PBL Netherlands Environmental
Assessment Agency

BIOSCORE 2.0

A species-by-species model to assess anthropogenic impacts on terrestrial biodiversity in Europe

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PBL Netherlands Environmental Assessment Agency is the national institute for strategic policy analysis in the fields of the environment, nature and spatial planning. We contribute to improving the quality of political and administrative decision-making by conducting outlook studies, analyses and evaluations in which an integrated approach is considered paramount. Policy relevance is the prime concern in all of our studies. We conduct solicited and unsolicited research that is both independent and scientifically sound.

Contents

Preface

The BioScore model (Biodiversity impact assessment using species sensitivity Scores) has been developed in order to provide a tool able to assess the impacts of policy measures on biodiversity in Europe. BioScore projects the spatial distribution of individual species (plants, invertebrates and vertebrates) in relation to a set of environmental factors related to climate, soil, land use and various human-induced pressures, including acidification, eutrophication and habitat fragmentation. The first version of the model was released in 2009, resulting from a research project funded by EC DG Research and Technological Development FP6 (www.bioscore.eu). The project was coordinated by the European Centre for Nature Conservation (ECNC) / Ben Delbaere and executed by a consortium of nine partners. PBL Netherlands Environmental Assessment Agency and Alterra Wageningen UR were in charge of the development of the BioScore database and web tool (Delbaere et al., 2009).

BioScore version 1.0 has been used for a number of Europe-wide scenario studies. PBL has been developing an improved version of the model (BioScore 2.0), based on the experiences with BioScore 1.0 and a list of proposed model improvements as identified in Delbaere et al. (2009). Compared to the previous version, BioScore 2.0 is based on improved species monitoring data and improved response relationships to describe species' probability of occurrence in relation to the environmental factors of concern. The following partners have been highly involved in the development of BioScore 2.0:

- European Bird Census Council / Henk Sierdsema, Sovon (NL);
- Butterfly Conservation Europe / Chris van Swaay, Vlinderstichting, (NL);
- European Vegetation Survey / Stephan Hennekens and Joop Schaminée, Alterra, (NL);
- Global Mammal Assessment / Luca Santini and Carlo Rondinini, Sapienza University, (IT).

An important application of BioScore 2.0 has been in PBL's Nature Outlook 2016. The Nature Outlook studies are produced every four years. They provide perspectives on nature and policy options for the next 30 to 40 years. Until now, these assessments have been limited to the Netherlands. However, as national nature policy is increasingly decided upon at EU level, the Dutch Government has requested PBL to expand the study area to cover the whole of the EU-28.

This report describes the model concept and methodology underlying BioScore 2.0, and illustrates the type of results that can be obtained with the model. Furthermore, it discusses both the methodology and the results.

Summary

BioScore 2.0 is a model which supports the analysis of potential impacts of future changes in human-induced pressures on European terrestrial biodiversity (e.g. mammals, vascular plants, breeding birds and butterflies). The model is based on large databases on species occurrences in Europe. The relationship between species observations and pressures is calculated through statistical analysis. By using output of models on future changes in pressures, BioScore 2.0 can be used for calculating changes in species occurences. In this way, BioScore 2.0 can be used for assessing policy plans or scenarios on the achievement of European biodiversity goals and on impacts of climate change. It models changes in both species abundance and habitat quality. This is of interest to policymakers and scientists.

BioScore 1.0, released in 2009, resulted from a research project funded by EC DG Research and Technological Development, FP6 (www.bioscore.eu). The project was coordinated by the European Centre for Nature Conservation (ECNC) and executed by a consortium of nine partners. PBL has been developing an improved version of the model (BioScore 2.0), together with European Bird Census Council (Sovon), Butterfly Conservation Europe (De Vlinderstichting), European Vegetation Survey and Sapienza University.

The driving variables included are climate change, land-use change, and local environmental pressures. The last include air pollution through nitrogen and sulphur deposition, agricultural intensification, water stress, habitat fragmentation, forest and nature management, and disturbance caused by roads and urbanisation. The model assesses the impacts on probability of occurrence for 1400 policy-relevant species, for each 5 x 5 km grid cell. Model calculations are executed in five consecutive steps. In the first step, climate, elevation and soil maps are used to project the distribution range of each species. The second step uses land-cover information to determine suitable habitats, per species, within their distribution range. In the third step, the relationships between local pressures (e.g. water stress and habitat fragmentation) and species occurrences are derived. In the fourth step, the relationships between local pressures and species occurrence are combined with species distribution ranges and species habitat suitability, in order to produce probability maps of species occurrence. In the final step, these maps are aggregated into species and ecosystem indicators.

This report provides detailed descriptions of the calculation procedures in the five steps and the data used in each step. It discusses the quality and applicability of BioScore 2.0.

1 Introduction

Global biodiversity is currently declining at an unusually high rate (Butchart et al., 2010; Barnosky et al., 2011; Pereira et al., 2012; Tittensor et al., 2014). This brings about a clear demand for quantitative models able to project future biodiversity in response to anthropogenic pressures as well as policy measures designed to counteract the decline (Pereira et al., 2010; Harfoot et al., 2014a). Common biodiversity modelling approaches range from descriptive correlative statistical models, such as species distribution models (SDMs) or species–area relationships (SARs), to more mechanistic, process-based models that simulate population or community dynamics (Boyce, 1992; Drakare et al., 2006; Elith and Leathwick, 2009; Harfoot et al., 2014b). As process-based models tend to be more data and computationally intensive, large-scale biodiversity assessments are commonly based on correlative models.

In general, there are two main approaches to correlative biodiversity modelling. In the first approach, biotic survey data are aggregated to location-specific estimates of assemblage-level biodiversity indicators, such as species richness or mean species abundance (MSA) (Thomas et al., 2004; Alkemade et al., 2009). These indicators are then used to establish quantitative cause–effect relationships by relating them to measurements or estimates of co-occurring environmental factors (‘assemble first, predict later’; (Ferrier and Guisan, 2006)). In the alternative approach, the environmental responses of the individual species are modelled first, by establishing so-called species distribution models (SDMs) or habitat suitability models (HSMs), i.e., quantitative relationships between the abundance or (potential) occurrence of a species on the one hand and a set of environmental factors on the other (Elith and Leathwick, 2009). The modelled species' or habitat distributions are then combined in order to derive multi-species biodiversity indicators (‘predict first, assemble later’ (Ferrier and Guisan, 2006)).

Modelling individual species is a very flexible approach to biodiversity modelling: once the distributions of the individual species are known, virtually any property of an assemblage and hence virtually any multi-species biodiversity indicator can be derived (Ferrier and Guisan, 2006). Moreover, species-specific models are expected to improve our understanding and predictive ability of ecological responses to global change, as they allow for evaluation of which species are at higher risk and why (Visconti et al., 2016b). So far, however, a species-by-species approach to biodiversity modelling has mostly been restricted to relatively few species, to particular taxonomic groups, or to relatively few environmental factors, mostly related to climate change and land use (Thuiller et al., 2005; Visconti et al., 2011; Feeley et al., 2012; Ficetola et al., 2015; Visconti et al., 2016b).

The BioScore model was developed with the aim to establish a large-scale species-specific biodiversity assessment model including species from multiple taxonomic groups and a set of environmental factors representative of a variety of anthropogenic pressures. The model was specifically designed to quantify the impacts of policy measures on biodiversity in Europe (Delbaere et al., 2009). A first version of the model was released in 2009. The present report describes version 2.0 of the BioScore model, which was developed based on the experiences with version 1.0 and a list of improvements proposed upon completion of version 1.0 (Delbaere et al., 2009). Compared to the previous version, BioScore 2.0 is based on improved species monitoring data and improved response relationships to describe species’ probability of occurrence in relation to the environmental factors of concern. BioScore 2.0 projects the spatial distribution of individual species belonging to four taxonomic groups (vascular plants, butterflies, breeding birds and mammals) in relation to a set of environmental factors related to climate, soil, land use and various human-induced pressures, including acidification, eutrophication and habitat fragmentation. It includes a total of 1320 policy-relevant species, of which 863 vascular plants, 95 butterflies, 284 breeding birds and 78 mammals.

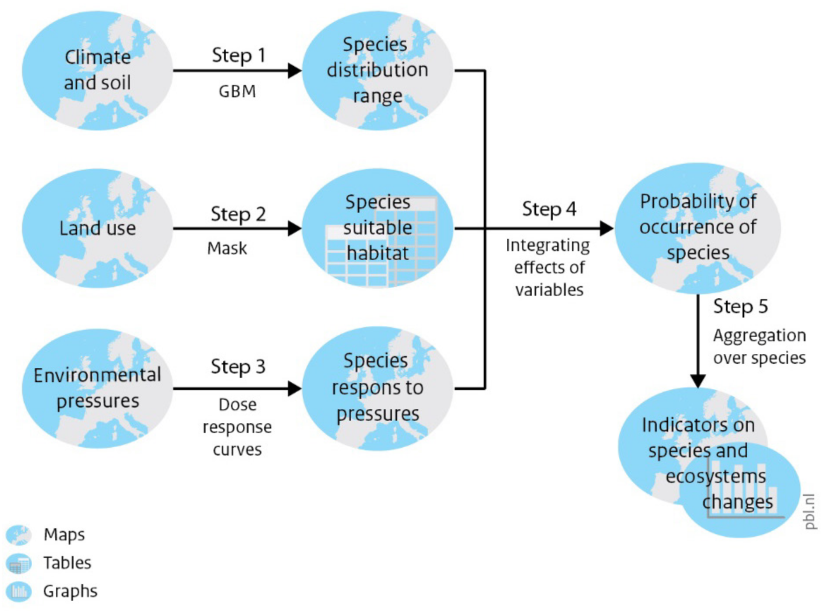
2 Methods

2.1 General approach

BioScore follows a hierarchical approach to species distribution modelling, assuming that the distribution of a species results from a set of nested environmental filters ranging from large-scale climatic and soil variables at the coarsest spatial resolution via land cover and land use to fine-grained habitat characteristics at the highest spatial resolution (Pearson and Dawson, 2003). First, the distribution range of each species is projected based on envelope models that estimate species' probability of occurrence in relation to large-scale climate and soil characteristics (Figure 2.1). From the projected envelopes, the areas with potentially suitable habitat for each species are selected based on its affinity to specific land-cover, land-use and/or land-management types. Thirdly, the species' probabilities of occurrence within the potentially suitable habitat are determined based on their responses to environmental factors indicative of various human pressures, including habitat fragmentation, eutrophication and acidification.

Model results are then aggregated by location and/or species, in order to obtain species and ecosystem indicators (Figure 2.1). Species indicators give an indication of the percentage of species changing, where change of a species is determined by the change in summed probability of occurrence over all grid cells. The ecosystem indicators give an indication of changes in ecosystem quality, where change of quality is determined by the sum of occurrence probability of all species per grid cell.

Model framework Bioscore 2.0



Source: PBL, 2014

Figure 2.1: Conceptual scheme of the BioScore model, showing a hierarchical approach to biodiversity modelling where the occurrence probability of each species is a function of a set of nested environmental filters including large-scale climate and soil characteristics (step 1), land use (step 2) and fine-grained environmental characteristics influencing habitat quality (step 3).

2.2 Species

2.2.1 Species selection

Selection of taxonomic groups

BioScore 2.0 focuses on species relevant for European policies, i.e. species mentioned in the Birds and Habitats Directives (or underlying lists of the Bern Convention) and/or Red Lists, or species considered to be characteristic for the selected Annex I habitat types. The Birds Directive aims to protect all European wild birds throughout their natural range within the EU. It also identifies 193 species and subspecies of wild birds naturally occurring in Europe as being in need of special conservation measures. These species, listed in Annex I of the directive, are considered to have the following characteristics: to be in danger of extinction, to be vulnerable to specific changes in their habitat, to be rare, or to require specific attention because of their habitats. The Habitats Directive aims at ensuring the conservation of a variety of rare, threatened, or endemic species, including more than 1250 species and subspecies and 237 habitat types. The quality of the habitat types are measured by so-called typical species. Full lists of typical species do not exist. However manuals are available to help Member States listing these species. Based on available information it is clear that most typical species are plant species, but also butterflies are often mentioned.

BioScore 2.0 focusses on terrestrial biodiversity and four groups which are of prime importance of the Birds and Habitats Directives, i.e. the vascular plants, butterflies, mammals and breeding birds. This of course holds for the breeding birds protected in the Birds Directive. Plants have the longest list of protected species in the Habitats Directive and mammals and arthropods (including Butterflies) are the next groups in size.

Within these four taxonomic groups, the species were selected based on both policy relevance and availability of monitoring data. A list of criteria specific to each taxonomic group is provided below:

Vascular plants
First, 40 protected terrestrial habitat types were selected (Hennekens et al., 2015);

- The habitat is terrestrial and listed in the Habitats Directive, and the habitat is not confined to local sites but relevant across Europe and well characterised from a phytosociological point of view. (Some habitats for which the Netherlands has an international responsibility, especially wetlands, dunes and heathland were also selected in order to enable Dutch assessments).
- The set of habitat types is selected to be representative of the variation in main habitat types across Europe (i.e., including coastal habitats, grasslands, fens and forests).
- The set of habitat types includes High Nature Value (HNV) Farmland (Paracchini et al., 2008).

Next, for each habitat type a set of typical species was selected, using the 'Interpretation manual of European habitats' as starting point (EC, 2013). If this did not provide sufficient and correct information on typical species, information was added from unpublished synoptic tables of alliances from the 'EuroVegChecklist' and other literature. More recently 5 extra habitat types were selected, with characteristic species, but these have not yet been included in the model. These habitat types are H1340 'Inland salt meadows', H5110 'Stable xerothermophilous formations with Buxus sempervirens on rock slopes (Berberidion p.p.)', H7140 'Transition mires and quaking bogs', H9110 'Luzulo-Fagetum beech forests' and H91H0 'Pannonian woods with Quercus pubescens'.

Butterflies
Butterfly species were selected when fulfilling at least one of the following criteria (Van Swaay et al., 2014):

- The species is listed in the annexes II and IV of the Habitats Directive or the species is a 'typical species' for at least one of the habitats mentioned in Annex I of the Habitats Directive.
- The species occurs on the European Red List as Near Threatened (NT), Vulnerable (VU), Endangered (EN) or Critically Endangered (CR).
- The species is used for the identification of High Nature Value (HNV) Farmland (Paracchini et al., 2008).
- Monitoring data should be available from at least 50 transects (see Section 2.2.2).

In addition;

- The species occurs in more than one biogeographic region throughout Europe. (Some species should be characteristic of one of the habitat types for which the Netherlands has an international responsibility, especially wetlands, dunes and heathland in order to enable Dutch assessments).
- The species has a high area under the ROC curve (AUC >0.75) in the climate models of Settele et al. (2008), and thus can be modelled using climate-change models.
- The species is assessed in BioScore 1 (see www.bioscore.eu).

Breeding birds
Breeding bird species were selected when fulfilling at least one of the following criteria (Sierdsema, 2014):

- The species is mentioned in the Birds Directive
- The species is a target species for the designation of Special Protection Areas (SPAs) according to the Birds Directive.
- The species is characteristic of High Nature Value Farmland Farmland (Paracchini et al., 2008).

In addition;

- The species is included in BioScore 1.0 (see www.bioscore.eu), except if it does not breed in the geographical range of interest (mainly species breeding in the Siberian arctic).
- Some species associated with old growth forest.
- Species can be modelled with climate-change models and are expected to be disproportionally impacted by climate change (mainly boreal, arctic and alpine species).

Mammals
Mammal species were selected when fulfilling at least one of the following criteria (Hennekens et al., 2015):

- The species is listed under the Habitats Directive.
- The species is listed under the Bern Convention.
- The species is listed under the Bonn Convention.
- The species is listed under CITES.
- The species is considered threatened according to the IUCN Red List (categories Vulnerable (VU), Endangered (EN) and Critically Endangered (CR)).

  And:
- species should be monitored in a sufficient number of high-quality presence points (see further Section 2.2.2).

Based on these criteria, a total of 1402 species were initially selected for inclusion in BioScore 2.0 (see Table 3.1).

2.2.2 Species monitoring data

Species observations were obtained from various sources, including point record databases, atlas data and range maps (Table 2.1). For butterflies and breeding birds, different data sources were used for the different modelling steps. For the first step, the distribution range modelling, atlas data with a 50 km resolution were used, covering the same time period as the data used for the climate-related predictor variables. For the second and third steps, which require species observations at higher resolution, point records were used. For vascular plants and mammals, point records were used for all three steps.

Point observations were retrieved/selected as follows:

- For plants species, observations in geo-referenced vegetation plots from the European Vegetation Archive (EVA) were used as a basis, supplemented with geo-referenced point observations from GBIF to complement data in regions where EVA has less data coverage (Hennekens et al., 2015).
- For butterflies, monitoring transect data were used from seven countries/regions engaging in Butterfly Monitoring Schemes: Finland, Germany, Netherlands, United Kingdom, France, Catalonia and Sweden. Data for in total 3000 transects were available for 2010–2012 (Van Swaay et al., 2014).
- For breeding birds, only point records were selected that were not further than 50 km from the species ranges as mapped by Birdlife International. To ensure that the observations concerned only breeding birds, for migratory species only observations were selected from a species-specific window representing the breeding season (Sierdsema, 2014).
- For mammals, a selection was made for records obtained after 1990, with a spatial precision of <10 km and falling within the species' geographic range as available from IUCN (www.iucn.org). This resulted in a total of 81 species for the analyses, with a minimum of 29 presence points and a maximum of 9,899 points per species (Hennekens et al., 2015).

Table 2.1: Data sources, number of species observations present in the database and modelling steps in which the data are used. Step 1 refers to the models describing the species' distribution range, step 2 refers to the selection of potential habitat, and step 3 refers to the calculation of the pressure–response curves (see also Figure 2.1).

Data source	**No. of observations**	**Used in step**
Vascular plants		
European Vegetation Archive (http://euroveg.org/eva-database)	20.5 million	1, 2, 3
Global Biodiversity Information Facility (www.gbif.org)	22 million	1, 2, 3
Butterflies		
LepiDiv database (UFZ, Leipzig-Halle) (Kudrna et al., 2011)	137 to 2119 per species	1
IUCN range maps (www.iucn.org)	Not applicable; polygons	1
- database created within project LOLA (www.cesab.org) - Svensk Dagfjärilsövervakning (www.dagfjarilar.lu.se/)	95,000	2, 3
Breeding birds		
EBCC Breeding Bird Atlas 1980–1995 (www.ebcc.info)	1,351,000	1
eBird (www.ebird.org)	23,706,000	2, 3
Global Biodiversity Information Facility (www.gbif.org)	1,351,000	2, 3

Data source	No. of observations	Used in step
Observado and waarneming.nl (www.observado.org)	23,706,000	2, 3
Distribution maps for EU N2000 reporting (Article 12 BirdsDirective) (www.eea.eu)	28,020,000	2, 3
Bulgarian bird counts (pc.trektellen.nl)	202,000	2, 3
Mammals		
Global Biodiversity Information Facility (www.gbif.org)	179,000	1, 2, 3
Observado (www.observado.org)	14,000	1, 2, 3
Silene database	8,000	1, 2, 3
Sicily atlas	2,700	1, 2, 3
Repertorio Naturalistico Toscana (re.na.to)	1,300	1, 2, 3
French national bat atlas	41,000	1, 2, 3
Derived from research papers	1,500	1, 2, 3
Private GMA database	4,600	1, 2, 3

2.3 Environmental variables

The usefulness of an assessment tool such as BioScore will increase when policy makers are informed about the potential effects of decisions. With respect to stopping the loss of biodiversity or reaching the targets of the Birds and Habitats Directives, it is not only important to look at the ecologically important factors, but also to incorporate factors mentioned in policy. In BioScore 1.0, 26 legislative documents were screened for mention of any environmental variable or pressure on biodiversity (Delbaere et al., 2009). At the same time, ecologically relevant factors were listed for modelling species occurrences.

Variables for modelling the distribution range (step 1)
For the envelope models, climate variables were selected according to the following criteria, which all needed to be fulfilled (Hennekens et al., 2015):

- Ecologically relevant, and used in other climate studies, for at least one of the species groups (Bakkenes et al., 2002; Huntley et al., 2007; Settele et al., 2008).
- Available at high resolution for EU28 (preferably 1 x 1 km).
- Computable with models, in order to facilitate climate-change projections.

Climate variables were retrieved from the BioClim database (Hijmans et al., 2005). Based on the four criteria listed above, seven climate variables were selected from the 19 variables available in BioClim (Table 2.2). To the BioClim data, temperature sum in the growing season and the annual ratio of actual to potential evaporation were added from the IMAGE model (Bouwman et al., 2006).

Soil variables are included to model the distribution range. Selected variables were acidity, soil moisture content, organic carbon content in the top soil, clay content in the top soil, silt content in the top soil and availability of salt. These soil factors were expected to be most important for the distribution of plants and habitats and indirect for the animal species living in those habitats. In addition, elevation was added to this list.

Variables to model the extent of suitable habitat (step 2)
Land-cover data, needed for the habitat modelling in step 2, was retrieved from the CORINE land-cover (CLC) map of the European Environment Agency for the year 2000, combined with information from the Pan-European Land Cover database (PELCOM) of Alterra and the Global Land Cover 2000 (GLC2000) map produced by the Joint Research Centre (Table 2.2) (Hazeu et al., 2008). The thematic classification of the map corresponds with the CLC classification (Appendix I). The map was aggregated from 100 metres to a resolution of 1 km by selecting the class which covered the majority within the 1km grid cell.

Variables to model the quality of the habitat: Pressure variables (step 3)

The selection of pressure variables (step 3) was based on the following criteria, which all needed to be fulfilled:

- The pressure is known to affect species' occurrence or habitat quality and/or the pressure is considered relevant in European policies and goals (Delbaere et al., 2009).
- High-resolution data is available for the pressure of concern.
- The pressure can be modelled, in order to facilitate scenario projections.

In BioScore 1.0, 26 legislative documents were scanned in order to identify policy-relevant instruments and drivers. This exercise resulted in a list of over 200 terms, ranging from 'abandonment of high-nature-value farmland' (EC Biodiversity Communication, 2006) to 'wind' (EC Biodiversity Strategy, 1998). The list contained very specific activities with direct pressures related to them, such as 'ammonia and nitrous oxide emissions to air' (Thematic Strategy on Air Pollution 2005). It also contained broader terms such as 'use of fossil fuels' (Thematic Strategy on the Urban Environment 2005) or even very general terms such as 'climate change' (various instruments). These different drivers and pressures were divided into 11 groups of policy-relevant drivers/environmental pressures, i.e. climate change, land-use change, pollution, fragmentation, disturbance, direct pressures, species interaction, management, water , water-related changes and miscellaneous (Delbaere et al., 2009). Ecologically relevant factors, such as natural geological events and catastrophes, were excluded. Because of data availability species interactions (e.g. effects of invasive and introduced species) were also excluded. Eventually 8 pressure variables were selected (Table 2.2). Total deposition of oxidised sulphur and total deposition of nitrogen were selected to incorporate the most important effects of pollution (eutrophication and acidification) on natural ecosystems. Acidification and eutrophication due to atmospheric sulphur and nitrogen deposition threatened Europe's natural areas and directly influences plant species occurrence (Galloway, 1984; Slootweg et al., 2014). These factors are also used for modelling effects in animals, as changes in vegetation may influence animal species occurrence. Nitrogen input was chosen as an indicator for agricultural intensification. Nitrogen input includes manure application (corrected for volatilisation losses), manure deposition by grazing animals and the application of mineral fertilizer. Desiccation was chosen as an indicator of influence of water use. Proximity of roads and urban land use was used as an indicator for various disturbances due to human activities which can't be modelled in detail, such as noise, light and traffic.

