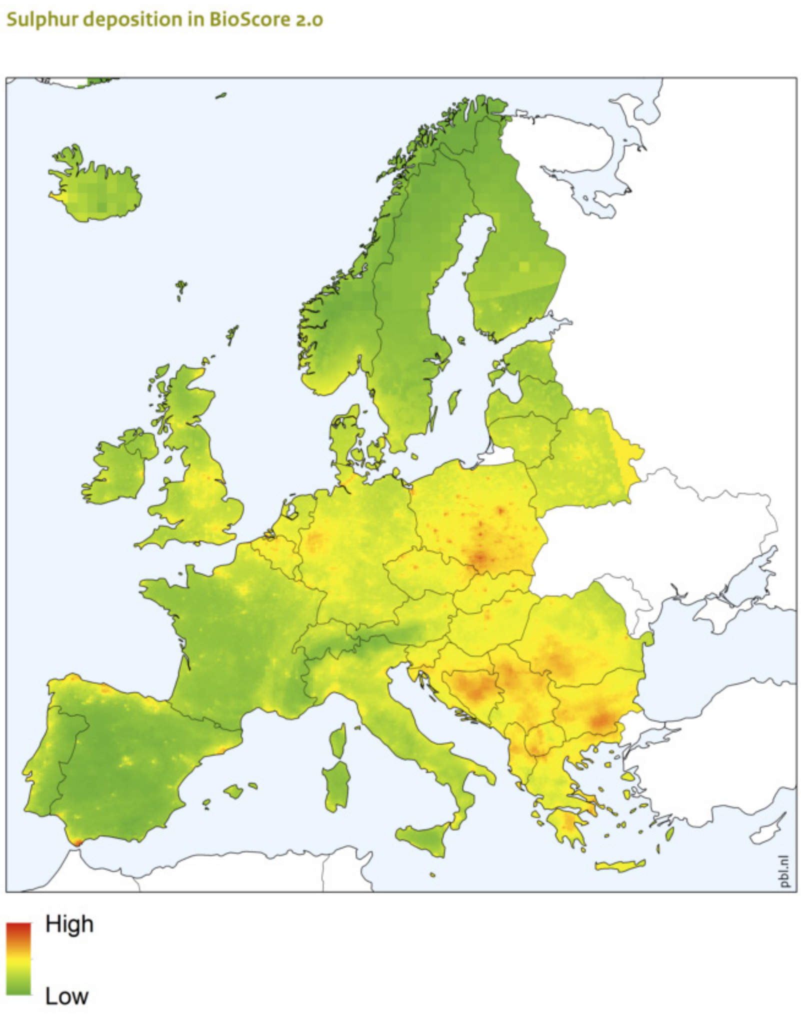
Year: 2009

Coverage: Europe, excluding northern part of Scandinavia

Website: -

Reference: C. Cuvilier *et al*. (2013). ScaleDep: Performance of European chemistry-transport models as function of horizontal spatial resolution
http://emep.int/publ/reports/2013/MSCW_technical_1_2013.pdf

Prepocessing/data adjustments: Outside the extent of the TNO data, EMEP-data (European Monitoring and Evaluation Programme) is added of the same year. This data was in the unit, but has a spatial resolution of 50x50 km.



Oxidized sulpher deposition. Values range from 0 to 6403 mg S/m^2

Nitrogen deposition in rural area

Content: Total nitrogen deposition

Description: Total reduced and oxidized nitrogen deposition.

Unit: mg N/m^2

Source: TNO; LOTOS-EUROS model

Spatial resolution: original: 1/16 degree, processed: 1x1 km, 5x5 km, 10x10 km

Year: 2009

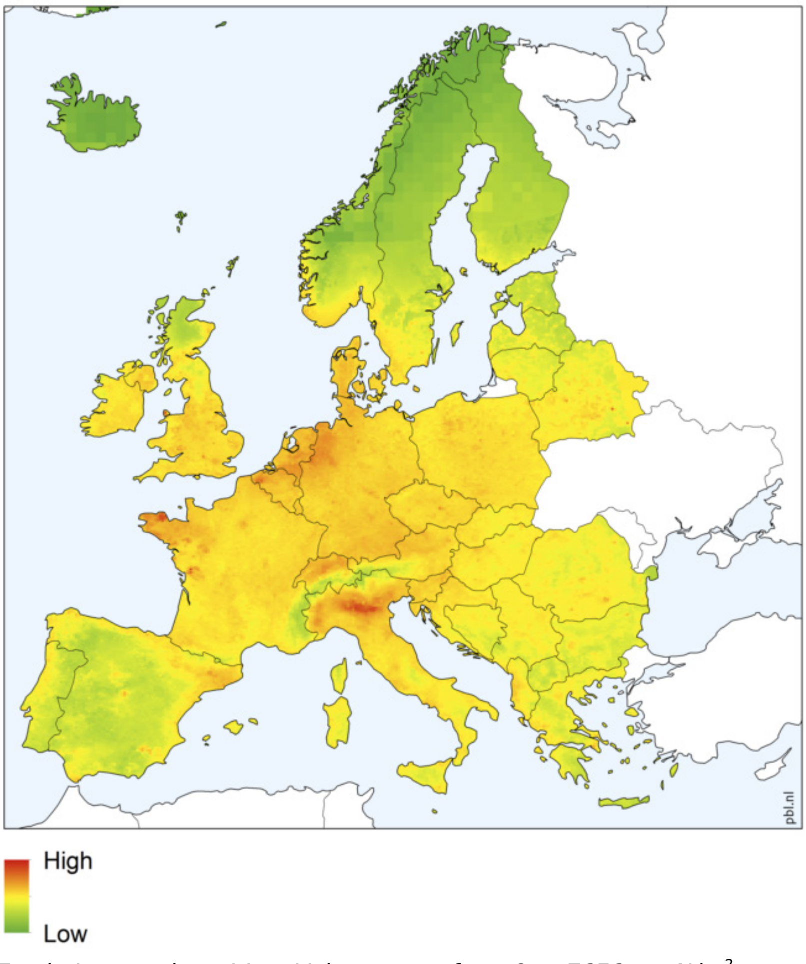
Coverage: Europe, excluding northern part of Scandinavia

Website: -

Reference: C. Cuvilier *et al*. (2013). ScaleDep: Performance of European chemistry-transport models as function of horizontal spatial resolution
http://emep.int/publ/reports/2013/MSCW_technical_1_2013.pdf

Prepocessing/data adjustments: Outside the extent of the TNO data, EMEP-data (European Monitoring and Evaluation Programme) is added of the same year. This data was in the unit, but has a spatial resolution of 50x50 km.

Nitrogen deposition in BioScore 2.0



Total nitrogen deposition. Values range from 0 to 7656 mg N/m^2

Nitrogen application in grasslands and agricultural area

Content: nitrogen application in agricultural area as a proxy for agricultural intensity

Description: Nitrogen application includes manure application (corrected for volatilization losses), manure deposition by grazing animals and application of mineral fertilizer manure. Nitrogen input is distributed over the spatial units on the following basis. Manure is distributed on the basis of the crops' N requirement and N-availability in vicinity of the spatial unit. Mineral fertilizer nitrogen is added according to crops' need. Total availability of nitrogen is exhausted by scaling regional application rates.

Unit: kg N per hectare of utilized agricultural area

Source: AFOLU Data Portal for European Terrestrial Modelling; JRC

Spatial resolution: Pixel cluster according to "homogeneity rules" - selection of clusters according to presence of agriculture. Resolution original data: $1km^2$. processed: 1x1 km, 5x5 km, 10x10 km

Year: 2002

Coverage: See figure 4

Website: http://afoludata.jrc.ec.europa.eu/index.php/dataset/parameter/218
Reference: Leip, A. (2011). Assessing the environmental impact of agriculture in europe: the indicator database for european agriculture, in: Guo, L., Gunasekara, A., McConnell, L. (Eds.), Understanding Greenhouse Gas Emissions from Agricultural Management. ASC, Washington DC, pp. 371–385. doi:10.1021/bk-2011-1072.ch019.

Prepocessing/data adjustments: The original dataset has a pixel size of 1 km^2. This data is downscaled by overlaying it with the CORINE land cover map of 2006 (spatial resolution of 100x100 m). All pixels from the CORINE land cover map not classified as agricultural areas or natural grasslands were removed. Natural grasslands not covered by the nitrogen application map were given a value of 0 kg nitrogen per hectare.
For upscaling the data to 1, 5 and 10 km resolution the average value of the agricultural areas is taken. Afterwards 0 kg N/ha is allocated to cells without agricultural areas.

Remarks: The current detailed data are approved to be the best available now by Hans van Grinsven. However the data year is 2002. Hans suspects there are more recent data but not on 1* 1 km grid. Interesting would be to know the trend in fertilizer application in EU for the past period. This could be used to update the current map in the future.
Furthermore, nitrogen gift is a proxy for intensification in agriculture and therefore will be a relevant parameter in scenarios. So it is worth to invest in developing N-trends for EU, and to retrieve regional trends. Koen Overmars has done related work and could be asked. Furthermore we can ask Leip for more recent data.
Henk van Zeijts mentioned a JRC project Volante that can be relevant. http://www.volante-project.eu/

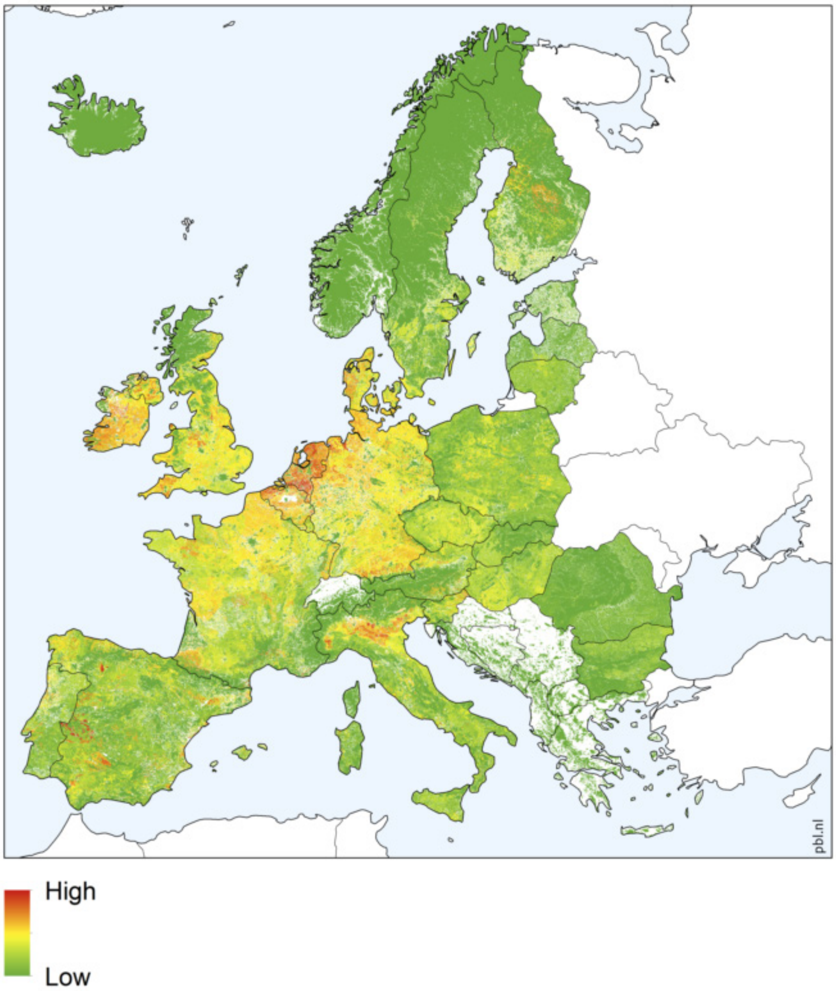
See also:

Kleijn, D., F. Kohler, A. Báldi, P. Batáry, E.D. Concepción, Y. Clough, M. Díaz, D. Gabriel, A. Holzschuh, E. Knop, A. Kovács, E.J.P. Marshall, T. Tscharntke & J. Verhulst (2009), 'On the relationship between farmland biodiversity and land-use intensity in Europe', *Proceedings of the Royal Society B: Biological Sciences* 276: 903-909.

Temme, A.J.A.M. & P.H. Verburg (2011), 'Mapping and modelling of changes in agricultural intensity in Europe', *Agriculture, Ecosystems & Environment* 140: 46-56.

Overmars, K.P., C.J.E. Schulp, R. Alkemade, P.H. Verburg, A.J.A.M. Temme & N. Omtzigt (2011), 'A species based and spatially explicit indicator for biodiversity on agricultural land in the EU', submitted to *Ecosystems*.

Agricultural intensity in BioScore 2.0



Nitrogen application in agricultural area. Values range from 0 to 1290 kg N/ha.

Forest management appoaches

Content: Map of potential forest management approaches (FMA's)

Description: Five FMA's are distinguished:

1. Short rotation forestry
2. Even-aged forestry
3. Combined objective forestry,
4. Close-to-nature,
5. Nature reserve.

The presented method calculates the suitability of a location to different forest management alternatives based on biotic, abiotic, socioeconomic, and political factors. The most suitable forest management approach is selected at a location. A comparison of the map with reference data shows that in general the forest management type applied is more intensive than the type predicted as most suitable.

Unit: not applicable

Source: ALTERRA – Wageningen UR and European Forest Institute

Spatial resolution: Original: 1 km^2. processed: 1x1 km, 5x5 km, 10x10 km

Year: Unknown

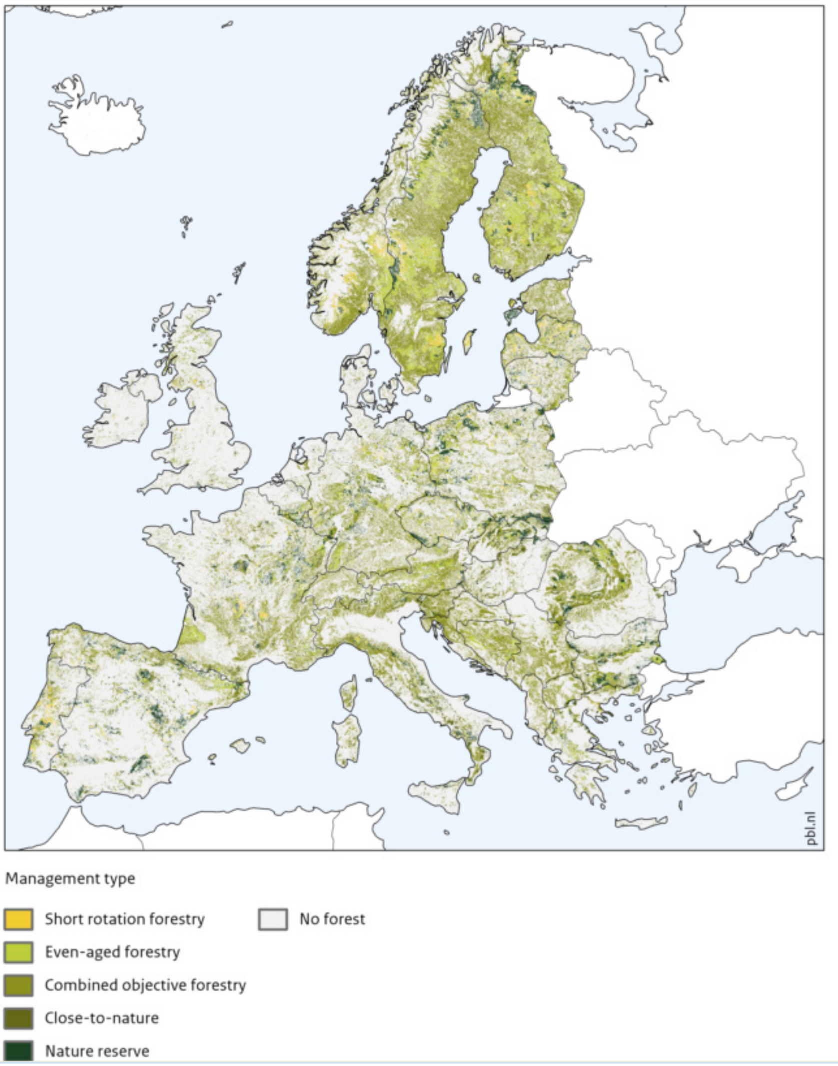
Coverage: See Figure 5

Website: -

Reference: Hengeveld, G.M., G.J. Nabuurs, M. Didion, I. van den Wyngaert, A.P.P.M. Clerkx and M.J. Schelhaas (2012). *A forest management map of European forests*. Ecology and Society 17(4): 53.

Prepocessing/data adjustments: The original dataset has a pixel size of 1 km^2. As the map shows *potential* forest types, locations without forest are also given a value. This data is downscaled by overlaying it with the CORINE land cover map of 2006 (spatial resolution of 100x100 m). All pixels from the CORINE land cover map not classified as forest were allocated the value 0 (no forest). In the original data a category is added where a potential forest management approach is unknown, because the potential area of forest is lower than 20% in the pixel. Pixels with an unknown FMA, which are categorized as forest in the CLC map are given the value 3 (combined objective forestry), based on the advice of G.M. Hengeveld. This situation occurs mainly in areas with agriculture and extensive grasslands, where forests cover consists of trees next to rivers, pastures, arable land and roads. Therefore an allocation of combined objective forestry is a save choice. This resulted in a map which names of all forests in Europe the potential forest management approach. Percentage cover per gridcell is calculated. Format is changed from shapefile to ascii grids.

Forest management type in BioScore 2.0



Forest management approach

Desiccation

Content: Map of annual total water abstraction as a fraction of available long-term freshwater resources. It is a proxy for waterscarscity.

Description: The warning threshold for the water exploitation index (WEI), which distinguishes a non-stressed region from a stressed region, is around 0.2. Severe water stress can occur where the WEI exceeds 0.4, indicating unsustainable water use.

WEI_abstraction = abstraction / (external inflow + internal flow)

Where:

- Internal flow = net generated water (rainfall – evapotranspiration + snowmelt)
- External inflow = inflow from upstream areas
- Abstraction = water abstraction in the region (including water return flow)

Abstraction includes public water withdrawals, industrial water withdrawals, energy water withdrawals, irrigation water requirements and water abstraction for livestock.

Unit: No unit

Source: JRC

Spatial resolution: original: sub-basis of rivers, processed: 1x1 km, 5x5 km, 10x10

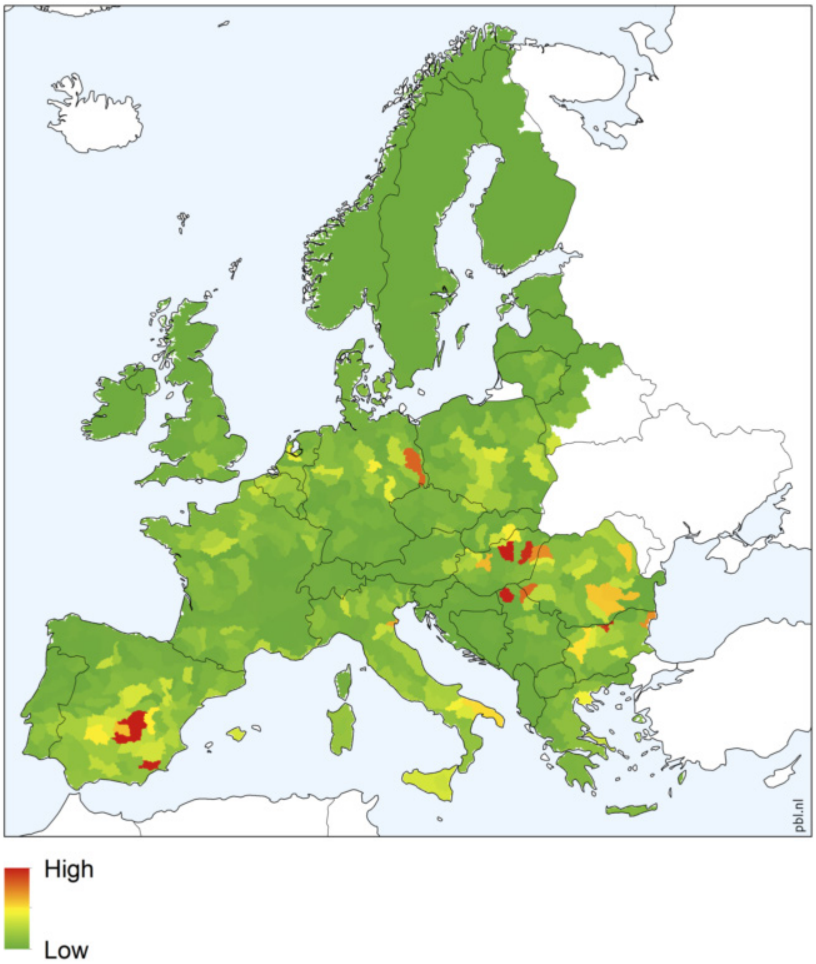
Year: 2006

Coverage: See figure 6

Website: -

Reference: de Roo, A., P. Burek, A. Gentile, A. Udias, F. Bouraoui, A. Aloe, A. Bianchi, A. La Notte, O. Kuik, J. Elorza Tenreiro, I. Vandecasteele, S. Mubareka, C. Baranzelli, M. van der Perk, C. Lavalle and G. Bidoqlio (2012). *A multi-criteria optimisation of scenarios for the protection of water resources in Europe.* JRC, Italy.

Prepocessing/data adjustments: No adjustments



Map of annual total water abstraction as a fraction of available long-term freshwater resources. High values indicate high water stress. Low values indicate no water stress.

Fragmentation

Content: 24 maps of the relative fragmentation of ecosystems in Europe.

Description: Spatial Cohesion of different ecosystems (level 2 Corine Land Cover; CLC) in Europe for four spatial scales (10 km, 20 km, 50 km and 100 km).
In database the names of the different maps have codes: first numbers refer to ecosystem (table 1), next number refers to dispersal capacity, '95' refers to parameter setting of LARCH-SCAN and 'div' or 'dv' refers to step 4 (see Preprocessing). F.e. forest species with a dispersal capacity of 20 km need to use the map div3_1_20_95.

Unit: - (ha / ha)

Source: LARCH-SCAN analyses (Groot Bruinderink *et al.*, 2003; IEEP & Alterra 2010) of aggregated map from Corine Land Cover.

Spatial resolution: original: 100 m x 100 m (CLC-map), processed: 1x1 km, 5x5 km, 10x10 km

Year: 2000

Coverage: Europe

Website: http://www.wageningenur.nl/nl/Expertises-Dienstverlening/Onderzoeksinstituten/Alterra/Faciliteiten-Producten/Software-en-modellen/LARCH.htm (very short description)

Reference: Groot Bruinderink, G., Van der Sluis, T., Lammertsma, D., Opdam, P. & Pouwels, R. (2003). Designing a coherent ecological network for large mammals in northwestern Europe. Conservation Biology, 17, 549-557.
IEEP & Alterra (2010) Reflecting environmental land use needs into EU policy: preserving and enhancing the environmental benefits of "land services": soil sealing, biodiversity corridors, intensification / marginalisation of land use and permanent grassland. Final report to the European Commission, DG Environment on Contract ENVB1/ETU/2008/0030. Institute for European Environmental Policy / Alterra Wageningen UR.
Pouwels, R., R. Jochem, M.J.S.M. Reijnen, S.R. Hensen en J.G.M. van der Greft (2002). LARCH voor ruimtelijk ecologische beoordelingen van landschappen. Alterra-rapport 492. Alterra, Research Instituut voor de Groene Ruimte, Wageningen.

Preprocessing/data adjustments:
Step 1: The Corine Land Cover (CLC) map is aggregated for each level 2 ecosystem (Table 1) at 1 km x 1 km. Each cell contains the amount of the ecosystem present (0-100 ha); count of 100 meter x 100 meter CLC input map.

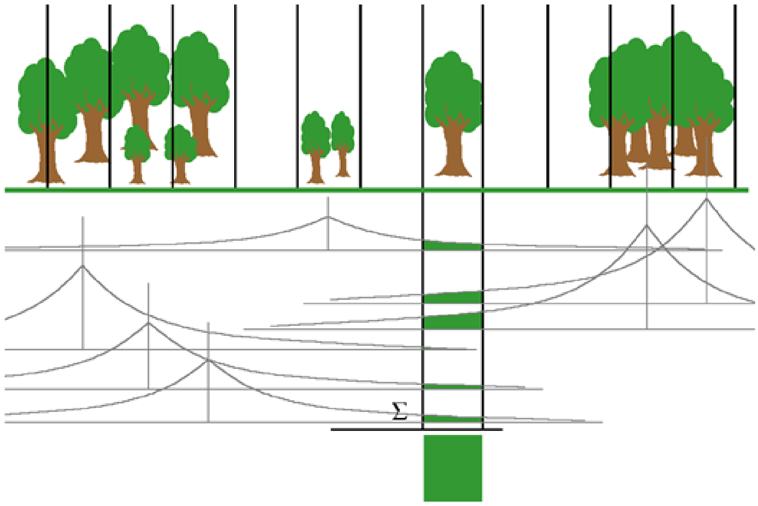
Step 2: LARCH-SCAN determines the Spatial Cohesion of nature areas. For this analyses it is used to determine the fragmentation of the ecosystem. For each cell the amount of habitat in its surrounding (almost twice the dispersal distance) is determined. Habitat further away is accounted for less than habitat close by, using Hanski's (1994) negative exponential function for cohesion ($e^{-\alpha d}$); α being the species specific dispersal capacity and d distance between cells or patches) (Figure 1). Dispersal classes used are 10, 20, 50 and 100 km. These correspond with α's of 0.230, 0.115, 0.046, 0.023.

Step 3: For a fictive landscape containing habitat the maximum values within non-fragmented landscapes are determined to scale the maps between 0 and 1. For the four dispersal classes the maximum values of LARCH-SCAN in a 1 km x 1 km grid are: 9473.4164, 37944.3358, 237054.1016 and 948295.7031. The percentage parameter in LARCH-SCAN is set at 95% to take into account habitat further away than the dispersal distance. When the percentage parameter is set at 90% the maximum values will be lower.

Step 4: LARCH-SCAN maps from step 2 are divided by thresholds from step 3. This results in maps containing values between 0 and 1. Zero meaning no habitat present in a circle of almost two times the dispersal distance and 1 meaning surroundings completely covered with the ecosystem. Based on the thresholds given by Rybicki and Hanski (2013) metapopulation processes start to occur when the ecosystem is less than 20% present in the landscape. This corresponds with values of 0.2 in the LARCH-SCAN output maps. Whether this is also a threshold useful for Bioscore needs to be decided after the regression analysis.

Ecosystems taken into account.

Code	Ecosystem
3.1	Forest
3.2	shrub and/or herbaceous vegetation associations
3.3	open spaces with little or no vegetation
4.1	inland wetlands
4.2	coastal wetlands
5.1	inland waters



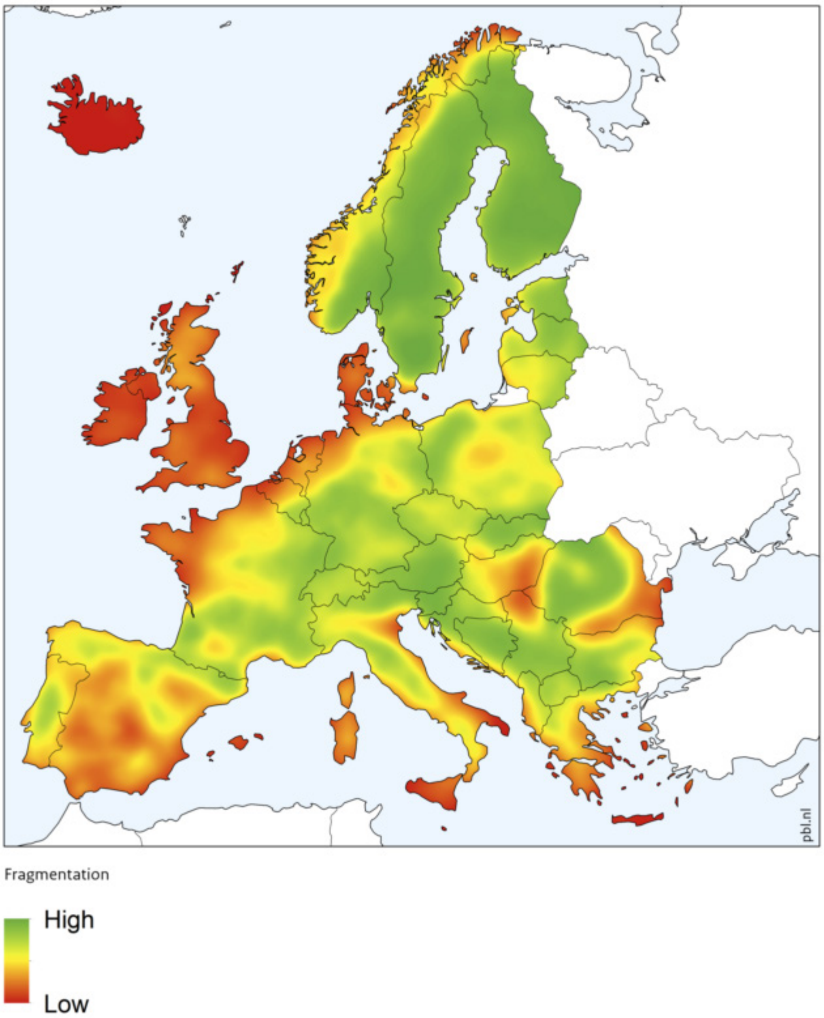
Schematic overview of LACRH-SCAN method

References

Hanski, I. (1994). A practical model of metapopulation dynamics. Journal of Animal Ecology 63: 151-162.

Rybicki, J. & Hanski, I. (2013) Species–area relationships and extinctions caused by habitat loss and fragmentation. Ecology Letters.

Fragmentation of forests in BioScore 2.0



Fragmentation of forests for species with a dispersal capacity of 10 km.