To assess the impact of fragmentation the spatial cohesion of ecosystems was used. This spatial cohesion was determined by LARCH-SCAN (Appendix II) (Groot Bruinderink et al., 2003; IEEP and Alterra, 2010). For fragmentation, for each species of plants, birds and butterflies out of a set of 24 maps one map was selected as a measure for the spatial cohesion of its habitat (see Section 2.4.3). The set of 24 maps covers six ecosystem types/land-cover classes and four possible dispersal distances (10, 20, 50 and 100 km). Land-cover classes include forests (class 3.1), shrub and/or herbaceous vegetation (class 3.2), open spaces with little vegetation (class 3.3), inland wetlands (class 4.1), coastal wetlands (class 4.2) and open water (class 5.1). To create the fragmentation maps, the land-cover map was aggregated to a resolution of 1 x 1 km to express the amount of each of the six ecosystem types per grid cell. Then, the degree of fragmentation of each ecosystem type in each grid cell was calculated based on the amount of the same ecosystem type within approximately twice the dispersal distance. For each mammal species, a unique fragmentation map was composed using LARCH-SCAN, land cover was synthesised of a set of the six ecosystem types/land-cover classes, depending on the habitat preferences of the species. The dispersal distance was selected based on the median dispersal distance as calculated in Santini et al.*(2013)*. Little information was available on dispersal distance for most bat species, but as they are known to have good dispersal abilities, it was assumed that all bats are associated to max-grain fragmentation (100 km).

To quantify road impact, a selection was made of the primary, secondary and tertiary roads as included in the GRIP database (Meijer, 2009). A buffer zone of 500 meters was created around the roads and the total area of the buffer zone per 5 x 5 km grid cell was used as road impact indicator. To quantify urbanisation a similar approach was followed. From the land-cover map, all grid cells classified as urban were selected, a 500 m buffer was made around these areas and the total area of the buffer per 5 x 5 km grid cell was used as indicator of urbanisation.

Information on forest management was available as a 1 x 1 km map showing per cell one of the five potential forest management categories (close to nature; combined objective forestry; even-aged forestry; nature reserve; short rotation forestry). As the original map shows potential management types, locations without forest are also given a value. To cover actual forest only, all grid cells from the CORINE land-cover map not classified as forest were removed. Next, for each forest management category a map on a resolution of 5 x 5 km was constructed by aggregation from the underlying scales, rendering information on the area covered (within the 5 x 5 km grid cell) by this forest management category.

Table 2.2: Overview of the data used to quantify the environmental variables used in BioScore 2.0. For each variable the unit of the values in the map, the resolution of the map, the year the data is representative for and the source of the data are mentioned. More information on these variables can be found in Hennekens et al. *(2015).*

Variable	Unit	Resolution	Year	Source
Climate variables				
Precipitation seasonality	Mm	30 arc seconds	~1950–2000	BioClim[1]
Precipitation of driest month	Mm	30 arc seconds	~1950–2000	BioClim[1]
Precipitation of warmest quarter	Mm	30 arc seconds	~1950–2000	BioClim[1]
Temperature seasonality	°C * 10	30 arc seconds	~1950–2000	BioClim[1]
Isothermality	°C * 10	30 arc seconds	~1950–2000	BioClim[1]
Min temperature of coldest month	°C * 10	30 arc seconds	~1950–2000	BioClim[1]
Mean temperature of driest quarter	°C * 10	30 arc seconds	~1950–2000	BioClim[1]
Temperature sum in growing season	°C	0.5 arc degrees	2010	IMAGE model (version 2.4)[2]
Annual ratio of actual to potential evapotranspiration	fraction	0.5 arc degrees	2010	IMAGE model (version 2.4)[2]
Soil variables				
pH-H_2O in top soil	-	5 x 5 km	[15]	HWSD[3]
Availability of salt	-	1 x 1 km	[15]	Sworld-soil map[4]
Organic carbon content in top soil	%	1 x 1 km	[15]	ESDB[5]
Clay content in top soil	%	1 x 1 km	[15]	ESDB[5]
Silt content in top soil	%	1 x 1 km	[15]	ESDB[5]
Elevation (elevation above sea level)	M	30 arc seconds	[15]	SRTM[6]
Annual mean moisture index	fraction	10 arc minutes	~1950–2000	BioClim[1]
Land cover and management				
Land cover	-	100 m	2000	PLCM2000[7]
Nature management of open vegetation	-	No resolution		Expert judgement[8]

Variable	Unit	Resolution	Year	Source
Pressure variables				
Total deposition of oxidised sulphur	mg S/m^2	1/16 degree	2009	LOTUS-EUROS[9] model
Total deposition of nitrogen	mg N/m^2	1/16 degree	2009	LOTUS-EUROS model[9]
Nitrogen input in agricultural area	kg N/ ha	1 x 1 km	2002	DNDC-CAPRI metamodel[10]
Desiccation (Water exploitation index per sub-basins of rivers)	fraction	sub-basins of rivers	2006	LISFLOOD[12]
Fragmentation	fraction	1 x 1 km	2000	LARCH-SCAN model[8]
Forest management approach	fraction	5 x 5 km	~2000–2008[14]	Derived from EFMM[11]
Impact of roads	ha	5 x 5 km	~2005	Derived from GRIP (version 1)[13]
Urbanisation	ha	5 x 5 km	2000	Derived from land-cover map

[1](Hijmans et al., 2005); [2](Bouwman et al., 2006); [3]Harmonized Soils World database (FAO/IIASA/ISRIC/ISSCAS/JRC, 2012); [4]Not yet published; [5]European Soil Database (Hiederer, 2013); [6]Shuttle Radar Topography Mission data (Farr et al., 2007); [7]Pan-European Land Cover Map (Hazeu et al., 2008); [8] Management of open vegetation, such as natural grasslands and shrubs, excluding agriculture (Hennekens et al., 2015); [9] (Cuvelier, 2013), supplemented with (Benedictow, 2010); [10] (Leip, 2011) [11]European Forest Management Map (Hengeveld et al., 2012); [12](De Roo et al., 2012); [13] (Meijer, 2009) [14] The forest management approach map is a map of potential forest management and is therefore not strictly representative for the forest management of this period. The input data on which the forest management approach map is based are mainly representative of the period 2000 to 2008. [15] Soil texture is assumed to not change within the time scale considered, between 2000 and 2050.

2.4 Species distribution modelling

2.4.1 Step 1: Species distribution range

In the first modelling step, the distribution range of each species within the study area is delineated based on envelope models that estimate species' probability of occurrence (PoO) in relation to large-scale climate and soil characteristics. The models relating species occurrence probability to climate and soil variables were obtained with the boosted regression trees technique (BRT) in the R environment (R Core Team, 2014). BRT constitutes a machine-learning non-parametric algorithm specifically suited to model nonlinear relationships and interactions between predictors (Elith et al., 2008). BRT output includes information on the relative importance of each predictor as well as its marginal effect on the response, expressed by so-called partial dependence plots. For each species a BRT model was built with TRIM-Maps (Hallmann et al., 2015), a suite of R-scripts for creating distribution maps from monitoring data and casual observations which employs functionality from related R-packages such as 'dismo' and 'gbm'. Climate and soil variable data layers were resampled to a resolution of 5 x 5 km for plants, 50 x 50 km for butterflies and birds, and 10 x 10 km for mammals (Sierdsema, 2014; Van Swaay et al., 2014; Hennekens et al., 2015), reflecting differences in the resolution and accuracy of the species records. For the plants, butterflies and birds, absence data were available (i.e., vegetation plots or atlas blocks with absence values). For the mammals, 10,000 pseudo-absences were generated across the study area (Barbet-Massin, 2012). Two sets of BRT models were established: one based on 10,000 randomly chosen pseudo-absences and one based on 10,000 pseudo-absences selected using a sampling bias grid representing locations where a given species was not observed despite other similar species were present (Ranc et al., 2016). Per species, the best performing model of the two was retained, based on visual inspection of the modelled distribution in comparison with the species' range as delineated by IUCN (www.iucn.org).

Because of the large number of species involved, a uniform set of default BRT parameters was employed, consisting of a learning rate of 0.01 (which is used to shrink the contribution of each tree when added to the model, according to the idea that it is better to improve a model by taking many small steps than by taking fewer large steps), tree complexity of 2 (to allow for second order interaction terms), bag fraction of 0.75 (i.e. the fraction of the original data set which is randomly drawn for training additive tree models in each iteration of the stage-wise gradient step search), and the Bernoulli distribution family (because of the binary response data). BRT models were tenfold cross-validated for birds and fivefold for plants, butterflies and mammals. The predictive performance of the BRT models was assessed based on estimates of the area under the ROC curve (AUC) and the explained deviance of the cross-validated models.

For all species the probabilities of occurrence as predicted by the BRT models were translated such that probabilities below a species-specific threshold were set to 0 and probabilities above this threshold were retained for use in further modelling steps (see Section 2.4.4). For each species a probability threshold was determined that maximised the true skill statistic (TSS), as TSS has been shown to be one of the best measures for determining the threshold value for SDMs (Allouche et al., 2006). A weighted version of the *TSS* was used, according to:

$$TSS_\lambda = \lambda \cdot \text{Sensitivity} + \text{Specificity} - 1 \qquad \text{(Eq. 1)}$$

whereby a weighting factor λ higher than 1 puts more emphasis on correctly predicting presences, while a λ smaller than 1 puts more emphasis on correctly predicting absences. The value of λ was determined per taxonomic group, based on visual similarity with the known distribution of the species. A weighting factor $\lambda = 1.1$ for birds and $\lambda = 1.2$ for butterflies was deemed suitable for an appropriate discrimination between presences and absences by the species experts, while for mammals and plants sensitivity and specificity were weighted equally ($\lambda = 1$).

2.4.2 Step 2: Species suitability habitat

Filtering based on land cover

In the second step in the modelling approach of BioScore 2.0, the envelopes modelled in step 1 (consisting of the grid cells with PoO larger than the threshold) are refined by selecting suitable habitats based on land cover. Species' habitat preferences in terms of land cover were identified as follows:

- For plant species, habitat preferences were derived from the frequency of occurrence of each of the 40 selected Annex I habitat types in relation to each land-cover type (based on level 3 of the CORINE land-cover classification). A threshold of 5% was applied to determine which land-cover types were suitable for each habitat type. The match between habitat type and land cover obtained in this manner was checked by an expert and further refined to exclude or include certain land-cover types per habitat type. The land-cover types suitable for each habitat types were then assumed to represent suitable habitat to all typical (i.e. habitat-related) species.

- For butterflies habitat preferences were determined by relating the species' point observations to the land-cover map and selecting as suitable habitat for a species those land-cover classes (CLC level 3 containing at least 3% of the observations). The habitat suitability classification thus obtained was then checked by an expert to 1) exclude land-cover types erroneously assigned as suitable due to geo-referencing errors in the observations and 2) add land-cover types containing less than 3% of the records but known to be suitable to the species.
- For birds, information on habitat suitability was derived from Van Kleunen (2003), who defined the habitat use of all European breeding birds, in terms of EUNIS codes from regional and European atlases and literature. For implementation in BioScore, the EUNIS codes were translated to the classes of the CORINE land-cover map (see Appendix III for the conversion).
- For mammals, habitat suitability information was derived from Rondinini et al. (2011), who assessed the suitability of land-cover types as represented in ESA's Global Land Cover map (Globcover) (version 2.1) for 5027 out of 5330 known terrestrial mammal species. For implementation in BioScore, the Globcover classes were translated to the classes of the CORINE land-cover map (see Appendix IV for the conversion). The land-cover classes that were classified as highly and medium preferred habitat by Rondinini et al. (2011) were considered suitable.

Influence of nature management of open vegetation

Because the suitability of any land-cover type for a particular species may depend on specific management measures (for example, some grassland species may occur only on grassland that is regularly mown), the extent of suitable habitat is further refined based on management. This only applies to management of natural open vegetation, as agricultural intensification is already included in nitrogen input and forest management. Nature management applies to future situations (scenarios) only, i.e., it is not included when predicting the present-day or reference distribution of species. If a given scenario assumes that management is stopped (for example, cessation of mowing in abandoned grassland), the corresponding grid cells are removed from the habitat area of species dependent on management. The dependency of species on management is expressed as so-called hemeroby level, which is an integer score ranging from 1 to 9 where 1 represents hemorobic (not dependent on human management) and 9 represents polyhemerobic (strongly dependent on human activity). The assignment of hemeroby levels to habitat types is based on expert judgement. For the quantification of hemeroby levels on species level, the same selection of plots was used as for the other pressures. Each plant species was assigned a hemeroby level based on the habitat type of the plots in which the species occurs (mean value, see Annex 5 in (Hennekens et al., 2015)). Species with a hemeroby level above 5 were then classified as being dependent on management. For butterflies and birds the hemeroby classification was based on expert judgement. Mammal species are considered as not being dependent on management, hence the hemeroby filter is not applied. See Appendix V for all species classified as dependent on management.

2.4.3 Step 3: Species response to pressures

Deriving pressure–response relationships

Pressure–response relationships were derived for each of the local-scale pressure variables nitrogen deposition, sulphur deposition, desiccation, nitrogen input, forest management, urbanisation, impact of roads, and fragmentation (Table 2.2). Variable maps were resampled to 5 x 5 km for plants, birds and butterflies and to 10 x 10 km for mammals taking the average value within a grid cell. Response relationships were obtained with logistic regression (logit link and binomial error distribution) in the R environment (R Core Team, 2014). Models with only a linear term as well as those with linear and quadratic terms were both considered, and the most parsimonious model per species and pressure was selected based on the Akaike information Criterion (AIC). Model performance was assessed by calculating AUC values based on a tenfold cross-validation.

Presence-absence data for this modelling step were retrieved as follows:

- For plant species, point records were selected located within the suitable habitat (determined in step 2) and within the limits of the binary map of the habitat type the species is characteristic for (determined in step 1). These occurrences were supplemented with a more or less equal number of randomly selected absences from the pool of vegetation plots located within the same mask (Hennekens et al., 2015). (i.e., no pseudo-absences were generated)
- For the birds and butterflies, presence-absence data were retrieved from point record data sources within the species distribution range that contained true absences (Sierdsema, 2014; Van Swaay et al., 2014)
- For mammals, presences and absences were selected from the grid cells representing suitable habitat within the envelopes, using the distribution maps resulting from steps 1 and 2.

The response functions on average were computed on 9547, 405, 5898 and 3710 presence values and 12130, 551, 5898 and 3722 absence values for respectively birds, butterflies, mammals and plants. The exact number varies among species and pressures.

To select the appropriate layer with fragmentation for breeding birds, butterflies and plants (see Section 2.3), first all established relationships for fragmentation were discarded if both the linear and the quadratic term were not significant ($p > 0.05$). Secondly, the ecosystem type/land-cover class was chosen with the largest number of observations, as a proxy for the most important habitat of a species. A corresponding dispersal distance was then selected based on the goodness-of-fit of the regression model, selecting for each species the fragmentation layer with the dispersal distance resulting in the model with the highest AUC.

Post-processing

Response relationships obtained for each species and pressure variable (excluding fragmentation, see above) were screened and selected/adjusted as follows:

- Relationships were only discarded if both the linear and the quadratic term were not significant ($p > 0.05$), indicating no significant response of the species to the variable of concern. Models with only a linear term relationships were discarded when the linear term was not significant ($p > 0.05$).
- Relationships including both a linear and quadratic term whereby the linear term was significant ($p < 0.05$) and the quadratic term resulted in a negative unimodal (U-shaped) response, were modified to include only the linear term (i.e., the coefficient for the squared term was set to zero). This was done for sulphur deposition, nitrogen deposition, nitrogen input, desiccation, impact of roads and urbanisation as these U-shaped types of responses are ecologically not expected for these pressures.

Based on the selected response relationships a probability of occurrence map per species per pressure was calculated.

Both the forest fragmentation maps and the maps of area covered per forest management approach are strongly correlated with the area of forest. To avoid that the effect of forest area shows up in two pressure–response relationships, thus acting as a clear confounder, the forest management maps have been aggregated to one forest management approach per 5 x 5 km grid. This correspond to the PoO with a 100% coverage of that management type from the pressure response curve. The forest management approach ‘combined objective forestry’ was much more abundant in the forest management map than the other approaches. To avoid that this category becomes even more abundant, out of the other four approaches the dominant one is selected. All other grid cells are appointed to ‘combined objective forestry’.

2.4.4 Step 4: Probability of occurrence of species

The final step consists of combining the results obtained from steps 1–3. First, the results of steps 1, 2 and 3 are aggregated per species. For each species this results in a probability of occurrence per grid cell as a function of all the included environmental variables.

In order to aggregate over the environmental variables, for each species the model results from step 1 are combined with those resulting from step 3 in grid cells with land cover that is representing suitable habitat (delineated in step 2), as follows:

$$\frac{Odds_{1\&3}}{SF_{1\&3}} := \frac{Odds_{step_1}}{SF_{step1}} \times \frac{Odds_{step_3}}{SF_{step3}} \qquad \text{(Eq. 2)}$$

where *Odds* represents the ratio p/(1-p) as calculated by the BRT (step 1) and logistic regression models (step 3). The use of odds enables to distinguish between the situation where a pressure decreases and where it increases the probability of occurrence. *SF* is a scaling factor calculated as the ratio N_1/N_0 of the number of presences and absences in the species distribution data used in the corresponding modelling step. It reflects the simple *null* model (constant) and is used as a reference point to express how the Odds change relative to its average value (null-model reference point) due to the individual influences of the pressures.

A similar strategy is used to determine the *Odds* (p/(1-p)) which results from the combined influence of the environmental pressures modelled in step 3:

$$\frac{Odds_{step3}}{SF_{step3}} := \prod_{k=1}^{p} \frac{Odds_k}{SF_{step3}} \qquad \text{(Eq. 3)}$$

where $Odds_k$ represents the ratio p/(1-p) for a given pressure *k*, according to the logistic model which is established in step 3 for this single pressure–response relationship.
The overall scaling $SF_{1\&3}$ is determined as the geometric mean of the separate scaling factors:

$$SF_{1\&3} = \sqrt{SF_{step1} \times SF_{step3}} = \sqrt{\frac{N_1}{N_0}_{step1} \times \frac{N_1}{N_0}_{step3}} \qquad \text{(Eq. 4)}$$

A more extensive explanation of the derivation of Equations 2 and 3 is provided in Appendix VI.

The overall Odds from combining Equations 2 to 4 is then translated into an overall probability of occurrence, as follows:

$$PoO = Odds_{1\&3} / (1 + Odds_{1\&3}) \qquad \text{(Eq. 5)}$$

Thus, the PoO represents the (conditionalised) probability of occurrence of a species in a specific land-cover type (step 2), under the prevailing conditions regarding climate and soil (step 1) and environmental pressures (step 3).

In the above integration, pressures are taken into account only in grid cells with land-cover types where the pressures are relevant. For example, forest management intensity is not relevant in agricultural areas. Table 2.3 shows the pressures included per land-cover type. Ecologically relevant pressures are included per land-cover type. For example forest management is only included in forests. Nitrogen, sulphur deposition and fragmentation are not included in agriculture because these effects are expected to be negligible compared to the effect of agricultural intensity (mapped as nitrogen input).

As a final step in this integration to calculate the species PoO for a specific grid cell, one first determines what fraction of the grid cell is covered by the various land-cover types and then one calculates a weighted average of the species PoOs for the land-cover types of interest, using the fractions as weight factors in this averaging.

Table 2.3: pressures taken into account per land-cover type

Variable	Urban area (CLC class 1.X)	Agriculture (CLC class 2.X)	Forests (CLC class 3.1)	Shrubs and open vegetation (CLC class 3.2–5.1)
Climate and soil	X	X	X	X
Sulphur deposition	X		X	X
Nitrogen deposition	X		X	X
Nitrogen input		X		
Forest management			X	
Desiccation		X	X	X
Fragmentation			X	X
Impact of roads	X	X	X	X
Urbanisation	X	X	X	X
Nature management		X		X

2.4.5 Step 5: Indicators on species and ecosystems changes

Biodiversity encompasses the overall biological variety found in the living world and includes the variation in genes, species and ecosystems. For this reason it is not possible to express biodiversity in one indicator only. Therefore a small number of complementary headline indicators were developed. The indicator at species level expresses the change in occurrence of species. The indicator at ecosystem level expresses the change in extent and quality of ecosystems, considering the change in probability of occurrence of all species occurring in that ecosystem. Four types of ecosystems were distinguished: shrubs and open vegetation (e.g. grassland), forests, urban areas and agricultural areas. Indicators can be presented as graphs or maps.

Maps with modelled probabilities of occurrence of each species for the reference year 2005 and a future scenario were then used to calculate indicators of biodiversity change on the level of species and ecosystems. In presenting the results the focus is on the relative change (change in the summed probability of occurrence between two scenarios).
Indicators can be calculated for specific selections of species (e.g. taxonomic groups, red list species) or a specific set of grid cells (e.g. Natura 2000 areas, countries, biogeographical regions) to increase policy relevance.

Species Indicator
Changes from the current situation to a future scenario in the summed probability of occurrence for each species was calculated. The proportion of species increasing or decreasing was expressed for the EU-28 plus Switzerland. The change in probability of occurrence per species was calculated as:

$$C_S = \left(\left(\sum_1^G PoO_{S,y} - \sum_1^G PoO_{S,0}\right) / \sum_1^G PoO_{S,0}\right) \qquad \text{(Eq. 6)}$$

where C_s is the relative change in probability of occurrence of species *S,* $PoO_{S,y}$ and $PoO_{S,0}$ are the probabilities of occurrence of species S in scenario year y and the reference year, respectively, and G refers to the number of grid cells in the study area. This is expressed in terms of percentage points.

Ecosystem indicator
In order to obtain an indicator on changes in the quality and extent of ecosystems, per grid cell, the relative change in summed probabilities of occurrence given the set of species considered was calculated between the current situation and a future scenario as follows:

$$C_G = \left(\left(\sum_1^S PoO_{G,y} - \sum_1^S PoO_{G,0}\right) / \sum_1^S PoO_{G,0}\right) \qquad \text{(Eq. 7)}$$

where C_G is the change in the sum of probability of occurrence in a grid cell G. All probability of occurrences of all species are summed per grid cell. Changes are expressed as a product of the number of species and their change in probability of occurrence per 5 x 5 km grid cell. For expressing the change in quality and extent of the four distinguished ecosystems, the latter product is multiplied by the fraction covered by the specific ecosystem in the grid cell.

3 Model results

3.1 Species selection and relationships derived in steps 1, 2 and 3

Species selection

Models were retained for 1320 of the 1402 species that were initially selected (Table 3.1). All results presented consist of this selection of species. Species excluded were those for which no adequate climate/soil envelope could be established in step 1, based on visual inspection of the modelled distribution, or for which no model could be established due to lack of observations. Furthermore species were excluded when no pressure–response models were retained. The butterfly species *Leptidea sinapis* was discarded as recent research shows that this is a species complex consisting of at least three species (Dincă et al., 2011).

Table 3.1: Numbers of species initially selected for BioScore 2.0 and the numbers eventually included. A list of the species included is provided in Appendix V.

Species group	Initial selection	Final selection
Vascular plants	884	863
Butterflies	100	95
Breeding birds	299	284
Mammals	81	78
Total	1402	1320

Distribution models (step 1) and pressure–response relationships (step 3)

It is only partially possible to validate the model results obtained from applying BioScore 2.0, to the scenarios to assess the impact on species and ecosystems. Since no data on the future is available, one cannot test whether the BioScore 2.0 relationships between environmental conditions and species occurrence that are calibrated based on the species monitoring data will also hold under future conditions. Also there is limited possibility to compare BioScore modelling results by backcasting with information of the past, since historical data on species occurrences is scarce. Comparing the modelled output with that from other models provides information on model differences, but not on the quality of BioScore 2.0. What is left as a means of validation is cross-validation or with expert knowledge to assess its plausibility. Special points of attention is given to the relationships established in steps 1 and 3. The higher the plausibility and accuracy of these relationships, the more confident one could be in the predictive value of the model. Of course also due care should be taken when extrapolating the relationships for combinations of values of explanatory variables outside the value range that has been used in estimating these relations.