Roads

Content: Area impacted by roads

Description: Area within a 5 by 5 km cell affected by the major roads within that cell

Unit: hectares

Source: Meijer J.R. and Klein Goldewijk C.G.M. (2009) Global Roads Inventory Project (GRIP) version 1. PBL Netherlands Environmental Assessment Agency,
Spatial resolution: 5 x 5km

Year:

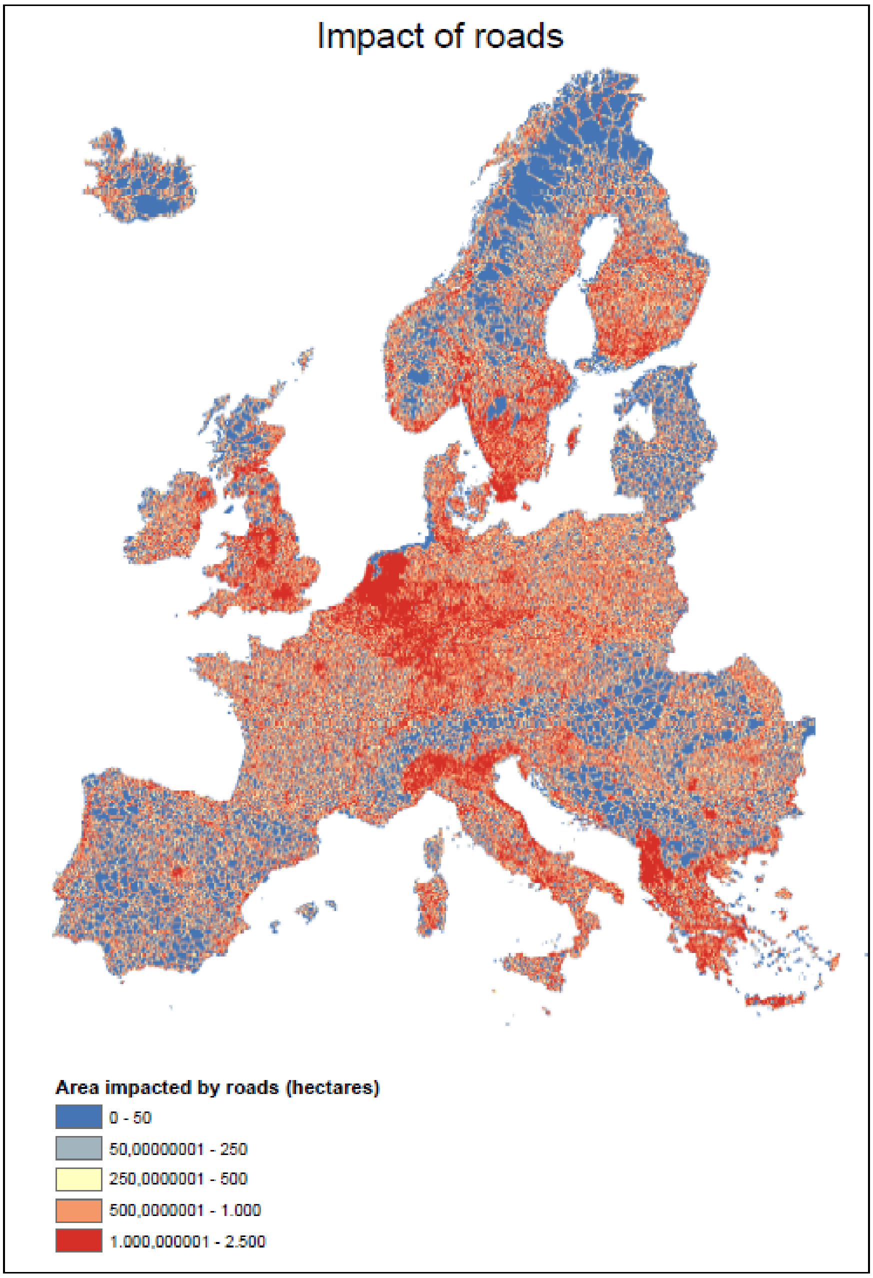
Coverage: see image

Website: http://geoservice.pbl.nl/website/GRIP

Reference: Work in progress

Prepocessing/data adjustments: All roads classified as highways, primary roads, secondary roads or tertiary roads are buffered with a 500 meter zone. Per grid cell the total area of this zone is calculated.

In alternative is to use the following version as a basis:
Meijer J.R., Schotten C.G.J. and Klein Goldewijk C.G.M. (2014) Global Roads Inventory Project (GRIP) version 3. PBL Netherlands Environmental Assessment Agency, http://geoservice.pbl.nl/website/GRIP


Impact of roads
Area impacted by roads (hectares)
0 - 50
50,00000001 - 250
250,0000001 - 500
500,0000001 - 1.000
1.000,000001 - 2.500

Urban

Content: Area impacted by urban area

Description: Area within a 5 by 5 km cell affected by artificial surface within that cell

Unit: hectares

Source: Corine Landcover map (see above for description)

Spatial resolution: 5 x 5km

Year: 2000

Coverage: see image

Website:

Reference:

Prepocessing/data adjustments: All cells in the Corine Landcover map classified as artificial surface (CLC Label 1, CLC codes 111 to 142) are buffered with a 500 meter zone. Per grid cell the total area of this zone is calculated.

Hemeroby-levels

The selected pressures in BioScore 2.0 (see Chapter 5) do not include the effects of management type and intensity. Management measures such as grazing or mowing influence the performance of plant species both directly (i.e. by biomass removal) and indirectly (i.e. through changes in environmental conditions and altered biotic interactions). Hence management has a strong influence on the local habitat suitability for plant species.

For many species, the persistence at the landscape scale depends on periodic disturbances, such as grazing, flooding, fire. These disturbances can be natural and/or human-induced. Human impacts are however so pervasive that in most European landscapes natural disturbance regimes have largely disappeared. Large-bodied animals (megaherbivores) are particularly affected, with massive prehistoric extinctions. As a consequence many plant species in man-made landscapes depend on some form of human induced management. Spatial data on management type and intensity are however not available (at least not with a sufficient resolution). The effects of management are therefore more difficult to implement in BioScore as compared to the selected pressures. As a pragmatic solution we use a proxy approach based on hemeroby-levels at the species level that can be applied as a *post-processing step*.

Hemeroby levels give a ranking of the degree of human impact (or inversely the degree of naturalness) and this approach can be used for the classification of both species and habitats. The hemeroby scale was developed by Jalas (1955), who proposed a four-point scale based largely on the degree of disturbance to the soil and vegetation. This scale was subsequently extended to a more detailed scale (with 7 to 9 classes). The system was intended for the ranking of species and habitats in a way comparable to Ellenberg's indicator values. The approach has been developed in central Europe and especially in the area around West Berlin (Kowarik 1990, 1999; Sukopp 1969, 1990) and the original classification cannot not be generalized to other regions (Hill *et al*., 2002). We therefore started with a new classification of habitat types according to hemeroby-levels and we subsequently used these data to assign hemeroby levels to the selected species.

Due to the different types of human-induced disturbances it is difficult to define hemeroby levels in a quantitative way. Rather the levels enable a *relative* ranking by expert judgement. The approach should therefore be regarded as a proxy approach. This chapter provides background information on the assignment of hemeroby-levels to habitat types and species.

Description of hemeroby levels. The hemeroby levels give an indication of the relative human influence on biotic and abiotic conditions in a given habitat type.

Hemeroby-level		Description
Code	*Name*	
1	ahemerobic (I)	Areas with almost no human influence such as rock outcrops, glaciers and remote parts in bogs
2		Intermediate between 1-3
3	oligohemerobic (II)	Weakly utilized areas such as tundras, steppic grasslands, grasslands and heaths in the alpine and boreal region, alluvial forests (PNV), and fens. Human impact is restricted: e.g. slight wood felling, grazing, emission from air (e.g. low levels of nitrogen- or sulphur dioxide deposition) and slightly altered hydrology (e.g. flooding of floodplains with eutrophic water)
4		Intermediate between 3-5
5	mesohemerobic (III)	Areas with a low-intensity of management measures, such as forests with a well-developed forb layer, heathlands, Juniperus shrubs, dry and nutrient poor grasslands, slightly utilized pastures and meadows. Many low-intensity management measures do have a more natural parallel, like pasturing (versus natural grazing), burning (versus fires after lightning), tree felling (versus windthrow)
6		Intermediate between 5-7

Hemeroby-level *Code*	*Name*	Description
7	euhemerobic (IV)	Areas with a strong human influence (i.e. a high intensity of management measures) such as hay meadows, intensely used pastures (e.g. machairs and dehesas)
8		Intermediate between 7-9
9	polyhemerobic (V)	Areas with a very strong human influence e.g. arable fields, ruderal weed communities, debris with pioneer communities. The proportion of non-native plant species is often high. Human impact includes deep ploughing, persistent and intense drainage (or intense irrigation), intense fertilization or application of biocides and planting or sowing of non-native species

Assignment of hemeroby levels to habitat types
The assignment of hemeroby levels to habitat types is based on expert judgement (by J.H.J. Schaminée, S.M. Hennekens & W.A. Ozinga, 2015). The results for the 40 selected Natura 2000 habitat types revealed that the lowest and highest hemeroby levels were underrepresented. This might bias the estimates of hemeroby levels at the species level and therefore a few additional habitat types were selected: five Annex I habitat types (with a low hemeroby level) and four EUNIS habitat types (with a high hemeroby level).

Overview of habitat types with their hemeroby level

Code	Name	Hemeroby
1330	Atlantic salt meadows (Glauco-Puccinellietalia maritimae)	2
2120	Shifting dunes along the shoreline with Ammophila arenaria ("white dunes")	2
2130	Fixed coastal dunes with herbaceous vegetation ("grey dunes")	5
2160	Dunes with Hippophaë rhamnoides	3
2210	Crucianellion maritimae fixed beach dunes	2
3110	Oligotrophic waters containing very few minerals of sandy plains (Littorelletalia uniflorae)	2
3130	Oligotrophic to mesotrophic standing waters with vegetation of the Littorelletea uniflorae and/or of the Isoëto-Nanojuncetea	2
3150	Natural eutrophic lakes with Magnopotamion or Hydrocharition - type vegetation	2
3260	Water courses of plain to montane levels with the Ranunculion fluitantis and Callitricho-Batrachion vegetation	2
4010	Northern Atlantic wet heaths with Erica tetralix	4
4030	European dry heaths	5
4060	Alpine and Boreal heaths	3
4070	Bushes with Pinus mugo and Rhododendron hirsutum (Mugo-Rhododendretum hirsuti)	3
5130	Juniperus communis formations on heaths or calcareous grasslands	5
5210	Arborescent matorral with Juniperus spp.	3
5420	Sarcopoterium spinosum phryganas	3
6110	Rupicolous calcareous or basophilic grasslands of the Alysso-Sedion albi	1
6120	Xeric sand calcareous grasslands	2
6150	Siliceous alpine and boreal grasslands	3
6170	Alpine and subalpine calcareous grasslands	4
6210	Semi-natural dry grasslands and scrubland facies on calcareous substrates (Festuco-Brometalia) (* important orchid sites)	6
6220	Pseudo-steppe with grasses and annuals of the Thero-Brachypodietea	3
6230	Species-rich Nardus grasslands, on silicious substrates in mountain areas (and submountain areas in Continental Europe)	3
6240	Sub-Pannonic steppic grasslands	3

Code	Name	Hemeroby
6410	Molinia meadows on calcareous, peaty or clayey-silt-laden soils (Molinion caeruleae)	7
6430	Hydrophilous tall herb fringe communities of plains and of the montane to alpine levels	5
6510	Lowland hay meadows (Alopecurus pratensis, Sanguisorba officinalis)	7
6520	Mountain hay meadows	7
7110	Active raised bogs	1
7130	Blanket bogs (if active bog)	1
7150	Depressions on peat substrates of the Rhynchosporion	3
7210	Calcareous fens with Cladium mariscus and species of the Caricion davallianae	3
7230	Alkaline fens	3
8210	Calcareous rocky slopes with chasmophytic vegetation	1
8220	Siliceous rocky slopes with chasmophytic vegetation	1
9150	Medio-European limestone beech forests of the Cephalanthero-Fagion	3
9160	Sub-Atlantic and medio-European oak or oak-hornbeam forests of the Carpinion betuli	4
9190	Old acidophilous oak woods with Quercus robur on sandy plains	4
9410	Acidophilous Picea forests of the montane to alpine levels (Vaccinio-Piceetea)	1
91E0	Alluvial forests with Alnus glutinosa and Fraxinus excelsior (Alno-Padion, Alnion incanae, Salicion albae)	3
	Additional Annex I habitat types	
1340	Inland salt meadows	2
5110	Stable xerothermophilous formations with Buxus	3
7140	Transition mires and quaking bogs	2
9110	Luzulo-Fagetum beech forests	2
91H0	Pannonian woods with Quercus pubescens	2
	Additional EUNIS habitat types	
H5.6a	Trampled areas	9
E5.1a	Anthropogenic herb stands (weeds)	9
I1.1a	Intensive unmixed crops	9
E5.1b	Anthropogenic herb stands (fringes)	8

Assignment of hemeroby levels to species

For the quantification of hemeroby levels of species we used the same selection of plots as used for the other pressures (see Chapter 6, step 3) supplemented with plots representing the nine additional habitat types. For each species the hemeroby levels were quantified based on the selection of plots in which the species occurs. The main differences with the approach used for the other pressures is that we only have one hemoroby value for a given habitat type, i.e. there is no spatial differentiation within a given habitat type. Moreover it is important to keep in mind that only a small fraction of habitat types in included. It was therefore not possible to use GLM's (Generalized Linear Models) to quantify dose-response functions. Instead we quantified mean, standard deviation and percentiles (25^{th}, 50^{th}, 75^{th} percentiles). The species-specific results presented in the next table should therefore be regarded as a first proxy, which can be improved by using a larger selection of habitat types.

References

Jalas, J. (1955) Hemerobe und hemerochore Pflanzenarten. Ein terminologischer Reformversuch. Acta Societatia Pro Fauna et Flora Fennica, 72, 1–15.

Hill, M. O., D.B. Roy, & K. Thompson (2002). Hemeroby, urbanity and ruderality: bioindicators of disturbance and human impact. Journal of Applied Ecology 39: 708-720.

Kowarik, I. (1990) Some responses of flora and vegetation to urbanization in Central Europe. Urban Ecology: Plants and Plant Communities in Urban Environments (eds H. Sukopp, S. Hejny & I. Kowarik), pp. 45–74. SPB Academic Publishing, Amsterdam, the Netherlands.

Kowarik, I. (1999) Natürlichkeit, Naturnähe und Hemerobie als Bewertungskriterien. Handbuch für Naturschutz und Landschaftspflege (eds W. Konold, R. Böcker &U. Hampicke), V-2·1, pp. 1–18. Ecomed, Landsberg, Germany.
Sukopp, H. (1969) Der Einfluss des Menschen auf die Vegetation. Vegetatio, 17, 360–371.
Sukopp, H. (1990) Stadtökologie: das Beispiel Berlin. Dietrich Reimer, Berlin, Germany.

Overview of species with their hemeroby level (mean, standard deviation, percentiles and number of observations)

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H91E0_Alnus_glutinosa	13819	3	3	5	4.263	2.061
H91E0_Alnus_incana	6791	3	3	5	4.278	2.000
H91E0_Angelica_sylvestris	15838	3	5	7	4.727	2.018
H91E0_Cardamine_amara	2714	3	3	5	4.126	1.981
H91E0_Carex_pendula	1481	3	3	3	3.695	1.800
H91E0_Carex_remota	4409	3	3	4	3.788	1.887
H91E0_Carex_strigosa	428	3	3	3	3.843	1.809
H91E0_Cirsium_oleraceum	9699	3	5	7	5.093	1.973
H91E0_Equisetum_telmateia	1239	3	3	5	4.022	1.810
H91E0_Festuca_gigantea	8383	3	3	8	4.629	2.304
H91E0_Fraxinus_excelsior	39104	3	3	5	4.088	2.066
H91E0_Geranium_robertianum	16718	3	3	8	4.443	2.508
H91E0_Geum_rivale	6634	3	5	7	4.703	1.958
H91E0_Geum_urbanum	18301	3	4	8	5.296	2.411
H91E0_Glechoma_hederacea	19126	3	7	8	6.098	2.261
H91E0_Humulus_lupulus	5733	3	3	8	5.021	2.325
H91E0_Impatiens_noli_tangere	8876	3	3	5	4.121	2.264
H91E0_Lysimachia_nemorum	6001	2	3	3	3.021	1.736
H91E0_Populus_nigra	1693	3	3	8	4.952	2.462
H91E0_Ranunculus_ficaria	6305	3	4	8	4.866	2.262
H91E0_Rumex_sanguineus	3113	3	3	8	4.748	2.296
H91E0_Salix_alba	2661	3	3	8	5.047	2.442
H91E0_Salix_purpurea	1908	3	3	8	4.876	2.364
H91E0_Salix_triandra	705	3	3	8	4.936	2.489
H91E0_Salix_viminalis	640	3	3	8	5.233	2.550
H91E0_Silene_dioica	8180	3	5	7	4.909	2.273
H91E0_Stellaria_nemorum	3713	3	3	5	4.176	2.125
H91E0_Ulmus_glabra	9609	3	3	4	3.960	2.087
H1330_Armeria_maritima	2353	2	2	2	2.154	0.688
H1330_Artemisia_maritima	1962	2	2	2	2.009	0.205
H1330_Blysmus_rufus	117	2	2	2	2.060	0.328
H1330_Carex_distans	969	2	3	7	3.710	2.170
H1330_Carex_extensa	746	2	2	2	2.028	0.195
H1330_Halimione_pedunculata	116	2	2	2	2.000	0.000
H1330_Halimione_portulacoides	3975	2	2	2	2.005	0.140
H1330_Juncus_gerardii	3493	2	2	2	2.137	0.696
H1330_Juncus_maritimus	866	2	2	2	2.127	0.485
H1330_Limonium_vulgare	4297	2	2	2	2.005	0.152
H1330_Lysimachia_maritima	4562	2	2	2	2.070	0.429
H1330_Plantago_maritima	5858	2	2	2	2.125	0.641
H1330_Puccinellia_distans	596	2	2	9	4.178	3.231
H1330_Puccinellia_fasciculata	54	2	2	2	2.130	0.944
H1330_Puccinellia_maritima	5284	2	2	2	2.006	0.193
H1330_Spergularia_media	4575	2	2	2	2.010	0.254

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H1330_Spergularia_salina	947	2	2	2	2.322	1.458
H1330_Suaeda_maritima	4264	2	2	2	2.002	0.108
H1330_Triglochin_maritima	5189	2	2	2	2.032	0.364
H1330_Tripolium_pannonicum	6313	2	2	2	2.063	0.643
H2120_Achillea_maritima = Otanthus maritimus	2396	2	2	2	2.057	0.423
H2120_Ammophila_arenaria	10709	2	2	3	2.760	1.268
H2120_Anthemis_maritima	1651	2	2	2	2.094	0.513
H2120_Calystegia_soldanella	4683	2	2	2	2.301	0.900
H2120_Cerastium_diffusum	782	2	5	5	3.614	1.526
H2120_Cutandia_maritima	1737	2	2	2	2.043	0.342
H2120_Cyperus_capitatus	2905	2	2	2	2.100	0.531
H2120_Echinophora_spinosa	5091	2	2	2	2.052	0.391
H2120_Elymus_pycnanthus	392	2	2	2	2.431	1.000
H2120_Eryngium_maritimum	8857	2	2	2	2.177	0.704
H2120_Euphorbia_paralias	4848	2	2	2	2.131	0.618
H2120_Honckenya_peploides	909	2	2	2	2.338	0.940
H2120_Leymus_arenarius	930	2	2	2	2.599	1.279
H2120_Medicago_marina	5614	2	2	2	2.107	0.550
H2120_Ononis_natrix	1442	2	6	6	4.413	1.916
H2120_Polygonum_glaucum	1231	2	2	2	2.098	0.572
H2130_Anacamptis_pyramidalis	2028	5	6	6	5.299	1.518
H2130_Artemisia_campestris_maritima	654	2	2	5	3.185	1.500
H2130_Calamagrostis_epigeios	9651	3	5	5	4.543	1.732
H2130_Calystegia_soldanella	4683	2	2	2	2.301	0.900
H2130_Carex_arenaria	9828	3	5	5	4.322	1.151
H2130_Cerastium_semidecandrum	8977	3	5	5	4.349	1.522
H2130_Cetraria_aculeata	2208	3	5	5	4.096	1.416
H2130_Cladonia_foliacea	4695	5	5	5	4.400	1.344
H2130_Cladonia_rangiformis	4761	3	5	5	4.363	1.472
H2130_Corynephorus_canescens	4048	3	5	5	4.197	1.357
H2130_Crucianella_maritima	3427	2	2	2	2.148	0.641
H2130_Erodium_cicutarium	2390	5	5	5	4.621	0.899
H2130_Erodium_lebelii	733	5	5	5	4.527	0.862
H2130_Eryngium_maritimum	8857	2	2	2	2.177	0.704
H2130_Galium_verum	29936	5	6	6	5.232	1.656
H2130_Gentiana_cruciata	1158	5	6	6	5.276	1.332
H2130_Gentianella_campestris	2036	3	4	6	4.403	1.400
H2130_Helichrysum_stoechas	4971	3	3	3	3.378	1.371
H2130_Koeleria_macrantha	16300	3	5	6	4.451	1.830
H2130_Myosotis_ramosissima	5010	3	5	5	4.554	1.637
H2130_Phleum_arenarium	4170	3	5	5	4.323	1.181
H2130_Sedum_acre	11836	2	5	5	3.986	1.893
H2130_Silene_conica	1156	2	5	5	3.694	1.596
H2130_Silene_otites	5146	2	5	6	3.998	1.994
H2130_Tortula_ruralis	2726	1	3	6	3.498	2.119
H2130_Trifolium_scabrum	2482	3	3	3	3.394	1.407
H2130_Tuberaria_guttata	306	3	3	3	3.180	0.786
H2130_Viola_curtisii	1749	5	5	5	4.533	0.899
H2160_Anthriscus_caucalis	414	3	3	5	4.321	1.904
H2160_Berberis_vulgaris	5120	3	3	5	3.737	1.742
H2160_Bryonia_cretica	12	3	3	3	2.833	0.553
H2160_Bryonia_dioica	1312	3	3	8	4.671	2.235

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H2160_Calamagrostis_epigeios	9651	3	5	5	4.543	1.732
H2160_Carex_arenaria	9828	3	5	5	4.322	1.151
H2160_Crataegus_monogyna	27308	3	3	6	4.255	1.979
H2160_Cynoglossum_officinale	3565	3	5	5	4.254	1.442
H2160_Euonymus_europaeus	12040	3	4	8	4.536	2.179
H2160_Hippophae_rhamnoides	5436	3	3	5	3.534	1.004
H2160_Ligustrum_vulgare	16170	3	3	5	3.796	1.702
H2160_Moehringia_trinervia	7329	3	4	8	4.426	2.395
H2160_Polygonatum_odoratum	8993	2	3	6	3.914	1.905
H2160_Rhamnus_catharticus	5993	3	3	6	3.914	1.941
H2160_Rosa_canina	8045	3	5	6	4.561	1.985
H2160_Rosa_rubiginosa	1953	3	5	6	4.511	1.658
H2160_Rubus_caesius	15211	3	5	8	5.031	2.116
H2160_Salix_repens	5110	3	3	5	3.690	1.371
H2160_Sambucus_nigra	12958	3	4	8	5.123	2.464
H2210_Ambrosia_crithmifolia	196	2	2	2	2.128	0.597
H2210_Calystegia_soldanella	4683	2	2	2	2.301	0.900
H2210_Crucianella_maritima	3427	2	2	2	2.148	0.641
H2210_Echium_sabulicola	56	2	2	2	2.250	0.634
H2210_Eryngium_maritimum	8857	2	2	2	2.177	0.704
H2210_Euphorbia_terracina	885	2	2	2	2.144	0.553
H2210_Helichrysum_stoechas	4705	3	3	3	3.396	1.399
H2210_Lotus_creticus	1499	2	2	2	2.061	0.381
H2210_Malcolmia_littorea	562	2	2	2	2.326	0.927
H2210_Maresia_nana	106	2	2	2	2.283	0.655
H2210_Matthiola_sinuata	1628	2	2	2	2.137	0.622
H2210_Pancratium_maritimum	4833	2	2	2	2.116	0.565
H2210_Scabiosa_atropurpurea	903	2	2	3	2.842	1.421
H2210_Scrophularia_frutescens	191	2	2	2	2.393	1.012
H2210_Scrophularia_ramosissima	217	2	2	2	2.041	0.260
H2210_Silene_nicaeensis	1349	2	2	2	2.119	0.580
H2210_Sonchus_bulbosus	1801	2	2	3	2.535	0.833
H2210_Teucrium_polium	3433	3	3	6	3.745	1.557
H3110_Deschampsia_setacea	259	2	2	2	2.112	0.420
H3110_Eleocharis_acicularis	381	2	2	2	2.436	1.631
H3110_Eleocharis_multicaulis	1736	2	2	4	2.667	0.982
H3110_Eriocaulon_aquaticum	208	2	2	2	2.168	0.374
H3110_Isoetes_echinospora	10	2	2	2	2.000	0.000
H3110_Isoetes_lacustris	34	2	2	2	2.000	0.000
H3110_Littorella_uniflora	697	2	2	2	2.072	0.565
H3110_Lobelia_dortmanna	349	2	2	2	2.092	0.458
H3110_Myriophyllum_alterniflorum	178	2	2	2	2.000	0.000
H3110_Potamogeton_polygonifolius	1088	2	2	3	2.560	0.899
H3110_Subularia_aquatica	3					
H3130_Anagallis_minima	327	2	3	9	5.309	3.321
H3130_Baldellia_ranunculoides	518	2	2	2	2.097	0.529
H3130_Cicendia_filiformis	185	2	2	2	2.141	0.793
H3130_Cyperus_fuscus	160	2	2	3	3.619	2.900
H3130_Cyperus_michelianus	32	2	2	2	2.656	2.040
H3130_Deschampsia_setacea	259	2	2	2	2.112	0.420
H3130_Elatine_hexandra	106	2	2	2	2.009	0.097
H3130_Elatine_hydropiper	76	2	2	2	2.289	1.244
H3130_Eleocharis_acicularis	381	2	2	2	2.436	1.631

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H3130_Eleocharis_multicaulis	1736	2	2	4	2.667	0.982
H3130_Eleocharis_ovata	188	2	2	2	2.229	1.232
H3130_Hypericum_elodes	817	2	2	2	2.278	0.784
H3130_Isolepis_antarctica	455	2	3	7	4.270	2.614
H3130_Isolepis_fluitans	522	2	2	2	2.046	0.273
H3130_Juncus_bulbosus	3189	2	3	4	3.028	1.469
H3130_Juncus_capitatus	165	2	3	3	3.376	2.164
H3130_Juncus_pygmaeus	144	2	2	2	2.111	0.356
H3130_Juncus_tenageia	154	2	2	2	2.273	1.265
H3130_Limosella_aquatica	215	2	2	2	3.633	2.955
H3130_Lindernia_procumbens	70	2	2	2	2.400	1.625
H3130_Littorella_uniflora	697	2	2	2	2.072	0.565
H3130_Luronium_natans	76	2	2	2	2.000	0.000
H3130_Pilularia_globulifera	135	2	2	2	2.000	0.000
H3130_Potamogeton_gramineus	169	2	2	2	2.012	0.108
H3130_Potamogeton_polygonifolius	1088	2	2	3	2.560	0.899
H3130_Pycreus_flavescens	29	2	2	2	2.586	1.791
H3130_Radiola_linoides	261	2	2	3	3.015	2.086
H3130_Schoenoplectiella_supina	32	2	2	2	2.000	0.000
H3130_Sparganium_natans	63	2	2	2	1.968	0.250
H3150_Aldrovanda_vesiculosa	39	2	2	2	2.000	0.000
H3150_Ceratophyllum_demersum	4658	2	2	2	2.002	0.091
H3150_Hydrocharis_morsus_ranae	3169	2	2	2	2.015	0.204
H3150_Lemna_trisulca	4430	2	2	2	2.022	0.296
H3150_Myriophyllum_spicatum	2378	2	2	2	2.007	0.084
H3150_Myriophyllum_verticillatum	930	2	2	2	2.018	0.255
H3150_Nuphar_lutea	3094	2	2	2	2.018	0.196
H3150_Nuphar_microphylla	8	2	2	2	2.000	0.000
H3150_Nymphaea_alba	1611	2	2	2	2.081	0.317
H3150_Nymphaea_candida	154	2	2	2	2.026	0.159
H3150_Nymphoides_peltata	1239	2	2	2	2.000	0.000
H3150_Potamogeton_illinoensis	1540	2	2	2	2.000	0.000
H3150_Potamogeton_natans	2001	2	2	2	2.017	0.152
H3150_Potamogeton_perfoliatus	907	2	2	2	2.001	0.033
H3150_Potamogeton_praelongus	29	2	2	2	2.000	0.000
H3150_Spirodela_polyrrhiza	4494	2	2	2	2.015	0.262
H3150_Stratiotes_aloides	1538	2	2	2	2.000	0.000
H3150_Stuckenia_pectinata	1926	2	2	2	2.003	0.076
H3150_Trapa_natans	446	2	2	2	2.004	0.067
H3150_Utricularia_vulgaris	1209	2	2	2	2.079	0.313
H3150_Wolffia_arrhiza	714	2	2	2	2.000	0.000
H3260_Potamogeton_alpinus	407	2	2	2	2.012	0.204
H3260_Potamogeton_nodosus	822	2	2	2	2.000	0.000
H3260_Ranunculus_fluitans	670	2	2	2	2.000	0.000
H3260_Ranunculus_penicillatus	272	2	2	2	2.000	0.000
H4010_Carex_panicea	17977	3	3	5	3.934	1.745
H4010_Dactylorhiza_maculata	7650	3	4	6	4.074	1.847
H4010_Drosera_intermedia	3523	3	3	4	3.245	0.881
H4010_Drosera_rotundifolia	8584	1	3	4	2.625	1.331
H4010_Erica_tetralix	12358	3	4	4	3.521	1.299
H4010_Eriophorum_angustifolium	12875	2	3	4	2.944	1.369
H4010_Gentiana_pneumonanthe	2009	3	4	5	4.218	1.438
H4010_Juncus_squarrosus	3375	3	4	4	3.609	1.107

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H4010_Narthecium_ossifragum	5803	1	4	4	3.054	1.357
H4010_Rhynchospora_alba	5758	2	3	4	2.934	1.205
H4010_Rhynchospora_fusca	1788	3	3	4	3.345	0.705
H4010_Sphagnum_compactum	1653	3	4	4	3.234	1.227
H4010_Sphagnum_tenellum	2615	1	4	4	2.699	1.472
H4010_Trichophorum_cespitosum	6937	3	3	4	3.056	1.254
H4030_Calluna_vulgaris	28497	3	3	5	3.522	1.422
H4030_Cistus_ladanifer	23	3	3	3	3.261	1.224
H4030_Cistus_salviifolius	2057	3	3	3	3.159	0.886
H4030_Daboecia_cantabrica	617	5	5	5	4.883	0.512
H4030_Erica_australis	46	5	5	5	4.565	1.014
H4030_Erica_cinerea	3121	4	5	5	4.368	1.199
H4030_Erica_mackaiana	77	1	4	4	3.000	1.604
H4030_Erica_tetralix	12358	3	4	4	3.521	1.299
H4030_Erica_umbellata	40	5	5	5	5.000	0.000
H4030_Galium_saxatile	8723	3	3	5	3.902	1.217
H4030_Genista_anglica	1858	3	5	5	4.391	0.967
H4030_Genista_germanica	949	3	5	6	4.274	1.630
H4030_Genista_pilosa	7697	3	5	6	4.236	1.606
H4030_Ulex_gallii	822	5	5	5	4.680	0.849
H4030_Ulex_minor	791	5	5	5	4.762	0.712
H4030_Vaccinium_myrtillus	45575	2	3	4	3.105	1.321
H4030_Vaccinium_vitis_idaea	20801	3	3	4	3.193	1.142
H4060_Arctostaphylos_uva_ursi	2019	3	3	4	3.586	1.311
H4060_Arctous_alpina	1085	3	3	4	3.272	0.657
H4060_Betula_nana	662	3	3	3	2.931	0.870
H4060_Bruckenthalia_spiculifolia	513	3	3	3	2.916	0.663
H4060_Calluna_vulgaris	28497	3	3	5	3.522	1.422
H4060_Carex_bigelowii	1251	3	3	3	3.090	0.470
H4060_Cassiope_tetragona	85	3	3	3	3.129	0.336
H4060_Cetraria_islandica	8113	3	3	3	3.087	0.640
H4060_Cornus_suecica	431	3	3	3	3.432	0.823
H4060_Dryas_octopetala	4977	3	4	4	3.540	1.067
H4060_Erica_herbacea	8500	3	3	4	3.294	1.398
H4060_Flavocetraria_nivalis	1148	3	3	3	3.122	0.543
H4060_Geum_montanum	9752	3	3	3	3.364	0.897
H4060_Homogyne_alpina	23219	3	3	3	3.062	1.114
H4060_Huperzia_selago	7863	2	3	3	2.718	1.090
H4060_Kalmia_procumbens	2713	3	3	3	3.085	0.423
H4060_Ligusticum_mutellina	9277	3	3	3	3.380	0.968
H4060_Phyllodoce_caerulea	333	3	3	3	3.150	0.498
H4060_Pleurozium_schreberi	15788	3	3	4	3.348	1.394
H4060_Potentilla_aurea	13041	3	3	4	3.519	1.132
H4060_Racomitrium_lanuginosum	3496	3	3	4	2.951	1.265
H4060_Rhododendron_ferrugineum	6207	3	3	3	3.139	0.790
H4060_Rhododendron_hirsutum	5204	3	3	4	3.060	1.080
H4060_Rhodothamnus_chamaecistus	1815	2	3	4	2.792	1.148
H4060_Vaccinium_myrtillus	45575	2	3	4	3.105	1.321
H4060_Vaccinium_uliginosum	7504	3	3	3	3.050	0.978
H4070_Calamagrostis_varia	12426	2	3	4	2.969	1.643
H4070_Calamagrostis_villosa	8657	2	3	3	2.997	1.336
H4070_Clematis_alpina	3493	1	3	3	2.554	1.408
H4070_Daphne_mezereum	15689	2	3	4	3.056	1.496

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H4070_Erica_herbacea	8500	3	3	4	3.294	1.398
H4070_Homogyne_alpina	23219	3	3	3	3.062	1.114
H4070_Luzula_sylvatica	13681	2	3	3	2.812	1.544
H4070_Pinus_mugo	8258	3	3	3	3.071	0.959
H4070_Rhododendron_ferrugineum	6207	3	3	3	3.139	0.790
H4070_Rhododendron_hirsutum	5204	3	3	4	3.060	1.080
H4070_Rhodothamnus_chamaecistus	1815	2	3	4	2.792	1.148
H4070_Vaccinium_myrtillus	45575	2	3	4	3.105	1.321
H4070_Vaccinium_vitis_idaea	20801	3	3	4	3.193	1.142
H4070_Valeriana_tripteris	9294	1	3	3	2.748	1.535
H4070_Viola_biflora	10503	2	3	4	3.341	1.609
H5130_Berberis_vulgaris	5120	3	3	5	3.737	1.742
H5130_Calluna_vulgaris	28497	3	3	5	3.522	1.422
H5130_Carex_flacca	32114	3	6	6	4.714	1.707
H5130_Crataegus_monogyna	27308	3	3	6	4.255	1.979
H5130_Dasiphora_fruticosa	9	3	3	3	3.000	0.000
H5130_Deschampsia_flexuosa	29750	3	3	4	3.360	1.257
H5130_Empetrum_nigrum	2443	3	3	5	3.185	1.421
H5130_Juniperus_communis	12964	3	4	6	4.171	1.625
H5130_Prunus_spinosa	13177	3	4	6	4.537	2.002
H5130_Rosa_canina	8045	3	5	6	4.561	1.985
H5130_Rosa_rubiginosa	1953	3	5	6	4.511	1.658
H5130_Sesleria_caerulea	6658	3	4	6	4.492	1.628
H5130_Sorbus_aucuparia	36588	2	3	4	3.170	1.653
H5130_Sorbus_intermedia	33	3	5	5	4.152	1.351
H5130_Vaccinium_myrtillus	45575	2	3	4	3.105	1.321
H5210_Berteroa_obliqua	15	3	3	6	4.933	2.323
H5210_Brachypodium_retusum	7827	3	3	3	2.987	0.634
H5210_Clematis_flammula	4584	3	3	3	3.046	0.954
H5210_Galium_album	10372	5	6	7	5.467	1.807
H5210_Genista_scorpius	1963	3	3	3	3.401	1.065
H5210_Jasminum_fruticans	854	3	3	3	2.974	0.914
H5210_Juniperus_communis	12964	3	4	6	4.171	1.625
H5210_Juniperus_drupacea	7	3	3	3	3.000	0.000
H5210_Juniperus_excelsa	48	3	3	3	2.958	0.200
H5210_Juniperus_foetidissima	44	3	3	3	2.773	0.794
H5210_Juniperus_oxycedrus	5896	3	3	3	3.150	1.064
H5210_Juniperus_phoenicea	2040	3	3	3	2.942	0.666
H5210_Juniperus_thurifera	108	3	3	6	3.806	1.848
H5210_Olea_europaea	1500	3	3	3	2.949	0.580
H5210_Phillyrea_angustifolia	3924	3	3	3	3.107	0.770
H5210_Pistacia_lentiscus	6001	3	3	3	3.021	0.717
H5210_Prasium_majus	793	3	3	3	2.941	0.285
H5210_Quercus_coccifera	3287	3	3	3	2.988	0.432
H5210_Rosmarinus_officinalis	4934	3	3	3	3.047	0.707
H5210_Stipa_bromoides	738	3	3	3	2.986	0.494
H5210_Teucrium_chamaedrys	32191	3	6	6	4.436	1.888
H5210_Teucrium_polium	3433	3	3	6	3.745	1.557
H5210_Thymus_sibthorpii	367	3	3	6	3.866	1.624
H5210_Thymus_vulgaris	8934	3	3	3	3.422	1.283
H5420_Anthyllis_hermanniae	210	3	3	3	2.781	0.552
H5420_Asparagus_acutifolius	6267	3	3	3	2.905	0.790
H5420_Ballota_pseudodictamnus	39	3	3	3	2.949	0.316

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H5420_Calicotome_villosa	773	3	3	3	2.997	0.309
H5420_Centaurea_spinosa	118	2	2	2	2.195	0.396
H5420_Cistus_parviflorus	30	3	3	3	3.000	0.000
H5420_Cistus_salviifolius	2057	3	3	3	3.159	0.886
H5420_Erica_manipuliflora	299	3	3	3	2.953	0.291
H5420_Euphorbia_acanthothamnos	165	3	3	3	2.988	0.155
H5420_Fumana_thymifolia	1448	3	3	3	3.209	0.826
H5420_Genista_acanthoclada	209	3	3	3	2.976	0.206
H5420_Lithodora_hispidula	34	3	3	3	3.000	0.000
H5420_Micromeria_graeca	278	3	3	3	3.050	0.868
H5420_Micromeria_juliana	216	3	3	3	2.968	0.223
H5420_Micromeria_nervosa	80	3	3	3	3.000	0.000
H5420_Phagnalon_rupestre	265	3	3	3	2.936	0.300
H5420_Pistacia_lentiscus	6001	3	3	3	3.021	0.717
H5420_Sarcopoterium_spinosum	660	3	3	3	2.977	0.149
H5420_Satureja_thymbra	118	3	3	3	2.966	0.258
H5420_Smilax_aspera	5323	3	3	3	2.955	0.850
H5420_Teucrium_brevifolium	30	3	3	3	3.000	0.000
H5420_Teucrium_divaricatum	121	3	3	3	2.967	0.220
H5420_Thymus_capitatus	71	2	3	3	2.676	0.623
H6110_Allium_lusitanicum	2929	1	3	6	3.229	2.250
H6110_Alyssum_alyssoides	4667	1	3	6	3.601	2.228
H6110_Arabidopsis_arenosa	2221	1	3	4	3.029	2.163
H6110_Arabis_auriculata	852	1	3	6	3.185	2.167
H6110_Arabis_hirsuta	7945	3	6	6	4.467	2.072
H6110_Arenaria_serpyllifolia	11670	2	6	6	4.683	2.867
H6110_Asperula_cynanchica	23310	3	6	6	4.650	1.942
H6110_Cerastium_pumilum	2609	1	3	6	3.366	2.069
H6110_Clinopodium_acinos	9963	1	4	6	3.722	2.311
H6110_Echium_vulgare	9876	1	6	6	4.283	2.485
H6110_Hornungia_petraea	1260	1	3	5	3.101	1.960
H6110_Koeleria_macrantha	16300	3	5	6	4.451	1.830
H6110_Poa_badensis	1738	1	3	6	3.415	2.183
H6110_Poa_compressa	4195	1	6	6	4.397	2.824
H6110_Potentilla_cinerea	13138	2	6	6	4.052	2.140
H6110_Potentilla_tabernaemontani	14187	3	6	6	4.943	1.890
H6110_Saxifraga_tridactylites	3336	1	5	5	3.613	2.025
H6110_Sedum_album	7542	1	3	6	3.219	2.269
H6110_Sedum_sexangulare	6509	1	5	6	3.930	2.350
H6110_Teucrium_botrys	1091	1	3	6	3.321	2.505
H6110_Thymus_pulegioides	11253	3	6	6	4.849	1.852
H6110_Tortella_tortuosa	11825	1	3	4	2.954	1.633
H6120_Allium_schoenoprasum	462	3	3	4	3.823	1.828
H6120_Alyssum_montanum	110	2	2	2	2.855	1.566
H6120_Arabidopsis_arenosa	2221	1	3	4	3.029	2.163
H6120_Artemisia_campestris	8052	2	4	6	3.854	2.151
H6120_Astragalus_arenarius	94	2	2	2	2.596	1.402
H6120_Carex_colchica	183	2	2	5	3.486	1.522
H6120_Carex_praecox	1075	2	5	6	4.398	2.196
H6120_Dianthus_arenarius	34	2	2	2	2.265	0.779
H6120_Dianthus_deltoides	1044	3	6	7	4.917	2.138
H6120_Euphorbia_seguieriana	1948	2	5	6	4.230	1.924
H6120_Festuca_psammophila	458	2	2	5	2.913	1.563

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H6120_Galium_verum	29936	5	6	6	5.232	1.656
H6120_Gypsophila_fastigiata	223	2	2	5	3.188	1.870
H6120_Helichrysum_arenarium	1616	2	2	5	3.347	1.783
H6120_Herniaria_glabra	780	2	5	9	4.977	3.053
H6120_Koeleria_glauca	1279	2	2	5	3.323	1.606
H6120_Koeleria_macrantha	16300	3	5	6	4.451	1.830
H6120_Petrorhagia_prolifera	3260	2	3	6	3.476	2.017
H6120_Sedum_acre	11836	2	5	5	3.986	1.893
H6120_Sedum_rupestre	2011	1	2	6	3.338	2.126
H6120_Silene_chlorantha	193	2	2	5	3.124	1.747
H6120_Silene_conica	1156	2	5	5	3.694	1.596
H6120_Thymus_praecox	8514	3	5	6	4.403	1.813
H6150_Agrostis_rupestris	6169	3	3	3	3.055	0.548
H6150_Campanula_alpina	3699	3	3	3	3.069	0.394
H6150_Carex_bigelowii	1251	3	3	3	3.090	0.470
H6150_Carex_sempervirens	18026	3	4	4	3.904	1.372
H6150_Cassiope_tetragona	85	3	3	3	3.129	0.336
H6150_Festuca_airoides	3396	3	3	3	3.056	0.531
H6150_Helictotrichon_versicolor	7041	3	3	3	3.149	0.632
H6150_Hieracium_alpinum	4568	3	3	3	3.040	0.363
H6150_Homogyne_alpina	23219	3	3	3	3.062	1.114
H6150_Juncus_trifidus	6508	3	3	3	3.031	0.596
H6150_Ligusticum_mutellina	9277	3	3	3	3.380	0.968
H6150_Luzula_alpinopilosa	3872	3	3	3	3.128	0.566
H6150_Oreochloa_disticha	3525	3	3	3	3.042	0.346
H6150_Potentilla_aurea	13041	3	3	4	3.519	1.132
H6150_Primula_minima	3607	3	3	3	3.119	0.468
H6150_Pulsatilla_alpina	3080	3	3	4	3.731	1.372
H6150_Soldanella_carpatica	3819	3	3	3	3.310	1.098
H6170_Achillea_clavennae	1070	3	4	4	3.363	1.161
H6170_Alchemilla_conjuncta	1					
H6170_Alchemilla_flabellata	594	3	3	4	3.591	1.220
H6170_Alchemilla_hoppeana	1130	3	4	4	3.726	1.473
H6170_Antennaria_carpatica	1028	3	4	4	3.439	0.788
H6170_Aster_alpinus	2676	3	4	4	3.942	1.530
H6170_Astragalus_alpinus	396	3	4	4	4.174	1.306
H6170_Campanula_scheuchzeri	13455	3	3	4	3.610	1.273
H6170_Carex_atrata	1427	3	3	4	3.473	0.713
H6170_Carex_brevicollis	42	4	4	8	5.405	2.279
H6170_Carex_capillaris	1674	3	3	4	3.455	0.742
H6170_Carex_ferruginea	7076	3	3	4	3.624	1.570
H6170_Carex_firma	3367	3	4	4	3.267	1.094
H6170_Carex_foetida	109	3	4	4	3.615	0.634
H6170_Carex_rupestris	533	3	4	4	3.405	1.140
H6170_Carex_sempervirens	18026	3	4	4	3.904	1.372
H6170_Daphne_striata	1259	3	3	4	3.469	0.951
H6170_Dianthus_glacialis	222	3	3	4	3.441	0.639
H6170_Draba_aizoides	1567	1	4	4	3.239	1.455
H6170_Dryas_octopetala	4977	3	4	4	3.540	1.067
H6170_Galium_anisophyllon	8966	3	4	4	3.600	1.298
H6170_Gentiana_nivalis	780	3	4	4	3.673	0.751
H6170_Geum_montanum	9752	3	3	3	3.364	0.897
H6170_Globularia_nudicaulis	3931	3	4	6	4.311	1.511

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H6170_Helianthemum_nummularium	3586	3	4	4	4.002	1.500
H6170_Helianthemum_oelandicum	3106	3	4	4	3.598	1.062
H6170_Hieracium_villosum	3229	3	4	4	3.997	1.523
H6170_Minuartia_sedoides	2347	3	4	4	3.366	0.869
H6170_Oxytropis_jacquinii	428	4	4	4	3.951	1.160
H6170_Paronychia_polygonifolia	112	2	3	4	3.098	1.433
H6170_Phyteuma_orbiculare	16765	3	4	6	4.451	1.674
H6170_Poa_variegata	1593	3	4	4	3.945	1.373
H6170_Polygala_alpestris	2135	3	4	4	3.927	1.257
H6170_Potentilla_nivea	1					
H6170_Primula_auricula	3049	1	3	4	2.859	1.551
H6170_Sagina_pilifera	49	4	4	4	3.510	1.109
H6170_Saussurea_nuda	538	3	3	4	3.478	0.877
H6170_Scabiosa_lucida	9151	3	4	6	4.226	1.532
H6170_Sibbaldia_procumbens	748	3	3	4	3.348	0.559
H6170_Stachys_alopecuros	2365	3	4	4	3.413	1.494
H6170_Thymus_pulcherrimus	1496	1	4	4	3.048	1.533
H6170_Trifolium_thalii	590	3	4	4	3.751	0.782
H6170_Veronica_alpina	1095	3	3	4	3.289	0.665
H6210_Adonis_vernalis	2474	3	6	6	4.646	1.857
H6210_Anthyllis_vulneraria	23246	4	6	6	5.087	1.675
H6210_Arabis_hirsuta	7945	3	6	6	4.467	2.072
H6210_Asperula_cynanchica	23310	3	6	6	4.650	1.942
H6210_Brachypodium_pinnatum	25994	5	6	6	5.287	1.552
H6210_Bromus_erectus	20750	6	6	6	5.260	1.645
H6210_Campanula_glomerata	8039	6	6	6	5.646	1.437
H6210_Carex_caryophyllea	18917	5	6	6	5.342	1.541
H6210_Carex_flacca	32114	3	6	6	4.714	1.707
H6210_Carlina_vulgaris	10495	5	6	6	5.265	1.474
H6210_Centaurea_scabiosa	17990	6	6	6	5.476	1.596
H6210_Cirsium_acaulon	14847	6	6	6	5.557	1.236
H6210_Dianthus_carthusianorum	9949	3	6	6	4.709	2.001
H6210_Dianthus_sylvestris	1720	4	6	6	4.903	1.787
H6210_Eryngium_campestre	17806	3	6	6	4.639	1.840
H6210_Euphorbia_cyparissias	33656	3	6	6	4.714	1.981
H6210_Festuca_valesiaca	8482	3	6	6	4.436	2.003
H6210_Fumana_procumbens	4251	3	6	6	4.619	1.919
H6210_Globularia_punctata	5550	3	6	6	4.876	1.819
H6210_Helictotrichon_pratense	8745	5	6	6	5.266	1.501
H6210_Hippocrepis_comosa	22455	4	6	6	5.157	1.567
H6210_Koeleria_pyramidata	13565	6	6	6	5.537	1.371
H6210_Medicago_falcata	11804	3	6	6	5.024	1.877
H6210_Neotinea_ustulata	3183	6	6	6	5.500	1.315
H6210_Ophrys_apifera	707	6	6	6	5.661	1.136
H6210_Ophrys_insectifera	1200	6	6	6	5.541	1.194
H6210_Orchis_militaris	1503	6	6	6	5.600	1.290
H6210_Phleum_phleoides	8168	3	6	6	4.530	2.038
H6210_Plantago_media	27421	6	6	6	5.698	1.401
H6210_Polygala_comosa	4051	6	6	6	5.779	1.237
H6210_Potentilla_cinerea	13138	2	6	6	4.052	2.140
H6210_Potentilla_pusilla	2622	6	6	6	5.450	1.494
H6210_Potentilla_tabernaemontani	14187	3	6	6	4.943	1.890
H6210_Primula_veris	15182	5	6	6	5.500	1.570

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H6210_Sanguisorba_minor	26798	5	6	6	5.125	1.799
H6210_Scabiosa_columbaria	16081	6	6	6	5.547	1.405
H6210_Scabiosa_ochroleuca	7693	3	6	6	4.539	2.058
H6210_Stipa_capillata	6363	3	5	6	4.205	1.975
H6210_Stipa_joannis	108	2	6	6	4.426	2.024
H6210_Teucrium_chamaedrys	32191	3	6	6	4.436	1.888
H6210_Teucrium_montanum	12661	3	6	6	4.690	1.880
H6220_Aira_cupaniana	502	3	3	3	3.004	0.641
H6220_Anthyllis_lotoides	20	1	4	4	3.250	1.299
H6220_Arenaria_modesta	15	1	1	3	1.667	0.943
H6220_Arenaria_retusa	0					
H6220_Asterolinon_linum_stellatum	1225	3	3	3	3.066	0.733
H6220_Brachypodium_distachyon	1569	3	3	3	3.159	0.966
H6220_Brachypodium_retusum	7827	3	3	3	2.987	0.634
H6220_Bromus_rubens	413	3	3	3	3.215	1.239
H6220_Campanula_fastigiata	11	3	3	3	3.000	0.000
H6220_Catapodium_rigidum	2361	3	3	3	3.276	1.391
H6220_Chaenorhinum_rubrifolium	122	3	3	3	2.885	0.925
H6220_Convolvulus_althaeoides	729	3	3	3	2.959	0.589
H6220_Euphorbia_exigua	2834	3	9	9	6.310	2.972
H6220_Filago_pyramidata	845	3	3	3	3.715	1.899
H6220_Helictotrichon_bromoides	4972	3	3	3	3.659	1.384
H6220_Hippocrepis_ciliata	347	3	3	3	2.988	0.626
H6220_Jasione_penicillata	0					
H6220_Linum_strictum	1754	3	3	3	3.278	0.999
H6220_Logfia_gallica	761	3	3	3	3.096	1.083
H6220_Medicago_minima	5750	2	3	6	3.616	1.884
H6220_Micropyrum_tenellum	299	1	3	3	2.605	1.617
H6220_Narduroides_salzmannii	5	1	3	3	2.600	0.800
H6220_Ornithopus_compressus	580	3	3	3	3.105	0.827
H6220_Phlomis_lychnitis	385	3	3	3	3.062	0.511
H6220_Plantago_lagopus	520	3	3	3	3.131	0.933
H6220_Reseda_stricta	9	3	3	3	3.000	0.000
H6220_Sedum_sediforme	4004	3	3	3	3.200	1.301
H6220_Teesdalia_coronopifolia	149	3	3	3	2.879	0.517
H6220_Thymus_vulgaris	8934	3	3	3	3.422	1.283
H6220_Trifolium_scabrum	2482	3	3	3	3.394	1.407
H6220_Tuberaria_guttata	306	3	3	3	3.180	0.786
H6220_Valantia_hispida	242	3	3	3	2.963	0.246
H6220_Vulpia_myuros	959	3	3	6	3.992	2.174
H6230_Antennaria_dioica	6974	3	3	5	3.912	1.374
H6230_Arnica_montana	8242	3	3	4	3.752	1.243
H6230_Campanula_barbata	5432	3	3	4	3.678	1.264
H6230_Campanula_scheuchzeri	13455	3	3	4	3.610	1.273
H6230_Carex_ericetorum	639	3	4	4	3.754	1.489
H6230_Carex_pallescens	6706	3	4	7	4.870	1.961
H6230_Carex_panicea	17977	3	3	5	3.934	1.745
H6230_Deschampsia_flexuosa	29750	3	3	4	3.360	1.257
H6230_Festuca_ovina	21570	3	6	6	4.745	1.706
H6230_Galium_saxatile	8723	3	3	5	3.902	1.217
H6230_Gentiana_pneumonanthe	2009	3	4	5	4.218	1.438
H6230_Geum_montanum	9752	3	3	3	3.364	0.897
H6230_Homogyne_alpina	23219	3	3	3	3.062	1.114

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H6230_Hypericum_maculatum	12830	3	4	7	4.552	1.899
H6230_Hypochaeris_maculata	2480	4	6	6	5.223	1.580
H6230_Lathyrus_linifolius	3594	3	4	5	4.115	1.713
H6230_Ligusticum_mutellina	9277	3	3	3	3.380	0.968
H6230_Meum_athamanticum	3478	3	3	5	4.236	1.564
H6230_Nardus_stricta	25832	3	3	4	3.606	1.269
H6230_Pedicularis_sylvatica	2565	3	3	4	3.696	1.523
H6230_Plantago_alpina	2660	3	3	4	3.644	1.119
H6230_Platanthera_bifolia	4982	3	3	5	3.805	1.693
H6230_Poa_alpina	9858	3	3	4	3.669	1.240
H6230_Polygala_vulgaris	12678	3	6	6	5.025	1.587
H6230_Potentilla_aurea	13041	3	3	4	3.519	1.132
H6230_Potentilla_erecta	42894	3	3	5	4.051	1.676
H6230_Pseudorchis_albida	1908	3	3	4	3.482	1.124
H6230_Selinum_pyrenaeum	1361	3	3	5	3.550	1.239
H6230_Soldanella_alpina	6254	3	3	4	3.542	1.264
H6230_Trifolium_alpinum	2620	3	3	3	3.356	0.846
H6230_Vaccinium_myrtillus	45575	2	3	4	3.105	1.321
H6230_Veronica_officinalis	12905	3	3	5	3.746	1.714
H6230_Viola_canina	5476	3	5	6	4.562	1.684
H6240_Allium_flavum	2958	1	3	6	3.619	2.096
H6240_Alyssum_alyssoides	4667	1	3	6	3.601	2.228
H6240_Artemisia_austriaca	362	3	3	6	4.323	2.203
H6240_Astragalus_austriacus	1258	3	6	6	4.383	1.776
H6240_Astragalus_exscapus	590	3	6	6	4.429	1.769
H6240_Bothriochloa_ischaemum	6011	3	6	6	4.254	1.935
H6240_Carex_humilis	16209	3	6	6	4.264	1.972
H6240_Chrysopogon_gryllus	2367	3	6	6	4.572	1.707
H6240_Daphne_cneorum	471	3	4	6	4.119	1.568
H6240_Eryngium_campestre	17806	3	6	6	4.639	1.840
H6240_Euphorbia_cyparissias	33656	3	6	6	4.714	1.981
H6240_Festuca_rupicola	9571	3	6	6	4.916	1.969
H6240_Festuca_valesiaca	8482	3	6	6	4.436	2.003
H6240_Gagea_pusilla	28	2	3	6	3.929	2.034
H6240_Globularia_cordifolia	3855	3	4	6	4.122	1.812
H6240_Helianthemum_canum	2900	3	6	6	4.242	1.982
H6240_Hesperis_tristis	231	3	3	6	3.957	1.984
H6240_Iris_humilis	82	1	3	6	3.512	1.971
H6240_Medicago_minima	5750	2	3	6	3.616	1.884
H6240_Oxytropis_pilosa	1161	3	5	6	4.176	1.984
H6240_Poa_badensis	1738	1	3	6	3.415	2.183
H6240_Potentilla_cinerea	13138	2	6	6	4.052	2.140
H6240_Ranunculus_illyricus	246	3	3	6	3.976	2.004
H6240_Scorzonera_austriaca	1341	3	5	6	4.108	2.011
H6240_Stipa_capillata	6363	3	5	6	4.205	1.975
H6240_Stipa_joannis	108	2	6	6	4.426	2.024
H6240_Teucrium_chamaedrys	32191	3	6	6	4.436	1.888
H6410_Carex_pallescens	6706	3	4	7	4.870	1.961
H6410_Cirsium_dissectum	1382	3	4	7	4.593	1.868
H6410_Cirsium_tuberosum	1164	3	6	7	5.357	1.641
H6410_Colchicum_autumnale	8756	6	7	7	6.222	1.325
H6410_Crepis_paludosa	9480	3	3	5	3.977	1.988
H6410_Dianthus_superbus	1568	3	4	6	4.577	1.699

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H6410_Galium_uliginosum	7009	3	3	7	4.417	2.100
H6410_Inula_salicina	2714	4	6	6	5.327	1.734
H6410_Juncus_conglomeratus	3333	3	7	7	5.299	2.001
H6410_Lotus_pedunculatus	4831	3	7	7	5.358	2.047
H6410_Luzula_multiflora	8620	3	4	6	4.349	1.736
H6410_Molinia_caerulea	22162	3	4	4	3.719	1.574
H6410_Ophioglossum_vulgatum	732	5	7	7	6.007	1.617
H6410_Potentilla_anglica	315	3	5	7	5.114	2.052
H6410_Sanguisorba_officinalis	9925	5	7	7	5.964	1.685
H6410_Selinum_carvifolia	2398	5	7	7	5.855	1.777
H6410_Serratula_tinctoria	2449	3	5	7	4.816	1.868
H6410_Silaum_silaus	2005	7	7	7	6.608	0.981
H6410_Succisa_pratensis	14300	3	4	7	4.582	1.866
H6410_Viola_palustris	3819	2	3	5	3.711	1.936
H6410_Viola_persicifolia	62	7	7	7	6.387	1.418
H6430_Aconitum_lycoctonum	1403	2	3	5	3.301	1.824
H6430_Aconitum_napellus	1767	3	5	5	4.320	1.525
H6430_Adenostyles_alliariae	7840	2	3	5	3.543	1.778
H6430_Angelica_archangelica	347	3	5	5	5.000	1.761
H6430_Angelica_sylvestris	15838	3	5	7	4.727	2.018
H6430_Athyrium_alpestre	2455	3	3	5	3.689	1.446
H6430_Calamagrostis_arundinacea	8385	2	3	5	3.224	1.845
H6430_Campanula_serrata	1083	3	4	5	4.221	1.648
H6430_Chaerophyllum_hirsutum	10852	3	5	6	4.474	2.064
H6430_Cirsium_helenioides	1214	5	5	7	5.557	1.655
H6430_Cirsium_oleraceum	9699	3	5	7	5.093	1.973
H6430_Digitalis_grandiflora	3172	2	3	5	3.631	2.036
H6430_Epilobium_hirsutum	2406	3	5	8	5.404	2.156
H6430_Filipendula_ulmaria	15774	3	5	7	4.949	2.008
H6430_Gentiana_asclepiadea	9697	2	3	4	2.975	1.617
H6430_Geranium_robertianum	16718	3	3	8	4.443	2.508
H6430_Geranium_sylvaticum	16673	3	5	7	4.804	1.834
H6430_Imperatoria_ostruthium	2503	3	4	5	4.054	1.533
H6430_Lactuca_alpina	3899	2	5	5	3.658	1.818
H6430_Lactuca_plumieri	409	5	5	5	4.951	1.611
H6430_Lilium_martagon	10221	3	3	5	3.794	1.811
H6430_Lysimachia_vulgaris	9146	3	4	5	4.324	1.933
H6430_Lythrum_salicaria	7619	3	4	5	4.359	2.061
H6430_Petasites_hybridus	2213	3	5	8	5.426	2.129
H6430_Ranunculus_platanifolius	3873	2	5	5	3.755	1.877
H6430_Senecio_nemorensis	230	3	5	8	5.361	2.241
H6430_Trollius_europaeus	10817	3	5	7	4.914	1.701
H6430_Valeriana_officinalis	6360	3	5	5	4.620	1.967
H6430_Veratrum_album	9088	3	3	5	3.765	1.720
H6510_Alopecurus_pratensis	9593	7	7	7	6.803	1.214
H6510_Arrhenatherum_elatius	24612	6	7	7	6.211	1.734
H6510_Campanula_patula	6497	6	7	7	6.308	1.507
H6510_Centaurea_jacea	20283	6	6	7	6.086	1.416
H6510_Centaurea_jacea_jacea (vervalt)	0					
H6510_Crepis_biennis	8630	7	7	7	6.823	0.867
H6510_Galium_mollugo	15342	4	6	7	5.499	1.924
H6510_Knautia_arvensis	19836	6	6	7	6.018	1.432
H6510_Lathyrus_pratensis	18965	6	7	7	6.233	1.506