Cross-validation can be used as a first test to assess the predictive quality of the BioScore 2.0 model parts, albeit in conditions which reflect the present monitoring data. Table 3.2 shows the AUC and explained deviance of the models established in steps 1 and 3. For step 3 only the relationships are shown which are left after post-processing (see Section 2.4.3). An overview of the numbers of linear and quadratic pressure–response relationships obtained and the numbers resulting from the post-processing is provided in Appendix VII. As the performance results in Table 3.2 show, the results of step 1 – where the influence of climate–soil conditions on species occurrence is determined – show typically high (>=0.9) to moderate (0.7–0.9) AUC values, while the deviance explained is in the order of 40% (butterflies) to 70 % (vascular plants), which indicates that a large part of the variation in the data on the scale under consideration can be explained already by the selected climate and soil variables. For the majority of the selected pressure–response relationships in step 3 the AUC values are lower than 0.7 and a mean explained deviance smaller than 10% (Table 3.2). These low explained deviance values are not surprising and are partly due to the fact that in each relationship only one variable was used, which describes generally less variation than a multitude of variables. Allowing for more complex model relations than the linear or quadratic forms which are used in the present single pressure logistic models could improve the statistical accuracy of these models.

When looking at the ecological plausibility of the pressure–response relationships of a few butterfly species the results are mixed (Swaay et al., 2016). Many relationships seem plausible, but there are also relations which seem unlikely. This means that a statistically inaccurate pressure–response relationship doesn't always lead to an ecologically implausible relationship. However, more statistically accurate relationships will probably lead to more ecologically plausible relationships.

Habitat preference (step 2)

Most species can occur in forest and other terrestrial nature areas (CLC code 311–333). Fewer species had a habitat preference for agricultural area (CLC code 211–244) or wetlands and open waters (CLC code 411–523). There were no plant species with a habitat preference for urban areas (CLC code 111–142) and few bird, mammal and butterfly species with this preference (Table 3.3).

Table 3.2: Overview of performance for the models established for steps 1 and 3 for each of the four taxonomic groups. For step 3 only the selected pressure–response relations are shown (see 'post-processing' in Section 2.4.3) The number of models is shown as well as the distribution of AUC values (cross-validated models), the average explained deviance (cross-validated models) and the standard deviation of the explained deviances. FMA refers to forest management approach, with 1 = close to nature, 2 = combined objective forestry, 3 = even-aged forestry, 4 = nature reserve, 5 = short rotation forestry).

	n	**AUC values**				**DevExpl (%)**
		< 0.6	**0.6– < 0.7**	**0.7 – < 0.9**	**>=0.9**	**mean (SD)**
Vascular plants						
Climate/soil	863	0	1	3	859	68.5 (13.8)
Desiccation	719	420	196	98	5	5.48 (9.14)
Nitrogen input	742	334	266	136	6	6.30 (8.82)
FMA 1	652	545	98	9	0	1.82 (3.12)
FMA 2	714	460	193	61	0	3,65 (5.29)
FMA 3	604	506	86	12	0	1.80 (3.46)
FMA 4	641	535	88	18	0	2.13 (4.62)
FMA 5	501	499	1	1	0	0,69 (1,19)
Fragmentation	544	214	211	112	7	7.39 (9.44)
N Deposition	786	325	256	184	21	9.50 (12.7)
Roads	739	465	221	52	1	4.26 (6.23)
S Deposition	774	328	258	171	17	8.68 (12.2)
Urban	733	451	221	61	0	3.81 (5.53)

	n	**AUC values**				**DevExpl (%)**
		< 0.6	**0.6– < 0.7**	**0.7 – < 0.9**	**>=0.9**	**mean (SD)**
Butterflies						
Climate	95	0	0	58	37	39.8 (9.30)
Desiccation	67	23	31	13	0	4.84 (4.20)
Nitrogen input	55	34	20	1	0	3.56 (3.36)
FMA 1	51	42	8	1	0	1.48 (1.20)
FMA 2	68	36	29	3	0	3.58 (3.72)
FMA 3	54	50	4	0	0	2.08 (1.85)
FMA 4	38	37	1	0	0	1.41 (1.16)
FMA 5	33	32	0	1	0	1.65 (3.52)
Fragmentation	55	9	21	25	0	10.8 (7.15)
N Deposition	81	31	25	25	0	7.19 (5.62)
Roads	76	26	35	15	0	5.39 (4.28)
S Deposition	75	21	38	16	0	5.56 (4.18)
Urban	73	31	31	11	0	3.95 (2.83)
Breeding birds						
Climate	284	0	0	26	258	56.0 (14.8)
Desiccation	259	147	90	20	2	3.67 (8.04)
Nitrogen input	260	135	104	21	0	3.96 (5.71)
FMA 1	250	228	20	2	0	1.12 (1.56)
FMA 2	259	170	80	8	1	2.83 (4.61)
FMA 3	250	225	25	0	0	1.44 (1.70)
FMA 4	243	220	19	4	0	1.52 (3.09)
FMA 5	198	198	0	0	0	0.48 (0.61)
Fragmentation	141	18	60	59	4	10.5 (10.4)
N Deposition	278	113	127	38	0	4.79 (5.36)
Roads	270	180	77	13	0	2.96 (3.91)
S Deposition	282	100	139	43	0	4.46 (5.01)
Urban	270	140	112	18	0	3.83 (4.02)
Mammals						
Climate	78	0	0	21	57	49.4 (22.8)
Desiccation	73	22	24	25	2	9.85 (11.5)
Nitrogen input	67	27	28	12	0	5,26 (6.24)
FMA 1	64	50	12	2	0	1.14 (1.55)
FMA 2	75	44	24	6	1	3.70 (5.42)
FMA 3	69	55	14	0	0	1.86 (2.07)
FMA 4	69	59	10	0	0	0.94 (1.54)
FMA 5	56	56	0	0	0	0.50 (0.81)
Fragmentation	75	28	26	20	1	8.42 (10.5)
N Deposition	74	25	20	27	2	10.0 (11.4)
Roads	68	49	14	5	0	3.17 (5.33)
S Deposition	75	25	22	26	2	9.85 (11.2)
Urban	71	32	25	14	0	5.60 (7.50)

Table 3.3: Number of species with a habitat preference per Corine land-cover class

Corine land-cover class	**CLC code**	**Vascular plants**	**Butterflies**	**Breeding birds**	**Mammals**
Continuous urban fabric	111	0	6	18	0
Discontinuous urban fabric	112	0	72	18	0
Industrial or commercial units	121	0	2	22	0
Road and rail networks and associated land	122	0	0	2	0
Port areas	123	0	0	2	0

Corine land-cover class	CLC code	Vascular plants	Butterflies	Breeding birds	Mammals
Airports	124	0	0	2	0
Mineral extraction sites	131	0	3	6	0
Dump sites	132	0	0	1	0
Construction sites	133	0	0	19	0
Green urban areas	141	0	16	21	28
Sport and leisure facilities	142	0	5	0	28
Non-irrigated arable land	211	397	97	30	37
Permanently irrigated land	212	0	6	31	37
Rice fields	213	0	0	19	37
Vineyards	221	0	6	25	40
Fruit trees and berry plantations	222	0	4	40	40
Olive groves	223	0	0	16	40
Pastures	231	518	73	52	0
Annual crops associated with permanent crops	241	0	0	30	55
Complex cultivation patterns	242	245	77	39	55
Land principally occupied by agriculture, with significant areas of natural vegetation	243	288	97	68	55
Agro-forestry areas	244	0	0	0	55
Broad-leaved forest	311	546	90	83	75
Coniferous forest	312	632	97	65	75
Mixed forest	313	577	87	48	75
Natural grasslands	321	544	69	82	77
Moors and heathland	322	276	22	65	77
Sclerophyllous vegetation	323	93	34	39	77
Transitional woodland shrub	324	133	75	63	77
Beaches, dunes, sands	331	99	7	57	60
Bare rocks	332	186	0	71	60
Sparsely vegetated areas	333	219	11	102	60
Burnt areas	334	0	0	18	60
Glaciers and perpetual snow	335	0	0	1	60
Inland marshes	411	1	2	110	0
Peat bogs	412	79	7	55	0
Salt marshes	421	20	0	13	48
Salines	422	0	0	7	48
Intertidal flats	423	20	0	12	48
Water courses	511	0	0	30	42
Water bodies	512	29	2	54	42
Coastal lagoons	521	0	0	18	42
Estuaries	522	0	0	5	42
Sea and ocean	523	104	0	16	42

3.2 Type of indicators

We illustrate two types of indicators on the level of species and ecosystems, as proposed in step 5 of BioScore (see Section 2.4.5). Next to these two types of indicators, other types are possible as well. For example the mean probability of occurrence as a proxy for ecosystem quality or the number of cells with a probability of occurrence larger than zero as a proxy for the extent of species. Important for a set of indicators is that it should show a spectrum of different types of change (e.g. change in number of species and change in extent of occurrence) and the indicators should be closely related to European nature policy goals.

Species indicator
The first indicator presents the fraction of assessed species which show a (strong) decrease or increase (in summed probability of occurrence), when comparing a reference year with a target year, given a scenario (Figure 3.1). These results can be considered as a proxy for the relative change in species occurrence.

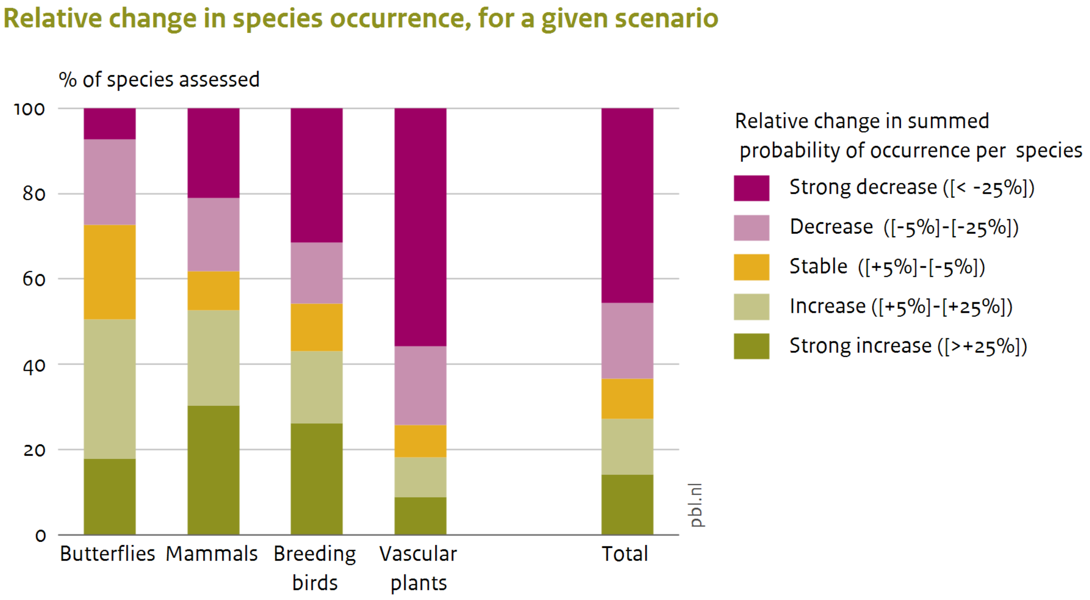


Figure 3.1. Indicator of the relative change in summed probability of occurrence for all assessed species and per taxonomic group.

Ecosystem indicator
The second type of indicator concerns the ecosystem level. Figure 3.2 shows the change in ecosystem quality within forests, agriculture, urban area and open vegetation and the area it concerns. This indicator type can also be visualised in map (Figure 3.3).

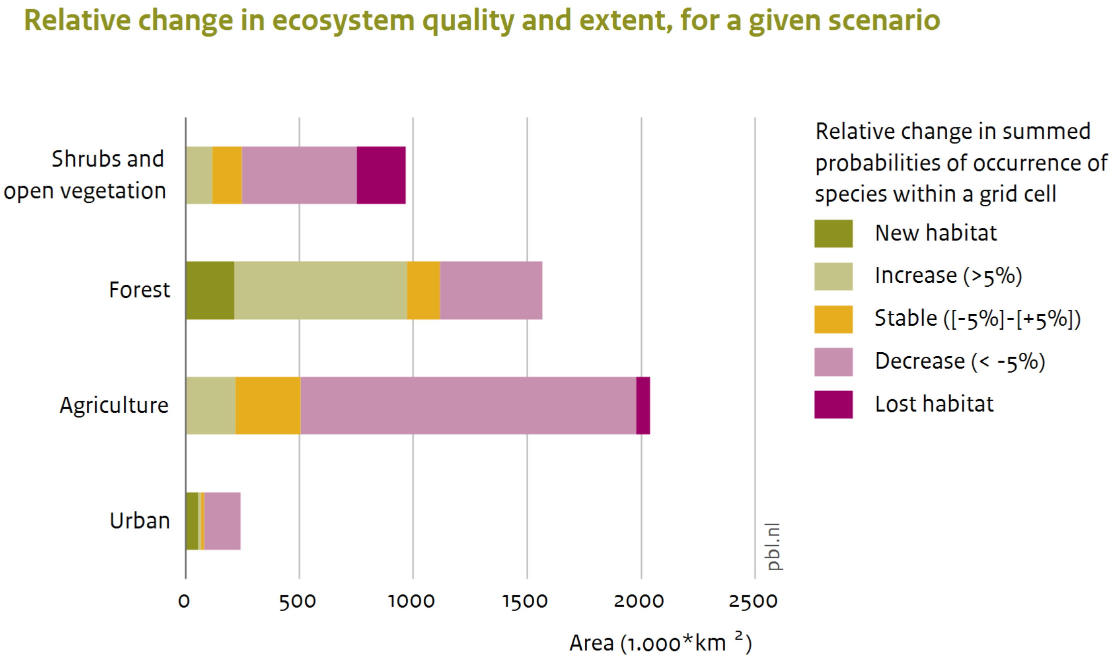


Figure 3.2. Indicator of relative change in summed probability of occurrence for shrubs and open vegetation, forests, agriculture and urban area.

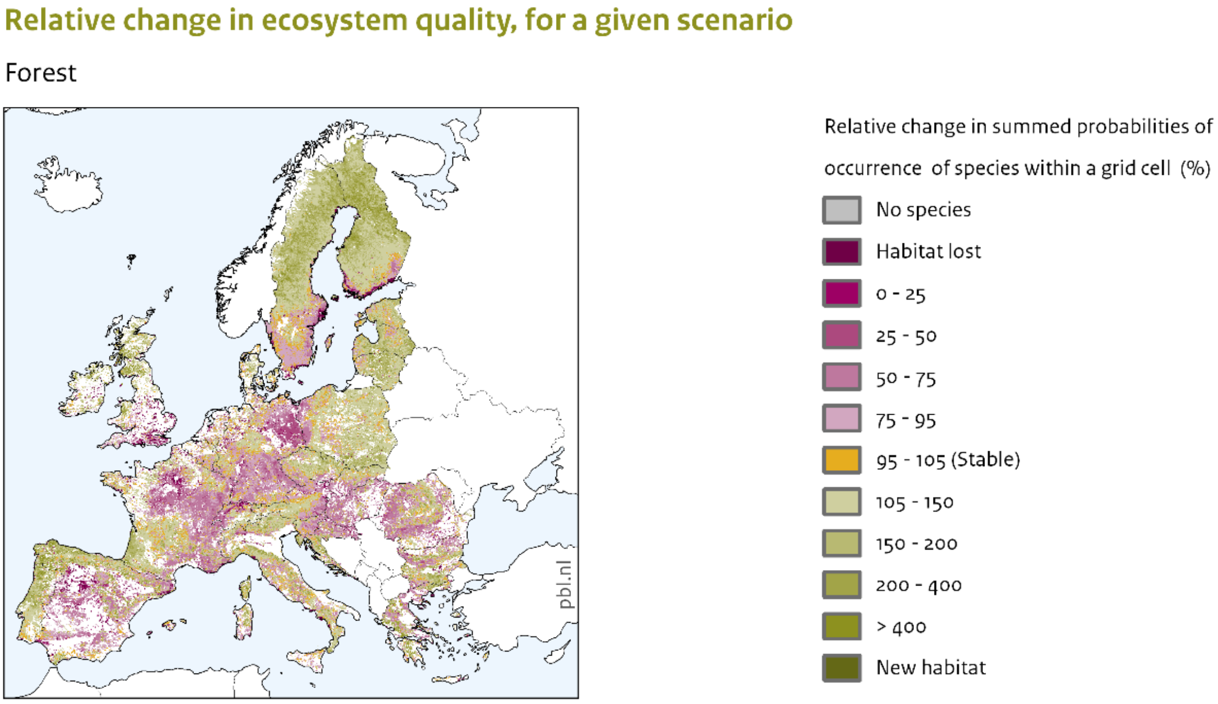
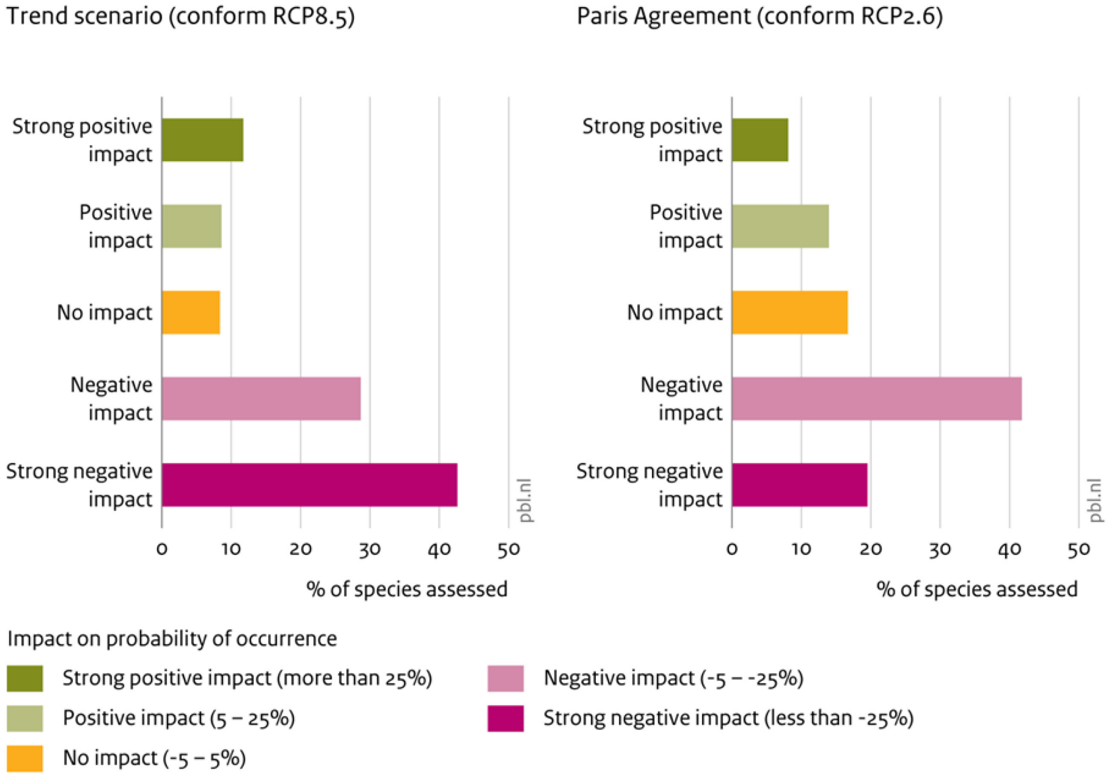


Figure 3.3: Indicator of the relative change in sum of probability of occurrence for forests

3.3 Modelled effect of climate change

The effect of climate change on European protected species is modelled using BioScore 2.0. The model has been used to assess the effect of the trend scenario for 2050 and a scenario directed towards achieving the Paris Agreement on Climate Change to keep temperature rise well below 2 degrees Celsius until 2100 – instead of 4 °C in 2100, or 2 °C in 2050 (Figure 3.4). A considerable share of the species assessed is strongly negatively impacted by the expected changes in climate. Achieving the objective of the Paris Agreement on climate change – to limit global temperature increase to well below 2 °C, instead of 4 °C by 2100 or 2 °C by 2050, as was assumed in the Trend scenario – decreases the strong negative impact for many species.

Impact of climate change on species in EU, 2005 – 2050



EU is EU28 and Switzerland

Source: PBL results from Bioscore 2.0 model

Figure 3.4: A sensitivity analysis has been carried out of the effects of achieving the Paris Agreement on Climate Change to keep temperature rise well below 2 degrees Celsius until 2100 – instead of 4 °C in 2100, or 2 °C in 2050, also see Van Zeijts et al. (forthcoming).

4 Discussion

Species distribution models

BioScore 2.0 uses a boosted regression tree method to calculate species distribution ranges. Within those ranges the habitat suitability is determined by correlating presence observations with the land-cover map, whereas the pressure–response relationships are based on logistic regression. In general, the correlative methodology of species distribution modelling has several important shortcomings that have been frequently criticised (Pearson and Dawson, 2003; Heikkinen et al., 2006; Botkin et al., 2007; Thuiller et al., 2008; Jarnevich et al., 2015). The main points of criticism for the derived bioclimatic models or habitat suitability models concern the missing elements, such as:
(1) biotic interactions (Pearson and Dawson, 2003; Guisan and Thuiller, 2008);
(2) dispersal limitations (Pyke et al., 2005; Heikkinen et al., 2006; Körner et al., 2010);
(3) possible changes in species responses due to adaptations (e.g. evolutionary or behavioural) (Davis and Shaw, 2001; Parmesan, 2006).

Furthermore, the correlative approach assumes that species are at equilibrium with the environmental conditions and thus typically do not consider transient dynamics, even though non-equilibrium conditions are highly relevant in environments with exceedance of critical loads of nitrogen and sulphur deposition (CCE, 2010) or climate change (Thuiller et al., 2008). Time lags in terms of damage delay time and/or recover response time have been reported in many studies (Galloway, 1995; Lindborg and Eriksson, 2004; Menéndez et al., 2006). The use of mechanistic population or even evolutionary dynamical and biogeochemical models, which try to describe underlying processes based on ecological theory instead of using correlative research, might be a future step and result in dynamic multi-stress models (De Vries et al., 2010). International scientific groups, such as the International Cooperative Programme on Modelling and Mapping of Critical Levels and Loads and Air Pollution Effects, Risks and Trends (ICP M&M) and the Coordination Centre of Effects of the UNECE Convention of Long Range Transboundary Air pollution, are currently developing European scale dynamical models for effects of air pollution and climatic change on plant species (Slootweg et al., 2014). At present the developed models do have a mechanistic chemical soil module (such as VSD+) but the effects on vegetation are still described with regression modules, such as PROPS and MOVE (De Vries et al., 2010; Slootweg et al., 2014). European-scale mechanistic dynamical models for a wider set of pressures (i.e. including e.g. population dynamics, dispersal) and species are currently not available. A review on bioclimatic modelling for species protection (Sieck et al., 2011) concluded that the current statistical, state-of-the-art, multi-species, bioclimatic models will remain useful as a first step in a broader modelling framework designed to evaluate the potential distributions of critical species in protected areas or protected area networks. This holds in spite of the described limitations (Sieck et al., 2011).

Three discussion points on the BioScore modelling approach

In order to evaluate the applicability and limitations of the BioScore modelling approach the model has been reviewed two times by an international group of scientists and potential users (http://www.ecnc.org/news201014/ and Appendix VIII). During the second review, the following three discussion points came forward as most important, concerning:
(1) the modelling framework concerning the hierarchical approach and in particular the approach of integrating multiple response relationships for single stressors or environmental factors into one combined effect;
(2) the selection of species and monitoring data;

(3) the selection and data of environmental variables.
These issues are discussed in more detail below.

Modelling framework

Hierarchical approach

BioScore 2.0 uses a hierarchical approach in species modelling, which combines different statistical methods to relate species occurrence to particular abiotic factors with knowledge on habitat preferences. This hierarchical approach offers the opportunity to use combinations of various and heterogeneous sources of knowledge, such as process knowledge, observational and experimental data, and expert judgement. At each level appropriate knowledge and data can be added.

The hierarchical approach assumes that the probability of occurrence of a species is the result of a set of nested and independent environmental factors. Both climate and geology/soil play a role at the coarsest spatial resolution and determine the potential distribution range of a species (Pearson et al., 2004; Guisan and Thuiller, 2005). At landscape scale, land cover determines where a species has potential habitat within its distribution range and at a local scale, local pressures determine the actual probability of occurrence of a species. This hierarchical approach holds when:
(1) climate and soil determine the potential distribution range of a species and do not affect local occurrence;
(2) land cover determines the distinction between potentially suitable and unsuitable habitat;
(3) pressures, such as nitrogen deposition and desiccation, are the most important factors determining local conditions and therefore the actual probability of occurrence;
(4) the variables are uncorrelated between the steps and their impacts can be considered as additive on the logistic scale.