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H6510_Leontodon_hispidus	31994	4	6	7	5.284	1.696
H6510_Leucanthemum_vulgare	11455	6	7	7	5.916	1.680
H6510_Malva_moschata	313	6	7	7	6.530	1.318
H6510_Oenanthe_pimpinelloides	238	2	2	3	3.017	1.883
H6510_Pastinaca_sativa	3513	7	7	8	7.081	1.285
H6510_Pimpinella_major	11638	4	6	7	5.566	1.831
H6510_Ranunculus_acris	24755	5	7	7	5.951	1.808
H6510_Rumex_acetosa	26099	6	7	7	6.043	1.721
H6510_Sanguisorba_officinalis	9925	5	7	7	5.964	1.685
H6510_Tragopogon_pratensis	6435	6	7	7	6.278	1.247
H6510_Trisetum_flavescens	18266	6	7	7	6.433	1.171
H6520_Astrantia_major	7758	3	5	7	4.901	1.918
H6520_Bistorta_officinalis	10622	3	5	7	4.924	1.870
H6520_Centaurea_nemoralis	429	6	6	6	5.939	0.697
H6520_Chaerophyllum_hirsutum	10852	3	5	6	4.474	2.064
H6520_Cirsium_helenioides	1214	5	5	7	5.557	1.655
H6520_Conopodium_majus	1381	3	4	7	4.552	2.023
H6520_Crepis_mollis	1951	4	7	7	5.681	1.668
H6520_Crepis_pyrenaica	2395	4	6	7	5.402	1.634
H6520_Crocus_caeruleus	1646	3	4	6	4.704	1.692
H6520_Geranium_phaeum	1690	3	5	8	5.534	2.229
H6520_Geranium_sylvaticum	16673	3	5	7	4.804	1.834
H6520_Narcissus_poeticus	371	6	7	7	6.067	1.679
H6520_Phyteuma_orbiculare	16765	3	4	6	4.451	1.674
H6520_Phyteuma_ovatum	1221	2	3	6	3.719	2.282
H6520_Phyteuma_spicatum	14692	2	3	5	3.585	1.961
H6520_Poa_chaixii	3934	3	4	7	4.482	1.833
H6520_Salvia_pratensis	18860	6	6	6	5.439	1.716
H6520_Sanguisorba_officinalis	9925	5	7	7	5.964	1.685
H6520_Trisetum_flavescens	18266	6	7	7	6.433	1.171
H6520_Trollius_europaeus	10817	3	5	7	4.914	1.701
H6520_Valeriana_repens	149	3	3	5	4.416	1.643
H6520_Viola_cornuta	128	5	7	7	6.078	1.482
H7110_Andromeda_polifolia	3744	1	1	2	1.617	1.105
H7110_Carex_limosa	2359	1	2	2	1.963	0.792
H7110_Carex_pauciflora	998	1	1	1	1.326	0.795
H7110_Chamaedaphne_calyculata	116	1	1	2	1.474	1.118
H7110_Drosera_anglica	1819	1	3	3	2.470	1.134
H7110_Eriophorum_vaginatum	6672	1	1	3	2.045	1.395
H7110_Narthecium_ossifragum	5803	1	4	4	3.054	1.357
H7110_Odontoschisma_sphagni	2814	1	3	4	2.537	1.497
H7110_Rhododendron_tomentosum	858	1	1	1	1.298	0.941
H7110_Scheuchzeria_palustris	774	1	1	2	1.487	0.687
H7110_Sphagnum_angustifolium	649	1	1	1	1.470	1.197
H7110_Sphagnum_balticum	80	1	1	1	1.100	0.406
H7110_Sphagnum_capillifolium	4606	1	3	4	2.483	1.391
H7110_Sphagnum_fuscum	607	1	1	1	1.338	0.863
H7110_Sphagnum_imbricatum	0					
H7110_Sphagnum_magellanicum	3732	1	1	1	1.587	1.129
H7110_Sphagnum_papillosum	3888	1	3	4	2.510	1.462
H7110_Vaccinium_oxycoccos	5347	1	1	2	1.821	1.226
H7130_Campylopus_atrovirens	1127	1	3	4	2.647	1.465
H7130_Diplophyllum_albicans	1308	1	3	4	3.017	1.463

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H7130_Erica_tetralix	12358	3	4	4	3.521	1.299
H7130_Eriophorum_vaginatum	6672	1	1	3	2.045	1.395
H7130_Mylia_taylorii	862	1	3	3	2.590	1.385
H7130_Narthecium_ossifragum	5803	1	4	4	3.054	1.357
H7130_Pinguicula_lusitanica	322	2	3	4	3.031	1.155
H7130_Pleurozia_purpurea	1663	1	3	4	2.541	1.468
H7130_Schoenus_nigricans	4376	2	3	4	3.004	1.278
H7130_Sphagnum_compactum	1653	3	4	4	3.234	1.227
H7130_Sphagnum_strictum	20	1	1	4	2.500	1.500
H7130_Sphagnum_tenellum	2615	1	4	4	2.699	1.472
H7130_Trichophorum_cespitosum	6435	2	3	4	3.062	1.293
H7150_Drosera_intermedia	3523	3	3	4	3.245	0.881
H7150_Drosera_rotundifolia	8584	1	3	4	2.625	1.331
H7150_Lycopodiella_inundata	777	3	3	4	3.290	0.742
H7150_Rhynchospora_alba	5758	2	3	4	2.934	1.205
H7150_Rhynchospora_fusca	1788	3	3	4	3.345	0.705
H7210_Cladium_mariscus	2238	3	3	3	2.920	0.517
H7230_Aneura_pinguis	2532	2	3	3	2.795	0.908
H7230_Bartsia_alpina	7510	3	3	4	3.499	1.045
H7230_Bellis_sylvestris	12295	3	3	4	3.264	1.448
H7230_Bryum_pseudotriquetrum	5039	2	3	3	2.818	1.053
H7230_Campylium_stellatum	7436	2	3	3	2.894	0.933
H7230_Carex_davalliana	4834	3	3	3	3.377	1.229
H7230_Carex_dioica	1691	2	3	3	2.917	1.014
H7230_Carex_flava	3421	3	3	3	3.445	1.426
H7230_Carex_hostiana	3681	3	3	3	3.653	1.473
H7230_Carex_pulicaris	2836	3	3	5	3.925	1.658
H7230_Carex_viridula	2843	2	3	3	3.017	1.154
H7230_Cinclidium_stygium	372	2	2	3	2.444	0.676
H7230_Ctenidium_molluscum	11888	2	3	4	3.183	1.738
H7230_Dactylorhiza_incarnata	2209	2	3	3	3.152	1.364
H7230_Dactylorhiza_russowii	19	3	3	3	3.211	0.893
H7230_Dactylorhiza_traunsteineri	410	2	3	3	2.980	1.251
H7230_Eleocharis_quinqueflora	1892	3	3	3	2.868	0.596
H7230_Epipactis_palustris	4010	3	3	3	3.357	1.341
H7230_Equisetum_variegatum	1043	3	3	3	3.054	0.641
H7230_Eriophorum_latifolium	4751	3	3	3	3.132	1.040
H7230_Liparis_loeselii	1004	2	3	3	2.650	0.782
H7230_Parnassia_palustris	10793	3	3	4	3.438	1.292
H7230_Pedicularis_sceptrum_carolinum	24	2	3	3	2.667	0.471
H7230_Pinguicula_vulgaris	3911	3	3	3	3.072	0.843
H7230_Primula_laurentiana	4432	3	3	3	3.447	1.128
H7230_Schoenus_ferrugineus	1282	3	3	3	3.105	0.876
H7230_Schoenus_nigricans	4376	2	3	4	3.004	1.278
H7230_Selaginella_selaginoides	7054	3	3	4	3.302	0.919
H7230_Tofieldia_calyculata	7124	3	3	4	3.539	1.316
H7230_Tomentypnum_nitens	1196	2	3	3	2.932	1.038
H7230_Valeriana_dioica	4898	3	3	6	3.934	1.883
H8210_Achillea_oxyloba	12	3	3	4	3.250	1.479
H8210_Androsace_cylindrica	0					
H8210_Androsace_helvetica	56	1	1	1	1.750	1.299
H8210_Antirrhinum_siculum	2					
H8210_Artemisia_umbelliformis	168	1	1	3	1.982	1.275

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H8210_Asperula_hirta	146	1	1	1	1.356	0.956
H8210_Asplenium_ceterach	1896	1	2	3	2.179	1.428
H8210_Asplenium_petrarchae	0					
H8210_Asplenium_ruta_muraria	4871	1	1	3	2.256	1.774
H8210_Asplenium_trichomanes	6366	1	1	3	2.167	1.666
H8210_Asplenium_trichomanes_ramosum	6682	1	2	3	2.424	1.459
H8210_Ballota_frutescens	5	1	1	1	1.400	0.800
H8210_Biscutella_laevigata	6762	3	3	4	3.656	1.585
H8210_Campanula_carpatica	278	1	1	3	1.935	1.458
H8210_Campanula_cochlearifolia	4387	1	2	4	2.449	1.480
H8210_Campanula_rupestris	0					
H8210_Campanula_versicolor	3					
H8210_Carex_mucronata	906	1	2	4	2.408	1.441
H8210_Chaenorhinum_origanifolium	92	1	1	1	1.315	1.010
H8210_Cheilanthes_acrostica	41	3	3	3	2.756	0.654
H8210_Cystopteris_fragilis	3924	1	2	3	2.478	1.904
H8210_Dianthus_rupicola	5	1	1	1	1.000	0.000
H8210_Draba_aizoides	1567	1	4	4	3.239	1.455
H8210_Draba_tomentosa	72	1	1	3	1.972	1.323
H8210_Erinus_alpinus	511	1	1	3	1.947	1.668
H8210_Erodium_petraeum	33	3	3	3	2.636	0.771
H8210_Globularia_repens	821	1	1	4	2.395	1.994
H8210_Gypsophila_petraea	4	1	1	1	1.000	0.000
H8210_Kernera_saxatilis	1699	1	1	4	2.394	1.700
H8210_Melica_minuta	1138	1	3	3	2.504	1.012
H8210_Minuartia_rupestris	44	1	1	1	1.227	1.041
H8210_Phyteuma_charmelii	67	1	1	1	1.104	0.602
H8210_Potentilla_alchimilloides	223	1	1	1	1.188	0.728
H8210_Potentilla_caulescens	666	1	1	3	1.728	1.280
H8210_Potentilla_nivalis	6	1	1	1	1.333	0.745
H8210_Potentilla_saxifraga	17	1	1	1	1.000	0.000
H8210_Primula_allionii	16	1	1	1	1.000	0.000
H8210_Primula_auricula	3049	1	3	4	2.859	1.551
H8210_Primula_marginata	267	1	1	1	1.273	0.889
H8210_Pteris_cretica	2					
H8210_Ramonda_myconi	85	1	1	1	1.153	0.744
H8210_Saxifraga_aretioides	57	1	1	1	1.439	0.974
H8210_Saxifraga_canaliculata	4	1	1	1	1.000	0.000
H8210_Saxifraga_cuneifolia	1205	1	2	3	2.200	1.356
H8210_Saxifraga_longifolia	115	1	1	1	1.148	0.749
H8210_Saxifraga_marginata	21	1	1	1	1.143	0.639
H8210_Saxifraga_media	74	1	1	1	1.095	0.619
H8210_Sedum_dasyphyllum	1062	1	1	3	1.820	1.565
H8210_Silene_campanula	38	1	1	1	1.158	0.670
H8210_Thymus_pulcherrimus	1496	1	4	4	3.048	1.533
H8210_Valeriana_globulariifolia	102	1	1	1	1.284	0.867
H8210_Woodsia_glabella	1					
H8220_Anarrhinum_bellidifolium	272	1	1	1	1.728	1.465
H8220_Androsace_pyrenaica	1					
H8220_Androsace_vandellii	150	1	1	1	1.187	0.786
H8220_Anogramma_leptophylla	87	1	1	1	1.632	1.407
H8220_Armeria_leucocephala	76	1	1	1	1.000	0.000

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H8220_Asarina_procumbens	69	1	1	1	1.029	0.239
H8220_Asplenium_adiantum_nigrum	1315	1	1	3	1.880	1.412
H8220_Asplenium_adulterinum	80	1	1	1	1.013	0.111
H8220_Asplenium_balearicum	0					
H8220_Asplenium_cuneifolium	145	1	1	1	1.303	1.066
H8220_Asplenium_forisiense	67	1	1	1	1.030	0.243
H8220_Asplenium_obovatum	22	1	1	1	1.000	0.000
H8220_Asplenium_onopteris	1373	1	3	3	2.241	1.087
H8220_Asplenium_septentrionale	1425	1	1	1	1.359	1.224
H8220_Carex_kitaibeliana	329	1	3	3	2.657	1.366
H8220_Cheilanthes_hispanica	0					
H8220_Cheilanthes_maderensis	81	1	1	3	1.778	1.066
H8220_Cheilanthes_tinaei	7	1	1	1	1.000	0.000
H8220_Cosentinia_vellea	3					
H8220_Dianthus_graniticus	85	1	1	1	2.000	1.916
H8220_Eritrichium_nanum	142	1	1	1	1.359	0.952
H8220_Galium_tendae	154	1	1	1	1.052	0.374
H8220_Haberlea_rhodopensis	17	1	1	1	1.471	1.242
H8220_Jovibarba_heuffelii	48	1	1	1	1.333	1.087
H8220_Murbeckiella_boryi	45	1	1	1	1.311	0.725
H8220_Paragymnopteris_marantae	139	1	1	3	2.079	1.513
H8220_Phyteuma_hemisphaericum	3174	3	3	3	2.930	0.829
H8220_Phyteuma_scheuchzeri	237	1	1	2	2.068	1.547
H8220_Polypodium_vulgare	5885	1	2	4	2.602	1.687
H8220_Potentilla_crassinervia	68	1	1	1	1.000	0.000
H8220_Primula_hirsuta	449	1	1	3	2.018	1.232
H8220_Rhodiola_rosea	1517	3	3	4	3.317	1.419
H8220_Saxifraga_aspera	106	1	1	1	1.330	1.044
H8220_Saxifraga_continentalis	139	1	1	1	1.410	1.296
H8220_Saxifraga_florulenta	114	1	1	1	1.070	0.434
H8220_Saxifraga_nevadensis	0					
H8220_Saxifraga_pedemontana	95	1	1	1	1.074	0.417
H8220_Silene_lerchenfeldiana	17	1	1	1	1.000	0.000
H8220_Silene_requienii	48	1	1	1	1.000	0.000
H8220_Umbilicus_rupestris	868	1	1	1	1.317	0.812
H9150_Acer_campestre	22388	3	3	4	3.992	1.894
H9150_Berberis_vulgaris	5120	3	3	5	3.737	1.742
H9150_Buxus_sempervirens	8312	3	3	3	3.254	1.132
H9150_Carex_alba	6377	2	3	3	2.716	1.289
H9150_Carex_digitata	14949	2	3	4	2.940	1.370
H9150_Carex_flacca	32114	3	6	6	4.714	1.707
H9150_Carex_montana	14196	3	6	6	4.742	1.659
H9150_Cephalanthera_damasonium	3859	3	3	3	3.310	1.220
H9150_Cephalanthera_rubra	2975	3	3	3	3.187	1.205
H9150_Epipactis_leptochila	14	3	3	3	3.571	1.178
H9150_Epipactis_microphylla	389	3	3	3	3.144	1.131
H9150_Fagus_sylvatica	67345	2	3	3	2.773	1.412
H9150_Hieracium_murorum	25918	2	3	4	2.924	1.519
H9150_Lactuca_muralis	14101	2	3	4	2.919	1.819
H9150_Lathyrus_vernus	9897	3	3	4	3.668	1.613
H9150_Lonicera_xylosteum	16083	3	3	4	3.418	1.511
H9150_Neottia_nidus_avis	6308	2	3	3	2.914	1.231
H9150_Sesleria_albicans	11815	2	3	4	3.335	1.627

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H9150_Solidago_virgaurea	25133	2	3	4	3.294	1.616
H9150_Sorbus_aria	18955	2	3	3	3.053	1.358
H9160_Acer_campestre	22388	3	3	4	3.992	1.894
H9160_Anemone_nemorosa	17924	3	3	4	3.881	1.830
H9160_Brachypodium_sylvaticum	18584	3	3	4	3.877	1.983
H9160_Carpinus_betulus	21562	3	4	4	4.130	1.752
H9160_Corylus_avellana	26678	3	3	4	3.846	1.867
H9160_Fragaria_vesca	28893	2	3	5	3.764	1.927
H9160_Galium_odoratum	15693	2	3	4	3.293	1.719
H9160_Galium_sylvaticum	4751	3	4	4	3.479	1.374
H9160_Melica_nutans	14338	2	3	4	3.357	1.686
H9160_Mercurialis_perennis	19742	2	3	4	3.270	1.759
H9160_Poa_chaixii	3934	3	4	7	4.482	1.833
H9160_Potentilla_sterilis	1731	3	4	6	4.688	1.785
H9160_Prunus_avium	13364	3	4	4	4.095	1.803
H9160_Stellaria_holostea	8843	3	4	6	4.646	2.029
H9160_Tilia_cordata	9884	3	4	4	4.354	1.954
H9160_Viola_reichenbachiana	21190	2	3	4	3.316	1.683
H9190_Amelanchier_lamarckii	978	4	4	4	4.125	0.626
H9190_Betula_pendula	11473	3	4	5	4.084	1.684
H9190_Ceratocapnos_claviculata	1284	4	4	4	4.121	0.783
H9190_Deschampsia_flexuosa	29750	3	3	4	3.360	1.257
H9190_Holcus_mollis	5275	4	4	7	5.096	2.158
H9190_Lonicera_periclymenum	6970	3	4	4	4.003	1.378
H9190_Maianthemum_bifolium	14919	2	3	4	2.954	1.557
H9190_Melampyrum_pratense	7582	3	3	4	3.502	1.358
H9190_Populus_tremula	6160	3	4	5	4.292	1.676
H9190_Pteridium_aquilinum	9124	2	4	5	3.704	1.655
H9190_Quercus_petraea	20657	3	4	4	3.746	1.496
H9190_Quercus_robur	17515	3	4	6	4.722	1.893
H9190_Sorbus_aucuparia	36588	2	3	4	3.170	1.653
H9190_Trientalis_europaea	2293	3	4	5	3.859	1.346
H9410_Abies_alba	34709	1	2	3	2.269	1.211
H9410_Calamagrostis_varia	12426	2	3	4	2.969	1.643
H9410_Gymnocarpium_dryopteris	9266	1	2	3	2.200	1.322
H9410_Luzula_luzuloides	12878	2	3	3	2.885	1.476
H9410_Luzula_sylvatica	13681	2	3	3	2.812	1.544
H9410_Melampyrum_sylvaticum	7258	1	3	3	2.693	1.464
H9410_Petasites_japonicus	6444	1	2	3	2.603	1.823
H9410_Picea_abies	57580	2	2	3	2.652	1.466
H9410_Picea_orientalis	1					
H9410_Polygonatum_verticillatum	15086	1	2	3	2.631	1.603
H9410_Prenanthes_purpurea	19606	1	2	3	2.368	1.311
H1340_Artemisia_santonicum	148	2	2	2	2.149	0.671
H1340_Aster_tripolium	6606	2	2	2	2.062	0.640
H1340_Atriplex_hastata	10	2	9	9	6.900	3.208
H1340_Bupleurum_tenuissimum	150	2	2	2	2.247	0.945
H1340_Carex_distans	969	2	3	7	3.710	2.170
H1340_Elymus_pycnanthus	392	2	2	2	2.431	1.000
H1340_Festuca_pseudovina	1125	2	3	6	4.064	1.995
H1340_Halimione_pedunculata	116	2	2	2	2.000	0.000
H1340_Hordeum_marinum	81	2	2	2	2.383	1.366
H1340_Juncus_gerardii	3493	2	2	2	2.137	0.696

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H1340_Lotus_tenuis	630	2	2	3	3.113	2.098
H1340_Plantago_coronopus	1590	2	2	3	3.016	1.858
H1340_Plantago_maritima	7769	2	2	2	2.631	1.317
H1340_Puccinellia_distans	895	2	2	2	3.450	2.830
H1340_Puccinellia_fasciculata	55	2	2	2	2.127	0.935
H1340_Salicornia_europaea	3525	2	2	2	2.003	0.120
H1340_Scorzonera_cana	360	2	2	2	2.644	1.564
H1340_Spergularia_marina	947	2	2	2	2.322	1.458
H1340_Spergularia_media	4575	2	2	2	2.010	0.254
H1340_Suaeda_maritima	4299	2	2	2	2.002	0.108
H1340_Triglochin_maritima	5189	2	2	2	2.032	0.364
H5110_Amelanchier_ovalis	7840	3	3	4	3.310	1.514
H5110_Berberis_vulgaris	5144	3	3	5	3.731	1.744
H5110_Buxus_sempervirens	8312	3	3	3	3.254	1.132
H5110_Cornus_mas	6662	2	3	4	3.187	1.694
H5110_Cornus_sanguinea	19470	3	3	6	4.185	1.915
H5110_Crataegus_monogyna	27809	3	3	6	4.263	1.987
H5110_Cytisus_sessilifolius	3441	3	3	3	3.289	1.339
H5110_Daphne_laureola	3509	3	3	3	3.037	1.004
H5110_Dictamnus_albus	2067	2	2	6	3.186	1.824
H5110_Euphorbia_amygdaloides	10029	2	3	4	3.197	1.529
H5110_Geranium_sanguineum	6008	2	6	6	4.255	2.081
H5110_Ligustrum_vulgare	16170	3	3	5	3.796	1.702
H5110_Lonicera_xylosteum	16083	3	3	4	3.418	1.511
H5110_Prunus_mahaleb	3457	2	3	6	3.601	1.811
H5110_Prunus_spinosa	13214	3	4	6	4.530	2.004
H5110_Rosa_rubiginosa	1953	3	5	6	4.511	1.658
H5110_Rubia_peregrina	10259	3	3	3	3.124	1.120
H5110_Ruscus_aculeatus	3547	2	3	3	2.782	1.143
H5110_Sorbus_aria	19006	2	3	3	3.051	1.358
H5110_Viburnum_lantana	12334	3	3	4	3.535	1.481
H5110_Vincetoxicum_hirundinaria	12656	2	3	6	3.924	1.996
H7140_Bryum_pseudotriquetrum	5039	2	3	3	2.818	1.053
H7140_Calliergon_giganteum	1548	2	2	2	2.262	0.711
H7140_Campylium_stellatum	7436	2	3	3	2.894	0.933
H7140_Carex_chordorrhiza	358	2	2	2	1.944	0.515
H7140_Carex_diandra	2397	2	2	2	2.234	0.825
H7140_Carex_lasiocarpa	3157	2	2	2	2.331	0.991
H7140_Carex_limosa	2359	1	2	2	1.963	0.792
H7140_Carex_rostrata	6235	2	2	3	2.544	1.312
H7140_Epilobium_palustre	4020	2	2	3	3.211	1.832
H7140_Equisetum_fluviatile	6614	2	2	3	2.807	1.537
H7140_Eriophorum_gracile	315	2	2	2	2.162	0.582
H7140_Hammarbya_paludosa	189	2	2	3	2.593	1.048
H7140_Liparis_loeselii	1004	2	3	3	2.650	0.782
H7140_Menyanthes_trifoliata	7225	2	2	3	2.493	1.145
H7140_Pedicularis_palustris	2686	2	2	3	2.662	1.085
H7140_Potentilla_palustris	4984	2	2	3	2.663	1.517
H7140_Rhynchospora_alba	5758	2	3	4	2.934	1.205
H7140_Rhynchospora_fusca	1788	3	3	4	3.345	0.705
H7140_Scheuchzeria_palustris	774	1	1	2	1.487	0.687
H7140_Scorpidium_revolvens	3239	2	3	3	2.723	0.778
H7140_Scorpidium_scorpioides	2116	2	2	3	2.471	0.708

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H9110_Abies_alba	34709	1	2	3	2.269	1.211
H9110_Calamagrostis_arundinacea	8385	2	3	5	3.224	1.845
H9110_Calamagrostis_villosa	8657	2	3	3	2.997	1.336
H9110_Fagus_sylvatica	68236	2	3	3	2.770	1.417
H9110_Gymnocarpium_dryopteris	9266	1	2	3	2.200	1.322
H9110_Ilex_aquifolium	5504	2	3	4	3.280	1.351
H9110_Leucobryum_glaucum	2995	2	3	4	2.918	1.372
H9110_Luzula_luzuloides	13798	2	3	4	2.985	1.532
H9110_Luzula_sylvatica	13739	2	3	3	2.814	1.543
H9110_Oxalis_acetosella	28617	2	2	3	2.853	1.690
H9110_Picea_abies	58284	2	2	3	2.672	1.490
H9110_Polygonatum_verticillatum	15086	1	2	3	2.631	1.603
H9110_Polytrichastrum_formosum	15262	2	2	3	2.669	1.274
H9110_Prenanthes_purpurea	19606	1	2	3	2.368	1.311
H9110_Pteridium_aquilinum	9636	2	4	5	3.729	1.647
H9110_Sambucus_racemosa	3926	2	2	4	2.885	1.897
H9110_Senecio_nemorensis	17441	2	2	4	2.948	1.891
H9110_Vaccinium_myrtillus	45575	2	3	4	3.105	1.321
H91H0_Amygdalus_nana	77	3	5	6	4.234	1.973
H91H0_Arabis_brassica	672	2	3	5	3.634	1.683
H91H0_Arabis_turrita	1493	2	2	3	2.856	1.783
H91H0_Astragalus_austriacus	1258	3	6	6	4.383	1.776
H91H0_Astragalus_monspessulanus	3131	3	6	6	4.557	1.658
H91H0_Buglossoides_purpurocaerulea	2986	2	2	3	2.894	1.516
H91H0_Campanula_bononiensis	648	2	3	6	3.991	2.104
H91H0_Carex_humilis	16209	3	6	6	4.264	1.972
H91H0_Carex_michelii	1240	2	4	6	4.027	2.049
H91H0_Colutea_arborescens	626	2	2	3	2.992	1.571
H91H0_Cornus_mas	6662	2	3	4	3.187	1.694
H91H0_Cotinus_coggygria	2406	2	3	3	3.096	1.508
H91H0_Dictamnus_albus	2067	2	2	6	3.186	1.824
H91H0_Euphorbia_angulata	241	2	3	5	3.726	1.516
H91H0_Fraxinus_ornus	6872	2	2	3	2.731	1.461
H91H0_Geranium_sanguineum	6008	2	6	6	4.255	2.081
H91H0_Lactuca_quercina	158	2	2	6	3.943	2.620
H91H0_Limodorum_abortivum	627	2	3	5	3.427	1.667
H91H0_Melittis_melissophyllum	8141	2	3	4	3.283	1.412
H91H0_Orchis_purpurea	960	3	6	6	4.557	1.731
H91H0_Potentilla_alba	951	4	6	7	5.411	1.800
H91H0_Potentilla_micrantha	840	2	3	4	3.171	1.747
H91H0_Pulmonaria_mollis	1071	3	5	7	5.041	2.029
H91H0_Pyrus_pyraster	2542	2	3	6	3.871	2.001
H91H0_Quercus_cerris	2909	2	2	4	3.142	1.898
H91H0_Quercus_pubescens	16742	2	3	3	3.171	1.531
H91H0_Sorbus_domestica	2484	2	3	3	2.961	1.311
H91H0_Sorbus_torminalis	8084	2	3	4	3.192	1.314
H91H0_Tanacetum_corymbosum	7707	2	3	6	3.658	1.813
H91H0_Viola_suavis	424	2	3	6	3.922	2.318
E5.1a_Anthemis_cotula	555	9	9	9	8.773	1.126
E5.1a_Artemisia_vulgaris	8450	8	9	9	8.280	1.536
E5.1a_Atriplex_nitens	721	9	9	9	8.895	0.567
E5.1a_Atriplex_patula	3887	9	9	9	8.933	0.430
E5.1a_Ballota_nigra	1916	8	9	9	8.185	1.572

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
E5.1a_Bromus_sterilis	3019	5	8	9	6.961	2.544
E5.1a_Chenopodium_album	12964	9	9	9	8.847	0.844
E5.1a_Cirsium_arvense	17255	7	9	9	7.710	1.996
E5.1a_Convolvulus_arvensis	13836	6	8	9	7.072	2.324
E5.1a_Conyza_canadensis	4999	6	9	9	7.419	2.565
E5.1a_Descurainia_sophia	1509	9	9	9	8.346	1.768
E5.1a_Elymus_repens	19710	7	9	9	7.718	1.964
E5.1a_Galinsoga_parviflora	2665	9	9	9	8.932	0.466
E5.1a_Geranium_pusillum	3093	9	9	9	8.547	1.476
E5.1a_Hordeum_murinum	1315	8	9	9	7.460	2.585
E5.1a_Lactuca_serriola	2924	9	9	9	8.008	2.148
E5.1a_Lepidium_ruderale	820	9	9	9	8.673	1.443
E5.1a_Malva_neglecta	1069	9	9	9	8.798	0.930
E5.1a_Matricaria_maritima	842	8	9	9	7.719	2.540
E5.1a_Matricaria_perforata	1850	9	9	9	8.735	1.164
E5.1a_Senecio_vulgaris	5172	7	9	9	7.684	2.326
E5.1a_Sisymbrium_loeselii	688	9	9	9	8.590	1.460
E5.1a_Sisymbrium_officinale	2485	9	9	9	8.660	1.079
E5.1a_Sonchus_asper	5532	9	9	9	8.247	1.905
E5.1a_Sonchus_oleraceus	5223	9	9	9	8.297	1.854
E5.1a_Tanacetum_vulgare	2541	7	9	9	7.867	1.749
E5.1a_Urtica_urens	1098	9	9	9	8.643	1.300
E5.1a_Verbena_officinalis	1042	6	9	9	7.196	2.382
E5.1b_Aegopodium_podagraria	16694	3	7	8	5.754	2.332
E5.1b_Alliaria_petiolata	8659	3	8	8	6.029	2.464
E5.1b_Anthriscus_sylvestris	12029	7	8	8	6.974	1.746
E5.1b_Arctium_lappa	1980	8	8	9	7.474	2.006
E5.1b_Arctium_tomentosum	1355	8	8	9	7.728	1.719
E5.1b_Bromus_sterilis	3019	5	8	9	6.961	2.544
E5.1b_Chelidonium_majus	3130	8	8	8	6.972	2.215
E5.1b_Elymus_repens	19710	7	9	9	7.718	1.964
E5.1b_Galium_aparine	21988	4	8	8	6.641	2.474
E5.1b_Geranium_robertianum	16886	3	3	8	4.437	2.510
E5.1b_Geum_urbanum	18301	3	4	8	5.296	2.411
E5.1b_Glechoma_hederacea	19281	3	7	8	6.096	2.263
E5.1b_Heracleum_sphondylium	23605	4	7	8	6.017	2.021
E5.1b_Lamium_album	3323	8	8	8	7.770	1.376
E5.1b_Lamium_maculatum	6864	3	8	8	6.010	2.406
E5.1b_Rumex_obtusifolius	7489	7	8	9	7.382	1.948
E5.1b_Urtica_dioica	29600	3	7	8	5.756	2.503
E5.1b_Veronica_chamaedrys	28249	4	6	7	5.546	2.034
H5.6a_Chamomilla_aurea	0					
H5.6a_Chamomilla_suaveolens	4723	9	9	9	8.931	0.507
H5.6a_Coronopus_didymus	123	9	9	9	8.707	1.330
H5.6a_Coronopus_squamatus	569	9	9	9	8.958	0.501
H5.6a_Gymnostyles_stolonifera	0					
H5.6a_Herniaria_glabra	824	2	5	9	5.117	3.080
H5.6a_Plantago_major	13356	8	9	9	8.093	1.898
H5.6a_Poa_annua	11757	9	9	9	8.339	1.697
H5.6a_Poa_infirma	13	3	3	9	5.308	2.919
H5.6a_Polycarpon_tetraphyllum	466	2	3	3	3.468	2.192
H5.6a_Polygonum_arenastrum	1344	9	9	9	8.938	0.527
H5.6a_Polygonum_aviculare	12972	9	9	9	8.789	1.045