Climate is often identified as the most important factor determining potential distribution ranges (Huntley et al., 2007; Settele et al., 2008). In terrestrial systems climate dominates distributions at the global scale (coarsest grain, largest extent), whereas at landscape scale (from a few to hundreds of kilometres) topography and soil type create the finer-scale variations in climate, nutrient availability, and water flows that influence species (Mackey and Lindenmayer, 2001). This suggests that the choice to include soil properties only in step 1, together with climate, might need to be reconsidered. Moreover, climate not only determines the coarse-scale distribution ranges but also has local impacts (Lassueur et al., 2006; Scherrer and Körner, 2011), which are not taken into account in the current model approach. Finally, interactions and correlations exist between climate, soil, pressures and land cover. Climate has a large impact on soil texture and land cover. For example, bogs can only develop with large amounts of rain throughout the year and nitrogen deposition is highest in Western European countries, which happen to have a relatively mild climate. Thus, the assumptions behind the hierarchical approach need further investigation.

Combining effects of single pressure–response relationships

Another point of concern is the approach behind step 4 to calculate the combined effects of the various single pressure–response relationships from step 3 and probability of occurrence from step 1 (see also Appendix VI). This hinges on a number of assumptions:
(1) interaction effects of pressures are negligible;
(2) correlations between the pressures are absent or small;
(3) a logistic regression model structure with only linear and/or quadratic terms is adequate to describe the pressure–response relationships.

Appendix X includes a tentative comparison between the results of the aggregation of the single pressure models with a (non-parametric) benchmark model where the responses to the various pressures are modelled simultaneously. This comparison, based on a selection of 11 butterfly species, shows that apparently there are interactions between the pressures, which are not accounted for in the aggregation of the single pressure models in step 4 (Appendix X). The ecological and statistical basis for these interactions require further study. Correlations among environmental pressure variables also exist, as illustrated in Appendix X. For example, there is a correlation between nitrogen application on agricultural land (e.g. fertiliser) and the fragmentation maps of forests (CLC class 3.1) and shrub and/or herbaceous vegetation associations (CLC class 3.2) as well as between nitrogen deposition and these fragmentation maps. Another example is the correlation between the impact of roads and urbanisation. The correlations among the pressures imply that single pressure models may reflect ecologically unrealistic (spurious) responses, as the relationships identified may be confounded by the effects of the correlated pressures. To reduce this risk, a pre-selection of pressure variables was performed in the construction of BioScore 2, discarding highly correlated pressure variables from the model. For example, the highest correlations were found among the various fragmentation maps, and therefore it was decided to include only one fragmentation relationship per species in step 4. Moreover, the correlations between nitrogen deposition and nitrogen application are accounted for, since nitrogen application is only used in grid cells with an agricultural land-cover class and nitrogen deposition is used in all the other cells (Table 2.3). Yet, despite these efforts to decrease correlations between pressures, small and large correlations still exist between numerous pressures, which implies that the approach to aggregate the impact of the pressures might need to be reconsidered.

Logistic regression is often used to describe pressure–response relationships (Guisan and Zimmermann, 2000; Rushton et al., 2004). Fitting simple unimodal Gaussian or sigmoid functions help in describing underlying ecological processes, because niche theory as applied to both plants and animals assumes Gaussian-shaped unimodal curves. In plant community ecology, niche theory has an intimate relationship with the continuum concept (Austin and Smith, 1989). Current evidence supports unimodal response curves with various skewed or symmetric shapes for plants (Austin, 2002). H owever, these relationships might be too simple to be used as an adequate basis for modelling pressure–response relationships for distal (i.e. indirect effect) rather than proximal (i.e., direct effect) environmental variables (Merow et al., 2014). Because relationships between indirect variables and more direct variables need not be linear, there is no theoretical expectation regarding the shape of species responses to indirect variables (Austin, 2007). For example, sulphur deposition is an indirect driver, which influences acidification of the soil, whereas the pH of the soil can be considered as the direct driver affecting plant species occurrence. Sulphur deposition and the pH of the soil are not linearly related, as the effect of sulphur deposition on acidification of the soil is dependent on the soil type. Hence, for distal environmental variables, more complex functions such as multi-modal curves, splines or U-shaped curves might be more appropriate. However, these are ecologically less easily explained. In BioScore 2, ecologically unrealistic negative unimodal (U-shaped) responses were modified a posteriori by setting the coefficient for the squared term to zero. This was done for pressures where U-shaped curves were regarded implausible, such as nitrogen deposition. However, in such cases it would be better to choose for linear or sigmoidal curves on beforehand, as simply removing a quadratic term and retaining the linear term neglects the fact that the linear and quadratic terms are conditional on each other. Given the fact that the pressure–response relationships are characterised by low accuracy (Table 3.2) and that not all assumptions are fulfilled on which the approach to aggregate the impact of the pressures is based, the single pressure–response relationships in BioScore 2.0 should be used with caution.

Impact of climate change on species

Despite these limitations, the results calculated by the BioScore 2.0 model on species change due to future climate (Figure 3.4) are considered fairly robust. First, these results are not significantly affected by the assumptions made in steps 2 to 4, because a BioScore run based on only step 1 resulted in the same conclusions regarding the share of declining species as runs including all modelling steps (see Appendix XI). The model simulations revealed that a considerable share of the species assessed is strongly negatively impacted by the expected changes in climate in 2050. Such large effects of climate change are also reported in various other European-scale studies on specific species groups. Studies on European butterflies and breeding birds show for example that the vast majority of species is expected to be negatively affected by climate change, because climate-induced range expansions (mainly at higher latitudes) do not compensate for climate induced range contractions (typically at lower latitudes) (Huntley et al., 2007; Settele et al., 2008). According to three scenarios explored in Huntley et al. (2007), the potential future distribution of breeding birds is reduced on average by 20%. In a study on European bumblebees, more than 75% of the modelled species were found to lose over 20% of their suitable area, even under a modest climate scenario (Rasmont et al., 2015).

It should be noted however, that BioScore 2.0 assumes that species are not restricted in their migration ability. Yet, land use and fragmentation inhibit species migration and modelling climate-change impacts without incorporating these factors may underestimate effects on species occurrences (Thomas et al., 2004; Thuiller et al., 2004; Schloss et al., 2012; Santini et al., 2016; Visconti et al., 2016a). New climatically suitable sites might not be reached. As a consequence, the calculated probability of occurrence in the 4 °C increase in 2100 scenario might be overestimated for species with limited dispersal ability (Hellmann et al., 2016). In the future, ecological realism might be added to the model by accounting for dispersal limitations.

Species selection and data

Species selection

In most species-based assessment models, the focus is on specific taxonomic groups and effects of individual pressures, such as climate-change models for birds or butterflies and air pollution models for plant species (Slootweg et al., 2014). These models are typically based on a random sample of species, in order to describe the effect of environmental change on the whole group, assuming that this random sample is representative. Although these models are also limited by data availability, e.g. less data is generally available on rare species, which impact the possibility to select a random sample. In BioScore the focus is on target species of the most important European biodiversity policies, i.e., the Birds and Habitats Directives. It is assumed that the sample of selected vascular plants, butterflies, breeding birds and mammals can be considered representative for the present European terrestrial target species and target habitats, because it includes the major taxonomic groups of the Directives (EEA, 2015) . Moreover, by including a wide range of different species sensitive to various environmental pressures (Delbaere et al., 2009), it is assumed to have covered a wide and unbiased range of sensitivities representative of all European terrestrial target species. However, this assumption has not yet been tested, and it is possible that species that could not be included in the model because of data limitations (particularly species in eastern Europe) are actually more sensitive than well-monitored species (mostly in Western Europe). Further, the target species of the European biodiversity policies might be relatively sensitive to changes in environmental conditions, therefore modelled species change should not be interpreted as representative for changes in terrestrial biodiversity as a whole.

Uncertainties in monitoring data
In general, species monitoring data are characterised by uncertainty due to monitoring intensity differences (taxonomic and spatial bias) and imperfect species detection, which hampers the interpretation and comparison of computed changes in probabilities of occurrence (Guillera-Arroita, 2016). For plants, central and northern Europe and the Atlantic region are better monitored than the Mediterranean region and eastern Europe. When more data will become available from Mediterranean and eastern regions, the model could be improved. Since databases such as GBIF and the European Vegetation Archive are still growing, the response functions in BioScore could be regularly improved. Nevertheless, the spatial and taxonomic biases in the monitoring data, the use of presence-only data (for mammals), and differences in detection probabilities among species imply that the aggregation and comparison of the results should be done with caution. In case of (partially unknown) imperfections in detection which cannot be adequately accounted for, the estimated model output for such species, strictly speaking, cannot be considered as a description of the occurrence for these species, but rather as the probability of observation (Gu and Swihart, 2004; Kéry, 2011; Lahoz-Monfort et al., 2014). This also holds for the output of models that are based on presence-only data, because the predicted probabilities by these models depend on the number of pseudo-absences selected (Guillera-Arroita et al., 2015). This stresses the need to interpret the modelled output as relative probabilities or habitat suitability rather than absolute occurrence probabilities (Guillera-Arroita et al., 2015). It also implies that stacked occurrence probabilities should not be interpreted as species richness, but used only in a comparative way, i.e., to compare changes between scenarios, under the assumption that the selected species are a random sample when it comes to the sensitivity to environmental pressures.

Finally, bias in species monitoring data may also affect the preferred land cover of the species as identified based on the distribution of records over the land-cover map. Moreover, land-cover types with a small extent, such as wetlands or open spaces in forests, are not well represented in the land-cover map. Consequently, observations of species that actually prefer for example open spaces in forests are likely to be erroneously associated with forest land-cover type. This stresses the importance of using (additional) expert knowledge in identifying potentially suitable and unsuitable land cover. Moreover, a land-cover map with a higher spatial accuracy may improve the quality of the habitat suitability mask (step 2).

Environmental variable selection and data

Environmental variable selection

In species distribution models observations of species occurrence or abundance are combined with information on environmental variables. Model realism and robustness are among other things influenced by selection of relevant environmental predictors. Incorporating more information on abiotic and biotic factors will yield more precise descriptions of both the potential and actual occurrence and range. Neglecting ecological knowledge in selecting environmental variables is often a limiting factor in the use of statistical modelling to predict future species distribution (Austin et al., 2006).

In BioScore 2.0, two lines of reasoning have guided the selection of environmental variables: one starting from the policy angle, by selecting policy-relevant factors for which effects needed to be assessed; and a second one starting from the species angle (Delbaere et al., 2009). A first problem arising is that possibly important factors are missing. For example, hunting is an important pressure for mammals (Maxwell et al., 2016), but is not included in BioScore 2.0. Secondly, variables are included only in the step in which they are assumed to have the most impact, whereas they may have effects also on other scales (see also the section on the hierarchical approach). Thirdly, all environmental factors were included for all species. Although this approach is helpful to explore and identify potential effects, it may also result in unexpected significant (spurious) correlations due to pure chance or multicollinearity. Identifying which relationships are spurious is not straightforward, because even unexpected relationships might have ecological meaning. Nitrogen deposition, for example, is known to have an effect on occurrences of plant species, but this effect is typically modified by biotic interactions. Nitrogen addition in the absence of competing plant species often leads to faster growth even for species adapted to nutrient-poor conditions (Chester and McGraw, 1983). However, in combination with competing plant species, slow-growing species from nutrient-poor conditions are outcompeted when nitrogen is applied (Bobbink and Hettelingh, 2011), which may change the response relationship. Indirect rather than direct effect of nitrogen deposition may also hold for fauna species, via changes in species composition and structure of the vegetation. For example, species from open sites might disappear when the vegetation becomes denser in response to eutrophication. These effects are quite plausible for various fauna species, including ants and wasps (Peeters et al., 2004), butterflies (Bink, 1992) different kinds of locusts (Lensink, 1963; Kleukers et al., 1997) and nesting birds (Van Turnhout et al., 2010). As such, nitrogen deposition might be an important indirect driver of change. Including drivers with such indirect effects might be important and easier than including direct drivers of change by including vegetation density in the modelling.

Still, a stricter a-priori selection of ecologically relevant environmental variables is expected to increase credibility, reduce the number of factors and decrease problems such as overfitting. Selection based on expert knowledge, as used in BioScore 1.0, could be extended by selection based on information from theoretic process models. In addition, attention should be paid to identify and distinguish between indirect and direct variables (Austin and Smith, 1989; Huston, 1994; Guisan and Zimmermann, 2000). Exploratory statistical analyses using more complex algorithms than logistic regression (e.g., non-parametric and machine-learning approaches) could be used to explore the influence of indirect variables (Merow et al., 2014), which should then be verified against ecological theory before actual inclusion in the model.

Uncertainties in environmental variables

Selection of environmental variables should also consider the quality of and uncertainties in the available maps. In this respect, especially the maps of road density and desiccation need attention. The roads map is incomplete and differs in the amount of detail represented per country. This makes it difficult to distinguish between roads which cause a high disturbance on the surrounding and roads which have a minor impact. A better alternative will become available soon (Meijer et al., in prep). The water exploitation index map is used in this study as a proxy for desiccation and has a spatial resolution of sub-river basins (De Roo et al., 2012). However, desiccation, especially important for vascular plants, plays a role at a more local scale. It should be checked whether a European map is available with more fine-grained information.

In the current version of BioScore, management of non-agricultural open vegetation (e.g. natural grasslands and shrubs) is incorporated, using a score for the dependency of a species on the presence of management. However, information on nature management of non-agricultural open vegetation with coverage of the whole of Europe is lacking for present or past years, whilst in the scenarios only assumptions are used to describe future nature management. This lack of information makes it difficult to analyse the impact of nature management of open vegetation on occurrence of species. More detailed information is required on the current status of management of open vegetation.

In BioScore 2.0, fragmentation was modelled by first compiling 24 fragmentation maps, based on combinations of six land-cover types with four potential dispersal distances. Each species of birds, butterflies and plants was then assigned one of these 24 fragmentation maps, based on its preferred land-cover type and AUC values of estimated response curves for each of the four dispersal distances. However, the identification of the species' preferred land-cover type, based on the distribution of species records over the land-cover map, is not flawless (see also the section on species selection and data). The representation of fragmentation maps for birds, butterflies and plant species might be improved by applying the procedure used for mammals, where species-specific fragmentation maps were constructed, accounting for all land-cover types on which the species is dependent and based on a species-specific dispersal distance class obtained from expert knowledge or literature (see step 5 in the preparation of fragmentation maps, Appendix II).

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Appendix I: CORINE land-cover classes

Table A1: Overview of CORINE land-cover classes and reclassification into four land-use types used in the ecosystem indicator.

Level 1	Level 2	Level 3	Ecosystem indicator
1 Artificial surfaces	1.1 Urban fabric	111 Continuous urban fabric	Urban
		112 Discontinuous urban fabric	
	1.2 Industrial, commercial and transport units	121 Industrial or commercial units	
		122 Road and rail networks and associated land	
		123 Port areas	
		124 Airports	
	1.3 Mine, dump and construction sites	131 Mineral extraction sites	
		132 Dump sites	
		133 Construction sites	
	1.4 Artificial, non-agricultural vegetated areas	141 Green urban areas	
		142 Sport and leisure facilities	
2 Agricultural areas	2.1 Arable land	211 Non-irrigated arable land	Agriculture
		212 Permanently irrigated land	
		213 Rice fields	
	2.2 Permanent crops	221 Vineyards	
		222 Fruit trees and berry plantations	
		223 Olive groves	
	2.3 Pastures	231 Pastures	
	2.4 Heterogeneous agricultural areas	241 Annual crops associated with permanent crops	
		242 Complex cultivation patterns	
		243 Land principally occupied by agriculture, with significant areas of natural vegetation	
		244 Agro-forestry areas	
3 Forest and semi natural areas	3.1 Forests	311 Broad-leaved forest	Forest
		312 Coniferous forest	
		313 Mixed forest	
	3.2 Scrub and/or herbaceous vegetation associations	321 Natural grasslands	Shrubs and open vegetation
		322 Moors and heathland	
		323 Sclerophyllous vegetation	
		324 Transitional woodland-shrub	
	3.3 Open spaces with little or no vegetation	331 Beaches, dunes, sands	
		332 Bare rocks	
		333 Sparsely vegetated areas	
		334 Burnt areas	
		335 Glaciers and perpetual snow	
4 Wetlands	4.1 Inland wetlands	411 Inland marshes	
		412 Peat bogs	
	4.2 Maritime wetlands	421 Salt marshes	
		422 Salines	
		423 Intertidal flats	
5 Water bodies	5.1 Inland waters	511 Water courses	Not included in indicator
		512 Water bodies	
	5.2 Marine waters	521 Coastal lagoons	
		522 Estuaries	
		523 Sea and ocean	

Appendix II: LARCH-SCAN – fragmentation maps

Fragmentation

Habitat loss and fragmentation are and will continue to be one of the major threats to biodiversity (Hanski, 2011; Pereira et al., 2010). Not only areas of natural habitats will be lost, but the remaining habitats will become smaller and more isolated (Fahrig, 2003; Opdam, 1991). Construction of transport infrastructure through natural landscapes will also contribute to a further fragmented landscape, especially for ground dwelling species (Forman and Alexander, 1998; Jaeger, 2000). The impact of fragmentation on species persistence will occur when the habitat covers roughly less than 20% of the landscape (Rybicki and Hanski, 2013).

Species persistence depends on four spatial characteristics of landscapes: size of habitat patches, number of habitat patches, quality of habitat patches and the connectivity between the patches (Hodgson, Moilanen, Wintle, and Thomas, 2011; Opdam, Verboom, and Pouwels, 2003). Margules and Pressey (2000) as well as Hodgson et al. (2011) conclude that the size and quality of habitats within these large patches should be the focus for nature conservation. However, in urbanised areas restoring habitat connectivity is still one of the main policies to counteract the impact of fragmentation due to infrastructure (Van Der Grift and Pouwels, 2006; C.C. Vos, Opdam, Steingröver, and Reijnen, 2007). Construction of road crossing structures has become a worldwide policy and many species use them to cross roads. However, the impact of these structures on the persistence of endangered species is unknown (Taylor and Goldingay, 2010).

Current methods

Currently there are many methods to quantify fragmentation of landscapes. Most methods use landscape indices derived from GIS-based tools (f.e. Fragstats (Neel, McGarigal, and Cushman, 2004; Riitters et al., 1995)). However, these indices are not ecologically scaled and therefore less suitable for predicting the impact on species persistence (C. C. Vos, Verboom, Opdam, and Ter Braak, 2001). The EEA also developed a method to assess the impact of fragmentation. This tool uses the method of Effective mesh size (Jaeger, 2000) and is only applicable for assessing the impact of transport infrastructure. At Alterra also several tools have been developed, f.e. LARCH (Groot Bruinderink, Van der Sluis, Lammertsma, Opdam, and Pouwels, 2003; Opdam, Pouwels, van Rooij, Steingrover, and Vos, 2008; Opdam et al., 2003). Also Population Viability Analyses (PVA) models (Beissinger and McCullough, 2002) are useful to assess the impact of fragmentation. However, these tools are less suitable for BioScore 2.0 as they need many parameters for each species and are not in line with the methods used for the other pressures.

In 2013 Alterra conducted a small research to compare the method used by the EEA and one of the Alterra methods (LARCH-SCAN, Groot Bruinderink et al., 2003) for several species of the Habitats Directive, and in particular large mammals (Wild cat, Pine marten, Beaver, Wolf, Brown bear, and Lynx). Results of both methods were compared with monitoring data of the species. Both methods proved to be limited in predicting the number of mammal species that are present in forest landscapes in Europe. Of both methods LARCH-SCAN explained a larger variation, up to 20%. Therefor we chose to use LARCH-SCAN to determine the fragmentation level of different ecosystems in Europe.

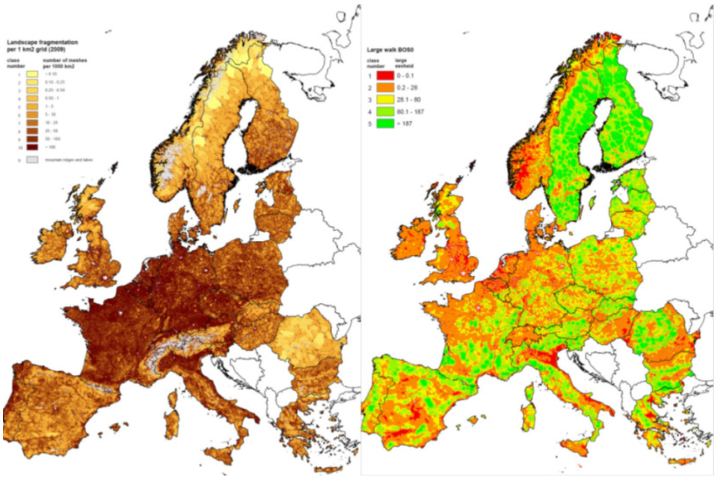

Figure 1 On the left the landscape fragmentation map based on the Effective mesh size (EEA/FOEN, 2011), and on the right the calculated landscape connectivity for a large forest species, calculated with the LARCH-SCAN model (IEEP and Alterra, 2010).

For each of the selected species groups in BioScore fragmentation can have an impact on the persistence of the group (Nilsson, Reidy, Dynesius, and Revenga, 2005; Ouborg, 1993; Schipper et al., 2008; Thomas and Hanski, 1997; Villard, Trzcinski, and Merriam, 1999). Regarding the scale of the model (between 1 x 1 and 10 x 10 square km within Europe) and the used input maps (e.g. CLC) fragmentation should be taken into account for birds and mammals to begin with. For most plant species (except ferns) and most butterflies the process of fragmentation already can occur on a finer scale than the size of the grid cells of the input maps, although it can be assumed that landscapes with a high connectivity have a low chance of being fragmented within a grid cell.

Preparation of input spatial cohesion maps

For each main ecosystem (level 2 of CLC) LARCH-SCAN will provide a map of the spatial cohesion. As an option in LARCH-SCAN it is possible to include the resistance regarding roads. However, in BioScore 2.0 this option is not used. To provide input maps for species with different dispersal capacity LARCH-SCAN is run for four dispersal classes (10, 20, 50, 100 km). Based on the dispersal class and the grain size used thresholds are determined to scale output maps between 0 and 1. Value 0 refers to situations with no habitat and maximum fragmentation, while value 1 refers to situations completely surrounded with habitat within dispersal distance and no fragmentation.

The preparation of the spatial cohesion maps consist of 5 steps:
Butterflies, vascular plants and breeding birds
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), counting the number of 100 meter x 100 meter CLC input map.
Step 2: LARCH-SCAN determines the Spatial Cohesion of nature areas. For each cell the amount of habitat in its surrounding 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* the distance between cells or patches) (Figure 2). Dispersal classes used are 10, 20, 50 and 100 km. These correspond with α's of 0.230, 0.115, 0.046, 0.023. To determine the spatial cohesion we also take into account habitat outside dispersal distance as habitat patches can be connected by other patches to one larger network. Therefore the 'percentage' parameter of LARCH-SCAN is set

to 95%. The default of this value is set at 90% resulting in the spatial cohesion where only habitat within dispersal distance is taken into account (for more information on the parameters see Groot Bruinderink et al., 2003 and Pouwels et al, 2002).

Step 3: For a continuous landscape of suitable habitat we determined the output of LARCH-SCAN. The maximum values in the output maps are used to scale all other values in the output maps. As distance is one of the parameters in the LARCH-SCAN model outputs for different dispersal capacity will have different maximum values: 9473.4164, 37944.3358, 237054.1016 and 948295.7031.

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. However the corresponding maps will be used as input in the regression analyses of BioScore and this will determine the magnitude of the impact.

Mammals

Step 5: Aggregation of output maps for mammals to combine several ecosystems. The values of different maps (within the same dispersal class) are added up to represent the spatial cohesion of the ecosystems that are suitable as habitat for the selected species. For each mammal a separate input map regarding the spatial cohesion is used in BioScore.

Table 1 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

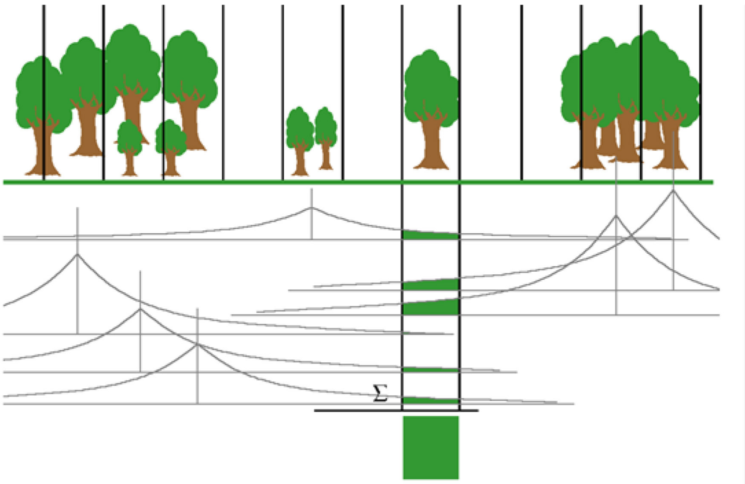

Figure 2 Schematic overview of LACRH-SCAN method

Technical data

Content: 24 maps (reflecting the combination of 4 dispersion classes with 6 ecosystem types) of the relative fragmentation of ecosystems in Europe and for each mammal species one map of the relative fragmentation of their habitat. Value 0 meaning no habitat and

maximum fragmentation (no spatial cohesion) and value 1 meaning completely surrounded with habitat within dispersal distance and no fragmentation (maximal spatial cohesion).
Description: Spatial Cohesion of different ecosystems (level 2 Corine Land Cover) in Europe for four spatial scales (10 km, 20 km, 50 km and 100 km).
In the 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 3-1_20_95_div. For mammal species the name of the mammal is included in the input map.
Unit: - (ha / ha)
Source: LARCH-SCAN analyses (Groot Bruinderink et al. 2003; IEEP and Alterra 2010) of aggregated map from Corine Land Cover.
Spatial resolution: 1 km x 1 km
Year: 2014
Coverage: Europe
Website: http://www.wageningenur.nl/nl/Expertises-Dienstverlening/Onderzoeksinstituten/Alterra/Faciliteiten-Producten/Software-en-modellen/LARCH.htm (very short description)

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Appendix III: Conversion of EUNIS to CLC classes

Table A2: Overview of EUNIS classes as used in the habitat suitability classification of Kleunen (2003) and reclassification into CORINE land-cover classes (level 2).

EUNIS class	Description	CLC class
A1	Littoral rock and other hard substrata	3.3.2.
A1	Littoral rock and other hard substrata	4.2.3.
A2	Littoral sediment	4.2.1.
A2	Littoral sediment	4.2.3.
A3	Infralittoral rock and other hard substrata	5.2.3.
A4	Circalittoral rock and other hard substrata	5.2.3.
A5	Sublittoral sediment	5.2.3.
A6	Deep-sea bed	5.2.3.
A7	Pelagic water column	5.2.3.
A8	Ice-associated marine habitats	5.2.3.
B1	Coastal dunes and sandy shores	2.3.1.
B1	Coastal dunes and sandy shores	3.1.1.
B1	Coastal dunes and sandy shores	3.1.2.
B1	Coastal dunes and sandy shores	3.2.3.
B1	Coastal dunes and sandy shores	3.3.1.
B2	Coastal shingle	3.3.1.
B3	Rock cliffs, ledges and shores, including the supralittoral	3.3.2.
C1	Surface standing waters	5.1.2.
C2	Surface running waters	4.1.1.
C2	Surface running waters	5.1.1.
C3	Littoral zone of inland surface waterbodies	3.3.1.
C3	Littoral zone of inland surface waterbodies	4.1.1.
D1	Raised and blanket bogs	4.1.2.
D2	Valley mires, poor fens and transition mires	4.1.1.
D3	Aapa, palsa and polygon mires	4.1.2.
D4	Base-rich fens and calcareous spring mires	4.1.1.
D5	Sedge and reedbeds, normally without free-standing water	4.1.1.
D6	Inland saline and brackish marshes and reedbeds	4.1.1.
E1	Dry grasslands	3.2.1.
E1	Dry grasslands	3.2.4.
E1	Dry grasslands	3.3.1.
E2	Mesic grasslands	1.4.1.
E2	Mesic grasslands	1.4.2.
E2	Mesic grasslands	2.3.1.
E2	Mesic grasslands	3.2.1.
E3	Seasonally wet and wet grasslands	3.2.1.
E4	Alpine and subalpine grasslands	3.2.1.
E4	Alpine and subalpine grasslands	3.3.3.
E5	Woodland fringes and clearings and tall forb stands	3.2.1.
E5	Woodland fringes and clearings and tall forb stands	3.2.2.

E5	Woodland fringes and clearings and tall forb stands	3.2.3.
E5	Woodland fringes and clearings and tall forb stands	3.2.4.
E6	Inland salt steppes	3.2.1.
E7	Sparsely wooded grasslands	2.3.1.
E7	Sparsely wooded grasslands	2.4.4.
F1	Tundra	3.3.3.
F2	Arctic, alpine and subalpine scrub	3.2.2.
F2	Arctic, alpine and subalpine scrub	3.3.3.
F3	Temperate and Mediterranean-montane scrub	3.2.2.
F3	Temperate and Mediterranean-montane scrub	3.3.1.
F4	Temperate shrub heathland	3.2.2.
F4	Temperate shrub heathland	3.3.1.
F5	Maquis, arborescent matorral and thermo-Mediterranean brushes	3.2.3.
F6	Garrigue	3.2.3.
F7	Spiny Mediterranean heaths (phrygana, hedgehog-heaths and related coastal cliff vegetation)	3.2.3.
F8	Thermo-Atlantic xerophytic scrub	3.2.3.
F9	Riverine and fen scrubs	3.2.2.
FA	Hedgerows	2.3.1.
FB	Shrub plantations	2.2.1.
FB	Shrub plantations	2.2.2.
G1	Broadleaved deciduous woodland	2.2.2.
G1	Broadleaved deciduous woodland	3.1.1.
G2	Broadleaved evergreen woodland	2.2.2.
G2	Broadleaved evergreen woodland	2.2.3.
G2	Broadleaved evergreen woodland	3.1.1.
G3	Coniferous woodland	3.1.2.
G4	Mixed deciduous and coniferous woodland	3.1.3.
G5	Lines of trees, small anthropogenic woodlands, recently felled woodland, early-stage woodland and coppice	3.2.2.
G5	Lines of trees, small anthropogenic woodlands, recently felled woodland, early-stage woodland and coppice	3.2.4.
H2	Screes	3.3.2.
H3	Inland cliffs, rock pavements and outcrops	1.3.1.
H3	Inland cliffs, rock pavements and outcrops	3.3.2.
H3	Inland cliffs, rock pavements and outcrops	3.3.3.
H4	Snow or ice-dominated habitats	3.3.5.
H5	Miscellaneous inland habitats with very sparse or no vegetation	3.3.1.
H5	Miscellaneous inland habitats with very sparse or no vegetation	3.3.3.
H5	Miscellaneous inland habitats with very sparse or no vegetation	3.3.4.
H6	Recent volcanic features	3.3.3.
I1	Arable land and market gardens	2.1.1.
I1	Arable land and market gardens	2.1.2.
I1	Arable land and market gardens	2.1.3.
I1	Arable land and market gardens	2.4.1.
I1	Arable land and market gardens	2.4.2.

I1	Arable land and market gardens	2.4.3.
I2	Cultivated areas of gardens and parks	1.4.1.
I2	Cultivated areas of gardens and parks	1.4.2.
I2	Cultivated areas of gardens and parks	2.4.2.
J1	Buildings of cities, towns and villages	1.1.1.
J1	Buildings of cities, towns and villages	1.1.2.
J2	Low density buildings	1.2.1.
J2	Low density buildings	1.3.1.
J2	Low density buildings	1.3.3.
J3	Extractive industrial sites	1.3.1.
J4	Transport networks and other constructed hard-surfaced areas	1.2.2.
J4	Transport networks and other constructed hard-surfaced areas	1.2.3.
J4	Transport networks and other constructed hard-surfaced areas	1.2.4.
J5	Highly artificial man-made waters and associated structures	1.2.1.
J5	Highly artificial man-made waters and associated structures	4.2.2.
J5	Highly artificial man-made waters and associated structures	5.1.1.
J5	Highly artificial man-made waters and associated structures	5.1.2.
J6	Waste deposits	1.3.2.
X1	Surface running waters	5.2.2.
X2_3	Sublittoral sediment	5.2.1.

Appendix IV: Conversion of Globcover to CLC classes

Table A2: Overview of Globcover classes as used in the habitat suitability classification of Rondinini et al. (2011) and reclassification into CORINE land-cover classes (level 2).

Globcover class	Description	CLC class
10	Cultivated and Managed areas	2.4
11	Post-flooding or irrigated croplands (or aquatic)	2.1
12	Post-flooding or irrigated shrub or tree crops	2.1
13	Post-flooding or irrigated herbaceous crops	2.1
14	Rainfed croplands	2.1
15	Rainfed herbaceous crops	2.1
16	Rainfed shrub or tree crops (cashcrops, vineyards, olive tree, orchards)	2.2
20	Mosaic cropland (50-70%) / vegetation (grassland/shrubland/forest) (20-50%)	2.4
21	Mosaic cropland (50-70%) / grassland or shrubland (20-50%)	2.4
22	Mosaic cropland (50-70%) / forest (20-50%)	2.4
30	Mosaic vegetation (grassland/shrubland/forest) (50-70%) / cropland (20-50%)	3.2
30	Mosaic vegetation (grassland/shrubland/forest) (50-70%) / cropland (20-50%)	3.1
31	Mosaic grassland or shrubland (50-70%) / cropland (20-50%)	3.2
32	Mosaic forest (50-70%) / cropland (20-50%)	3.1
40	Closed to open (>15%) broadleaved evergreen or semi-deciduous forest (> 5m)	3.1
41	Closed (>40%) broadleaved evergreen and/or semi-deciduous forest	3.1
42	Open (15-40%) broadleaved semi-deciduous and/or evergreen forest with emergents	3.1
50	Closed (>40%) broadleaved deciduous forest (>5m)	3.1
60	Open (15-40%) broadleaved deciduous forest/woodland (>5m)	3.1
70	Closed (>40%) needle-leaved evergreen forest (>5m)	3.1
80	Closed (>40%) needle-leaved deciduous forest (>5m)	3.1
90	Open (15-40%) needle-leaved deciduous or evergreen forest (>5m)	3.1
91	Open (15-40%) needle-leaved deciduous forest (>5m)	3.1
92	Open (15-40%) needle-leaved evergreen forest (>5m)	3.1
100	Closed to open (>15%) mixed broadleaved and needleaved forest	3.1
101	Closed (>40%) mixed broadleaved and needleaved forest	3.1
102	Open (15-40%) mixed broadleaved and needleaved forest	3.1
110	Mosaic forest or shrubland (50-70%) and grassland (20-50%)	3.1
120	Mosaic grassland (50-70%) and forest or shrubland (20-50%)	3.2
130	Closed to open (>15%) (broadleaved or needle-leaved, evergreen or deciduous) shrubland (<5m)	3.2
131	Closed to open (>15%) broadleaved or needle-leaved evergreen shrubland (<5m)	3.2
132	Closed to open (>15%) broadleaved evergreen shrubland (<5m)	3.2
133	Closed to open (>15%) needle-leaved evergreen shrubland (<5m)	3.2
134	Closed to open (>15%) broadleaved deciduous shrubland (<5m)	3.2
135	Closed (>40%) broadleaved deciduous shrubland (<5m)	3.2
136	Open (15-40%) broadleaved deciduous shrubland (<5m)	3.2
140	Closed to open (>15%) herbaceous vgt (grassland, savannas or Lichens/Mosses)	3.2
141	Closed (>40%) grassland	3.2
142	Closed (>40%) grassland with sparse (<15%) trees or shrubs	3.2
143	Open (15-40%) grassland	3.2
144	Open (15-40%) grassland with sparse (<15%) trees or shrubs	3.2
145	Lichens or Mosses	3.3
150	Sparse (<15%) vegetation	3.3
151	Sparse (<15%) grassland	3.3
152	Sparse (<15%) shrubland	3.3
153	Sparse (<15%) trees	3.3

Globcover class	Description	CLC class
160	Closed to open (>15%) broadleaved forest regularly flooded (semi-permanently or temporarly), fresh or brakish water	5.1
160	Closed to open (>15%) broadleaved forest regularly flooded (semi-permanently or temporarly), fresh or brakish water	4.2
160	Closed to open (>15%) broadleaved forest regularly flooded (semi-permanently or temporarly), fresh or brakish water	5.2
161	Closed to open broadleaved forest on (semi-)permanently flooded land, fresh water	3.1
162	Closed to open broadleaved forest on temporarly flooded land, fresh water	3.1
170	Closed (>40%) broadleaved forest or shrubland permanently flooded, saline or brackish water	3.1
170	Closed (>40%) broadleaved forest or shrubland permanently flooded, saline or brackish water	3.2
180	Closed to open (>15%) grassland or woody vgt on regularly flooded or waterlogged soil, fresh, brakish or saline water	4.2
180	Closed to open (>15%) grassland or woody vgt on regularly flooded or waterlogged soil, fresh, brakish or saline water	5.2
181	Closed to open (>15%) woody vgt on regularly flooded or waterlogged soil, fresh or brakish water	5.1
182	Closed to open (>15%) woody vgt on temporarily flooded land	3.1
183	Closed to open (>15%) woody vgt on permanently flooded land	3.1
184	Closed to open (>15%) woody vgt on waterlogged soil	3.1
185	Closed to open (>15%) grassland on regularly flooded or waterlogged soil, fresh or brakish water	3.2
186	Closed to open (>15%) grassland on temporarily flooded land	3.2
187	Closed to open (>15%) grassland on permanently flooded land	3.2
188	Closed to open (>15%) grassland on waterlogged soil	3.2
190	Artificial surfaces and associated areas (Urban areas >50%)	1.4
200	Bare areas	3.3
201	Consolidated bare areas (hardpands, gravels, bare rock, stones, boulders)	3.3
202	Non-consolidated bare areas (sandy desert)	3.3
203	Salt hardpands	4.2
210	Inland Water Bodies	5.1
220	Permanent Snow and Ice	3.3

Appendix V: List of species included in BioScore 2.0

Species names and their management dependencies (M)

Birds (284)
Species name
Accipiter brevipes
Accipiter gentilis
Acrocephalus arundinaceus
Acrocephalus melanopogon
Acrocephalus paludicola (M)
Acrocephalus scirpaceus
Aegolius funereus
Aegypius monachus (M)
Alauda arvensis (M)
Alcedo atthis
Alectoris barbara (M)
Alectoris chukar (M)
Alectoris graeca (M)
Alectoris rufa (M)
Anas acuta
Anas clypeata (M)
Anas penelope
Anas querquedula (M)
Anas strepera
Anser erythropus
Anthus campestris
Anthus cervinus
Anthus pratensis (M)
Anthus trivialis
Apus caffer
Aquila adalberti
Aquila chrysaetos
Aquila fasciata
Aquila heliaca
Ardea alba
Ardea purpurea
Ardeola ralloides
Asio flammeus
Athene noctua
Aythya ferina
Aythya fuligula
Aythya nyroca
Botaurus stellaris
Branta leucopsis
Bubo bubo
Burhinus oedicnemus (M)
Buteo lagopus
Buteo rufinus
Calandrella brachydactyla
Calandrella rufescens
Calcarius lapponicus
Calidris alpina
Calidris maritima
Calidris minuta
Caprimulgus europaeus (M)
Caprimulgus ruficollis
Cecropis daurica
Charadrius alexandrinus
Charadrius morinellus
Chersophilus duponti
Chlidonias hybrida
Chlidonias niger
Chroicocephalus genei
Ciconia ciconia (M)
Ciconia nigra
Circaetus gallicus (M)
Circus aeruginosus
Circus cyaneus
Circus macrourus
Circus pygargus
Clamator glandarius
Clanga clanga
Clanga pomarina
Clangula hyemalis
Coloeus monedula (M)
Columba oenas (M)
Columba palumbus (M)
Coracias garrulus (M)
Corvus corax
Corvus frugilegus (M)
Coturnix coturnix
Crex crex
Cygnus cygnus
Dendrocopos leucotos
Dendrocopos major
Dendrocopos medius
Dendrocopos minor
Dendrocopos syriacus
Dryocopus martius
Egretta garzetta
Elanus caeruleus (M)
Emberiza caesia
Emberiza calandra
Emberiza cia
Emberiza cineracea
Emberiza cirlus
Emberiza citrinella
Emberiza hortulana
Emberiza melanocephala
Emberiza pusilla
Emberiza rustica
Emberiza schoeniclus
Eremophila alpestris
Falco biarmicus
Falco cherrug
Falco columbarius
Falco eleonorae
Falco naumanni (M)
Falco peregrinus
Falco rusticolus
Falco subbuteo
Falco tinnunculus (M)
Falco vespertinus (M)
Ficedula albicollis
Ficedula parva
Ficedula semitorquata
Fulica atra
Fulica cristata
Galerida cristata (M)
Galerida theklae (M)
Gallinago gallinago (M)
Gallinago media
Gavia arctica
Gavia immer
Gavia stellata
Gelochelidon nilotica
Glareola nordmanni
Glareola pratincola
Glaucidium passerinum
Grus grus
Gypaetus barbatus
Gyps fulvus
Haematopus ostralegus (M)
Haliaeetus albicilla
Hieraaetus pennatus (M)
Himantopus himantopus
Hippolais icterina
Hippolais olivetorum
Hippolais polyglotta
Hirundo rustica (M)
Hydrobates pelagicus
Hydrocoloeus minutus
Hydroprogne caspia
Ichthyaetus audouinii
Ichthyaetus melanocephalus
Ixobrychus minutus
Jynx torquilla (M)
Lagopus lagopus
Lagopus muta
Lanius collurio
Lanius excubitor
Lanius minor
Lanius nubicus
Lanius senator
Larus canus
Limosa lapponica
Limosa limosa (M)
Linaria cannabina
Locustella fluviatilis
Locustella luscinioides
Locustella naevia
Lophophanes cristatus
Loxia curvirostra
Loxia leucoptera
Loxia pytyopsittacus
Loxia scotica
Lullula arborea (M)
Luscinia luscinia
Luscinia megarhynchos
Luscinia svecica
Lyrurus tetrix
Marmaronetta angustirostris
Melanitta fusca
Melanitta nigra
Melanocorypha calandra (M)
Mergellus albellus
Mergus merganser
Merops apiaster
Microcarbo pygmeus
Milvus migrans (M)
Milvus milvus (M)
Monticola saxatilis
Monticola solitarius
Motacilla alba (M)
Motacilla cinerea
Motacilla citreola
Motacilla flava (M)
Muscicapa striata
Neophron percnopterus
Netta rufina
Nucifraga caryocatactes
Numenius arquata (M)

Numenius phaeopus
Nycticorax nycticorax
Oenanthe hispanica
Oenanthe isabellina
Oenanthe leucura
Oenanthe oenanthe
Oenanthe pleschanka
Oriolus oriolus
Otis tarda (M)
Otus scops
Oxyura leucocephala
Pandion haliaetus
Panurus biarmicus
Passer hispaniolensis (M)
Passer montanus (M)
Pelecanus crispus
Pelecanus onocrotalus
Perdix perdix
Perisoreus infaustus
Pernis apivorus
Phalaropus lobatus
Philomachus pugnax (M)
Phoenicopterus roseus
Phoenicurus phoenicurus
Phylloscopus bonelli
Phylloscopus borealis
Phylloscopus collybita
Phylloscopus sibilatrix
Phylloscopus trochilus
Picoides tridactylus
Picus canus
Picus viridis
Platalea leucorodia
Plectrophenax nivalis
Plegadis falcinellus
Pluvialis apricaria
Podiceps auritus
Podiceps cristatus
Poecile cinctus
Poecile lugubris
Poecile montanus
Poecile palustris
Porphyrio porphyrio
Porzana parva
Porzana porzana
Porzana pusilla
Prunella collaris
Prunella modularis
Pterocles alchata
Pterocles orientalis (M)
Pyrrhocorax graculus
Pyrrhocorax pyrrhocorax
Recurvirostra avosetta
Regulus ignicapilla
Regulus regulus
Saxicola rubetra
Saxicola torquatus
Scolopax rusticola
Sitta europaea
Sitta krueperi
Sitta neumayer
Stercorarius longicaudus
Sterna dougallii
Sterna hirundo
Sterna paradisaea
Sternula albifrons
Streptopelia turtur
Strix aluco
Strix nebulosa
Strix uralensis
Sturnus unicolor (M)
Sturnus vulgaris (M)
Surnia ulula
Sylvia atricapilla
Sylvia borin
Sylvia cantillans
Sylvia communis
Sylvia curruca
Sylvia hortensis
Sylvia melanocephala
Sylvia nisoria
Sylvia rueppelli
Sylvia sarda
Sylvia undata
Tachybaptus ruficollis
Tadorna ferruginea
Tetrao urogallus
Tetrastes bonasia
Tetrax tetrax
Thalasseus sandvicensis
Tringa glareola
Tringa totanus (M)
Turdus viscivorus
Tyto alba
Upupa epops (M)
Uria aalge
Vanellus vanellus (M)

Butterflies (95)
Aglais io (M)
Aglais urticae (M)
Anthocharis cardamines (M)
Anthocharis euphenoides (M)
Apatura ilia
Apatura iris
Aphantopus hyperantus (M)
Aporia crataegi
Araschnia levana (M)
Arethusana arethusa (M)
Argynnis adippe (M)
Argynnis aglaja (M)
Argynnis niobe (M)
Argynnis paphia
Aricia agestis (M)
Aricia artaxerxes
Aricia eumedon
Boloria aquilonaris
Boloria dia (M)
Boloria euphrosyne
Boloria selene (M)
Brenthis daphne
Brenthis ino
Brintesia circe (M)
Callophrys rubi
Carcharodus alceae (M)
Carterocephalus palaemon
Carterocephalus silvicolus
Celastrina argiolus
Charaxes jasius
Coenonympha arcania (M)
Coenonympha glycerion (M)
Coenonympha pamphilus (M)
Coenonympha tullia
Colias alfacariensis (M)
Cupido argiades (M)
Cupido minimus (M)
Cyaniris semiargus (M)
Erebia ligea
Erynnis tages (M)
Euphydryas aurinia (M)
Euphydryas maturna
Favonius quercus
Glaucopsyche alexis (M)
Gonepteryx cleopatra
Gonepteryx rhamni (M)
Hamearis lucina (M)
Hesperia comma (M)
Heteropterus morpheus
Hipparchia semele (M)
Hipparchia statilinus (M)
Iphiclides podalirius (M)
Issoria lathonia (M)
Lampides boeticus (M)
Lasiommata maera (M)
Lasiommata megera (M)
Libythea celtis
Limenitis camilla
Limenitis reducta
Lycaena dispar (M)
Lycaena hippothoe (M)
Lycaena phlaeas (M)
Lycaena tityrus (M)
Lycaena virgaureae (M)
Maniola jurtina (M)
Melanargia galathea (M)
Melitaea athalia
Melitaea cinxia (M)
Melitaea diamina
Melitaea didyma (M)
Melitaea phoebe (M)
Nymphalis antiopa
Ochlodes sylvanus
Papilio machaon (M)
Pararge aegeria (M)
Phengaris alcon (M)
Phengaris arion (M)
Plebejus argus (M)
Plebejus idas (M)
Plebejus optilete
Polygonia calbum (M)
Polyommatus amandus
Polyommatus bellargus (M)
Polyommatus coridon (M)
Polyommatus escheri (M)
Polyommatus icarus (M)
Pyronia tithonus (M)
Satyrium ilicis
Satyrium pruni
Satyrium spini
Spialia sertorius (M)
Thecla betulae
Thymelicus acteon (M)
Thymelicus lineola (M)
Thymelicus sylvestris (M)