SPECIES_NAME	OBSER-VATIONS	25‰	MEDIAN	75‰	MEAN	STDDEV
H5.6a_Sagina_apetala	720	3	9	9	6.389	2.956
H5.6a_Sagina_procumbens	2226	5	9	9	7.402	2.535
H5.6a_Sclerochloa_dura	127	9	9	9	7.724	2.490
H5.6a_Spergularia_rubra	932	9	9	9	8.150	2.183
H5.6a_Trifolium_suffocatum	199	3	3	3	3.884	2.118
I1.1a_Alopecurus_myosuroides	1107	9	9	9	8.833	0.940
I1.1a_Anagallis_arvensis	7447	9	9	9	8.015	2.227
I1.1a_Apera_spica-venti	4884	9	9	9	8.887	0.755
I1.1a_Centaurea_cyanus	5092	9	9	9	8.885	0.801
I1.1a_Chamomilla_recutita	4003	9	9	9	8.716	1.238
I1.1a_Chenopodium_album	12964	9	9	9	8.847	0.844
I1.1a_Chrysanthemum_segetum	537	9	9	9	8.503	1.773
I1.1a_Consolida_regalis	2241	9	9	9	8.417	1.718
I1.1a_Euphorbia_exigua	2844	3	9	9	6.301	2.971
I1.1a_Euphorbia_helioscopia	4955	9	9	9	8.739	1.186
I1.1a_Fallopia_convolvulus	12085	9	9	9	8.387	1.798
I1.1a_Galeopsis_bifida	1804	4	8	9	6.609	2.773
I1.1a_Galeopsis_tetrahit	9918	3	8	9	6.110	2.795
I1.1a_Lamium_amplexicaule	3637	9	9	9	8.319	1.944
I1.1a_Lamium_hybridum	260	9	9	9	8.665	1.292
I1.1a_Lamium_purpureum	4620	9	9	9	8.667	1.235
I1.1a_Myosotis_arvensis	9660	7	9	9	8.089	1.734
I1.1a_Papaver_argemone	1615	9	9	9	8.670	1.419
I1.1a_Papaver_dubium	1772	9	9	9	7.917	2.360
I1.1a_Papaver_rhoeas	4849	9	9	9	8.573	1.507
I1.1a_Polygonum_lapathifolium	4911	9	9	9	8.720	1.265
I1.1a_Polygonum_persicaria	4954	9	9	9	8.650	1.292
I1.1a_Raphanus_raphanistrum	3779	9	9	9	8.675	1.414
I1.1a_Scleranthus_annuus	3953	9	9	9	7.962	2.274
I1.1a_Sinapis_arvensis	4619	9	9	9	8.902	0.617
I1.1a_Solanum_nigrum	2272	9	9	9	8.755	1.151
I1.1a_Sonchus_arvensis	5079	9	9	9	7.920	2.282
I1.1a_Spergula_arvensis	3875	9	9	9	8.942	0.565
I1.1a_Stellaria_media	15208	8	9	9	8.126	1.904
I1.1a_Thlaspi_arvense	4475	9	9	9	8.909	0.626
I1.1a_Veronica_persica	6641	9	9	9	8.899	0.621
I1.1a_Vicia_sativa	9665	6	7	9	6.995	2.213
I1.1a_Viola_arvensis	10647	9	9	9	8.475	1.709

Annex 6 R-script for running GBM under TRIMmaps

Parts in the script indicated with bold characters should be changed according to user settings.

```
##################################################################################
#
#  Multiivariate models
#
#  Author: Henk Sierdsema, Christian Kampichler
#
#  Last update 1-10-2014
#
##################################################################################

library(TRIMmaps)
setwd("D:/BioScore2/Additionele_bestanden/")
outdir <- "d:/BioScore2/Data/Output5x5/H91E0/"
dir.create(outdir)
Maxent <- "D:/BioScore2/Maxent/maxent.jar"

## set coordinate reference information of the data
# choose.crs()       # use this command without the hash to select your own
                     # coordinate reference system and retrieve its
                     # parameters
crs <- "+proj=laea +lat_0=52 +lon_0=10 +x_0=4321000 +y_0=3210000 +ellps=GRS80 +units=m
+no_defs"
# Make a TRIMdata object
  trimdata <- data2TRIMmaps(
       plot.data="D:/BioScore2/Data/Input/H91E0_habtype.csv", # name of plot data
##obs.dir = NULL   # in this case because observations are included in plotdata
       crs=crs,           # coordinate reference
       named="trimdata",  # name of the data (for saving purposes)
       outdir=outdir,     # name of output-directory
       add.zeroes=FALSE,  # Add zeroes by species/plot combi? (FALSE= no, TRUW=yes)
          generate.zeroes=TRUE,
          gen.zer.options=                                              # Opions for
generaing random zeroes... a list.
                      list(yearspecific=FALSE,                                 #    For
each year sperately?
                              way="maxent",                                       #
by which way? "enfa", "madifa", or "maxent"
                              n=10000,  #NULL,                                    #
How many zeroes (NULL equals number of presences)
                              add.to.csv=TRUE,                                    #
add to the csv's (we are dealing with a small dataset)
                              extended.output=TRUE,                               #
Provide extended output of maxent results?
                              tdir=outdir,                                        #
Where will this extended output be saved?
                              maxent.options=maxentTRIMOptions(path2maxent=Maxent)   #
Modify default options of maxent.TRIM : see maxent.TRIM.options()
                      ),
       user.dir="D:/BioScore2/Layers5x5/",  # points to folder with covariate maps
       user.crs=crs,
       user.all.question = FALSE)
  save(trimdata, file = "D:/BioScore2/H91E0_habtype.trimdata.RData")

  trim.gbm <- TRIMmaps(
     TRIMdata = trimdata,
     gbm = TRUE,
     gb.control = gbmTRIMOptions(tree.complexity = 2),
     count = FALSE,
     presence = TRUE,
        resid.int.method = NULL,
     # resid.int.method = "IDW",
        #inttype="response",
        #int.args=list(block=c(5000,5000)),
     driver = "asc",
     out.dir = "D:/BioScore2/Data/Output/GBM/H91E0_habtype",
     vars.subs = "-YEAR"
  )
  save(trim.gbm, file="D:/BioScore2/H91E0_habtype.trim.gbm.RData")

  modelSummary(trim.gbm)
```

R-script for determining thresholds for creating absence/presence maps

Annex 7 R-script for determining thresholds for creating absence/presence maps

Parts in the script indicated with bold characters should be changed according to user settings.

```
#################################################################################
#
#  Cutlevel optimisation
#
#  Author: Henk Sierdsema, Christian Kampichler
#
#  Last update 1-10-2014
#
#################################################################################

#source("Cutoff_Optimised.r")
library(raster)
library(sp)
library(maptools)
gpclibPermit()
FACTOR = 1
Cutoff.Optimised <- function (Obs, Fit)
{
    SumObs <- sum(Obs)
    LengObs <- length(Obs)
    tt <- c(100)
    Cut <- c(0, 0, 0)
    if (length(unique(Fit)) == 1) {
        Cut[1] <- unique(Fit)
        Cut[2] <- 100 * sum((Fit >= Cut[1])[Obs == 1])/SumObs
        Cut[3] <- 100 * sum((Fit < Cut[1])[Obs == 0])/(LengObs -
            SumObs)
        Cut <- t(Cut)
    }
    else {
        if (min(Fit) < 0)
            Fit[Fit < 0] <- 0
        Quant <- quantile(Fit)
        i <- Quant[1]
        a <- 2
        while (i <= Quant[5]) {
            se <- sum((Fit >= i)[Obs == 1])/SumObs
            sp <- sum((Fit < i)[Obs == 0])/(LengObs - SumObs)
            tt[a] <- abs(FACTOR*se - sp)   ## specifity is FACTOR as important as
sensitivity
            if (tt[a] > tt[a - 1])
                break
            i <- i + ((Quant[5] - Quant[1])/1000)
            a <- a + 1
        }
        b <- (i - ((Quant[5] - Quant[1])/1000))
        Cut[1] <- b
        Cut[2] <- 100 * sum((Fit >= b)[Obs == 1])/SumObs
        Cut[3] <- 100 * sum((Fit < b)[Obs == 0])/(LengObs - SumObs)
        Cut <- t(Cut)
        dimnames(Cut) = list(NULL, c("CutOff", "se", "sp"))
    }
    return(Cut)
}

## choose directory


setwd("D:/Projecten/BioScore 2.0/TrimmapsOutput/Habtypen")

filenames <- list.files(getwd(), pattern="RData$", recursive=TRUE, full=TRUE)
filenames <- sub(".RData", "", filenames)
filenames <- filenames[grep("preds", filenames, invert = TRUE)]
filenames <- filenames[grep("cutoff", filenames, invert = TRUE)]
filenames
progbar <- winProgressBar(title = "Progress", min = 0, max = length(filenames))
counter <- 1
for (i in filenames[1:length(filenames)]) {
```

```
  ## load dataframe with results from BRT-analysis
  gbm.model <- get(load(paste(i,".RData", sep="")))
  rm(list = ls(pattern= "gbm.TRIM"))
  gc()
  memory.size()
  Obs <- gbm.model$data$y
  Fit <- gbm.model$fitted

  par(mfrow=c(1,2))
  hist(Obs)
  hist(Fit)
  par(mfrow=c(1,1))
  cutoffs <- Cutoff.Optimised(Obs,Fit)
  cutoffs <- data.frame(cutoffs)
  save(cutoffs, file = paste(i, "_cutoff.RData", sep = ""))
  cutoffs$Species <- i
  if(!file.exists("all.cutoffs.csv")) {
    write.table(cutoffs, file = "all.cutoffs.csv", row.names = FALSE, sep=",")
  } else {
    write.table(cutoffs, file = "all.cutoffs.csv", append = TRUE,
                row.names = FALSE, col.names = FALSE, sep=",")
  }
  info <- sprintf("% of %i species done", counter, length(filenames))
  setWinProgressBar(progbar, counter, label = info)
  counter <- counter + 1
}
close(progbar)
# setwd("D:/Projecten/BioScore 2.0/TrimmapsOutput/Habtypen")
filenames <- list.files(getwd(), recursive=TRUE, full=TRUE)
filenames <-filenames[grep(".asc",tolower(filenames),fixed=T)]
filenames <-filenames[grep("predictedr_",tolower(filenames),fixed=T)]
filenames <-filenames[grep("presabs",tolower(filenames),fixed=T, invert = TRUE)]
filenames
progbar <- winProgressBar(title = "Progress", min = 0, max = length(filenames))
counter <- 1
for(i in filenames)
{
     speciescode <- sub(".asc$", "", i)
     speciescode <- sub("predictedr_presence_", "", speciescode)
     #load(paste("cutoff_gbm.TRIM_presence_",speciescode,".RData", sep="") )
        SPLIT <- unlist(strsplit(speciescode, "/"))
        PATH <- paste(SPLIT[1:(length(SPLIT)-1)], collapse = "/")
        load(paste(PATH, "/", "gbm.TRIM_presence_", SPLIT[length(SPLIT)], "_cutoff.RData",
sep = ""))
     grd <- read.asciigrid(fname=i)
     grd[[1]] <- ifelse(grd[[1]] < cutoffs$CutOff,0,1)
     filename <- sub(".asc$", "", i)
     write.asciigrid(grd,paste(filename,"_presabs_raw.asc",sep=""))
        info <- sprintf("% of %i species done", counter, length(filenames))
     setWinProgressBar(progbar, counter, label = info)
     counter <- counter + 1
}
close(progbar)
```

Annex 8 R-script for running GLM's

Parts in the script indicated with bold characters should be changed according to user settings.

```
################################################################################
#
#  Univariate models
#
#  Authors: Henk Sierdsema, Stephan Hennekens, Christian Kampichler
#
#  Last update 1-10-2014
#
################################################################################

library(tcltk)
library(cvAUC)
library(beepr)

## Define directory with csv-files containing observations and covariate date

setwd("D:/Projecten/BioScore 2.0/TrimmapsInput/WithCovars")
filenames <- list.files(getwd(), recursive=FALSE, full=FALSE)
filenames <- filenames[grep(".csv",tolower(filenames),fixed=T)]
filenames
wd <- getwd()  ## capture working directory


## Select to limut data or not
## TRUE: Equal number of 0 and 1
LIMITDATA   <- FALSE
FILEEXT     <- ifelse(LIMITDATA,"_datlim", "_nodatlim")

## Create directory to hold results

modeldir <- "Models"
dir.create(paste(getwd(),modeldir,sep="/"))
#modeldir <- "Models_no_step"
#dir.create(paste(getwd(),modeldir,sep="/"))
bootdir  <- "Models_boot"
dir.create(paste(getwd(),bootdir,sep="/"))


START <- 1

#for (i in filenames[1:length(filenames)]) {
for (i in filenames[1:1]) {
#for (i in selection[1:length(selection)]) {
  Dataset <- read.table(i,sep=",",header=T,as.is=T)
  str(Dataset)
  ## change name of field with observed numbers into 'observed'
  names(Dataset)[names(Dataset)=="Number"] <- "observed"
  ## Select only observations within the range
#  Dataset <- Dataset[Dataset$range==1,]
  ## Change observed numbers in presence and absence (or better: detection and non-
detection)
  Dataset$observed <- ifelse(Dataset$observed==0,0,1)
  ## Retrieve species name from file name
  SPECIES <- gsub(".csv","",i)
  SPECIES

  # setWindowTitle(suffix="",title=paste("Univariate models:",SPECIES))  ## remove hash to
see species file name in R-console
                                                                          ## however, this
stalls the sending of commands from Tinn-R

  ## Set paths for output
  PATH1 <- paste(getwd(),"/",modeldir,"/",SPECIES,"/",sep="")
  dir.create(PATH1)
  PATH2 <- paste(getwd(),"/",bootdir,"/",SPECIES,"/",sep="")
#  dir.create(PATH2)

  ## Make text-file for output
  SUMMnames <-
c("species","variable","rownames","Estimate","Std..Error","z.value","Pr...z..","Expldev","AI
C","AUC","AUCmin","AUCmax","AUCmean","NAbs","Npres","Ntot")
```

```
  write(SUMMnames, file=paste(PATH1,SPECIES, "_glm_summary",FILEEXT,".csv", sep =
""),ncolumns=length(SUMMnames), sep=";")

  FACTORS <- names(Dataset)[6:length(names(Dataset))]  ## Adjust according to your file
  FACTOR <- FACTORS[1] # for testing
  for(FACTOR in FACTORS) {
             ## MAKE SUBSET FOR CHOSEN VARIABLE
             #hist(get(eval(FACTOR)), data = Dataset)
             TEMP <- Dataset[,c("observed", FACTOR)]
             TEMP <- na.omit(TEMP)  ## removes all lines with missing values

             TEMP0 <- TEMP[TEMP$observed == 0,]
             TEMP1 <- TEMP[TEMP$observed >= 1,]

             #dim(TEMP0)
             #dim(TEMP1)
             #SELECT <- sample(1:nrow(TEMP1), nrow(TEMP0), replace = F)
             #SubData <- rbind(TEMP0, TEMP1[SELECT,])

             ## assumption: there are more lines with 1 than with 0

             if(LIMITDATA) {
                    if(nrow(TEMP1) > nrow(TEMP0)) {
                           SELECT <- sample(1:nrow(TEMP1), nrow(TEMP0), replace = F)
                           SubData <- rbind(TEMP0, TEMP1[SELECT,])
                    }
                    ## but when there are more lines with 0 than with 1 do this:
                    if(nrow(TEMP1) < nrow(TEMP0)) {
                       # tk_messageBox(type = c("ok"),
                       #            "yes", caption = "", default = "")
                       SELECT <- sample(1:nrow(TEMP0), nrow(TEMP1), replace = F)
                       SubData <- rbind(TEMP0[SELECT,], TEMP1)
                    }
                    if(nrow(TEMP1) == nrow(TEMP0)) {
                           SubData <- TEMP
                    }
             } else {
                    SubData <- TEMP
             }

        if(nrow(SubData)>= 10) {

          ## step to next factor if only postive or negative observations are available
          if(mean(SubData[,1], na.rm=T)%in% c(0,1)  )  {next}

          ## step to next FACTOR if no covariate information available
          if(mean(SubData[,2], na.rm=T)==0  )  {next}
          if (length(is.na(SubData[,2])) < 10) {next}

          # calculate squared version of FACTOR
               SubData$squared <- SubData[,2]^2

          ## stepwise variable selection
          #    glm.model <- step(glm(observed ~ get(eval(FACTOR)) + squared, family =
binomial(logit), data = SubData),direction="both")  ##
                    glm.model1 <- glm(observed ~ get(eval(FACTOR)) , family =
binomial(logit), data = SubData)
                    glm.model2 <- glm(observed ~ get(eval(FACTOR)) + squared, family =
binomial(logit), data = SubData)
          AIC1 <- AIC(glm.model1)
          AIC2 <- AIC(glm.model2)
          AICs <- data.frame(rbind(AIC1, AIC2))
          names(AICs) <- "AIC"
          # str(AICs)
          bestmodel <- which(AICs$AIC == min(AICs$AIC))
          if (bestmodel == 1)
             {glm.model <- glm.model1}
          if (bestmodel == 2)
             {glm.model <- glm.model2}

          SUMM <- summary(glm.model)
          SUMM

          ## Tenfold cross validation on 10% independent data
          AUC <- as.numeric()
          for (j in 1:10) {
            data <- glm.model$data
            rnd <- runif(dim(data)[1],0,1)
            # add random number
            data$rnd <- runif(dim(data)[1],0,1)
            # select 90% of data for modelling
            data.model <- data[data$rnd > 0.1, 1:(dim(data)[2]-1)]
```

```
            # select model to run
            ifelse (dim(data.model)[2]==2,
               glm.model.subset <- glm(observed ~ get(eval(FACTOR)), family =
binomial(logit), data = data.model),
               glm.model.subset <- glm(observed ~ get(eval(FACTOR)) + squared, family =
binomial(logit), data = data.model)
            )
            # select 10% indepent data and make predictions
            dat.independent <- data[data$rnd <= 0.1, 1:(dim(data)[2]-1)]
            if (length(table(dat.independent$observed))==2) {
               dat.independent$pred <-
predict(glm.model.subset,dat.independent[,2:dim(dat.independent)[2]], type="response")
               # calculate AUC
               AUC[j] <- cvAUC(dat.independent$pred,dat.independent[,1])$cvAUC
             } # end if
          } ## end cv AUC
          AUC
                                                    c
         glm_summary          <- data.frame(SUMM$coefficients)
          glm_summary$rownames <- row.names(glm_summary)
          glm_summary$species  <- SPECIES
          glm_summary$variable <- FACTOR
          glm_summary$AIC      <- AIC(glm.model)
          glm_summary$Expldev  <- (glm.model$null.deviance -
glm.model$deviance)/glm.model$null.deviance *100
          glm_summary$AUC      <- cvAUC(glm.model$fitted.values,glm.model$y)$cvAUC
          glm_summary$AUCmin   <- min(AUC)
          glm_summary$AUCmax   <- max(AUC)
          glm_summary$AUCmean  <- mean(AUC)
          glm_summary$NAbs     <- length(subset(glm.model$y,glm.model$y==0))
          glm_summary$NPres    <- length(subset(glm.model$y,glm.model$y==1))
          glm_summary$Ntot     <- length(glm.model$y)
          glm_summary
          glm_summary    <- subset(glm_summary, select =
c(species,variable,rownames,Estimate,Std..Error,z.value,
                   Pr...z..,Expldev,AIC,AUC,AUCmin,AUCmax,AUCmean,NAbs,NPres,Ntot))

          write.table(glm_summary, file=paste(PATH1,SPECIES, "_glm_summary",FILEEXT,".csv",
sep = ""),sep=";",row.names=F,col.names=F,append=T)

               ## PREDICTIE
               newdata <- SubData[,2:3]
               newdata <- newdata[order(newdata[,1]),]
               preds <- predict(glm.model, newdata = newdata, type = "response")
               plot(preds ~ newdata[,1], type = "l",col="blue",
                        xlab = FACTOR, ylab = "Presence", ylim = c(0,1)
                        )
               points(x = SubData[,2], y = SubData$observed, cex = 0.25)

               ## MAKE PREDICTION PLOTS
               png(paste(PATH1, SPECIES, "_", FACTOR, FILEEXT, ".png", sep = ""),
width=1000, height=800)
               plot(preds ~ newdata[,1], type = "l", col="blue",
                        xlab = FACTOR, ylab = "Presence", ylim = c(0,1),
                        main = paste(SPECIES, ":  ", FACTOR, "
(",gsub("_","",FILEEXT),")",sep=""))
               points(x = SubData[,2], y = SubData$observed, cex = 0.25)
               dev.off()
        #}

### REMOVE HASHES BEFORE FOLLOWING THREE LINES TO RUN MODELS WITHOUT BOOTSTRAPPING

    #  } # temporary end for 'species end for if(nrow(SubData)>= 10)'
    # } # temporary end for 'FACTORS'
  # } #  temporary end for 'species'



        ########################################################################
        #
        # model bootstrapping
        #
        ########################################################################

         nboots <- 20

         j <- 1      # for testing

          for (j in 1:nboots) {
            data <- glm.model$data
            rnd <- runif(dim(data)[1],0,1)
            # add random number
```

```
            data$rnd <- runif(dim(data)[1],0,1)
            # select 90% of data for modelling
            data.model <- data[data$rnd >= 0.5, 1:(dim(data)[2]-1)]
            # select model to run
#                            try(assign(paste("glm.model.boot",j,sep=""),
step(glm(observed ~ get(eval(FACTOR)) + squared, family = binomial(logit), data =
data.model),
#                 direction="both")),silent=T)
                      try(glm.model.boot.1 <-  glm(observed ~ get(eval(FACTOR)), family =
binomial(logit), data = data.model) ,silent=T)
                      try(glm.model.boot.2 <-  glm(observed ~ get(eval(FACTOR)) + squared,
family = binomial(logit), data = data.model),silent=T)
            try(AIC1 <- AIC(glm.model.boot.1),silent=T)
            try(AIC2 <- AIC(glm.model.boot.2),silent=T)

            try(AICs <- data.frame(rbind(AIC1, AIC2)),silent=T)
            try(names(AICs) <- "AIC", silent=T)
            # str(AICs)
            try( bestmodel <- which(AICs$AIC == min(AICs$AIC)),silent=T)
            if (bestmodel == 1)
              {assign(paste("glm.model.boot",j,sep=""), glm.model.boot.1)}
            if (bestmodel == 2)
              {assign(paste("glm.model.boot",j,sep=""), glm.model.boot.2)}


            # calculate model predictions
                 newdata <- SubData[,2:3]
                 newdata <- newdata[order(newdata[,1]),]
                 assign(paste("preds",j,sep=""),
predict(get(paste("glm.model.boot",j,sep="")), newdata = newdata, type = "response"))
            assign(paste("preds",j,sep=""), cbind(newdata[,1],get(paste("preds",j,sep=""))))
            } # end for 1:nboots

          ## make plot
               png(paste(PATH2, SPECIES, "_", FACTOR, FILEEXT, "_boot.png", sep = ""),
width=1000, height=800)
                      newdata <- SubData[,2:3]
                      newdata <- newdata[order(newdata[,1]),]
                      preds <- predict(glm.model, newdata = newdata, type = "response")
                      plot(preds ~ newdata[,1], type = "l",col="blue",
                               xlab = FACTOR, ylab = "Predictions", ylim = c(0,1), main =
paste(SPECIES, ":  ", FACTOR, "   (",gsub("_","",FILEEXT),")",sep="")

                               )
            for (j in 1:nboots) {
                points(get(paste("preds",j,sep=""))[,2] ~ newdata[,1], type =
"l",col="grey")
            }
                      points(preds ~ newdata[,1], type = "l",col="red",lwd=2)
            legend("topright",col=c("red","grey"),lwd=2,legend= c("complete
model","bootstraps" ))
          dev.off()

        } # end for if(nrow(SubData)>= 10)

         ## combine bootstraps
          try(assign(paste(FACTOR,".preds.boot",sep=""),data.frame(preds1)), silent=T)
          if (length(get(paste(FACTOR,".preds.boot",sep="")))>0 ) {
            for (j in 2:nboots) {
              assign(paste(FACTOR,".preds.boot",sep=""),
rbind(get(paste(FACTOR,".preds.boot",sep="")),data.frame(get(paste("preds",j,sep=""))) )  )
            } # end for boots
            tmp <- get(paste(FACTOR,".preds.boot",sep=""))
            tmp$sample.id <- row.names(tmp)
            tmp$species   <- SPECIES
            names(tmp) <- c(FACTOR,"pred","sample.id","species")
            assign(paste(FACTOR,".preds.boot",sep=""), tmp)
          } # end for if

          # tail(tmp)

          ## save bootstrap predictions to table

write.table(get(paste(FACTOR,".preds.boot",sep="")),paste(PATH2,SPECIES,"_",FACTOR,"_bootstr
aps.csv",sep=""),sep=";",row.names=F)


          ## bootstrap summaries
          boot.summaries <- aggregate(tmp[,2] ~ tmp[,1], data= tmp, mean )
          names(boot.summaries) <- c("value", "mean")
          boot.summaries.sd <- aggregate(tmp[,2] ~ tmp[,1], data= tmp, sd)
          names(boot.summaries.sd) <- c("value", "sd")
```

```
          boot.summaries <- merge(boot.summaries, boot.summaries.sd, by="value")
          head(boot.summaries)

          boot.summaries$min     <- boot.summaries$mean - boot.summaries$sd
          boot.summaries$max     <- boot.summaries$mean + boot.summaries$sd
          boot.summaries$range   <- boot.summaries$max - boot.summaries$min
          boot.summaries$ratio   <- boot.summaries$sd/boot.summaries$mean
          boot.summaries$species <- SPECIES

               png(paste(PATH2, SPECIES, "_", FACTOR, FILEEXT, "_bootstrapsummaries.png",
sep = ""), width=1000, height=800)
            plot(boot.summaries$value,boot.summaries$max, col="grey",
                ylim=c( min(boot.summaries$min)-0.05,max(boot.summaries$max)+0.05),
ylab="bootstrap predictions", xlab=FACTOR,
                                              main = paste(SPECIES, ":  ", FACTOR,"
(",gsub("_","",FILEEXT),")",sep=""))
            points(boot.summaries$value,boot.summaries$mean, col="red")
            points(boot.summaries$value,boot.summaries$min, col="grey")
            #lines(boot.summaries$value,boot.summaries$ratio, col="blue", xlab=FACTOR,
main=FACTOR )
            legend("topright",col=c("red","grey"),lwd=2,legend= c("bootstrap
mean","bootstrap sd" ))
            abline(h = 0, col = "gray60", lty="dashed")
          dev.off()

          ## local regressions
          # declare groups by quantiles
          boot.summaries$groups  <- cut(boot.summaries[,1],
quantile(boot.summaries[,1],probs = seq(0, 1, 0.05), na.rm = T))
          boot.summaries$groupnr <- as.numeric(boot.summaries$groups)

          k <- 1
          coeff.max <- coeff.min <- NA
          for (k in 1:length(na.omit(unique(boot.summaries$groupnr)))) {
            dat.sel <- boot.summaries[boot.summaries$groupnr==k,]
            ff1 <- try(coeff.max[k] <- coefficients(lm(max~value,data=dat.sel
))[2],silent=T)
            ff2 <- try(coeff.min[k] <- coefficients(lm(min~value,data=dat.sel
))[2],silent=T)

          } # end for 1:length(na.omit(unique(boot.summaries$groupnr)))
          if (class(ff1) != "try-error" | class(ff2) != "try-error") {
            quants <- quantile(boot.summaries[,1],probs = seq(0, 1, 0.05), na.rm = T)
            coeff.max
            coeff.min
            local.coefficients <- data.frame(cbind(quants[1:20],coeff.max,coeff.min))
            names(local.coefficients) <- c("break","coeff.max","coeff.min")
            local.coefficients$quantile <- row.names(local.coefficients)
            local.coefficients$variable <- FACTOR
            bootstraps.cutoffs <- try(local.coefficients[(local.coefficients$coeff.max <= 0
& local.coefficients$coeff.min >= 0) |
                               (local.coefficients$coeff.max >= 0 &
local.coefficients$coeff.min <= 0),], silent=T)
            if (dim(bootstraps.cutoffs)[1]>0) {
               local.coefficients <- merge(local.coefficients,bootstraps.cutoffs,
by="break",all.x=T)

write.table(local.coefficients,paste(PATH2,SPECIES,"_",FACTOR,"_boot_cutoffs.csv",sep=""),se
p=";",row.names=F)
            } # end if (dim(bootstraps.cutoffs)[1]>0)
          } ## end if (class(ff1) != "try-error" & class(ff2) != "try-error")

        }

               } ## end for FACTORS per species

       } ## end for i in filenames[1:length(filenames)] (all species files)



beep("fanfare")


## Combine the csv-files into one file
################################################################

CSV_PATH1 <- paste(getwd(),"/",modeldir,"/","_csv","/",sep="")
dir.create(CSV_PATH1)

dirs <- list.dirs(path = paste(getwd(),"/",modeldir,"/",".",sep=""), full.names = FALSE,
recursive = FALSE)
dirs
```

```
dirswd <- paste(getwd(),"/",modeldir,"/",sep="")  ## capture model directory
dirswd

outfile="Univariate_models_all.csv"

filenames <- list.files(paste(dirswd,dirs[2],sep="/"), recursive=FALSE, full=FALSE)
csvfile <- filenames[grep(".csv",tolower(filenames),fixed=T)]
csvfile
dat <- read.table(paste(dirswd,dirs[2],csvfile,sep="/"),sep=";", header=T, as.is=T )
str(dat)
write.table(dat,paste(getwd(),"/",modeldir,"/_csv/",outfile,sep=""),sep=";",row.names=F)

for (i in dirs[3:length(dirs)]) {
   filenames <- list.files(paste(dirswd,i,sep="/"), recursive=FALSE, full=FALSE)
   csvfile <- filenames[grep(".csv",tolower(filenames),fixed=T)]
   csvfile
   try(dat <- read.table(paste(dirswd,i,csvfile,sep="/"),sep=";", header=T, as.is=T ),
silent=T)
   if (class(dat) != "try-error") {
   write.table(dat, paste(getwd(),"/",modeldir,"/_csv/",outfile,sep=""), sep=";", col.names
= FALSE,
              row.names = F, append = TRUE)
              } ## end for try
}


## Crostabulate estimates per variable
#######################################################
models <- read.table(paste(getwd(),"/",modeldir,"/_csv/",outfile,sep=""), sep=";", header=T,
as.is=T)
str(models)

## part1
part1 <- subset(models, select=c(species,variable,rownames,
Estimate,Std..Error,z.value,Pr...z..))
str(part1)
part1$id <- paste(part1$species,"_",part1$variable,sep="")

part1.1 <- part1[part1$rownames=="(Intercept)",]
head(part1.1)
names(part1.1) <-
c("Species","Variable","rowname","Intercept_estimate","Intercept_SE","Intercept_zval","Inter
cept_Pval","id")
part1.1 <- part1.1[,-3]

part1.2 <- part1[part1$rownames=="get(eval(FACTOR))",]
head(part1.2)
names(part1.2) <-
c("Species","Variable","rowname","Variable_estimate","Variable_SE","Variable_zval","Variable
_Pval","id")
part1.2 <- part1.2[,-3]

part1.3 <- part1[part1$rownames=="squared",]
head(part1.3)
names(part1.3) <-
c("Species","Variable","rowname","Varsquared_estimate","Varsquared_SE","Varsquared_zval","Va
rsquared_Pval","id")
part1.3 <- part1.3[,-3]

part1.tot <- merge(part1.1,part1.2[,3:7], by="id",all.x=T)
part1.tot <- merge(part1.tot,part1.3[,3:7], by="id",all.x=T)
head(part1.tot)

## part 2
part2 <- unique(subset(models,
select=c(species,variable,Expldev,AIC,AUC,AUCmin,AUCmax,AUCmean,NAbs,Npres,Ntot)))
part2$id <- paste(part2$species,"_",part2$variable,sep="")
str(part2)

#3 combine two parts
models.xtab <- merge(part1.tot,part2[3:12], by="id",all.x=T)
str(models.xtab)
models.xtab <- models.xtab[,2:24]

## write to csv-file
write.table(models.xtab,paste(getwd(),"/",modeldir,"/_csv/","Univariate_models_all_xtab.csv"
,sep=""),sep=";",row.names=F)
```