Mammals (78)
Canis lupus
Capra ibex
Capra pyrenaica
Capreolus capreolus
Castor fiber
Chionomys nivalis
Crocidura sicula
Dama dama
Eliomys quercinus
Eptesicus nilssonii
Erinaceus europaeus
Felis silvestris
Galemys pyrenaicus
Genetta genetta
Gulo gulo
Herpestes ichneumon
Hystrix cristata
Lepus castroviejoi
Lepus corsicanus

Lepus europaeus
Lepus granatensis
Lepus timidus
Lutra lutra
Lynx lynx
Lynx pardinus
Marmota marmota
Martes foina
Martes martes
Alces alces
Meles meles
Microtus cabrerae
Miniopterus schreibersii
Muscardinus avellanarius
Mustela erminea
Mustela lutreola
Mustela nivalis
Mustela putorius
Myotis alcathoe
Myotis bechsteinii
Myotis blythii
Myotis brandtii
Myotis capaccinii
Myotis daubentonii
Myotis emarginatus
Myotis myotis
Myotis mystacinus
Myotis nattereri
Myotis punicus
Neomys anomalus
Neomys fodiens
Nyctalus lasiopterus
Nyctalus leisleri
Nyctalus noctula
Pipistrellus kuhlii
Pipistrellus nathusii
Pipistrellus pipistrellus
Pipistrellus pygmaeus
Pipistrellus savii
Plecotus auritus
Plecotus austriacus
Plecotus macrobullaris
Rhinolophus euryale
Rhinolophus ferrumequinum
Rhinolophus hipposideros
Rhinolophus mehelyi
Rupicapra rupicapra
Sciurus vulgaris
Sorex araneus
Sorex coronatus
Sorex granarius
Sorex minutus
Spermophilus citellus
Suncus etruscus
Tadarida teniotis
Barbastella barbastellus
Ursus arctos
Atelerix algirus
Vespertilio murinus

Plants (863)
H1330 Armeria maritima
H1330 Artemisia maritima
H1330 Blysmus rufus
H1330 Carex distans (M)
H1330 Carex extensa
H1330 Halimione pedunculata
H1330 Halimione portulacoides
H1330 Juncus gerardii
H1330 Juncus maritimus
H1330 Limonium vulgare
H1330 Lysimachia maritima
H1330 Plantago maritima
H1330 Puccinellia distans (M)
H1330 Puccinellia fasciculata
H1330 Puccinellia maritima
H1330 Spergularia media
H1330 Spergularia salina
H1330 Suaeda maritima
H1330 Triglochin maritima
H1330 Tripolium pannonicum
H2120 Achillea maritima
H2120 Ammophila arenaria
H2120 Anthemis maritima
H2120 Calystegia soldanella
H2120 Cerastium diffusum (M)
H2120 Cutandia maritima
H2120 Cyperus capitatus
H2120 Echinophora spinosa
H2120 Elymus pycnanthus
H2120 Eryngium maritimum
H2120 Euphorbia paralias
H2120 Honckenya peploides
H2120 Leymus arenarius
H2120 Medicago marina
H2120 Ononis natrix (M)
H2120 Polygonum glaucum
H3130 Anagallis minima (M)
H3130 Baldellia ranunculoides
H3130 Cicendia filiformis
H3130 Cyperus fuscus
H3130 Cyperus michelianus
H3110 Deschampsia setacea
H3130 Elatine hexandra
H3130 Elatine hydropiper
H3110 Eleocharis acicularis
H3110 Eleocharis multicaulis
H3130 Eleocharis ovata
H3130 Hypericum elodes
H3130 Isolepis antarctica (M)
H3130 Isolepis fluitans
H3130 Juncus bulbosus
H3130 Juncus capitatus
H3130 Juncus pygmaeus
H3130 Juncus tenageia
H3130 Limosella aquatica
H3130 Lindernia procumbens
H3110 Littorella uniflora
H3130 Luronium natans
H3130 Pilularia globulifera
H3130 Potamogeton gramineus
H3110 Potamogeton polygonifolius
H3130 Pycreus flavescens
H3130 Radiola linoides
H3130 Schoenoplectiella supina
H3130 Sparganium natans
H4010 Carex panicea (M)
H4010 Dactylorhiza maculata (M)
H4010 Drosera intermedia
H4010 Drosera rotundifolia
H4010 Erica tetralix
H4010 Eriophorum angustifolium
H4010 Gentiana pneumonanthe (M)
H4010 Juncus squarrosus
H4010 Narthecium ossifragum
H4010 Rhynchospora alba
H4010 Rhynchospora fusca
H4010 Sphagnum compactum
H4010 Sphagnum tenellum
H4010 Trichophorum cespitosum
H4030 Calluna vulgaris (M)
H4030 Cistus ladanifer
H4030 Cistus salviifolius
H4030 Daboecia cantabrica (M)
H4030 Erica australis (M)
H4030 Erica cinerea (M)
H4030 Erica mackaiana
H4030 Erica umbellata (M)
H4030 Galium saxatile (M)
H4030 Genista anglica (M)
H4030 Genista germanica (M)
H4030 Genista pilosa (M)
H4030 Ulex gallii (M)
H4030 Ulex minor (M)
H4030 Vaccinium myrtillus
H4030 Vaccinium vitis idaea
H4060 Arctostaphylos uva ursi
H4060 Arctous alpina
H4060 Betula nana
H4060 Carex bigelowii
H4060 Cassiope tetragona
H4060 Cetraria islandica
H4060 Cornus suecica
H4060 Dryas octopetala
H4060 Erica herbacea
H4060 Flavocetraria nivalis
H4060 Geum montanum
H4060 Homogyne alpina
H4060 Huperzia selago
H4060 Kalmia procumbens
H4060 Ligusticum mutellina
H4060 Phyllodoce caerulea
H4060 Pleurozium schreberi
H4060 Potentilla aurea
H4060 Racomitrium lanuginosum
H4060 Rhododendron ferrugineum
H4060 Rhododendron hirsutum
H4060 Rhodothamnus chamaecistus
H4060 Vaccinium uliginosum
H4070 Calamagrostis varia
H4070 Calamagrostis villosa
H4070 Clematis alpina
H4070 Daphne mezereum
H4070 Luzula sylvatica
H4070 Pinus mugo
H4070 Valeriana tripteris
H4070 Viola biflora
H6170 Achillea clavennae
H6170 Alchemilla flabellata
H6170 Alchemilla hoppeana
H6170 Antennaria carpatica

H6170 Aster alpinus
H6170 Astragalus alpinus
H6170 Campanula scheuchzeri
H6170 Carex atrata
H6170 Carex brevicollis (M)
H6170 Carex capillaris
H6170 Carex ferruginea
H6170 Carex firma
H6170 Carex foetida
H6170 Carex rupestris
H6150 Carex sempervirens
H6170 Daphne striata
H6170 Dianthus glacialis
H6170 Draba aizoides
H6170 Galium anisophyllon
H6170 Gentiana nivalis
H6170 Globularia nudicaulis (M)
H6170 Helianthemum nummularium
H6170 Helianthemum oelandicum
H6170 Hieracium villosum
H6170 Minuartia sedoides
H6170 Oxytropis jacquinii
H6170 Paronychia polygonifolia
H6170 Phyteuma orbiculare (M)
H6170 Poa variegata
H6170 Polygala alpestris
H6170 Potentilla nivea
H6170 Primula auricula
H6170 Saussurea nuda
H6170 Scabiosa lucida (M)
H6170 Sibbaldia procumbens
H6170 Stachys alopecuros
H6170 Thymus pulcherrimus
H6170 Trifolium thalii
H6170 Veronica alpina
H6510 Alopecurus pratensis (M)
H6510 Arrhenatherum elatius (M)
H6510 Campanula patula (M)
H6510 Centaurea jacea (M)
H6510 Centaurea jacea jacea
H6510 Crepis biennis (M)
H6510 Galium mollugo (M)
H6510 Knautia arvensis (M)
H6510 Lathyrus pratensis (M)
H6510 Leontodon hispidus (M)
H6510 Leucanthemum vulgare (M)
H6510 Malva moschata (M)
H6510 Oenanthe pimpinelloides
H6510 Pastinaca sativa (M)
H6510 Pimpinella major (M)
H6510 Ranunculus acris (M)
H6510 Rumex acetosa (M)
H6410 Sanguisorba officinalis (M)
H6510 Tragopogon pratensis (M)
H6510 Trisetum flavescens (M)
H6520 Astrantia major (M)
H6520 Bistorta officinalis (M)
H6520 Centaurea nemoralis (M)
H6430 Chaerophyllum hirsutum (M)
H6430 Cirsium helenioides (M)
H6520 Conopodium majus (M)
H6520 Crepis mollis (M)
H6520 Crepis pyrenaica (M)
H6520 Crocus caeruleus (M)
H6520 Geranium phaeum (M)
H6430 Geranium sylvaticum (M)
H6520 Narcissus poeticus (M)
H6520 Phyteuma ovatum (M)
H6520 Phyteuma spicatum (M)
H6520 Poa chaixii (M)
H6520 Salvia pratensis (M)
H6430 Trollius europaeus (M)
H6520 Valeriana repens (M)
H6520 Viola cornuta (M)
H91E0 Festuca gigantea (M)
H2130 Anacamptis pyramidalis (M)
H2130 Carex arenaria (M)
H2130 Cerastium semidecandrum (M)
H2130 Cladonia foliacea (M)
H2130 Cladonia rangiformis (M)
H2130 Corynephorus canescens (M)
H2130 Crucianella maritima
H2130 Erodium cicutarium (M)
H2130 Erodium lebelii (M)
H2130 Galium verum (M)
H2130 Gentiana cruciata (M)
H2130 Gentianella campestris (M)
H2130 Helichrysum stoechas
H2130 Koeleria macrantha (M)
H2130 Myosotis ramosissima (M)
H2130 Phleum arenarium (M)
H2130 Sedum acre (M)
H2130 Silene conica (M)
H2130 Silene otites (M)
H2130 Trifolium scabrum
H2130 Tuberaria guttata
H2160 Anthriscus caucalis (M)
H2160 Berberis vulgaris (M)
H2160 Crataegus monogyna (M)
H2160 Cynoglossum officinale (M)
H2160 Euonymus europaeus (M)
H2160 Hippophae rhamnoides (M)
H2160 Ligustrum vulgare (M)
H2160 Moehringia trinervia (M)
H2160 Polygonatum odoratum (M)
H2160 Rhamnus catharticus (M)
H2160 Rosa canina (M)
H2160 Rosa rubiginosa (M)
H2160 Rubus caesius (M)
H2160 Salix repens (M)
H2160 Sambucus nigra (M)
H2210 Echium sabulicola
H2210 Euphorbia terracina
H2210 Lotus creticus
H2210 Malcolmia littorea
H2210 Maresia nana
H2210 Matthiola sinuata
H2210 Pancratium maritimum
H2210 Scabiosa atropurpurea
H2210 Scrophularia frutescens
H2210 Scrophularia ramosissima
H2210 Silene nicaeensis
H2210 Teucrium polium (M)
H3110 Eriocaulon aquaticum
H3110 Isoetes echinospora
H3110 Isoetes lacustris
H3110 Lobelia dortmanna
H3110 Myriophyllum alterniflorum
H3110 Subularia aquatica
H3150 Aldrovanda vesiculosa
H3150 Ceratophyllum demersum
H3150 Lemna trisulca
H3150 Myriophyllum spicatum
H3150 Myriophyllum verticillatum
H3150 Nuphar lutea
H3150 Nymphaea alba
H3150 Nymphaea candida
H3150 Nymphoides peltata
H3150 Potamogeton natans
H3150 Potamogeton perfoliatus
H3150 Potamogeton praelongus
H3150 Stratiotes aloides
H3150 Trapa natans
H3150 Utricularia vulgaris
H3150 Wolffia arrhiza
H3260 Potamogeton alpinus
H3260 Potamogeton nodosus
H3260 Ranunculus fluitans
H3260 Ranunculus penicillatus
H5130 Carex flacca (M)
H5130 Deschampsia flexuosa
H5130 Empetrum nigrum (M)
H5130 Juniperus communis (M)
H5130 Prunus spinosa (M)

H5130 Sesleria caerulea (M)
H5130 Sorbus aucuparia
H5130 Sorbus intermedia (M)
H5210 Berteroa obliqua (M)
H5210 Brachypodium retusum
H5210 Clematis flammula
H5210 Galium album (M)
H5210 Genista scorpius
H5210 Jasminum fruticans
H5210 Juniperus excelsa
H5210 Juniperus foetidissima
H5210 Juniperus oxycedrus
H5210 Juniperus phoenicea
H5210 Juniperus thurifera (M)
H5210 Olea europaea
H5210 Phillyrea angustifolia
H5210 Pistacia lentiscus
H5210 Prasium majus
H5210 Quercus coccifera
H5210 Rosmarinus officinalis
H5210 Stipa bromoides
H5210 Teucrium chamaedrys (M)
H5210 Thymus sibthorpii (M)
H5210 Thymus vulgaris
H5420 Anthyllis hermanniae
H5420 Asparagus acutifolius
H5420 Ballota pseudodictamnus
H5420 Calicotome villosa
H5420 Cistus parviflorus
H5420 Erica manipuliflora
H5420 Euphorbia acanthothamnos
H5420 Fumana thymifolia
H5420 Genista acanthoclada
H5420 Lithodora hispidula
H5420 Micromeria graeca
H5420 Micromeria juliana
H5420 Micromeria nervosa
H5420 Sarcopoterium spinosum
H5420 Satureja thymbra
H5420 Smilax aspera
H5420 Teucrium divaricatum
H6110 Alyssum alyssoides (M)
H6110 Arabis hirsuta (M)
H6110 Arenaria serpyllifolia (M)
H6110 Asperula cynanchica (M)
H6110 Cerastium pumilum (M)
H6110 Echium vulgare (M)
H6110 Hornungia petraea (M)
H6110 Poa badensis (M)
H6110 Poa compressa (M)
H6110 Potentilla cinerea (M)
H6110 Potentilla tabernaemontani (M)
H6110 Saxifraga tridactylites (M)
H6110 Sedum album (M)
H6110 Sedum sexangulare (M)
H6110 Teucrium botrys (M)
H6110 Thymus pulegioides (M)
H6110 Tortella tortuosa
H6120 Allium schoenoprasum
H6120 Artemisia campestris (M)
H6120 Astragalus arenarius
H6120 Carex praecox (M)
H6120 Dianthus arenarius
H6120 Dianthus deltoides (M)
H6120 Festuca psammophila (M)
H6120 Gypsophila fastigiata (M)
H6120 Helichrysum arenarium (M)
H6120 Herniaria glabra (M)
H6120 Koeleria glauca (M)
H6120 Petrorhagia prolifera (M)
H6120 Sedum rupestre (M)
H6120 Silene chlorantha (M)
H6150 Agrostis rupestris
H6150 Campanula alpina
H6150 Festuca airoides
H6150 Hieracium alpinum
H6150 Juncus trifidus
H6150 Luzula alpinopilosa
H6150 Oreochloa disticha
H6150 Primula minima
H6150 Pulsatilla alpina
H6150 Soldanella carpatica
H6210 Adonis vernalis (M)
H6210 Anthyllis vulneraria (M)
H6210 Brachypodium pinnatum (M)
H6210 Bromus erectus (M)
H6210 Campanula glomerata (M)
H6210 Carex caryophyllea (M)
H6210 Carlina vulgaris (M)
H6210 Centaurea scabiosa (M)
H6210 Dianthus carthusianorum (M)
H6210 Dianthus sylvestris (M)
H6210 Eryngium campestre (M)
H6210 Euphorbia cyparissias (M)
H6210 Festuca valesiaca (M)
H6210 Fumana procumbens (M)
H6210 Globularia punctata (M)
H6210 Hippocrepis comosa (M)
H6210 Koeleria pyramidata (M)
H6210 Medicago falcata (M)
H6210 Ophrys apifera (M)
H6210 Ophrys insectifera (M)
H6210 Orchis militaris (M)
H6210 Phleum phleoides (M)
H6210 Plantago media (M)
H6210 Polygala comosa (M)
H6210 Potentilla pusilla (M)
H6210 Primula veris (M)
H6210 Sanguisorba minor (M)
H6210 Scabiosa columbaria (M)
H6210 Scabiosa ochroleuca (M)
H6210 Stipa capillata (M)
H6210 Stipa joannis (M)
H6210 Teucrium montanum (M)
H6220 Aira cupaniana
H6220 Anthyllis lotoides
H6220 Arenaria modesta
H6220 Arenaria retusa
H6220 Brachypodium distachyon
H6220 Bromus rubens
H6220 Campanula fastigiata
H6220 Chaenorhinum rubrifolium
H6220 Convolvulus althaeoides
H6220 Euphorbia exigua (M)
H6220 Filago pyramidata
H6220 Hippocrepis ciliata
H6220 Jasione penicillata
H6220 Linum strictum
H6220 Logfia gallica
H6220 Medicago minima (M)
H6220 Micropyrum tenellum
H6220 Narduroides salzmannii
H6220 Ornithopus compressus
H6220 Phlomis lychnitis
H6220 Plantago lagopus
H6220 Reseda stricta
H6220 Sedum sediforme
H6220 Teesdalia coronopifolia
H6220 Valantia hispida
H6220 Vulpia myuros (M)
H6230 Antennaria dioica (M)
H6230 Arnica montana
H6230 Campanula barbata
H6230 Carex ericetorum
H6230 Carex pallescens (M)
H6230 Festuca ovina (M)
H6230 Hypericum maculatum (M)
H6230 Lathyrus linifolius (M)
H6230 Meum athamanticum (M)
H6230 Nardus stricta
H6230 Pedicularis sylvatica
H6230 Plantago alpina
H6230 Platanthera bifolia (M)
H6230 Poa alpina
H6230 Polygala vulgaris (M)
H6230 Potentilla erecta (M)
H6230 Pseudorchis albida
H6230 Selinum pyrenaeum (M)
H6230 Soldanella alpina
H6230 Trifolium alpinum
H6230 Veronica officinalis (M)
H6230 Viola canina (M)
H6240 Allium flavum (M)

H6240 Artemisia austriaca (M)
H6240 Astragalus austriacus (M)
H6240 Astragalus exscapus (M)
H6240 Carex humilis (M)
H6240 Chrysopogon gryllus (M)
H6240 Festuca rupicola (M)
H6240 Gagea pusilla (M)
H6240 Globularia cordifolia (M)
H6240 Helianthemum canum (M)
H6240 Hesperis tristis (M)
H6240 Iris humilis (M)
H6240 Oxytropis pilosa (M)
H6240 Ranunculus illyricus (M)
H6240 Scorzonera austriaca (M)
H6410 Cirsium dissectum (M)
H6410 Cirsium tuberosum (M)
H6410 Colchicum autumnale (M)
H6410 Crepis paludosa (M)
H6410 Dianthus superbus (M)
H6410 Galium uliginosum (M)
H6410 Inula salicina (M)
H6410 Juncus conglomeratus (M)
H6410 Lotus pedunculatus (M)
H6410 Luzula multiflora (M)
H6410 Molinia caerulea
H6410 Ophioglossum vulgatum (M)
H6410 Potentilla anglica (M)
H6410 Selinum carvifolia (M)
H6410 Serratula tinctoria (M)
H6410 Silaum silaus (M)
H6410 Succisa pratensis (M)
H6410 Viola palustris (M)
H6410 Viola persicifolia (M)
H6430 Aconitum lycoctonum (M)
H6430 Aconitum napellus (M)
H6430 Adenostyles alliariae (M)
H6430 Angelica archangelica (M)
H6430 Angelica sylvestris (M)
H6430 Calamagrostis arundinacea (M)
H6430 Campanula serrata (M)
H6430 Cirsium oleraceum (M)
H6430 Digitalis grandiflora (M)
H6430 Epilobium hirsutum (M)
H6430 Filipendula ulmaria (M)
H6430 Gentiana asclepiadea
H6430 Geranium robertianum (M)
H6430 Lilium martagon (M)
H6430 Lysimachia vulgaris (M)
H6430 Lythrum salicaria (M)
H6430 Petasites hybridus (M)
H6430 Ranunculus platanifolius (M)
H6430 Valeriana officinalis (M)
H6430 Veratrum album (M)
H7110 Carex limosa
H7110 Carex pauciflora
H7110 Chamaedaphne calyculata
H7110 Drosera anglica
H7110 Eriophorum vaginatum
H7110 Odontoschisma sphagni
H7110 Scheuchzeria palustris
H7110 Sphagnum angustifolium
H7110 Sphagnum balticum
H7110 Sphagnum capillifolium
H7110 Sphagnum fuscum
H7110 Sphagnum imbricatum
H7110 Sphagnum magellanicum
H7110 Sphagnum papillosum
H7110 Vaccinium oxycoccos
H7130 Campylopus atrovirens
H7130 Diplophyllum albicans
H7130 Mylia taylorii
H7130 Pinguicula lusitanica
H7130 Pleurozia purpurea
H7130 Schoenus nigricans
H7130 Sphagnum strictum
H7150 Lycopodiella inundata
H7210 Cladium mariscus
H7230 Aneura pinguis
H7230 Bartsia alpina
H7230 Bryum pseudotriquetrum
H7230 Campylium stellatum
H7230 Carex davalliana
H7230 Carex dioica
H7230 Carex flava
H7230 Carex hostiana
H7230 Carex pulicaris (M)
H7230 Cinclidium stygium
H7230 Ctenidium molluscum
H7230 Dactylorhiza incarnata
H7230 Dactylorhiza traunsteineri
H7230 Eleocharis quinqueflora
H7230 Epipactis palustris
H7230 Equisetum variegatum
H7230 Eriophorum latifolium
H7230 Liparis loeselii
H7230 Parnassia palustris
H7230 Pinguicula vulgaris
H7230 Schoenus ferrugineus
H7230 Selaginella selaginoides
H7230 Tofieldia calyculata
H7230 Tomentypnum nitens
H7230 Valeriana dioica (M)
H8210 Androsace cylindrica
H8210 Androsace helvetica
H8210 Antirrhinum siculum
H8210 Asperula hirta
H8210 Asplenium ceterach
H8210 Asplenium petrarchae
H8210 Asplenium trichomanes
H8210 Ballota frutescens
H8210 Biscutella laevigata
H8210 Campanula carpatica
H8210 Campanula cochlearifolia
H8210 Campanula versicolor
H8210 Carex mucronata
H8210 Chaenorhinum origanifolium
H8210 Cheilanthes acrostica
H8210 Cystopteris fragilis
H8210 Dianthus rupicola
H8210 Draba tomentosa
H8210 Erinus alpinus
H8210 Erodium petraeum
H8210 Globularia repens
H8210 Kernera saxatilis
H8210 Melica minuta
H8210 Minuartia rupestris
H8210 Phyteuma charmelii
H8210 Potentilla alchimilloides
H8210 Potentilla caulescens
H8210 Potentilla nivalis
H8210 Potentilla saxifraga
H8210 Primula allionii
H8210 Primula marginata
H8210 Pteris cretica
H8210 Ramonda myconi
H8210 Saxifraga aretioides
H8210 Saxifraga canaliculata
H8210 Saxifraga cuneifolia
H8210 Saxifraga longifolia
H8210 Saxifraga marginata
H8210 Saxifraga media
H8210 Sedum dasyphyllum
H8210 Silene campanula
H8210 Valeriana globulariifolia
H8220 Anarrhinum bellidifolium
H8220 Androsace pyrenaica
H8220 Androsace vandellii
H8220 Anogramma leptophylla
H8220 Armeria leucocephala
H8220 Asarina procumbens
H8220 Asplenium adulterinum
H8220 Asplenium balearicum
H8220 Asplenium cuneifolium
H8220 Asplenium onopteris
H8220 Asplenium septentrionale
H8220 Carex kitaibeliana
H8220 Cheilanthes hispanica