Annex 9 Multivariate analysis of vascular plants in 2 habitat types

Results CCA habitat type H4010

Assessment of relative effect of the environmental variables on species composition

Method: Canonical Correspondence Analysis (CCA)
Number of plots (active cases): 5061
Number of species: 160
Explanatory variables account for 20.0% (adjusted explained variation is 19.1%)

Summary table with ordination results:

Statistic	Axis 1	Axis 2	Axis 3	Axis 4
Eigenvalues	0.4195	0.2817	0.2306	0.1612
Explained variation (cumulative) 3.85	6.43	8.54	10.02	
Pseudo-canonical correlation	0.9405	0.9148	0.8878	0.8562
Explained fitted variation (cumulative)	19.21	32.12	42.68	50.07

Variable *Name*	Conditional Effect *Explains %*	Marginal Effect *Explains %*	Comment
R_avg (Acidity Ellenberg)	3.4	3.4	
N_avg (Nitrogen Ellenberg)	0.9	3.3	
L_avg (LightEllenberg)	0.7	2.5	
M_avg (Moisture Ellenb)	2.4	2.4	
bio_4 (Temperature seasonality)	1.6	2.1	Strong correlation with Bio6 (min temp coldest month; >0.7)
bio_6 (min temp cold. month)	0.2	2	Large decrease from marginal (simple) effect to conditional effect (indicative for a high degree of multicollinearity with other variables); strong corr. Bio4 en Alt
Alt	1	1.9	Strong correlation with Bio6 (min temp coldest month)
S_avg (Salinity Ellenberg)	0.6	1.8	
bio_9	0.2	1.5	Strong correlation with Bio4 (temp.seas; >0.7)
bio_3	0.2	1.5	Strong corr. Bio6 (min temp cold. month)
ndep_mean_5km	0.1	1.5	Large decrease from marginal (simple) effect to conditional effect (indicative for a high degree of multicollinearity with other variables); Very low correlation with Nitrogen-Ell (0.08); Low corr. With R-Ell (-0.12); high corr. Bio28, Bio14, Bio4, Div4_1 (>0.5)
T_avg (T Ellenberg)	1.4	1.4	
C_avg	0.4	1.4	Moderate corr. with Bio6 (min temp cold. Month)
bio_28	0.2	1.4	Strong correlation with Bio14 and Bio18
div4_1_10_mean_5km (Fragm. inland wetlands)	0.1	1.4	Very strong correlation with div4_1_20
div3_1_20_mean_5km (Frag.forest)	0.1	1.4	
div4_1_20_mean_5km (Fragm. inl. wetlands)	0.5	1.3	Very strong corr. with div*_10 (given low LDD ability of plants we prefer *_10)

Variable *Name*	Conditional Effect *Explains %*	Marginal Effect *Explains %*	Comment
bio_14 (Precipit.driest month)	0.2	1.2	
bio_18 (Precipit.warmest quarter)	0.2	1	Strong correlation with Bio14 (precipit.driest month) and Bio28
tsum	<0.1	1	
div3_2_20_mean_5km (Fragment.shrub/herb.veg.)	0.4	0.9	Very strong corr. with div*_10 (given low LDD ability of plants we prefer *_10)
sdep_mean_5km	0.1	0.9	Moderate corr. With Ndep
soil_silt	<0.1	0.9	
desic_mean_5km	<0.1	0.9	Very low correlation with Moisture-Ell (<0.01)
napplication_5km	<0.1	0.8	Low correlation with Nitrogen-Ell (-0.15) and R-Ell (-0.19)
soil_clay	<0.1	0.8	
soil_oc	0.1	0.7	
fma_f1_5km	0.3	0.6	
div5_1_20_mean_5km (Fragment. inland waters)	0.2	0.5	
soil_salt	<0.1	<0.1	
soil_ph	0.1		
div5_1_10_mean_5km	0.1		
apet	<0.1		

Response curves H4010

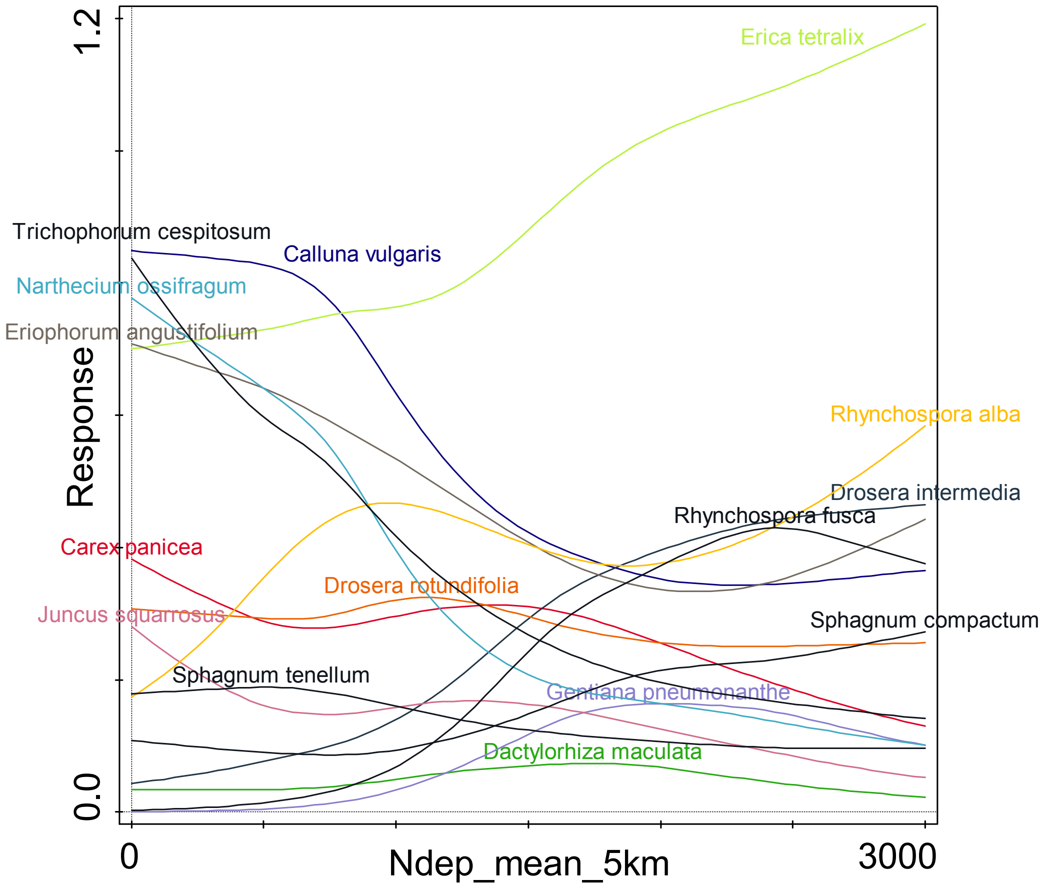
Nitrogen deposition (log-abundance)

Summary of fitted Generalized Additive Models (GAM; log-abundance):

Predictors	ndep_mean_5km
Distribution	Poisson
Link function	log

GAM fitted for 15 response variables (species in blue = $R^2 \geq 5\%$):

Response	**Type**	**R2[%]**	**F**	**p**
Calluna vulgaris	s3	10.2	152.4	<0.00001
Carex panicea	s3	1.2	14.0	<0.00001
Dactylorhiza maculata	s3	2.5	11.8	<0.00001
Drosera intermedia	s3	17.5	186.2	<0.00001
Drosera rotundifolia	s3	0.9	7.8	0.00003
Erica tetralix	s3	4.6	42.0	<0.00001
Eriophorum angustifolium	s3	6.2	64.5	<0.00001
Gentiana pneumonanthe	s3	28.7	151.0	<0.00001
Juncus squarrosus	s3	1.7	17.2	<0.00001
Narthecium ossifragum	s3	16.6	231.4	<0.00001
Rhynchospora alba	s3	2.2	32.7	<0.00001
Rhynchospora fusca	s3	29.9	348.4	<0.00001
Sphagnum compactum	s3	4.4	46.6	<0.00001
Sphagnum tenellum	s3	1.6	17.8	<0.00001
Trichophorum cespitosum	s3	9.7	148.8	<0.00001



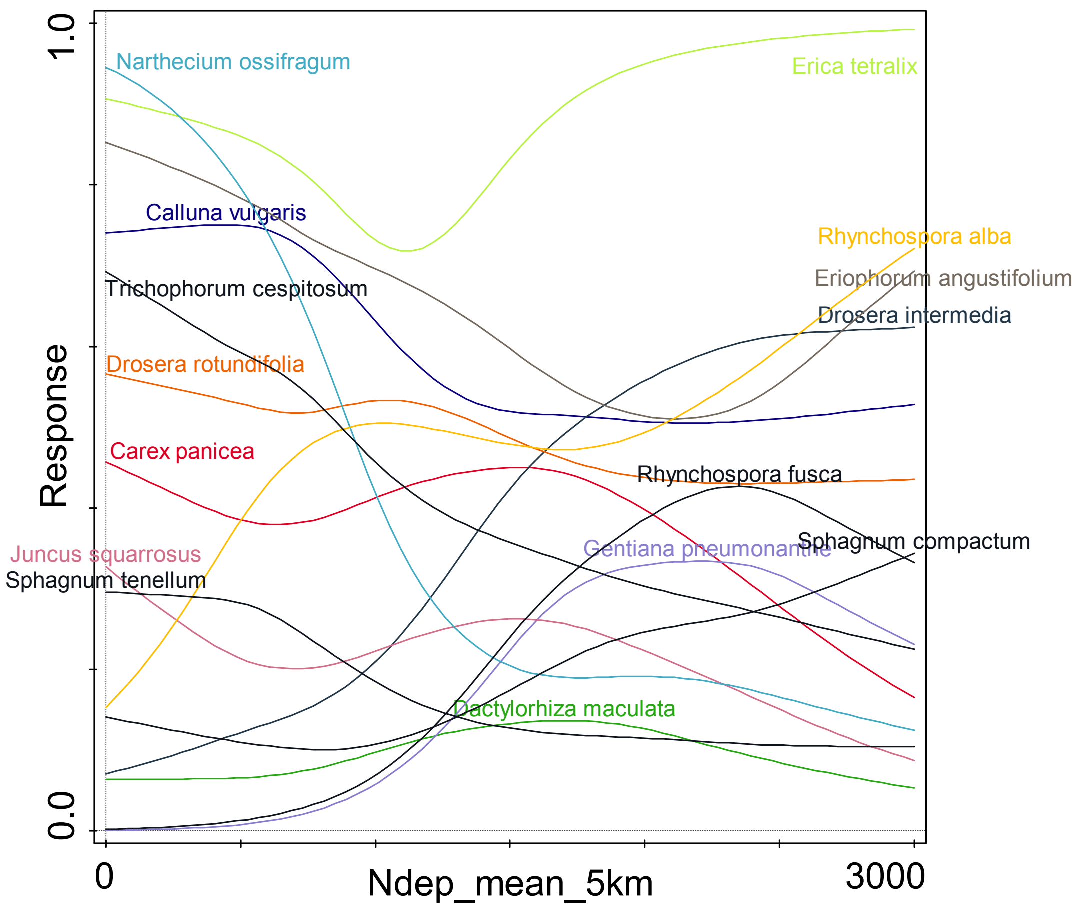
Nitrogen deposition (Presence /Absence)

Summary of fitted Generalized Additive Models:

Predictors	ndep_mean_5km
Distribution	binomial
Link function	logit

GAM fitted for 15 response variables (species in blue = R2≥5):

Response	**Type**	**R2[%]**	**F**	**p**
Calluna vulgaris	s3	4.4	111.0	<0.00001
Carex panicea	s3	0.9	22.7	<0.00001
Dactylorhiza maculata	s3	1.8	22.2	<0.00001
Drosera intermedia	s3	14.2	345.1	<0.00001
Drosera rotundifolia	s3	0.7	19.6	<0.00001
Erica tetralix	s3	7.3	134.5	<0.00001
Eriophorum angustifolium	s3	4.0	99.9	<0.00001
Gentiana pneumonanthe	s3	24.6	351.3	<0.00001
Juncus squarrosus	s3	1.2	27.5	<0.00001
Narthecium ossifragum	s3	21.6	646.6	<0.00001
Rhynchospora alba	s3	2.4	67.2	<0.00001
Rhynchospora fusca	s3	25.5	428.1	<0.00001
Sphagnum compactum	s3	3.8	65.5	<0.00001
Sphagnum tenellum	s3	3.4	70.7	<0.00001
Trichophorum cespitosum	s3	4.6	124.5	<0.00001



Comment

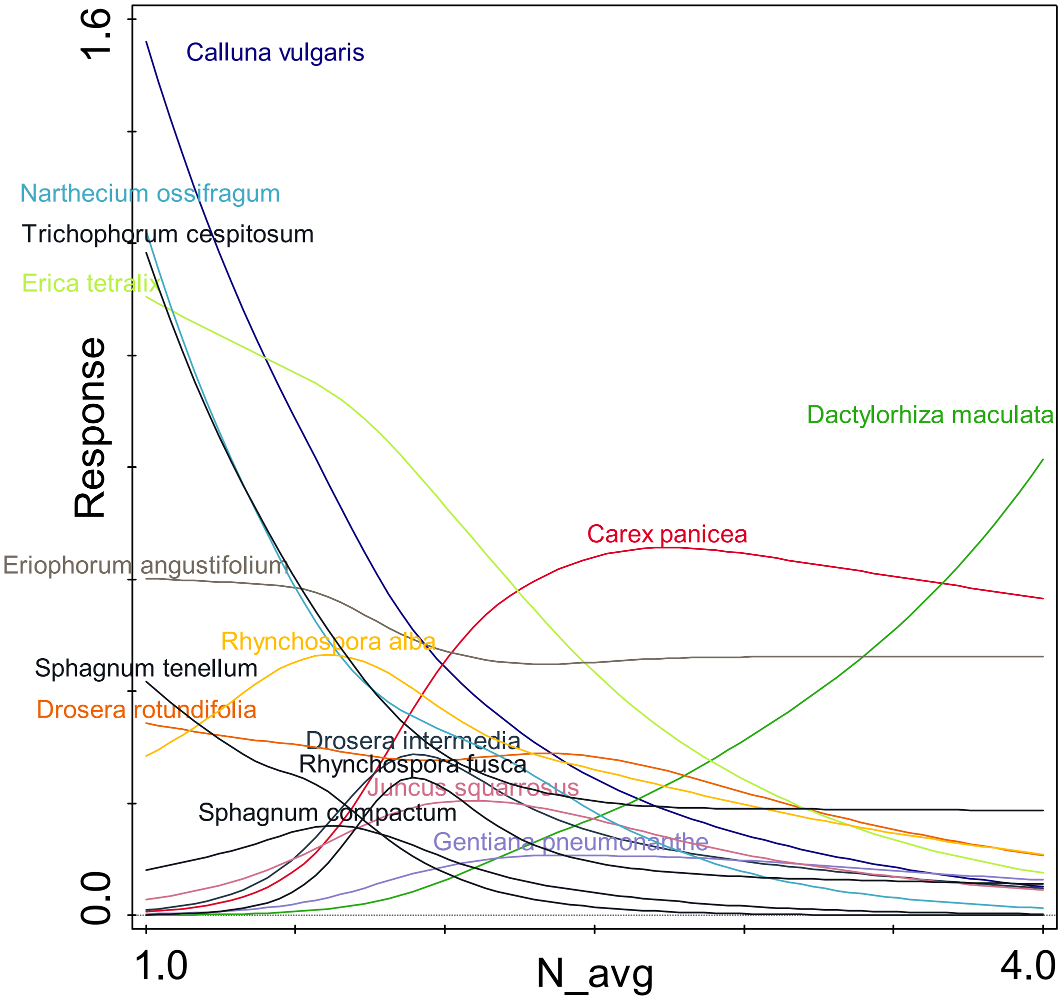
- Log abundance vs. Presence/absence: consistent patterns; log-abundance has better fit for 11 out of 15 species (for the exceptions the fit was in general poor)
- Response curve for Erica tetralix (increase with N)is unlikely, but R^2 low; For Nitrogen-Ellenberg this species has a decline with N (see below)

Nitrogen Ellenberg (log- abundance)

Summary of fitted Generalized Additive Models:

Predictors N_avg
Distribution Poisson
Link function log
GAM fitted for 15 response variables (species in blue = R2≥5):

Response	**Type**	**R2[%]**	**F**	**p**
Calluna vulgaris	s3	14.3	207.6	<0.00001
Carex panicea	s3	28.1	336.6	<0.00001
Dactylorhiza maculata	s3	25.5	120.9	<0.00001
Drosera intermedia	s3	9.7	106.9	<0.00001
Drosera rotundifolia	s3	0.3	3.1	0.02509
Erica tetralix	s3	10.2	95.3	<0.00001
Eriophorum angustifolium	s3	1.3	13.7	<0.00001
Gentiana pneumonanthe	s3	9.2	48.2	<0.00001
Juncus squarrosus	s3	3.4	35.4	<0.00001
Narthecium ossifragum	s3	9.2	127.6	<0.00001
Rhynchospora alba	s3	2.3	35.0	<0.00001
Rhynchospora fusca	s3	13.4	154.3	<0.00001
Sphagnum compactum	s3	3.3	35.0	<0.00001
Sphagnum tenellum	s3	11.6	127.6	<0.00001
Trichophorum cespitosum	s3	8.9	135.8	<0.00001

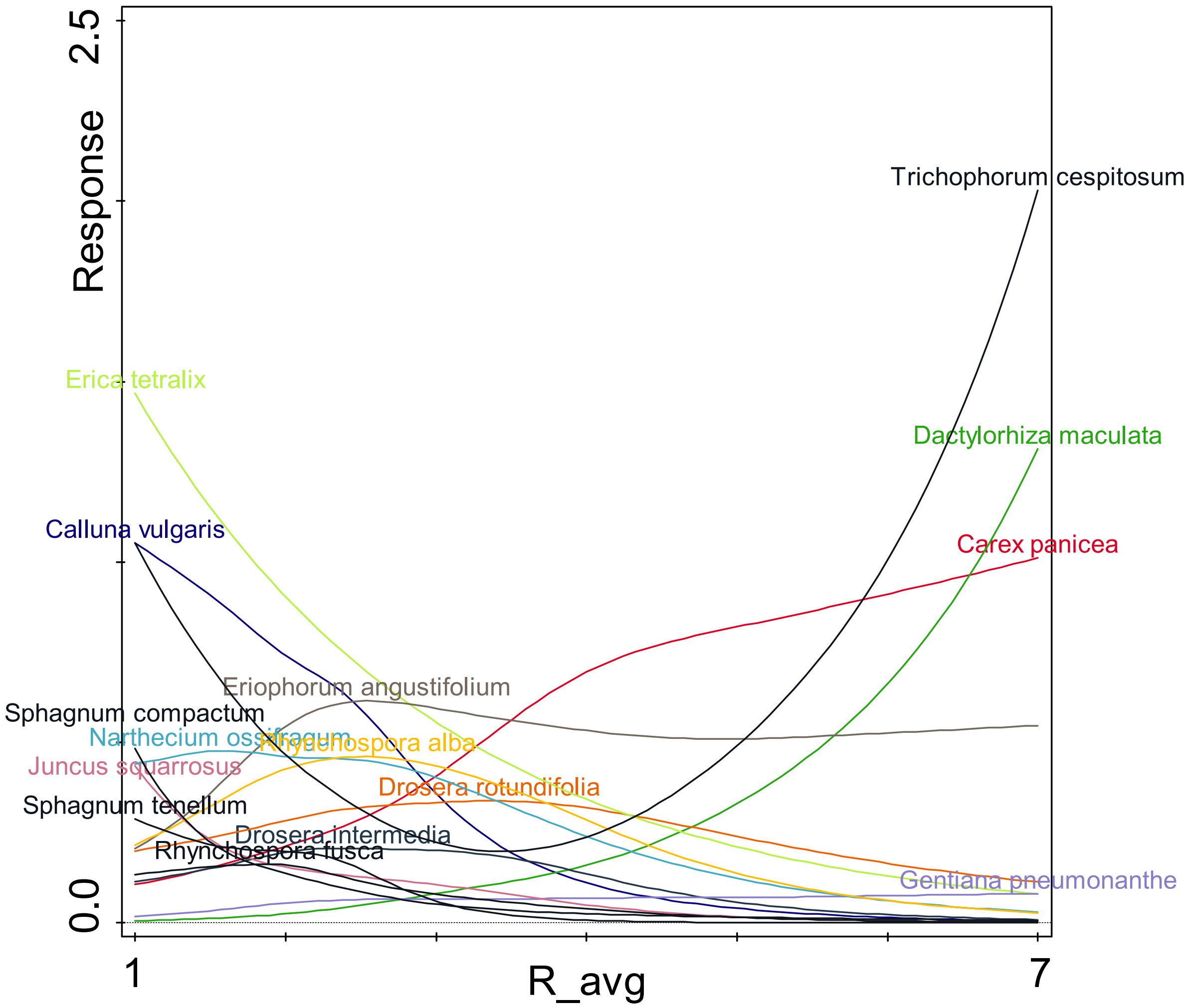


Soil Acidity Ellenberg (log abundance)

Summary of fitted Generalized Additive Models:

Predictors R_avg
Distribution Poisson
Link function log
GAM fitted for 15 response variables (species in blue = R2≥5):

Response	**Type**	**R2[%]**	**F**	**p**
Calluna vulgaris	s3	14.9	217.5	<0.00001
Carex panicea	s3	10.9	137.0	<0.00001
Dactylorhiza maculata	s3	14.8	69.4	<0.00001
Drosera intermedia	s3	1.3	13.9	<0.00001
Drosera rotundifolia	s3	1.2	10.6	<0.00001
Erica tetralix	lin	16.5	445.2	<0.00001
Eriophorum angustifolium	s3	5.2	53.7	<0.00001
Gentiana pneumonanthes3	1.6	8.4	0.00002	
Juncus squarrosus	s3	4.2	44.4	<0.00001
Narthecium ossifragum	s3	2.0	29.0	<0.00001
Rhynchospora alba	s3	2.0	32.2	<0.00001
Rhynchospora fusca	s3	2.9	33.0	<0.00001
Sphagnum compactum	s3	7.2	80.0	<0.00001
Sphagnum tenellum	s3	8.1	89.8	<0.00001
Trichophorum cespitosum	s3	10.3	160.3	<0.00001

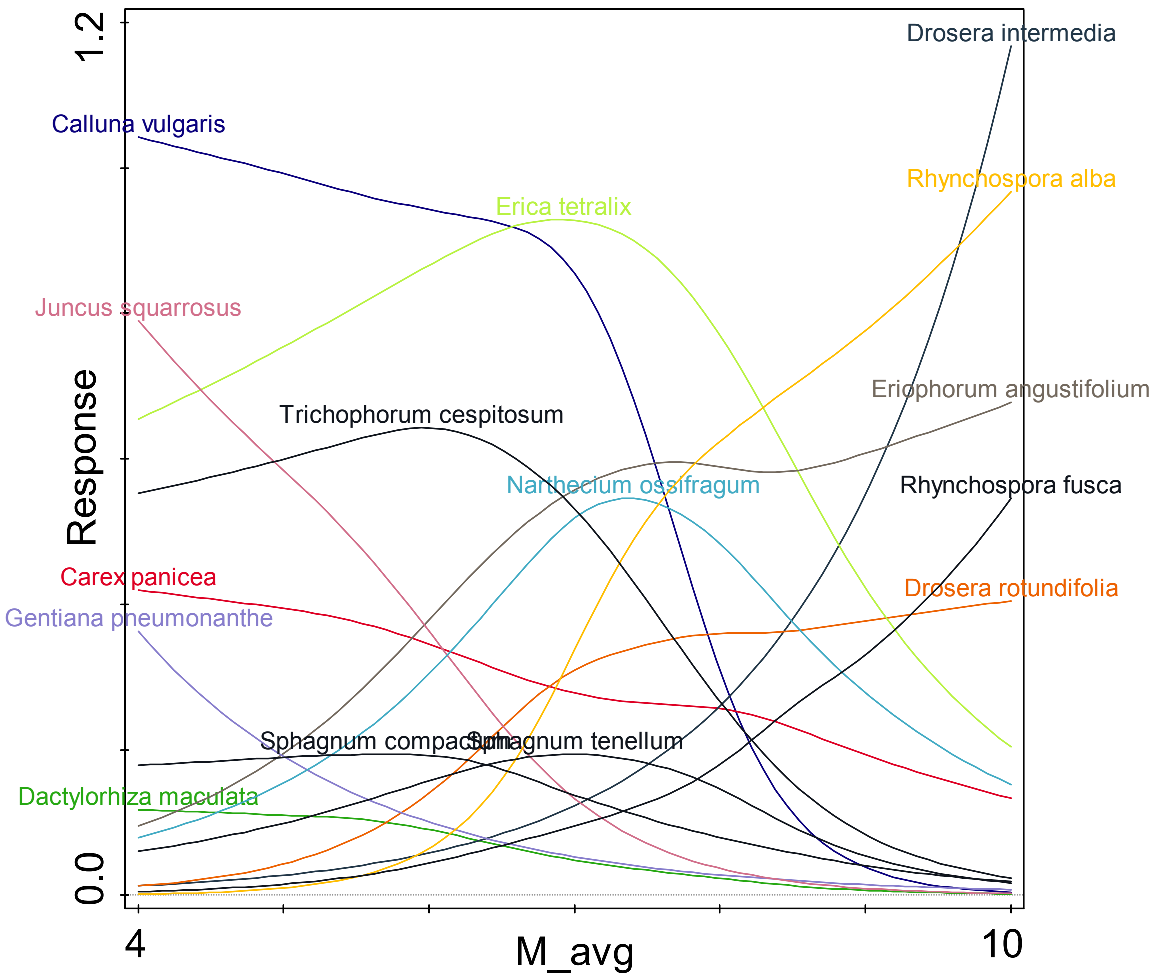


Moisture Ellenberg (log-abundance)

Summary of fitted Generalized Additive Models:

Predictors M_avg
Distribution Poisson
Link function log
GAM fitted for 15 response variables (species in blue = R2≥5):

Response	**Type**	**R2[%]**	**F**	**p**
Calluna vulgaris	s3	33.1	483.3	<0.00001
Carex panicea	s3	1.4	16.9	<0.00001
Dactylorhiza maculata	s3	7.7	36.3	<0.00001
Drosera intermedia	lin	15.7	497.5	<0.00001
Drosera rotundifolia	s3	8.9	80.6	<0.00001
Erica tetralix	s3	7.1	64.7	<0.00001
Eriophorum angustifolium	s3	5.1	53.4	<0.00001
Gentiana pneumonanthe	lin	8.2	126.8	<0.00001
Juncus squarrosus	s3	24.9	250.7	<0.00001
Narthecium ossifragum	s3	5.2	72.3	<0.00001
Rhynchospora alba	s3	24.3	372.7	<0.00001
Rhynchospora fusca	s3	8.6	99.2	<0.00001
Sphagnum compactum	s3	4.0	43.6	<0.00001
Sphagnum tenellum	s3	2.9	33.2	<0.00001
Trichophorum cespitosum	s3	12.0	184.1	<0.00001

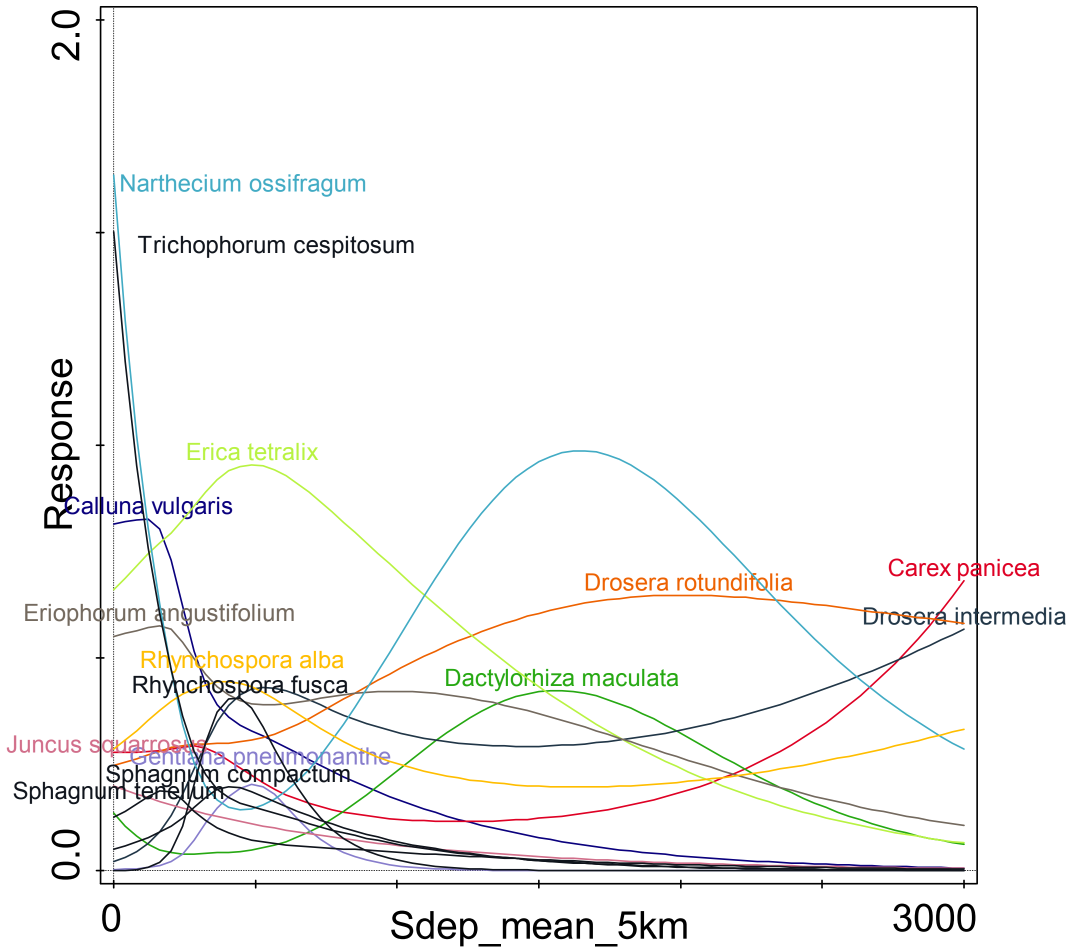


Sulphur deposition (log-abundance)

Summary of fitted Generalized Additive Models:

Predictors sdep_mean_5km
Distribution Poisson
Link function log

Response	**Type**	**R2[%]**	**F**	**p**
Calluna vulgaris	s3	8.2	117.0	<0.00001
Carex panicea	s3	0.5	6.2	0.00033
Dactylorhiza maculata	s3	2.5	12.0	<0.00001
Drosera intermedia	s3	14.5	163.4	<0.00001
Drosera rotundifolia	s3	0.2	2.3	0.07637
Erica tetralix	s3	1.3	12.6	<0.00001
Eriophorum angustifolium	s3	2.4	24.9	<0.00001
Gentiana pneumonanthe	s3	23.8	125.2	<0.00001
Juncus squarrosus	lin	0.5	11.5	0.00033
Narthecium ossifragum	s3	19.3	275.3	<0.00001
Rhynchospora alba	s3	0.5	7.2	0.00009
Rhynchospora fusca	s3	27.8	329.3	<0.00001
Sphagnum compactum	s3	2.7	29.4	<0.00001
Sphagnum tenellum	s3	2.5	26.9	<0.00001
Trichophorum cespitosum	s3	11.9	186.4	<0.00001



Comment

- Very weak conditional effect in ordination model (see “Summary table with ordination results”)
- Carex panicea (with unplausible positive effect of high S) has very low R2

Bio 4 (temperature seasonality)

Summary of fitted Generalized Additive Models:

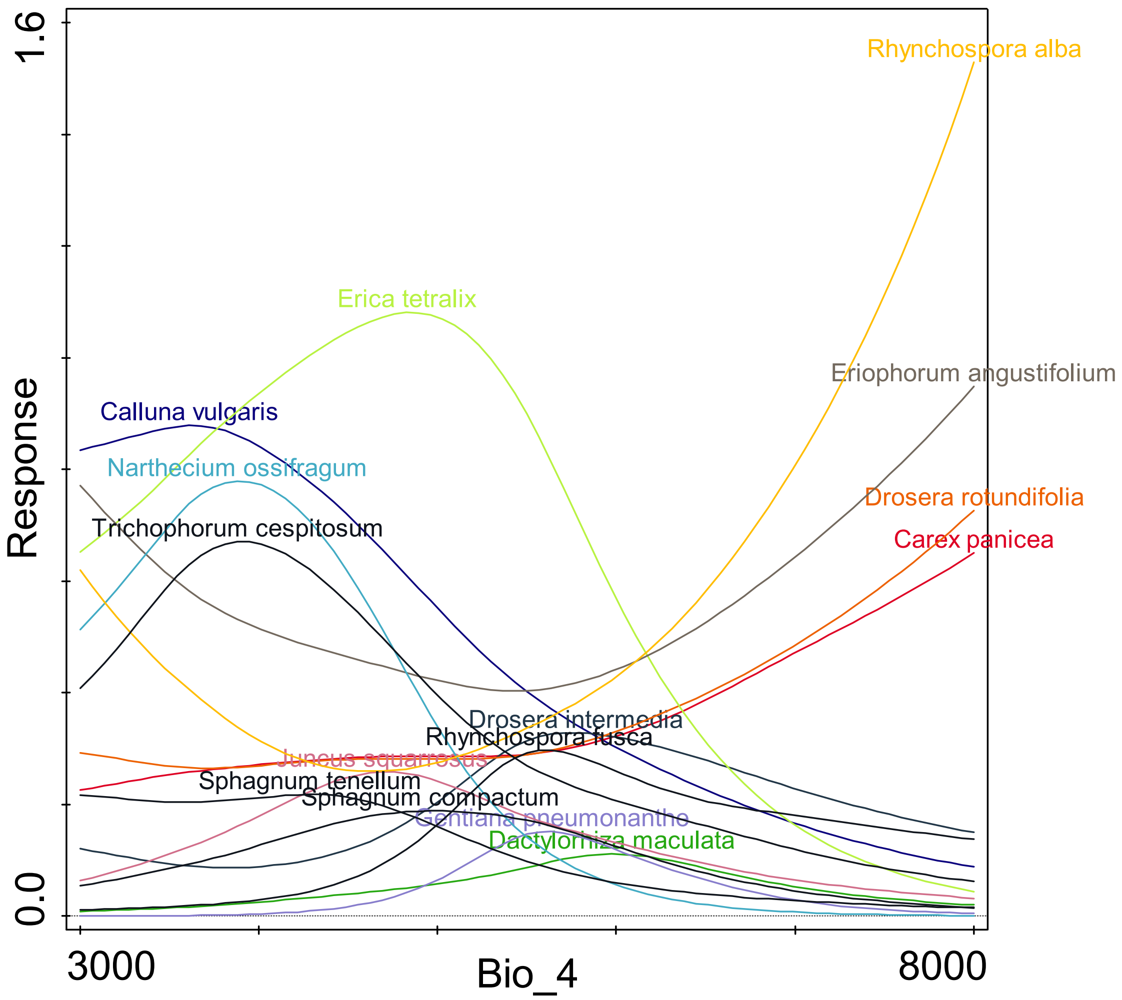
Predictors bio_4

Distribution Poisson

Link function log

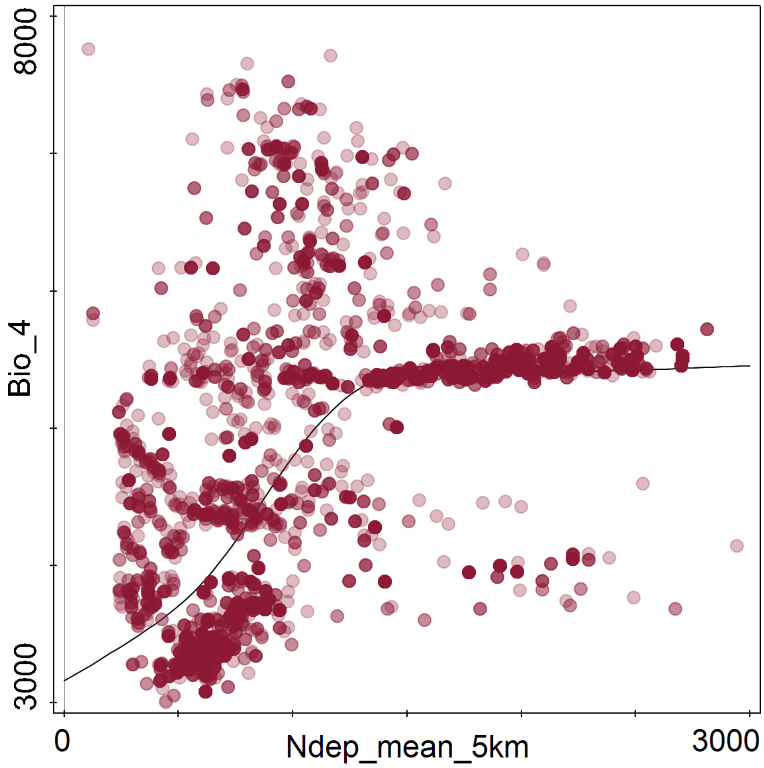
GAM fitted for 15 response variables:

Response	Type	R2[%]	F	p	
Calluna vulgaris	s3	14.4	219.3	<0.00001	
Carex panicea	s3	1.5	18.2	<0.00001	
Dactylorhiza maculata	s3	12.4	57.8	<0.00001	
Drosera intermedia	s3	12.8	137.1	<0.00001	
Drosera rotundifolia	s3	1.8	16.1	<0.00001	
Erica tetralix	s3	16.1	150.4	<0.00001	
Eriophorum angustifolium	s3	5.7	58.3	<0.00001	
Gentiana pneumonanthe	s3	35.2	188.0	<0.00001	
Juncus squarrosus	s3	5.3	54.0	<0.00001	
Narthecium ossifragum	s3	31.7	438.3	<0.00001	
Rhynchospora alba	s3	5.9	88.4	<0.00001	[unlikely]
Rhynchospora fusca	s3	25.4	300.5	<0.00001	
Sphagnum compactum	s3	4.4	48.4	<0.00001	
Sphagnum tenellum	s3	5.6	64.1	<0.00001	
Trichophorum cespitosum	s3	10.7	162.1	<0.00001	



Relationship between Nitrogen-depostion (N-Ell) and temperature seasonlity (Bio4)

For Nitrogen deposition there is a moderate correlation with several BioClim variables (e.g. Bio4, Bio14, Bio28: r>0.5-0.7) which is reflected in a relatively large decline in its conditional effect relative to its marginal effect. An example of the relation between N-depotition and Bio4 is given below. The figure shows that high values of Nitrogen deposition (Ndep) occur in a limited range of the continentalility gradient (bio4).



Results CCA habitat type H6520

Selection of species

- Excl. species groups with difficult / cryptic taxa that are represented in the dataset with multiple taxa (e.g. Alchemilla, Festuca, Hieracium, Taraxacum, Thymus)
- Extra species for response curves: Calluna vulgaris (also H4010 and H4030), Antennaria dioica and a few species that are typical for H6510
- Taxonomy:
  - Centaurea nemoralis = Centaurea debeauxii subsp nemoralis (According to GBIF)
  - Crocus caeruleus = Crocus albiflorus (GBIF)
- Number of plots too low for the following typical species: Centaurea nemoralis (29); Valeriana repens (30)

Assessment of relative effect of the environmental variables on species composition

Method: Canonical Correspondence Analysis (CCA)
Explanatory variables account for 13.7% (adjusted explained variation is 13.4%)

Summary table with ordination results:

CCA axis	Axis 1	Axis 2	Axis 3	Axis 4
Eigenvalues	0.5779	0.4232	0.2950	0.2405
Explained variation (cumulative) 2.99	5.18	6.70	7.95	
Pseudo-canonical correlation	0.9709	0.9758	0.9554	0.9074
Explained fitted variation (cumulative)	21.84	37.83	48.97	58.06

Variable	Condit. eff. *Explains %*	Marg. eff. *Explains %*	Comment
L_avg (Light Ellenberg)	2.4	2.4	
S_avg (Salinity Ellenberg)	0.3	2.1	
M_avg (Moisture Ellenberg)	1.9	2	
T_avg (Temperature Ellenberg)	1.8	2	
N_avg (Nitrogen Ellenberg)	1.2	1.9	
R_avg (Acidity Ellenberg)	1.4	1.7	
bio_18 (precipitation warmest quarter)	0.2	1.4	Strong corr. Bio6 (min temp cold. month) and Bio28
alt	0.2	1.4	
bio_28	0.2	1.1	Strong corr. Bio14 and Bio18
bio_6 (min temp cold. month)	0.1	1.1	Strong corr. Bio3 (Isothermality)
sdep_mean_5km	0.7	0.8	Strong corr. Bio15
C_avg	0.6	0.8	
bio_9 (Mean temp driest quarter)	0.3	0.8	Moderate correlation with Bio15 (precipitation seasonality)
bio_14 (Precipit.driest month)	0.2	0.8	Strong correlation with Bio15 (precipitation seasonality)
bio_4 (Temp.seasonality)	0.2	0.8	Strong correlation with Bio9 (Mean temp driest quarter) and Bio15 (Precipitation seasonality)
tsum	0.2	0.8	
soil_ph	0.1	0.8	
div3_2_10_mean_5km	0.1	0.8	Strong correlation with Alt
ndep_mean_5km	0.4	0.7	Very low correlation with Nitrogen-Ell; Low corr. with R-Ell; moderate correlation with Altitude

Variable	Condit. eff. *Explains %*	Marg. eff. *Explains %*	Comment
bio_15 (Precipitation seasonality)	0.2	0.7	
bio_3 (Isothermality)	0.3	0.6	Strong corr. Bio6 (min temp cold. month)
soil_clay	0.1	0.5	
napplication_5km	<0.1	0.5	Very low correlation with Nitrogen-Ell; Low corr. With R-Ell
soil_silt	0.1	0.2	
desic_mean_5km	<0.1	0.2	Very low correlation with Moisture-Ell
soil_oc	<0.1	0.1	
apet	<0.1	<0.1	

Response curves H6520

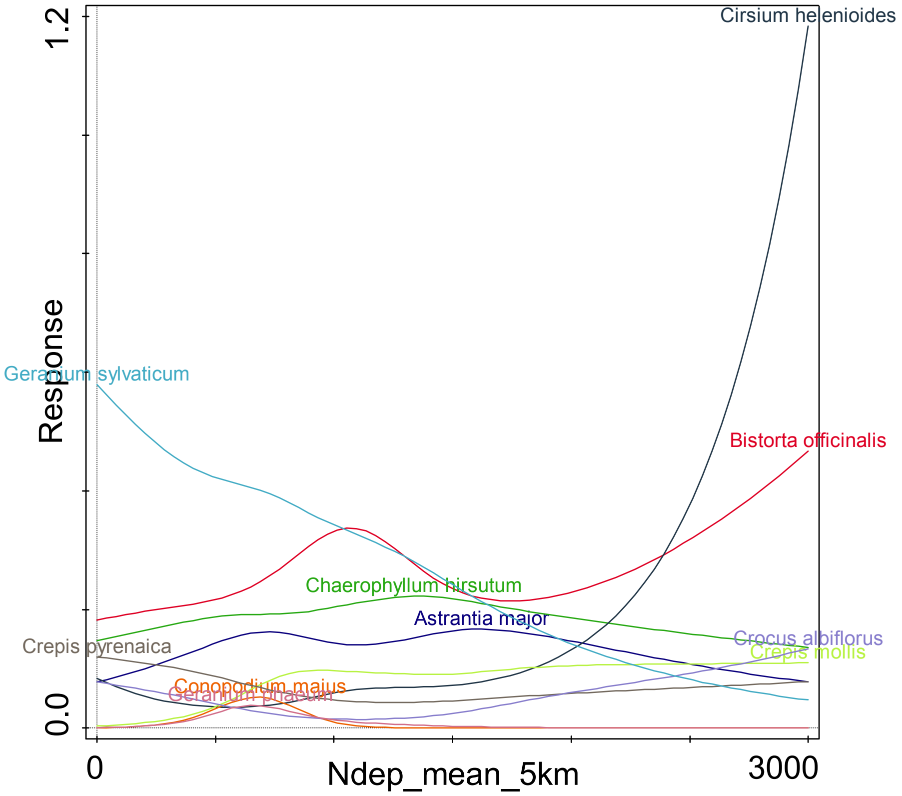
Nitrogen deposition

Summary of fitted Generalized Additive Models (GAM; log-abundance):

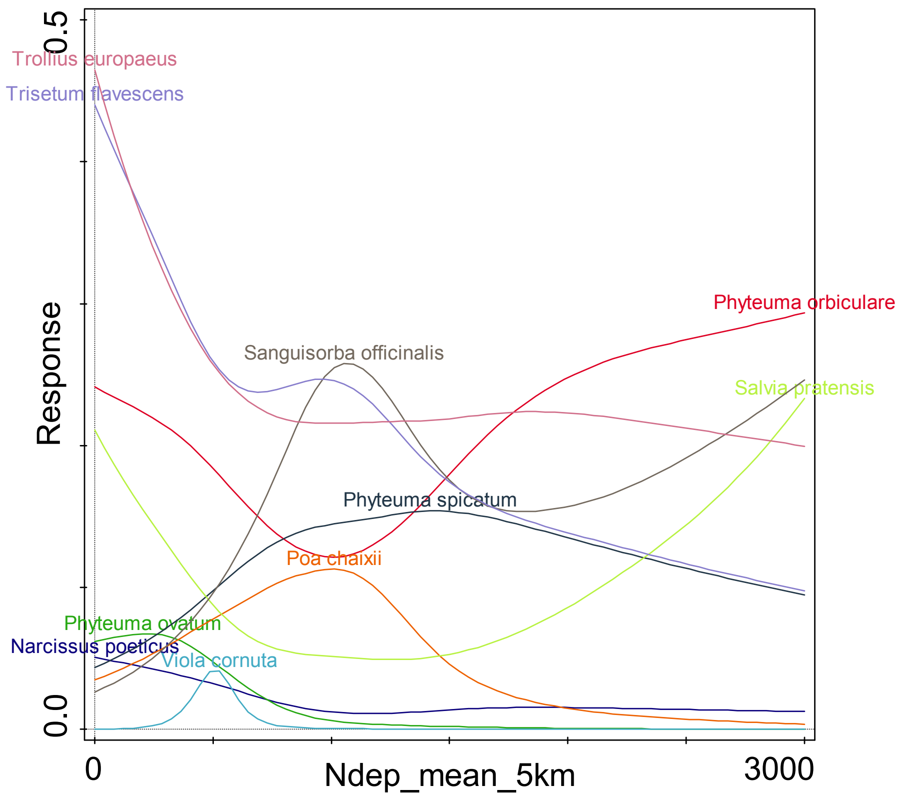
Predictors	ndep_mean_5km
Distribution	Poisson
Link function	log

GAM fitted for response variables (species in blue = $R^2 \geq 5$):

Response	**Type**	**R2[%]**	**F**	**p**
Astrantia major	s3	1.1	17.5	<0.00001
Bistorta officinalis	s3	3.0	58.1	<0.00001
Chaerophyllum hirsutum	s3	0.3	6.1	0.00038
Cirsium helenioides	s3	3.7	41.9	<0.00001
Conopodium majus	s3	15.7	71.7	<0.00001
Crepis mollis	s3	5.9	61.8	<0.00001
Crepis pyrenaica	s3	2.2	23.4	<0.00001
Crocus albiflorus	s3	5.4	29.3	<0.00001
Geranium phaeum	s3	8.4	35.8	<0.00001
Geranium sylvaticum	s3	2.4	42.1	<0.00001
Narcissus poeticus	s3	3.6	16.9	<0.00001
Phyteuma orbiculare	s3	2.5	33.6	<0.00001
Phyteuma ovatum	s3	15.6	66.4	<0.00001
Phyteuma spicatum	s3	1.7	20.8	<0.00001
Poa chaixii	s3	2.3	31.1	<0.00001
Salvia pratensis	s3	3.2	34.0	<0.00001
Sanguisorba officinalis	s3	6.3	118.1	<0.00001
Trisetum flavescens	s3	1.5	30.5	<0.00001
Trollius europaeus	s3	0.9	15.7	<0.00001
Viola cornuta	s3	29.7	64.3	<0.00001



1.2
Response
0.0
0
Ndep_mean_5km
3000
Cirsium helenioides
Geranium sylvaticum
Bistorta officinalis
Chaerophyllum hirsutum
Astrantia major
Crepis pyrenaica
Crocus albiflorus
Crepis mollis
Conopodium majus
Geranium phaeum

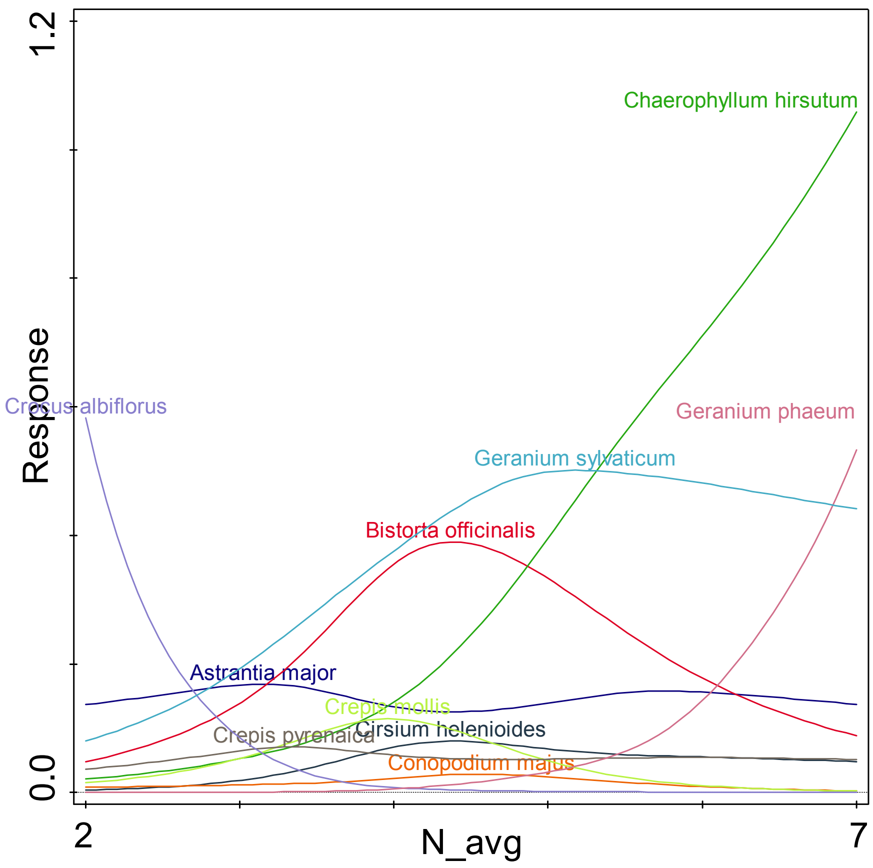


0.5
Response
0.0
0
Ndep_mean_5km
3000
Trollius europaeus
Trisetum flavescens
Phyteuma orbiculare
Sanguisorba officinalis
Salvia pratensis
Phyteuma spicatum
Poa chaixii
Phyteuma ovatum
Narcissus poeticus
Viola cornuta

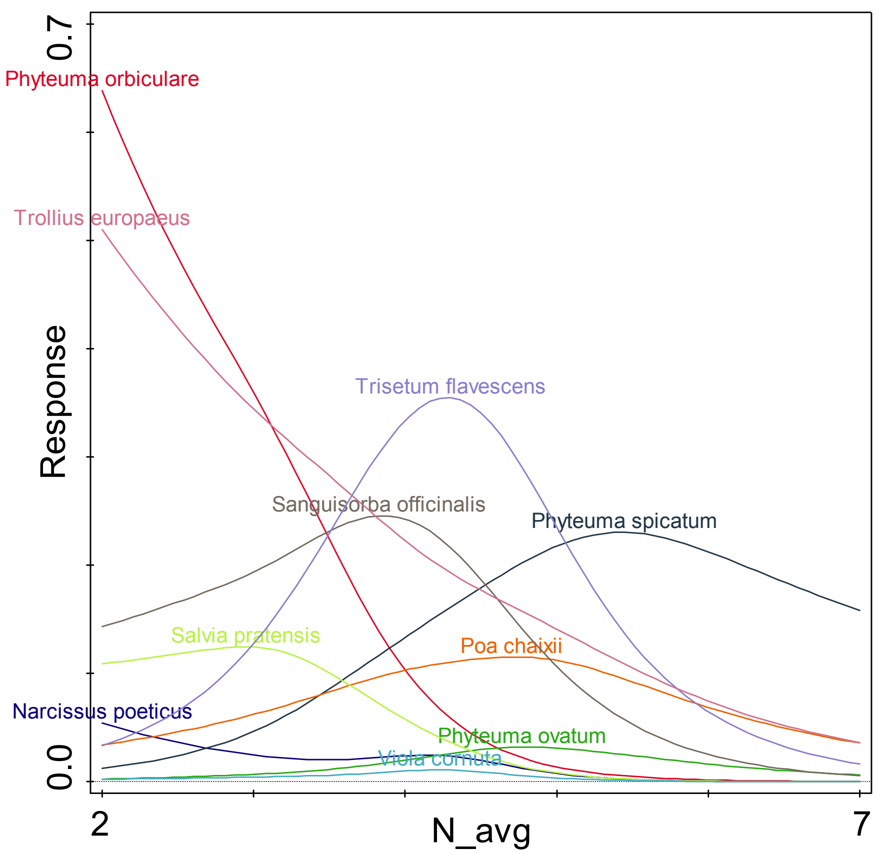
Nitrogen Ellenberg (log-abundance)

Predictors N_avg
Distribution Poisson
Link function log
Summary of fitted Generalized Additive Models (species in blue = R2≥5): :

Response	**Type**	**R2[%]**	**F**	**p**
Astrantia major	s3	1.0	14.4	<0.00001
Bistorta officinalis	s3	6.5	128.3	<0.00001
Chaerophyllum hirsutum	s3	22.7	432.6	<0.00001
Cirsium helenioides	s3	3.7	40.1	<0.00001
Conopodium majus	s3	2.1	9.7	<0.00001
Crepis mollis	s3	5.5	57.6	<0.00001
Crepis pyrenaica	s3	0.8	7.6	0.00004
Crocus albiflorus	s3	24.2	141.5	<0.00001
Geranium phaeum	s3	29.9	127.8	<0.00001
Geranium sylvaticum	s3	7.2	131.9	<0.00001
Narcissus poeticus	s3	4.2	19.7	<0.00001
Phyteuma orbiculare	s3	29.5	400.4	<0.00001
Phyteuma ovatum	s3	3.9	17.3	<0.00001
Phyteuma spicatum	s3	8.9	111.4	<0.00001
Poa chaixii	s3	1.3	18.5	<0.00001
Salvia pratensis	s3	12.0	131.6	<0.00001
Sanguisorba officinalis	s3	5.7	108.1	<0.00001
Trisetum flavescens	s3	7.9	161.8	<0.00001
Trollius europaeus	s3	5.6	99.0	<0.00001
Viola cornuta	s3	3.7	8.2	0.00002



1.2
0.0
Response
Chaerophyllum hirsutum
Crocus albiflorus
Geranium phaeum
Geranium sylvaticum
Bistorta officinalis
Astrantia major
Crepis mollis
Crepis pyrenaica
Cirsium helenioides
Conopodium majus
2
N_avg
7



0.7
0.0
Response
Phyteuma orbiculare
Trollius europaeus
Trisetum flavescens
Sanguisorba officinalis
Phyteuma spicatum
Salvia pratensis
Poa chaixii
Narcissus poeticus
Phyteuma ovatum
Viola cornuta
2
N_avg
7

Moisture Ellenberg (log-abundance)

Summary of fitted Generalized Additive Models:

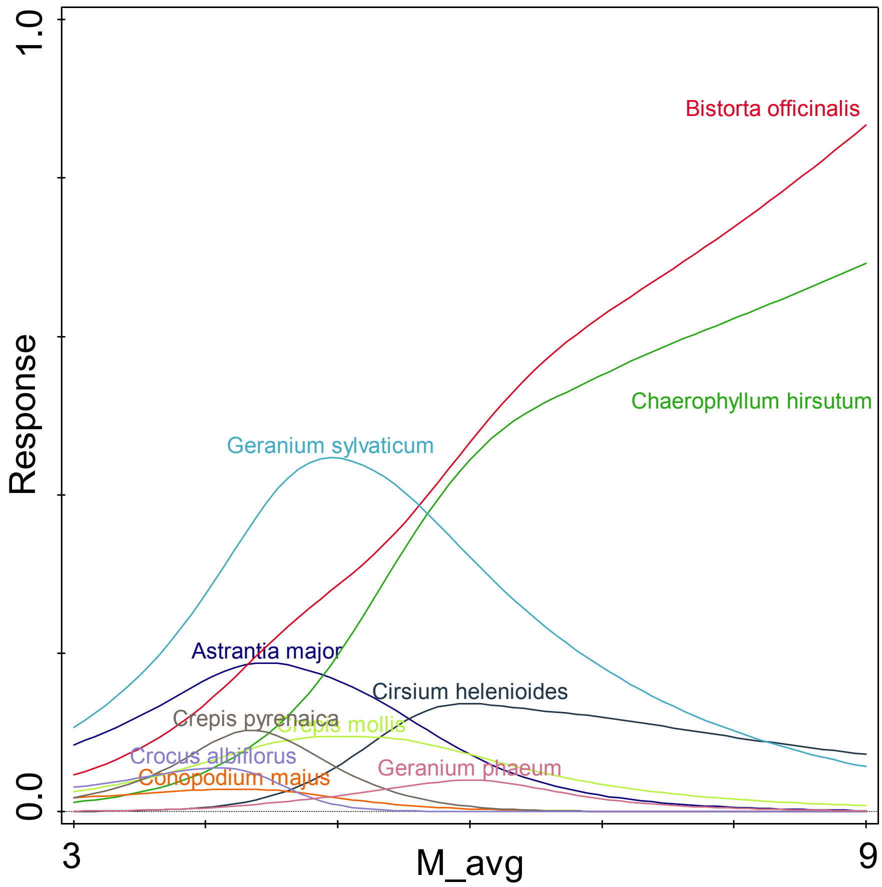
Predictors M_avg

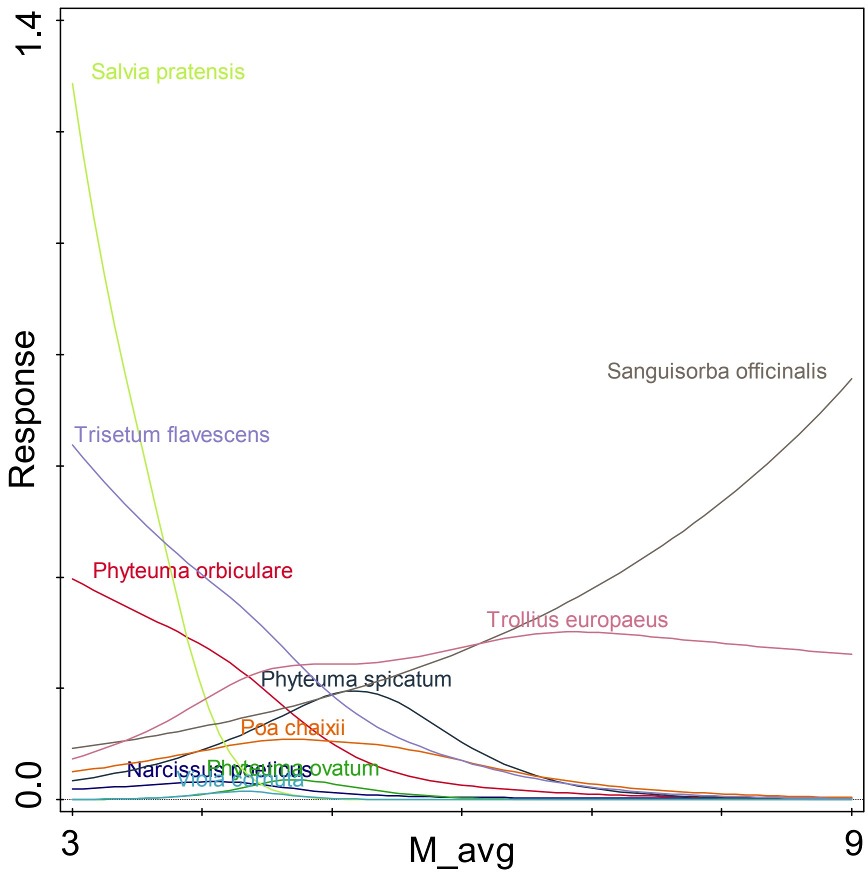
Distribution Poisson

Link function log

GAM fitted for response variables (species in blue = R2≥5):