H8220 Cheilanthes maderensis
H8220 Cheilanthes tinaei
H8220 Cosentinia vellea
H8220 Dianthus graniticus
H8220 Eritrichium nanum
H8220 Galium tendae
H8220 Haberlea rhodopensis
H8220 Jovibarba heuffelii
H8220 Murbeckiella boryi
H8220 Phyteuma hemisphaericum
H8220 Phyteuma scheuchzeri
H8220 Potentilla crassinervia
H8220 Primula hirsuta
H8220 Rhodiola rosea
H8220 Saxifraga aspera
H8220 Saxifraga continentalis
H8220 Saxifraga florulenta
H8220 Saxifraga nevadensis
H8220 Saxifraga pedemontana
H8220 Silene requienii
H8220 Umbilicus rupestris
H9150 Acer campestre
H9150 Buxus sempervirens
H9150 Carex alba
H9150 Carex digitata
H9150 Carex montana (M)
H9150 Cephalanthera damasonium
H9150 Cephalanthera rubra
H9150 Epipactis leptochila
H9150 Epipactis microphylla
H9150 Fagus sylvatica
H9150 Hieracium murorum
H9150 Lactuca muralis
H9150 Lathyrus vernus
H9150 Lonicera xylosteum
H9150 Sesleria albicans
H9150 Solidago virgaurea
H9150 Sorbus aria
H9160 Anemone nemorosa
H9160 Brachypodium sylvaticum
H9160 Carpinus betulus
H9160 Corylus avellana
H9160 Fragaria vesca (M)
H9160 Galium odoratum
H9160 Galium sylvaticum
H9160 Melica nutans
H9160 Mercurialis perennis
H9160 Potentilla sterilis (M)
H9160 Prunus avium
H9160 Stellaria holostea (M)
H9160 Tilia cordata
H9160 Viola reichenbachiana
H9190 Amelanchier lamarckii
H9190 Betula pendula (M)
H9190 Ceratocapnos claviculata
H9190 Holcus mollis (M)
H9190 Lonicera periclymenum
H9190 Maianthemum bifolium
H9190 Melampyrum pratense
H9190 Populus tremula (M)
H9190 Pteridium aquilinum (M)
H9190 Quercus petraea
H9190 Quercus robur (M)
H91E0 Alnus glutinosa (M)
H91E0 Alnus incana (M)
H91E0 Cardamine amara (M)
H91E0 Carex pendula
H91E0 Carex remota
H91E0 Carex strigosa
H91E0 Equisetum telmateia (M)
H91E0 Fraxinus excelsior (M)
H91E0 Geum rivale (M)
H91E0 Geum urbanum (M)
H91E0 Glechoma hederacea (M)
H91E0 Humulus lupulus (M)
H91E0 Impatiens noli tangere (M)
H91E0 Lysimachia nemorum
H91E0 Populus nigra (M)
H91E0 Ranunculus ficaria (M)
H91E0 Rumex sanguineus (M)
H91E0 Salix alba (M)
H91E0 Salix purpurea (M)
H91E0 Salix triandra (M)
H91E0 Salix viminalis (M)
H91E0 Silene dioica (M)
H91E0 Stellaria nemorum (M)
H91E0 Ulmus glabra
H9410 Abies alba
H9410 Gymnocarpium dryopteris
H9410 Luzula luzuloides
H9410 Melampyrum sylvaticum
H9410 Picea abies
H9410 Polygonatum verticillatum
H9410 Prenanthes purpurea
H2130 Artemisia campestris maritima (M)
H2130 Calamagrostis epigeios (M)
H2130 Calystegia soldanella
H2130 Cetraria aculeata (M)
H2130 Eryngium maritimum
H2130 Viola curtisii (M)
H2160 Bryonia dioica (M)
H2160 Calamagrostis epigeios (M)
H2160 Carex arenaria (M)
H2210 Calystegia soldanella
H2210 Crucianella maritima
H2210 Eryngium maritimum
H2210 Helichrysum stoechas
H2210 Sonchus bulbosus
H3130 Deschampsia setacea
H3130 Eleocharis acicularis
H3130 Eleocharis multicaulis
H3130 Littorella uniflora
H3130 Potamogeton polygonifolius
H3150 Hydrocharis morsus ranae
H3150 Nuphar microphylla
H3150 Potamogeton illinoensis
H3150 Spirodela polyrrhiza
H3150 Stuckenia pectinata
H4030 Erica tetralix
H4060 Calluna vulgaris (M)
H4060 Vaccinium myrtillus
H4070 Erica herbacea
H4070 Homogyne alpina
H4070 Rhododendron ferrugineum
H4070 Rhododendron hirsutum
H4070 Rhodothamnus chamaecistus
H4070 Vaccinium myrtillus
H4070 Vaccinium vitis idaea
H5130 Berberis vulgaris (M)
H5130 Calluna vulgaris (M)
H5130 Crataegus monogyna (M)
H5130 Dasiphora fruticosa
H5130 Rosa canina (M)
H5130 Rosa rubiginosa (M)
H5130 Vaccinium myrtillus
H5210 Juniperus communis (M)
H5210 Teucrium polium (M)
H5420 Cistus salviifolius
H5420 Phagnalon rupestre
H5420 Pistacia lentiscus
H6120 Alyssum montanum
H6110 Allium lusitanicum (M)
H6110 Arabidopsis arenosa
H6110 Arabis auriculata (M)
H6110 Clinopodium acinos (M)
H6110 Koeleria macrantha (M)
H6120 Arabidopsis arenosa
H6120 Carex colchica (M)
H6120 Euphorbia seguieriana (M)
H6120 Galium verum (M)
H6120 Koeleria macrantha (M)
H6120 Sedum acre (M)
H6230 Potentilla aurea
H6230 Vaccinium myrtillus
H6240 Alyssum alyssoides (M)
H6240 Bothriochloa ischaemum (M)
H6240 Eryngium campestre (M)
H6240 Euphorbia cyparissias (M)
H6240 Festuca valesiaca (M)
H6240 Medicago minima (M)
H6240 Poa badensis (M)
H6240 Potentilla cinerea (M)
H6240 Stipa capillata (M)
H6120 Silene conica (M)
H6120 Thymus praecox (M)
H6150 Carex bigelowii
H6150 Cassiope tetragona
H6150 Helictotrichon versicolor
H6150 Homogyne alpina
H6150 Ligusticum mutellina
H6150 Potentilla aurea
H6170 Carex sempervirens
H6170 Dryas octopetala

H6170 Geum montanum
H6210 Arabis hirsuta (M)
H6210 Asperula cynanchica (M)
H6210 Carex flacca (M)
H6210 Cirsium acaulon (M)
H6210 Helictotrichon pratense (M)
H6210 Neotinea ustulata (M)
H6210 Potentilla cinerea (M)
H6210 Potentilla tabernaemontani (M)
H6210 Teucrium chamaedrys (M)
H6220 Asterolinon linum stellatum
H6220 Brachypodium retusum
H6220 Catapodium rigidum
H6220 Helictotrichon bromoides
H6220 Thymus vulgaris
H6220 Trifolium scabrum
H6220 Tuberaria guttata
H6230 Campanula scheuchzeri
H6230 Carex panicea (M)
H6230 Deschampsia flexuosa
H6230 Galium saxatile (M)
H6230 Gentiana pneumonanthe (M)
H6230 Geum montanum
H6230 Homogyne alpina
H6230 Hypochaeris maculata (M)
H6230 Ligusticum mutellina
H6240 Stipa joannis (M)
H6240 Teucrium chamaedrys (M)
H6410 Carex pallescens (M)
H6430 Athyrium alpestre (M)
H6430 Imperatoria ostruthium (M)
H6430 Lactuca alpina (M)
H6430 Lactuca plumieri (M)
H6430 Senecio nemorensis (M)
H6510 Sanguisorba officinalis (M)
H6520 Chaerophyllum hirsutum (M)
H6520 Cirsium helenioides (M)
H6520 Geranium sylvaticum (M)
H6520 Phyteuma orbiculare (M)
H6520 Sanguisorba officinalis (M)
H6520 Trisetum flavescens (M)
H6520 Trollius europaeus (M)
H7110 Andromeda polifolia
H7110 Narthecium ossifragum
H7110 Rhododendron tomentosum
H7130 Erica tetralix
H7130 Eriophorum vaginatum
H7130 Narthecium ossifragum
H7130 Sphagnum compactum
H7130 Sphagnum tenellum
H7130 Trichophorum cespitosum
H7150 Drosera intermedia
H7150 Drosera rotundifolia
H7150 Rhynchospora alba
H7150 Rhynchospora fusca
H7230 Bellis sylvestris
H7230 Carex viridula
H7230 Pedicularis sceptrum carolinum
H7230 Primula laurentiana
H7230 Schoenus nigricans
H8210 Achillea oxyloba
H8210 Artemisia umbelliformis
H8210 Asplenium ruta muraria
H8210 Asplenium trichomanes ramosum
H8210 Draba aizoides
H8210 Primula auricula
H8210 Thymus pulcherrimus
H8220 Asplenium adiantum nigrum
H8220 Asplenium forisiense
H8220 Asplenium obovatum
H8220 Paragymnopteris marantae
H8220 Polypodium vulgare
H9150 Berberis vulgaris (M)
H9150 Carex flacca (M)
H9150 Neottia nidus avis
H9160 Acer campestre
H9160 Poa chaixii (M)
H9190 Deschampsia flexuosa
H9190 Sorbus aucuparia
H9190 Trientalis europaea (M)
H91E0 Angelica sylvestris (M)
H91E0 Cirsium oleraceum (M)
H91E0 Geranium robertianum (M)
H9410 Calamagrostis varia
H9410 Luzula sylvatica
H9410 Petasites japonicus

Appendix VI: Derivation of odds approach

The individual pressure–response relationships per species (see Section 2.4.3) were derived by single pressure logistic regression, with an associated simple GLM model (generalised linear model) of the form:

$$Logit(PoO)=log(PoO/(1-PoO))=log(Odds)=a+b\cdot x+c\cdot x^2 \qquad (1)$$

where *PoO* denotes the probability of species occurrence and *x* refers to the values of the specific pressure. The *Odds*, defined as *PoO/(1-PoO),* is the ratio of the probability of species presence and the probability of species absence.
The corresponding pressure–response relationship for this single pressure logistic model is:

$$PoO=exp(a+b\cdot x+c\cdot x^2)/(1+exp(\ a+b\cdot x+c\cdot x^2)) \qquad (2)$$

As a step towards combining these single pressure–response relations into an estimate of the multivariable effect we use an approach which has its basis in this logistic regression model. In cases where a general multivariable logistic regression model of the form

$$logit(PoO)=F(x), \qquad (3a)$$

with $x= (x_1,x_2,\dots,x_p)$ being the multivariable predictor variables, has an additive character, i.e.

$$F(x)=F_1(x_1)+F_2(x_2)+ \dots + F_p(x_p) \qquad (3b)$$

this additivity would suggest that an arbitrary single pressure model, if it has a similar basic form as $F_i(x_i)$:

$$logit(PoO)= \widetilde{F_i}(x_i) \qquad (4)$$

can be used to assess the combined influences of the x_i, simply by summing at the *logit-scale* the relative contribution of the separate predictors.

Based on this rationale we propose the following approach to ‘reconstruct’ a multivariable model from these single pressure ones:

$$[logit(PoO) - E(logit(PoO))]_{multi} := \sum_{k=1}^{p}[logit(PoO) - E(logit(PoO))]_{uni_k} \qquad (5)$$

Where $[logit(PoO) - E(logit(PoO))]_{multi}$ refers to the multivariable logistic regression model. The individual terms $[logit(PoO) - E(logit(PoO))]_{uni_k}$ indicate the net influence of the separate explanatory variables x_k on logit scale according to the single pressure model in (1). The additive model warrants this contribution as a sum. The *E(logit(PoO))-term* reflects the base case, which is used as a reference point to express the influence of specific variables over their range on the logit(P*oO*).
We use the log(N_1/N_0) as an estimate of this term, where N_1 is the number of presences in the data sample, and N_0 the number of absences. In fact the ratio N_1/N_0 expresses an estimate of the average odds of the species occurrence in the range where data collection took place.

$log(N_1/N_0)$ for $E(logit(PoO))$ in Equation (5) – concisely rewrite how the reconstruction of the multivariable model out of the single pressure models takes place:

$$log\left(\frac{Odds_{multi}}{N_1/N_0}\right) := \sum_{k=1}^{p}\left[log\left(\frac{Odds}{N_1/N_0}\right)\right]_{uni_k} = \log\left(\prod_{k=1}^{p}\frac{Odds_{uni_k}}{N_1/N_0}\right) \tag{6}$$

which means that the *scaled* version of the Odds for the multivariable case is the product of the *scaled* versions of the separate Odds associated to the individual variables.

$$\frac{Odds_{multi}}{N_1/N_0} := \prod_{k=1}^{p}\frac{Odds_{uni_k}}{N_1/N_0} \tag{7}$$

The value for the multivariable $Odds_{multi}$ which is obtained in this way can be simply transformed in a value for the multivariable probability of occurrence due to all environmental pressures $(x_1,x_2,\ldots,x_p)$ of interest by

$$PoO_{multi} := Odds_{multi}/(1+Odds_{multi}) \tag{8}$$

Remark: We hasten to say that the above Odds approach – which is set-up in analogy with dealing with separate additive models in ordinary regression – only renders a tentative and very first order approximation of the multivariable model, and is in fact limited in its validity and scope:

(a) This has first to do with the *additivity* assumption underlying the multivariable model of Equation (3a), where $F(x) = F_1(x_1) + \cdots + F_p(x_p)$ as denoted by Equation (3b). In fact additivity implies that *interactions* between predictor variables (pressures) are assumed to be negligible, and the question is whether this adequately describes the reality.

(b) Secondly also a hidden assumption on the mutual *independence* of the various individual predictors x_i is at the basis of the approach, to ensure that the single pressure models $\widetilde{F_i}(x_i)$ (in Equation (4)) provide direct information on the separate additive terms $F_i(x_i)$ in the multivariable model of Equation (3a-b).

(c) And the final assumption is that the single pressure model $\widetilde{F_i}(x_i)$ is of sufficient complexity to cover the functional form $F_i(x_i)$ in the multivariable model: e.g. when the single pressure model is linear while the multivariable counterpart also shows higher order terms in x, then the single pressure model will inevitably miss these features, and give incomplete and biased information on the real dose–response relation.

All this makes clear that the use of the odds approach will require a decent validation, e.g. comparing the outcomes according to Equation (8) with the results of a full multivariable benchmark model for the various pressure variables. In Appendix X, we offer some insights in this issue.

Appendix VII: Pressure–response relationships

Table A4: Numbers of quadratic pressure–response relationships per taxonomic group

Environmental variable	Birds	Butterflies	Mammals	Plants
Desiccation	237	60	65	663
Fertilisation	237	50	62	652
FMA: Short rotation forestry	194	54	59	524
FMA: Even Aged Forestry	214	43	57	570
FMA: Combined Objective Forestry	222	40	53	556
FMA: Close to nature	209	26	57	554
FMA: Nature Reserve	171	22	47	445
Fragmentation	253	79	68	672
N Deposition	244	61	61	704
Road impact	232	56	55	609
S Deposition	249	52	65	705
Urbanisation	234	40	59	602

Table A5: Numbers of pressure–response relationships retained after excluding non-significant relationships (included are both linear and quadratic term with $p < 0.05$ for quadratic relations and for linear relation only linear term with $p < 0.05$).

Environmental variable	Birds (284)	Butterflies (95)	Mammals (78)	Plants (863)
Desiccation	91%	71%	92%	83%
Fertilisation	91%	58%	85%	86%
FMA: Short rotation forestry	88%	54%	81%	76%
FMA: Even Aged Forestry	91%	72%	95%	83%
FMA: Combined Objective Forestry	88%	57%	89%	70%
FMA: Close to nature	86%	40%	87%	74%
FMA: Nature Reserve	70%	35%	72%	58%
Fragmentation	50%	58%	95%	63%
N Deposition	97%	85%	94%	91%
Road impact	95%	80%	86%	86%
S Deposition	99%	79%	95%	90%
Urbanisation	95%	77%	90%	85%

Table A6: Numbers of quadratic pressure–response relationships, where the quadratic term was set to zero

Environmental variable	Birds (284)	Butterflies (95)	Mammals (78)	Plants (863)
Desiccation	29%	24%	0%	41%
Fertilisation	31%	17%	20%	27%
FMA: Short rotation forestry	0%	0%	0%	0%
FMA: Even Aged Forestry	0%	0%	0%	0%
FMA: Combined Objective Forestry	0%	0%	0%	0%
FMA: Close to nature	0%	0%	0%	0%
FMA: Nature Reserve	0%	0%	0%	0%
Fragmentation	0%	0%	0%	0%
N Deposition	39%	35%	28%	32%
Road impact	30%	6%	33%	11%
S Deposition	34%	38%	33%	37%
Urbanisation	12%	27%	51%	41%

Appendix VIII: Review results

Review of Piero Visconti and Wilfried Thuiller on BioScore 2.0 and the minutes of the workshop.

1. Preface

PBL Netherlands Environmental Assessment Agency produces a Nature Outlook every four years for the ministry of environment. The theme of the Nature Outlook of 2016 is Europe. For this study a European biodiversity model was needed. BioScore 1.0 and Globio were thought to be to coarse for the expected usages. Therefore BioScore 1.0 was rigorously improved in terms of resolution, quantification of pressure–response relationships and use of monitoring data. The goal of BioScore 2.0 is to produce insights and indicators relevant for European nature policy, by assessing the impact of European policy measures on European terrestrial biodiversity.

On 21 June 2016, PBL organised a workshop which was attended by 25 persons. The primary goal of the workshop was to identify strengths and weaknesses in the model in order to
1) be able to improve the model and
2) determine which type of conclusions can be drawn with the current version of the model.
The participants received beforehand a description of the technical aspects of BioScore 2.0 (in the form of a Draft report). This note contains the minutes and the outcomes of the workshop.

The program of the workshop was as follows.
10:00 Welcome chairman (Lawrence Jones-Walters)
10:15 Presentation BioScore modelling concept and approach (Marjon Hendriks)
10:45 Presentation BioScore application (‘Nature Outlook’) (Anne Gerdien Prins)
11.15 Coffee break
11.30 Presentations Feedback reviewers (Wilfried Thuiller + Piero Visconti)
12:00 Discussion related to feedback of reviewers
12:30 Lunch
13:30 Discussion session 1: Content of BioScore model
14:30 Discussion session 2: Applicability of BioScore
15:00 Coffee break
15:30 Plenary discussion: evaluation BioScore, application NVK, main recommendations for improvement
16:15 Drinks

2. Presentations

2.1 Presentation on BioScore 2.0 by Marjon Hendriks

Marjon Hendriks gave a presentation about BioScore 2.0. It is a species-by-species model which assesses the impact of human induces pressures on future changes in mammals, breeding birds, vascular plants and butterflies. The model is developed to make policy-relevant indicators.
The model consists of three steps. In the first step the distribution range is calculated for each species, based on climate and soil variables by means of a multivariate analysis using BRT. In the second step, a species-specific land-use mask selects the potential habitat within the distribution range. The land-use mask consists of a land-cover map and a nature management map (presence/absence). In the third step univariate pressure response relationships are calculated using GLM per species per pressure. These univariate models are aggregated into a species-specific probability of occurrence map.

Indicators show the change between the base year (2005) and a scenario. Three types of indicators are shown: one with the number of species increasing and decreasing; a second showing the change in sum of probability of occurrence of all species within a grid cell; and a third indicator shows the relative contributions of climate change, land-use change and changes in pressures to the calculated changes in biodiversity.

2.2 Presentation on Nature Outlook by Anne Gerdien Prins

Anne Gerdien Prins presented the Nature Outlook. It explores multiple perspectives on nature and has the objective to inspire the agenda for policies beyond 2020.
Nature protection is considered important by EU citizens, but only 1 in 4 knows Natura 2000. What is considered as natural differs a lot, many people also consider city parks and large crop fields as having a high degree of naturalness.
Towards 2050 trends are expected to differ regionally in a business as usual scenario. Differences are expected in temperature and precipitation patterns, urbanisation and abandonment. With BioScore 2.0 the impact on mammals, breeding birds, butterflies and vascular plants of this scenario was calculated. The largest number of assessed species is expected to decrease in this scenario. Calculations of the contributions of climate change, land-use change and changes in pressures show that climate change is expected to contribute for a large part to this change.
Three challenges are formulated towards 2050. Four normative perspectives were developed that cover a variety of guiding values to nature. These perspectives are Strengthening Cultural Identity (SCI), allowing Nature to Find its Way (NFW), Going with the Economic Flow (GEF) and Working With Nature (WWN). Each of the perspectives has a different approach to the three challenges, which leads to four points for debate in developing a policy strategy beyond 2020. Furthermore, a semi-quantitative analysis shows the expected impact of the four perspectives on common and endangered species, regulating services and recreational services.

The discussion focused on the impact of climate change in the business as usual scenario with respect to the other pressures (land use and environmental conditions). Impacts of climate change are uncertain due to adaptation of species to climate change (and adaptation measures that can be taken), assumption on migration possibilities of species and the scale of the land-use maps included.

2.3 Review results of Wilfried Thuiller

Wilfried Thuiller summarises a couple of points from his review.
First there are conceptual issues related to the nested scales, such as the local impacts of soil and climate and biotic interactions. Second there are methodological issues, related to uncertainty in each step, which is not propagated to the next step and the resolution of the data, which varies between variables.
He suggests two solutions. In the first solution the three steps are combined in a single step with climate, soil and pressures variables and a common resolution. A land-cover mask should be applied afterwards. A multi-response SDM (‘joint SDM’) can model all species at once and account for species interaction. A problem with this method could be the different scales of the data.
The second solution separates large scale and local scale models using Bayesion technique. The results from an SDM with all variables using large scale observations is combined with results from an SDM with all variables using fine resolution observations and monitoring data. Wilfried prefers to apply land use as a mask afterwards, but it can also be used as a variable in the model.

Other issues he addresses relate to the use of elevation, which he recommends not to use, as it does not vary in time. He also questions the aggregation of probabilities of occurrence per species. He recommends to avoid this aggregation as it only reflects the sampling design and the selected species. When aggregating it should be made very clear that it only reflects a subset.

2.4 Review results of Piero Visconti

Piero Visconti summarises the most important issues raised in his review.
He discusses the approach to species selection. The current plant species selection does not reflect the diversity in Europe which is highest in south and Balkan. Butterflies should not be selected based on high AUC. Selection of birds and mammals species look fine.
He urges to look for the variation in environmental variables which is covered by the selected species. This can have a large impact on the importance of the variables.
Thirdly, he suggests to include the Corine land-cover map directly as predictor of a statistical model.
The inclusion of all variables for all species should be done with care, as relationships which come up as important, may be only statistical and not ecological. He recommends to use a custom set of variables for different taxa.
Furthermore he mentions that some mammals are dependent on management, while now all mammals are assumed to have no dependence on nature management.

The third step in the modelling procedure he recommends to skip for now, as a short term solution. Steps 1 and 2 are already important enough. Information which is included in step 3 is not usable for mammals due to the devious approach used for that taxonomic group. As an alternative method he recommends the use of a joint probability or Bayesian Hierarchical Models.

1. Results of workshop

3.1 Session 1

In session 1 three groups are formed which each discuss the BioScore modelling concept and approach.

Most important outcomes as identified by the group, moderated by Lawrence Jones-Walters in a plenary feedback round.

- Try a Bayesian multivariate analysis for a few species and compare the outcomes with the BioScore method. How do the impacts of the pressures differ between the methods? When comparing the methods, consider the Explained Deviance, expert evaluation, computational time, etcetera. Bayesian methods proposed are a 1 step method, 2 step method or 2 step method (see for more details the reviews of Piero Visconti and Wilfried Thuiller). The third step of the modelling procedure can be improved by including more expert knowledge. This can also be compared with the other modelling methods.
- Do not use all variables for all species. Use more expert knowledge on selecting environmental variables for species/taxonomic groups. For example, soil factors should only be included for plants.
- Exclude the soil maps in the first step, but include them in step 3 as it is a variable that has a local effect.
- Improve the data quality of the variables.

- Check bias in results caused by different data sources by comparing the sum of probability maps with other data sources, such as the IUCN ranges. A possibility to deal with the bias is to mimic the sampling bias with the background data selection.
- Improve the selection of species and decide what is the message you want to get across. Is the policy relevance a good criteria? Policy relevancy of species might change in the future. You can make different maps for e.g. rare species and common species. Select a much broader set of species.