Response	**Type**	**R2[%]**	**F**	**p**
Astrantia major	s3	4.9	72.8	<0.00001
Bistorta officinalis	s3	10.7	210.8	<0.00001
Chaerophyllum hirsutum	s3	20.3	387.3	<0.00001
Cirsium helenioides	s3	14.9	162.0	<0.00001
Conopodium majus	s3	5.2	23.5	<0.00001
Crepis mollis	s3	1.7	18.0	<0.00001
Crepis pyrenaica	s3	10.1	100.5	<0.00001
Crocus albiflorus	s3	15.7	85.7	<0.00001
Geranium phaeum	s3	6.9	30.7	<0.00001
Geranium sylvaticum	s3	4.9	85.1	<0.00001
Narcissus poeticus	s3	5.8	28.2	<0.00001
Phyteuma orbiculare	s3	18.1	242.2	<0.00001
Phyteuma ovatum	s3	8.5	37.7	<0.00001
Phyteuma spicatum	s3	6.8	82.9	<0.00001
Poa chaixii	s3	1.6	20.8	<0.00001
Salvia pratensis	s3	49.6	543.0	<0.00001
Sanguisorba officinalis	lin	3.4	165.9	<0.00001
Trisetum flavescens	s3	13.6	279.1	<0.00001
Trollius europaeus	s3	2.0	35.4	<0.00001
Viola cornuta	s3	10.7	23.2	<0.00001


1.0
Response
0.0
Bistorta officinalis
Chaerophyllum hirsutum
Geranium sylvaticum
Astrantia major
Cirsium helenioides
Crepis pyrenaica
Crepis mollis
Crocus albiflorus
Conopodium majus
Geranium phaeum
3
M_avg
9


1.4
Response
0.0
Salvia pratensis
Sanguisorba officinalis
Trisetum flavescens
Phyteuma orbiculare
Trollius europaeus
Phyteuma spicatum
Poa chaixii
Narcissus poeticus
Phyteuma ovatum
Viola cornuta
3
M_avg
9

Desiccation (log-abundance)

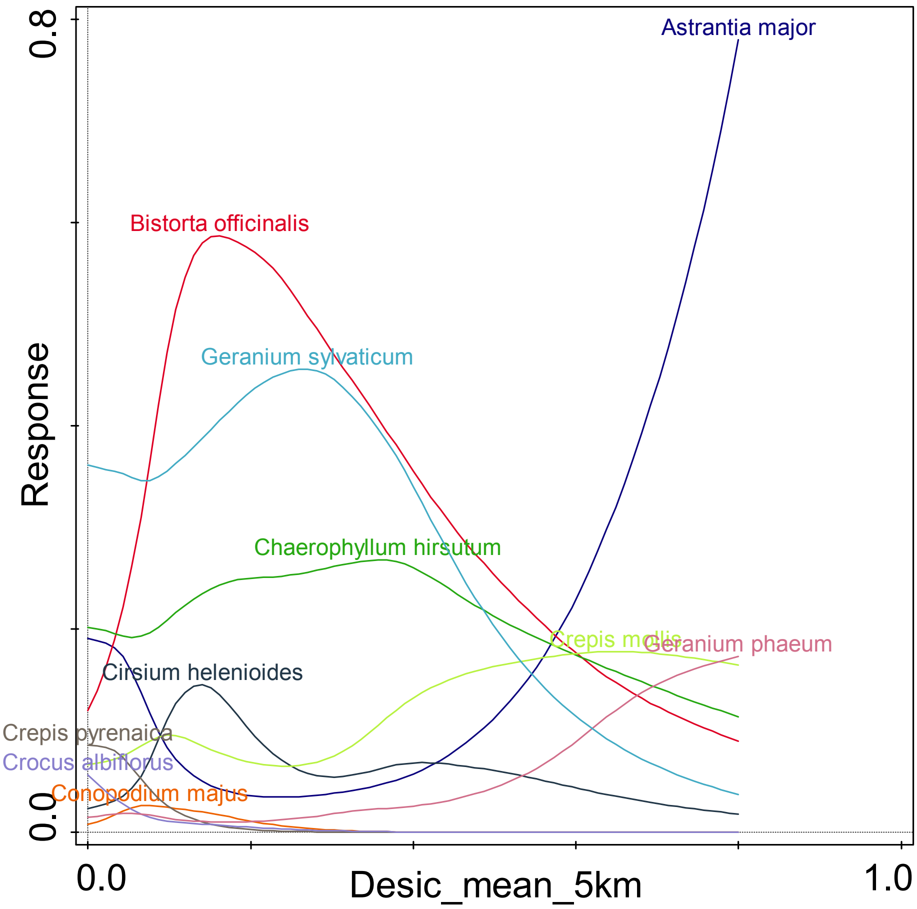
Summary of fitted Generalized Additive Models:

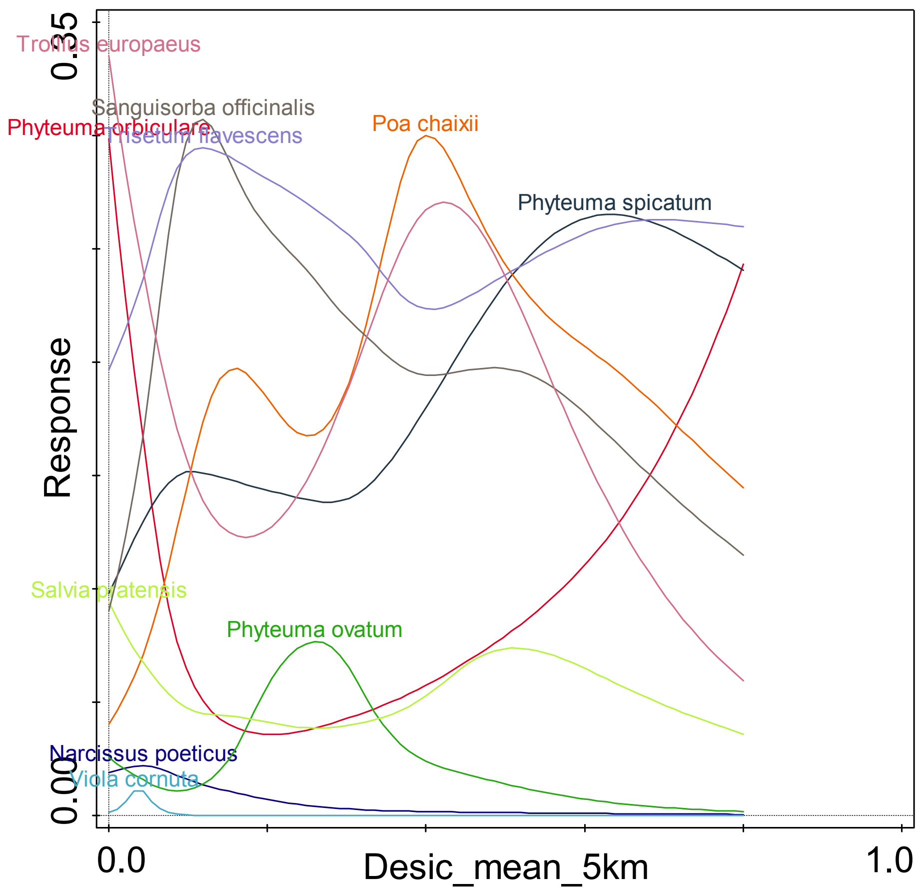
Predictors desic_mean_5km
Distribution Poisson
Link function log
GAM fitted for response variables (species in blue = R2≥5):

Response	Type	R2[%]	F	p
Astrantia major	s3	11.4	78.1	<0.00001
Bistorta officinalis	s3	12.2	95.1	<0.00001
Chaerophyllum hirsutum	s3	1.3	10.3	<0.00001
Cirsium helenioides	lin	16.7	76.6	<0.00001
Conopodium majus	s2	9.9	33.8	<0.00001
Crepis mollis	s2	3.5	14.6	<0.00001
Crepis pyrenaica	lin	11.3	99.0	<0.00001
Crocus albiflorus	lin	7.8	32.3	<0.00001
Geranium phaeum	lin	4.8	8.3	<0.00001
Geranium sylvaticum	s2	1.8	13.8	<0.00001
Narcissus poeticus	lin	3.1	7.7	<0.00001
Phyteuma orbiculare	s3	12.6	78.6	<0.00001
Phyteuma ovatum	lin	13.0	23.0	<0.00001
Phyteuma spicatum	lin	1.4	7.0	<0.00001
Poa chaixii	s2	8.4	41.6	<0.00001
Salvia pratensis	lin	2.5	12.0	<0.00001
Sanguisorba officinalis	s3	7.1	54.1	<0.00001
Trisetum flavescens	s3	1.7	13.5	<0.00001
Trollius europaeus	s2	3.1	25.9	<0.00001
Viola cornuta	s2	11.4	2.6	<0.00001

Comment:

- Poor correspondence with curve shapes for Moisture based on Ellenberg indicator values


Astrantia major
Bistorta officinalis
Geranium sylvaticum
Chaerophyllum hirsutum
Crepis mollis
Geranium phaeum
Cirsium helenioides
Crepis pyrenaica
Crocus albiflorus
Conopodium majus
0.8
0.0
Response
0.0
Desic_mean_5km
1.0


Trollius europaeus
Sanguisorba officinalis
Phyteuma orbiculare
Trisetum flavescens
Poa chaixii
Phyteuma spicatum
Salvia pratensis
Phyteuma ovatum
Narcissus poeticus
Viola cornuta
0.35
0.00
Response
0.0
Desic_mean_5km
1.0

Annex 10 Report on mammals

Author : Luca Santini, Sapienza Università di Roma

Data collection

We performed an extensive data collection on occurrence points for European mammal species of conservation concern, i.e. those listed under the Habitat Directive, the Bern Convention, the Bonn Convention, the CITES, and considered threatened under the Global and European IUCN Red List. We collected data points from various sources for a total of more than 252,100 records (Table A10.1).

Table A10.1

Sources and number of data points

Source	Records
GBIF	179000
Observado	14000
Silene database	8000
Sicily atlas	2700
Repertorio Naturalistico Toscano (re.na.to)	1300
French national bat atlas	41000
Derived from research papers	1500
Private GMA database	4600

From this data collection, we selected only those points collected after 1990, with a spatial precision of <10 km and falling within the species' geographic range available from IUCN Red List (IUCN 2013). A total of 81 species were filtered for analyses, having a minimum of 27 presence points and a maximum of 9,899 points per species, for a total of more than 163,000 records (Table A10.2; Fig. A10.1).

Table A10.2.

Mammal species with a sufficient number of high-quality presence points

Order	Family	Species	Records
Cetartiodactyla	Cervidae	*Alces alces*	937
Eulipotyphla	Erinaceidae	*Atelerix algirus*	567
Chiroptera	Vespertilionidae	*Barbastella barbastellus*	2506
Carnivora	Canidae	*Canis lupus*	2573
Cetartiodactyla	Bovidae	*Capra ibex*	137
Cetartiodactyla	Bovidae	*Capra pyrenaica*	1249
Cetartiodactyla	Cervidae	*Capreolus capreolus*	8401
Rodentia	Castoridae	*Castor fiber*	681
Rodentia	Cricetidae	*Chionomys nivalis*	409
Eulipotyphla	Soricidae	*Crocidura sicula*	154
Cetartiodactyla	Cervidae	*Dama dama*	1595
Rodentia	Gliridae	*Eliomys quercinus*	2028
Chiroptera	Vespertilionidae	*Eptesicus nilssonii*	526
Chiroptera	Vespertilionidae	*Eptesicus serotinus*	4843
Eulipotyphla	Erinaceidae	*Erinaceus europaeus*	9249
Carnivora	Felidae	*Felis silvestris*	3697
Eulipotyphla	Talpidae	*Galemys pyrenaicus*	969
Carnivora	Viverridae	*Genetta genetta*	5298
Carnivora	Mustelidae	*Gulo gulo*	35
Carnivora	Herpestidae	*Herpestes ichneumon*	1473

Order	Family	Species	Records
Rodentia	Hystricidae	*Hystrix cristata*	197
Lagomorpha	Leporidae	*Lepus castroviejoi*	128
Lagomorpha	Leporidae	*Lepus corsicanus*	203
Lagomorpha	Leporidae	*Lepus europaeus*	3273
Lagomorpha	Leporidae	*Lepus granatensis*	5712
Lagomorpha	Leporidae	*Lepus timidus*	1482
Carnivora	Mustelidae	*Lutra lutra*	9899
Carnivora	Felidae	*Lynx lynx*	86
Carnivora	Felidae	*Lynx pardinus*	651
Rodentia	Sciuridae	*Marmota marmota*	451
Carnivora	Mustelidae	*Martes foina*	5176
Carnivora	Mustelidae	*Martes martes*	1408
Carnivora	Mustelidae	*Meles meles*	7374
Rodentia	Cricetidae	*Microtus cabrerae*	503
Chiroptera	Vespertilionidae	*Miniopterus schreibersii*	2011
Rodentia	Gliridae	*Muscardinus avellanarius*	112
Carnivora	Mustelidae	*Mustela erminea*	1870
Carnivora	Mustelidae	*Mustela lutreola*	388
Carnivora	Mustelidae	*Mustela nivalis*	5963
Carnivora	Mustelidae	*Mustela putorius*	3233
Chiroptera	Vespertilionidae	*Myotis alcathoe*	557
Chiroptera	Vespertilionidae	*Myotis bechsteinii*	1533
Chiroptera	Vespertilionidae	*Myotis blythii*	900
Chiroptera	Vespertilionidae	*Myotis brandtii*	457
Chiroptera	Vespertilionidae	*Myotis capaccinii*	356
Chiroptera	Vespertilionidae	*Myotis daubentonii*	5235
Chiroptera	Vespertilionidae	*Myotis emarginatus*	2360
Chiroptera	Vespertilionidae	*Myotis myotis*	3502
Chiroptera	Vespertilionidae	*Myotis mystacinus*	2863
Chiroptera	Vespertilionidae	*Myotis nattereri*	3805
Chiroptera	Vespertilionidae	*Myotis punicus*	79
Eulipotyphla	Soricidae	*Neomys anomalus*	1337
Eulipotyphla	Soricidae	*Neomys fodiens*	848
Chiroptera	Vespertilionidae	*Nyctalus lasiopterus*	263
Chiroptera	Vespertilionidae	*Nyctalus leisleri*	2554
Chiroptera	Vespertilionidae	*Nyctalus noctula*	2155
Chiroptera	Vespertilionidae	*Pipistrellus kuhlii*	3186
Chiroptera	Vespertilionidae	*Pipistrellus nathusii*	1327
Chiroptera	Vespertilionidae	*Pipistrellus pipistrellus*	9784
Chiroptera	Vespertilionidae	*Pipistrellus pygmaeus*	4612
Chiroptera	Vespertilionidae	*Pipistrellus savii*	1230
Chiroptera	Vespertilionidae	*Plecotus auritus*	3133
Chiroptera	Vespertilionidae	*Plecotus austriacus*	2908
Chiroptera	Vespertilionidae	*Plecotus macrobullaris*	88
Chiroptera	Rhinolophidae	*Rhinolophus blasii*	44
Chiroptera	Rhinolophidae	*Rhinolophus euryale*	1085
Chiroptera	Rhinolophidae	*Rhinolophus ferrumequinum*	4790
Chiroptera	Rhinolophidae	*Rhinolophus hipposideros*	4719
Chiroptera	Rhinolophidae	*Rhinolophus mehelyi*	342
Cetartiodactyla	Bovidae	*Rupicapra rupicapra*	447
Rodentia	Sciuridae	*Sciurus anomalus*	29
Rodentia	Sciuridae	*Sciurus vulgaris*	6326
Eulipotyphla	Soricidae	*Sorex araneus*	940
Eulipotyphla	Soricidae	*Sorex coronatus*	956

Order	Family	Species	Records
Eulipotyphla	Soricidae	*Sorex granarius*	339
Eulipotyphla	Soricidae	*Sorex minutus*	1212
Rodentia	Sciuridae	*Spermophilus citellus*	59
Eulipotyphla	Soricidae	*Suncus etruscus*	1475
Chiroptera	Molossidae	*Tadarida teniotis*	1968
Carnivora	Ursidae	*Ursus arctos*	553
Chiroptera	Vespertilionidae	*Vespertilio murinus*	110

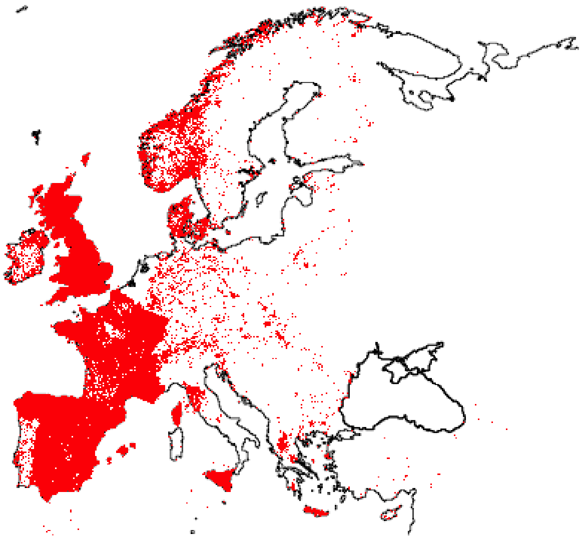


Figure A10.1 *Distribution of data points for mammals.*

We used a set of spatial variables for the subsequent distribution modelling, divided into the following main classes:

1. Climate and soils, elevation (alt), evapotranspiration (apet), several bioclimatic variables (bio3, bio4, bio6, bio9, bio14, bio15, bio18, bio28), soil characteristics (soil PH, salt1, salt2, salt3, soil silt, soil clai, soil oc), temperature sum (tsum);
2. Land cover, we used habitat suitability models published by Rondinini *et al.* (2011) for filtering the results of bioclimatic models according to species habitat preferences.
3. Threat proxies, desiccation (desic), forest management type (fma f1, fma f2, fma f3, fma f4, fma f5), nitrogen application (napplication), nitrogen deposition (ndep), sulfur deposition (sdep), fragmentation (div 1, div 2, div 3).

Since fragmentation data are divided into different classes according to the grain of fragmentation (10 km, 20 km, 50 km, 100 km), we assigned species in our dataset to the appropriate level of fragmentation to which they are sensitive, according to their median dispersal distance, as calculated in Santini *et al*. (2013). Since little precise information is available on dispersal distances for most species of bats, but they are known to have good dispersal abilities, we assumed that all bats were associated to max-grain fragmentation (100km).

Distribution modeling

Distribution modelling has been performed following 4 steps.

Step 1 - TriMmaps. We performed species distribution modelling based on bioclimatic and soil variables in TriMmaps using Generalised Boosted Models (GBM) at a resolution of 10 km. Our dataset consisted of only presence points, hence we had to generate pseudo-absence points to run TriMmaps. We repeated the modelling exercise twice, first by generating 10,000 random pseudo-absences for each species (i.e. random points across the study region), and then by using target sampling groups to identify locations where a given species was not observed despite other similar species were present (Phillips *et al*., 2009) (Fig. A10.2).

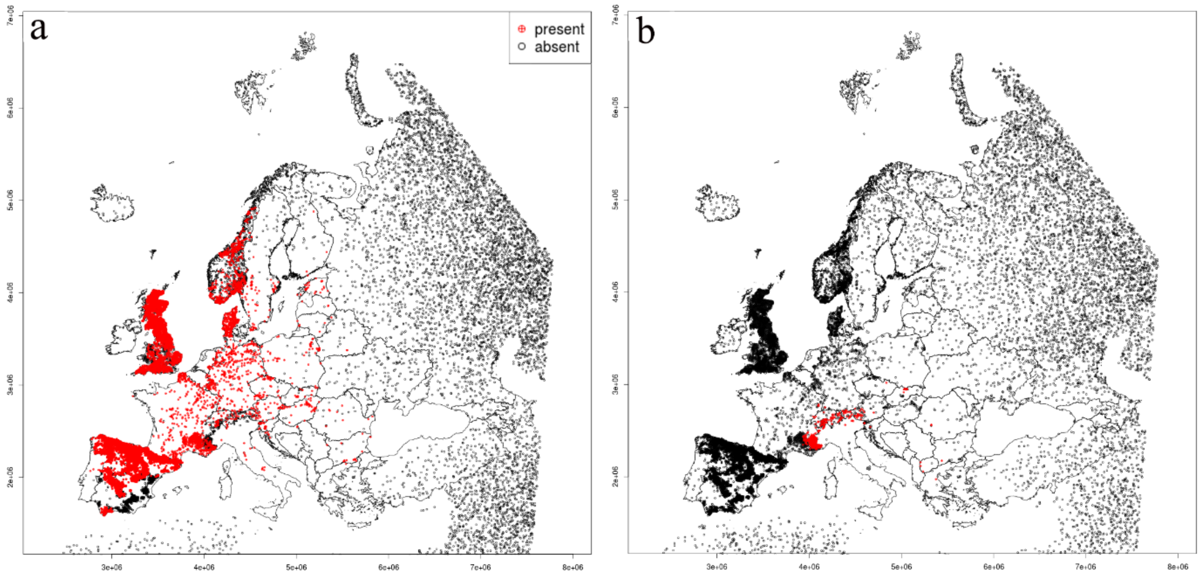


Figure A10.2 *Species presences and sampled pseudo-absences for Caproleus caproleus (a) and Rupicapra rupicapra (b).*

We aggregated species in the following target groups:

- bats;
- small insectivores (shrews, water shrews, desman);
- meso/large-carnivores (wolf, bear, lynxes, wolverine, arctic fox, golden jackal);
- large herbivores (bison, chamois, ibexes, deer, elk);
- small carnivores (mustelids and the genet);
- small herbivores (hares, hedgehogs, porcupine, marmot, beaver);
- small rodents.

For each species we performed a check of the model performances, comparing the random absences model and the target group-absence model, and retained the best performing model. After the check, two species were eliminated due to low model performance, probably due to excessive bias in presence points: *Eptesicus serotinus* and *Rhinolophus blasii*. A total of 79 species were retained for subsequent analyses. The main output of Step 1 is a set of species distribution models spanning the whole study region and reporting continuous probabilities of species presence (in the range 0-1; Fig. A10.3).

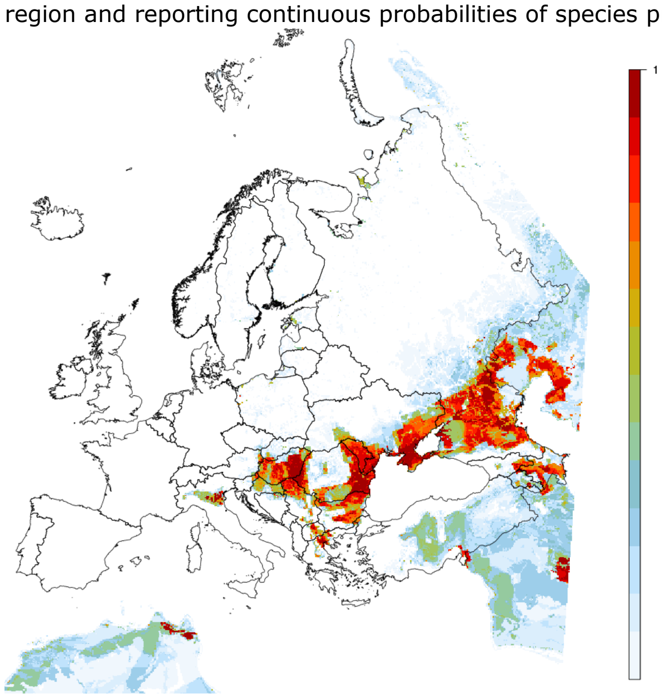


Figure A10.3 *Predicted probability of presence for Spermophilus citellus.*

Step 2 - For each species, we converted continuous model values (Step 1) into boolean suitable/non-suitable values, by defining species-specific cutoffs, i.e. threshold values above which a given grid cell in the region is considered to be suitable for the species. Cutoff values are calculated to maximise the relationship between model sensitivity (ability to classify species presence) and specificity (ability to classify species absences). The main output of Step 2 is a set of species distribution models spanning the whole study region and reporting boolean suitability values (suitable/non-suitable; Fig. A10.4).

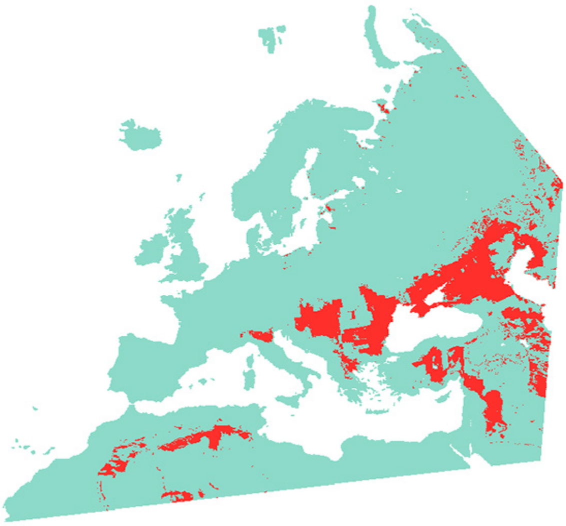


Figure A10.4 *Binary map of predicted presence for Spermophilus citellus obtained by equally weighting model specificity and sensitivity.*

Step 3 - We overlaid distribution models obtained in Step 2 with habitat suitability models obtained from Rondinini *et al.* (2011). This step allowed to filter the species bioclimatic distribution, obtained in Step 2, with species habitat suitability (based on expert-based species-land cover association). As the habitat suitability models are already filtered by the IUCN range polygons of the species, we also filter out all predicted presence cells outside the observed extent of occurrence of the species. Thus, we re-classified as non-suitable all grid cells occurring outside the species extent of occurrence and/or occurring in non suitable land-cover types. The main output of Step 3 is a set of species distribution models representing the suitable habitat, soil and bioclimatic conditions in which a species is expected to occur (Fig. A10.5).

Figure A10.5 *Binary map for Spermophilus citellus filtered by expert based habitat suitability model and species extent of occurrence. Yellow = cells of the IUCN range polygon where the species is predicted to be absent; Red = cells of the IUCN range polygon where the species is predicted to be present.*

Step 4 - We used the output models from step 3 to extract presence/absence values from the distribution range of the species (thus excluding all other cells of the study area). This boolean variable was then used as response variable in a binomial generalized linear model (GLM) using a logit link function. We performed a separate GLM using each of the pressure variable as predictor (those described in Data collection paragraph), both with and without an additional quadratic term. The AIC values of the two GLMs for each of the pressure variable (with and without the quadratic term) were then compared and the one with the lowest AIC was retained. The GLMs were used to predict response curves of species distribution with respect to the threat proxies (see Fig. A10.6). The main outputs of Step 4 are: (i) a set of response curves (to the various threat proxy variables) for each species, with coefficients of each curve parameters and (ii) a set of figures representing species responses to each threat proxy. Given that species are sensitive to different grain of fragmentation, due to their dispersal ability, we classified species into broad dispersal classes, based on Santini *et al*. (2013), and applied appropriate fragmentation maps to each of them.

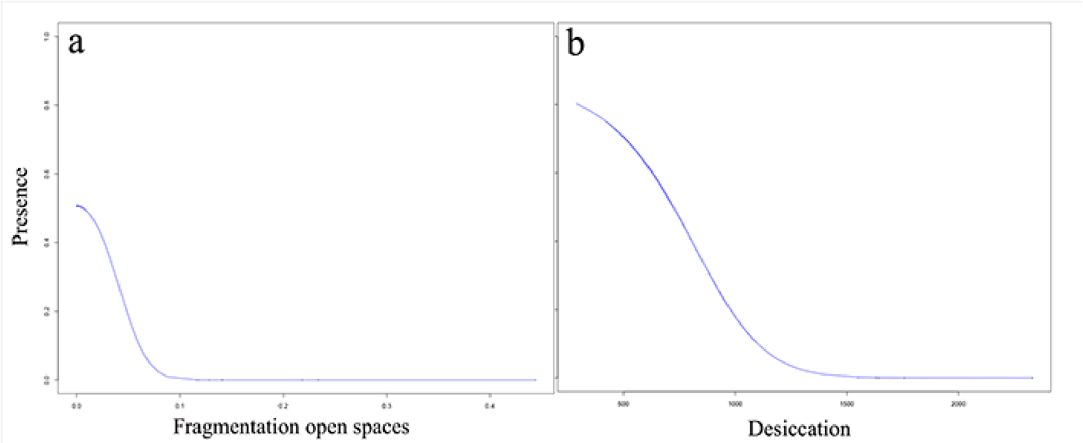


Figure A10.6 *Examples of dose-response curves to fragmentation to open spaces (a) and Desiccation (b).*

Summary of the key produced outputs
- Species distribution models: 79 raster models (one per each species) at a 10 km resolution.
- Species response curves: 17 response curves for each of 79 species, graphical representation of each curve and model parameters (formula).

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