Other opinions on and suggestions for on the general modelling concept/approach

- Compare results based on presence/absence with results based on densities.
- Analyse the interactions between the variables.
- Biotic interactions are not included in the model. It is not recommended to include it in the model as it is very difficult to model. Recommended is to exclude species which have a strong interaction with other species. Another suggestion is to differentiate between specialist and generalist species. Acknowledge the lack of biotic interactions in the model and communicate this in the report.
- Exclude variables which are locally not explicit enough, which do not contain certain data, which do not change over time or which do not have a direct impact on the species. Altitude is recommended to be excluded.
- The modelling procedure and the environmental variables used in the third step are not very good. Therefore it is an option to not publish this part of the results. A short term solution would be to focus on the results of steps 1 and 2: land use and climate.

Other opinions on and suggestions for the climate/soil modelling (step 1)

- Dispersal capacity of species is assumed to be perfect, as in reality this is impossible.

Other opinions on and suggestions for on the habitat filtering (step 2)

- Land use is expected to have a higher impact in the BAU scenario. Therefore the suggestion is to improve the land-use map.

Other opinions on and suggestions for the pressure–response relationships (step 3)

- See suggestions on model concept.

Other opinions and suggestions

- Improve regional specificity as this is interesting for policy makers. Consider to use different models for each region.

Strong points on the BioScore 2.0 model:

- It is the first model that includes a wide range of species and environmental factors;
- Its stepwise approach makes sense, especially when looking at data availability and policy response;
- A model such as BioScore is needed to see what the contributions of the pressures are;
- Its habitat filtering;
- The link between interventions and effects on taxonomic groups.

3.2 Session 2

In session 2, groups of three are formed to identify the major issues on the application of BioScore.

Opinions on and suggestions for the presentation of the results

- Account for uncertainties throughout the model. Do not pretend to be precise. Calculate for some aspects the uncertainties or show uncertainties in graphs by for example using a big dot instead of a small dot.
- Present maps based on policy-relevant issues.
- If regions will be used to aggregate the results, use the biogeographical regions, as these are policy-relevant.
- Present results in a relative way by comparing the change between scenarios.
- Present messages which are easy and to the point.
- Put information in context of policy targets, such as N2000 and CBD 2020 strategy.
- Use storylines to illustrate the results. Explain what factors cause the observed effects and illustrate this with maps and stories. Relate it to relevant targets and measures.
- Do not (only) use species richness maps.
- Place the results in a historical context to make visible what are the impacts of the future, compared to the impacts of the past.
- Ensure clarity of the message by placing the results in the context of overall knowledge on biodiversity and policy.

Opinions on and suggestions for the type of conclusions which can be drawn with the model

- BioScore plays a key role in combining agricultural and biodiversity policy.
- When comparing scenarios, distinguish pressures that are most important for each scenario.
- Showing outcomes of different choices on biodiversity policy
- Doing a strength analysis of factors, such as land use vs climate, and assessing what is the strongest driver.
- The effect of climate is overestimated compared to the effect of land use. In the Nature Outlook the focus is too much on the effect of climate change, while land-use change is has had a major impact on biodiversity in the past and it is cheaper to alter to increase biodiversity.
- Understand what you do not know. Communicate the assumptions that are made in the model.

3.3 Plenary discussion

- Presentation of relative changes is preferred. Publish results in overall context of biodiversity knowledge and policy.
- Circulate questions on BioScore 3.0.
- Evaluate the results of the 4 normative scenarios. Use it to experiment with presenting results.
- What are the key issues that still need to be addressed? Include this in question for feedback on BioScore 3.0.
- PBL explains how BioScore relates to GLOBIO. PBL wants to have a consistent approach between the two models.

2. Participants

Name	**Organisation**
Alkemade, Rob	PBL Netherlands Environmental Assessment Agency
Benitez Lopez, Ana	Radboud University
Condé, Sophie	European Topic Centre on Biological Diversity (ETC/BD)

Erhard, Markus	European Environment Agency (EEA)
Hendriks, Marjon	PBL Netherlands Environmental Assessment Agency
Hennekens, Stephan	Alterra Wageningen UR
Hettelingh, Jean-Paul	Coordination Centre for Effects (CCE)
Hinsberg, van Arjen	PBL Netherlands Environmental Assessment Agency
Huijbregts, Mark	PBL Netherlands Environmental Assessment Agency and Radboud University
Janssen, Peter	PBL Netherlands Environmental Assessment Agency
Jones-Walters, Lawrence (moderator)	Alterra Wageningen UR
Knegt, Bart de	Alterra Wageningen UR
Knol, Onno	PBL Netherlands Environmental Assessment Agency
Mylius, Sido	PBL Netherlands Environmental Assessment Agency
Ozinga, Wim	Alterra Wageningen UR
Prins, Anne Gerdien	PBL Netherlands Environmental Assessment Agency
Remenska, Daniela	Netherlands eScience Center
Rost, Jasmijn	PBL Netherlands Environmental Assessment Agency
Santini, Luca	Laboratoire d'Ecologie Alpine (LECA), Univ. Grenoble Alpes
Schaminée, Joop	Alterra Wageningen UR
Schipper, Aafke	PBL Netherlands Environmental Assessment Agency
Sierdsema, Henk	Sovon Centre for Field Ornithology
Swaay, Chris van	Dutch Butterfly Conservation
Thuiller, Wilfried (reviewer)	National Center for Scientific Research (CNRS)
Visconti, Piero (reviewer)	Zoological Society of London

Review by Piero Visconti

Thank you for the opportunity to review this project. You'll see that while I think the objectives are very good, I have reservations on some aspects of the modelling approach. My recommendations are by no means prescriptive (except for step 3), and I look forward to discuss my comments and that of the other reviewer at the workshop next week.

What is your opinion on and do you have suggestion for the general modelling concept/approach, e.g.:

a) The three step approach (Climate/soil, land use, pressure factors)
Hierarchical distribution models makes sense to me as different environmental and ecological factors affect species distribution at different scales. For terrestrial vertebrate species for instance, regional and local climate regulate species geographic ranges while vegetation type, human disturbance, micro-climate, slope, etc. regulate local occurrence (Pearson and Dawson 2003; Pearson et al. 2004). However, there are several issues with the approach taken that need resolving.

1. I don't understand the choice of using surrogacy (habitat types for plant species), expert opinion (mammals), or a mix of expert opinion and frequency of points in land-cover types (birds and butterflies). For species for which you had sufficient points representative of the environmental space (I clarify what I mean by that in point *d* below) you could have directly fitted a Bayesian hierarchical model or a series of structured equation models. Doing hierarchical, data-driven models would have allowed you direct control over collinearity and interactions between variables and better understanding of the nestedness of climatic and habitat suitability.

2. For mammals at least, you seem to use the outputs of steps 1 and 2 to fit the pressure models at step 3. This is incorrect. The outputs of steps 1 and 2 are models of suitable climate and habitats, to some extent driven by data and to some extent by expert opinions. These model outputs are not observations that you can use to constraint another model. All the signal of human pressure in the pattern of occurrences would have been lost after steps 1 and 2. Therefore, it comes by no surprise to me that you have low AUC values for models of step 3 for most species. I wouldn't put much confidence even into models with decent AUC values as it might just be that climate or land-cover types co-vary with some of the pressures you use in step 3. That is, there would be no causality in the pressure–response model and the models would be right for the wrong reason.

For species other than mammals, I am not clear if you select empirical observation points from extrapolated suitable areas or you sample new points from extrapolated suitable areas (which would be conceptually the same as for mammals). Even in the first case there would be a problem as the observation points are used to train the model used in step 1 so the model used for filtering them in step 3 is not independent of them.

Based on these points I would recommend using a hierarchical model of species distribution in which all parameters are estimated at once. You could use Bayesian Hierarchical Models for this, as the Bayes theorem allows you to treat the local occurrence based on pressures as conditional on the habitat being suitable and the climate being suitable. This could be a 2 or 3 steps hierarchical model. Structural equation models might also be suitable.

b) The combination / distinction of BRT and GLM

There is no consensus on what statistical technique is best suited to model what type of ecological responses. This is especially true for modelling species distribution where one can find both support and criticism of the same modelling technique.
Boosted Regression Trees were flagged by Elith and colleagues as having high predictive power under various combination of species prevalence and quantity of data (Elith et al. 2006). However, a more recent paper questioned the unsupervised use of machine-learning methods as the large number of features they can fit, can easily overfit to the noise inherent in occurrence data, and turn this noise into a spurious pattern (Merow et al. 2014). I agree with Merow and colleague that the choice of modelling technique depends on the question answered. While I don't have anything directly against BRT, I question their unsupervised use, and I think it would be useful to look at the type of response curves you obtain. If you get complex response curves, with no apparent biological sense, then these are likely spurious responses which may give wrong predictions under alternative scenarios. If this is the case at least for some species, I recommend using GLM or GAMs with user-defined predictors based on a-priori ecological understanding of the species. These could include interactions and non-linear terms, and could be as complex in terms of number of parameters to those deriving from machine-learning methods, but this complexity would be understood and justified. Step functions do exist in response curves due to ecological threshold, e.g. thermal tolerance, but they are a minority (Guisan and Zimmermann 2000).

I would note here that using information-theoretic approaches for model selection (e.g. AIC) may not warrant avoiding spurious responses by overfitting to noise. Again, these models would fit the data well (according to AIC) but for the wrong reasons. Also, given the variance in predictions across alternative models, I wanted to ask why you have discarded the use of Ensemble forecasting (Araújo and New 2007). This would give insight in just how much uncertainty there might be in applying one approach over the other. You could then explicitly account for that uncertainty in your model prediction, while retaining a consensus model for your main findings and recommendations. I am happy to discuss the pros and cons of ensemble forecasting at the workshop, we might find reasons why this would not work for you as well as using just one method.

c) Species selection (selection criteria, representativeness)
Plants: I don't understand why you have chosen typical species of widespread habitat types only. I would have thought that rare and restricted habitat types have great ecological and conservation value. This criterion is also in contrast with one of the rationales for selecting butterflies (typical of a Habitat in Annex I). Also, it would be useful to add the list of 40 habitat types and the typical species to the appendices and include the name of the 5 habitat types that were later added to the analyses.

Butterflies: Some of the criteria for selection seem rather arbitrary. For instance why do you choose the species with AUC>0.75 in the models from Settele et al? Also, what is the rationale for choosing species occurring in more than one European bioregion? I don't mean that you shouldn't have these criteria, but that they don't seem immediately important to me and more generally all criteria should have their rationale explicitly stated to justify their consideration. This applies to all taxonomic groups. Also, the monitoring data criterion may worth consideration of being mandatory as the result of this project may be of relevant for monitoring (see point below about EU biodiversity policy).

Birds: the same applies as to Butterflies
Mammals: From a conservation and policy-relevance perspective these seems to be the most sensible criteria and I suggest they were considered for all species. Governments, NGOs,

scientist and the general public would want to know what is the status of species identified as of importance under some international convention.

d) Environmental variables (relevance, number of variables, data quality)
I don't understand the rationale for having soil variables for species other than plants. You might get spurious results of some sort of correlation and explanatory power of, say, PH, only because the preferred habitat type of an animal species was on acid soil. However, this doesn't make any acid soil suitable for the animal species.

I would drop all variables for which you don't have reasons to suspect a direct relationship. I note here that one could argue that climate affect animal species distribution also indirectly through habitats. However, other factors that directly affect animal species distribution are also mediated by climate, e.g. total NPP and its seasonality that affect species distribution and abundance. Finally, thermal tolerance, especially for cold-blooded organisms, directly affect species distribution. Therefore, having climate as a predictor of SDMs for animal species is justifiable, however I don't see a reason to have soil variables, except for some exceptions (e.g. bee-eaters and sand-martin requiring sandbanks for nesting).

What is your opinion on and do you have suggestion for the climate/soil modelling (step 1) , e.g.:
a) The statistical techniques (GBM / Trimmaps)
See my general point above. I haven't used these R packages myself, and I don't think the specific package used matter, my concern is over using BRT without checking for the time of response curves produced. With regards to the use of a common set of parameters for each species (lr, tc, etc.) I understand the pragmatism required when dealing with many species, but I would recommend adding references to justify they use of these particular values.

b) The use of cut-off values
I think it makes sense to zero the values below a TSS-defined threshold and retain the probability above. You retain useful information while discarding grid cell with predicted values too low to be considered.

c) The quality of the data sources
I appreciate the use of different types of occurrence data, including from citizen science such as E-birds, but I wonder if you have checked for the representativeness in environmental space of the occurrence data. A simple ordination such as a PCA could reveal whether there is a sampling bias somewhere along the multi-dimensional environmental space that could affect model accuracy. See for instance Bystriakova et al. (2012) for the potential implications of sampling bias in your occurrence data.

d) The derivation of absence locations (zeros)
I don't have concerns with the methods used, which appear to be best-practice with the available data.

e) Ability to track climate change
I am curious to know why you didn't consider it. It appears that you assume that species can track colonise any new suitable habitat regardless of distance from present ranges as no mention is made of dispersal limitation in range expansion. I don't think this assumption is valid, except possibly for long-dispersal species, e.g. wind-dispersed plants.

f) Definitions

I recommend renaming Extent of Occurrence into range maps, as EOOs is commonly referred to as the geographic spread of the occurrences, typically calculated as a minimum convex polygon around the species' range (IUCN Standards and Petitions Subcommittee 2016).

What is your opinion on and do you have suggestion for on the habitat filtering (step 2) , e.g.:
a) The use of CORINE Land Cover as starting point
It seems appropriate to me.

b) The resolution of the analysis
The choice of different resolution for different taxa wasn't motivated. I think this is necessary information. Also, I think it is worth considering testing the implications of running Step 1 at different resolutions unless there is an obvious ecological reason for choosing one resolution. For instance, if both a resolution of 10 x 10 and 5 x 5 could be plausible, it would make sense to test the implications of those for the models. In my experience, increasing the resolution increases the size of the data sets and enables more species to be modelled. The counter-argument is that this apparent increase in training data, might be just a result of pseudo-replications as observations close in space might not be truly independent. The decision on the resolution, would also depend on the species considered, e.g. whether they are sessile or they move.

c) The potential and relevance for scenario development
I am convinced that predictive models are necessary to understand the impact of exploratory scenarios, such as the Trend scenario assessed here, but also to build normative scenarios that are designed to achieve sustainability goals. Especially valuable are good rules of thumbs or good analytical solutions to ecological models that can be run to evaluate the ecological impact of given land-use configurations.
Therefore, an improved version of these models could be used to design normative scenarios or to assess the implications of planned policies (ex-ante scenarios), or assess the impacts of exploratory scenarios for policy-agenda setting.
I would have liked to see these models applied to the normative scenarios of PBL Nature Outlook. It is mentioned that four were prepared, but none has been evaluated here.

d) Step 2 across taxa
Besides the fact that for plants, birds and butterflies, and possibly some mammals, you might have had enough points to formally constraint a hierarchical model of habitat preferences, which would have been the correct way to do this in my opinion, I also don't understand why you used different methods for different groups. This is essentially my point 1 with regards to the 3-step approach.
e) Management

I think the attribution of management is important enough as to need its own appendix could, as opposed to referring to the paper by Hennekens, Hendriks et al.
Also, I am not convinced that no mammal species require management. The Iberian lynx, for instance is strongly dependent on management (rabbits reintroduction and habitat protection), and many other mammal species require strict habitat protection as they are hunted legally or illegally outside protected areas. This is especially the case for large carnivores. If we agree that protected areas can be considered a form of management, this could be added and considered for all species.

What is your opinion on and do you have suggestion for the pressure–response relationships (step 3) , e.g.:

a) The derivation of pressure–response relationships.
As said above, the outputs of steps 1 and 2 cannot be used to derive the pressure–response relationship. Any signal of the pressures that might have been in the occurrence data would have been lost or distorted through modelling those occurrence as a function of climate, soil and land use in steps 1 and 2. This is therefore conceptually and technically wrong. Again, this is certainly true for mammals for which suitable grid cells instead of occurrence points are used in step 3.

If you had used the occurrence data directly to perform the pressure–response model, you would have certainly found a stronger pattern and much higher AUCs. Still I think the best way would have been to consider all variables in a Bayesian hierarchical framework as suggested above.

b) The selection of relevant pressure–response models
I don't think all pressures are relevant to all taxa. For instance, Nitrogen and Sulphur deposition should not be of concern to mammals.
Also, I think it wasn't very clear to me how you measure fragmentation. It seems to be the proportion of suitable habitat within a given distance, varying among species. But this sentence confused me "To select the appropriate layer with fragmentation for breeding birds, butterflies and plants, first all relationships were discarded if both the linear and the quadratic term were not significant". I am not clear what relationship this refers to.

c) The use of odds-normalisation – approach in aggregating the effects of pressure factors.
Since the outputs of steps 1 and 2 are used to derive step 3, the odds cannot be combined as they are not independent of each other (as a multiplication would imply). More generally, this approach would not be necessary if you had a hierarchical approach in which all parameters were fitted at once as I suggest.

How relevant are the indicators that BioScore currently produces to EU biodiversity policy? Do you have suggestions on increasing relevance, e.g. focus more specific on Natura 2000 habitats?
Of the results shown, the stacked bars of % of species increasing or decreasing is the most relevant for EU biodiversity policies as it speaks directly to the goal of halting biodiversity declines. EU is also committed to achieve the Aichi targets, therefore I recommend considering calculating the projected trends in total suitability and extent of suitable areas for threatened species as indicator of progress towards Aichi target 12.

A geometric mean of % changes relative to a reference year could be used to synthetise results across species, this is common to both the farmland bird index and the Living Planet Index, both metrics commonly used to track progress towards international biodiversity targets.
One modelling issues are resolved, the results of this project could be used to make recommendations about priority species for monitoring, e.g. those expected to lose more suitable habitat.

Which criteria can be used to determine whether a species is modelled well enough for the planned application?
Generally I think TSS is a good predictor and it is the one I use for my models, and I see used most of the time. This metric is also used in BioScore 2.0 to identify cut-off values of the occurrence model, and it makes sense. Since the threshold in the probability selected is that one that maximises this metric, I think it is sensible to use this metric.

What is critical is that the data used to evaluate sensitivity and specificity (from which TSS is derived), are truly independent data, and do not suffer of any geographic or environmental bias. Only this can give predictive power, as otherwise the same (possibly distorted) pattern present in the training data set would be also in the evaluation data set, and high TSS values would be misleading.

What type of European nature policy scenarios can the current BioScore analyse and compare?
An assessment of the implementation of the recently revised Common Agricultural Policy would be useful. An independent impact assessment of the CAP revisions was never done before the CAP was discussed and eventually agreed. There is still time to evaluate what benefits to species the so-called greening measures will have. Scenario assessment of the CAP may influence its future revisions towards a more evidence-based approach. PBL involvement in those might also mobilise funding for the BioScore group to improve the model and pursue further research on this.

I will think of other policy-relevant assessments and will bring the ideas to the workshop.

Which important policy-relevant environmental factors are missing in BioScore and do you have suggestions on their implementation? Do you have suggestions on improvement of current environmental factors?
Specifically accounting for land use (e.g. crop types) by using level 3 of Corine land cover in step 2 would be helpful to improve predictive accuracy of the model, and assess alternative land-use policies and scenarios.

On which level of spatial detail can BioScore be used? Are spatially explicit (single species) estimates representative or should results be aggregated across species and/or study area?
See above with regards to the effect of spatial resolution of model training. With regards to the appropriate scale for informing decision, I think anything from 5 to 50 x 50 km would be appropriate. Finer resolution would be unrealistic in terms or reliability of the land use, climate and pressure data, especially with regards to future projections; a resolution coarser than 50 x 50 would be meaning losing important spatial heterogeneity, for instance, countries of the size of Netherland would be covered by ~4 grid cells of 100 x 100 km.

Which type of conclusions can be drawn with the model?
Clear conclusions can be made about the projected impacts of climate change. I don’t think much can be said about the impact of land-use change, type of management and pressures, as the models are not properly constrained to be sensitive to those, as I explain above. Addressing my concern on the hierarchical models could give you a model with very high potential to answer both ecological and policy-relevant questions.

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Review by Wilfried Thuiller

What is your opinion on and do you have suggestion for the general modelling concept/approach, e.g.:

a) The three step approach (Climate/soil, land use, pressure factors)

The approach looks interesting so far. The approach is presented as hierarchical. A proper hierarchical framework will take of uncertainty propagation, which is not the case here.
I am wondering about plant modelling since this is highly linked (or even explained) to land use, but also land cover and human pressure. Those aspects are intertwined and thus difficult to disentangle.
The main issue I see with the entire framework is that it assumes that the large spatial scale distributions of the species are not influenced by land cover and human pressure but only their local appearance. While it has been shown to be true in some extent (see Thuiller et al. 2015 Ecology Letters), others have found the opposite and strong effects of biotic interactions or other drivers on large-scale ranges (see Araujo and Rozenfeld 2015 Ecography, Gotelli et al. 2010 PNAS).

b) The combination / distinction of BRT and GLM

Instead of having a three step procedure, I will rather suggest to use only one. Either by directly going straight to Step 3 but including climate and land cover, or even better to use a hierarchical Bayesian approach where Step 1 is used a prior in Step 3 (where BRT or GAM should be used rather than simple sequential GLMs). See Talluto et al. 2015 for a model integration of that sort.

c) Species selection (selection criteria, representativeness)

Selection of plants based on forty habitat type. Where do they come from? Why focusing on common habitats? Perhaps the most threatened are the rare ones?
Need to the list of habitats.

Table list of species:
Mammals: Silene database? Mistake I guess. The Silene database is a plant database as far as I know.

d) Environmental variables (relevance, number of variables, data quality)

Extent of occurrence - variables

Surprised that all those climatic variables are not correlated. What are the correlations?
Soil variables: % of clay or organic carbon content are not available as it is in the European soil database. How were they derived? Are those data available?
Pressure variables: Are those data widely available and have they been checked? Are they reliable?
Land cover: Why were CORINE and the other land-cover data put together? Need an explanation on how they were combined.
Why different models was run for extracting the fragmentation maps? Are they available?

What is your opinion on and do you have suggestion for the climate/soil modelling (step 1) , e.g.:

a) The statistical techniques (GBM / Trimmaps)
b) The use of cut-off values
c) The quality of the data sources
d) The derivation of absence locations (zeros)

10000 pseudo-absence for mammals. It is lot in respect to the study area right?
How many total point in EU-28 at 10′ resolution?
How ‘similar species’ were selected for mammals? I do not really like the idea since similar species might not be in the same pixel for other reasons. That does not mean it is a true absence that should be included in a ‘climate’ model.
Cross-validation: Weird to have different sets of CV for the 4 groups that do not correspond to the size of the data. Would have been more sensible to have higher CV for the largest data (mammals at 10′), and a lower CV for other groups.
Is it really CV or rather split-sampling? A bit weird. If this is split-sampling, was then a full model run?

ROC is fairly optimistic. I would rather use TSS, or even better a combination of the two. For presence data only, better to use the Boyce Index to double-check.
This is quite illogical to then use TSS for deciding about the optimal threshold to filter the probability of occurrence, while ROC was used to test the predictive ability of the models.
'visual similarity with the know distribution of the species'. What does it mean?
I potentially like the weighing. Perhaps better to put a higher rate for mammals presence for which no true absence are used.

What is your opinion on and do you have suggestion for on the habitat filtering (step 2) , e.g.:

a) The use of CORINE Land Cover as starting point
b) The resolution of the analysis
c) The potential and relevance for scenario development

For plant species: Is it not a bit circular to use land cover in the models and then refine again with it?
How does the filtering is influenced by the distribution of the sampling points? Are the sampling efforts regular and random, or are they bias? If they are bias, could be then that the filtering is also biased.
Hemorobic level. Where does it come from? Validated? Need more than a simple ref in the report.
Mammals species not influenced by management? Is that true?
Need the published report to understand.

What is your opinion on and do you have suggestion for the pressure–response relationships (step 3) , e.g.:

a) The derivation of pressure–response relationships.
b) The selection of relevant pressure–response models
c) The use of odds-normalisation – approach in aggregating the effects of pressure factors.

I am not entirely comfortable with this whole part because it should be included in the overall framework and not as a last part. See my comment to rather use a single complete model or Bayesian hierarchical model.

How relevant are the indicators that BioScore currently produces to EU biodiversity policy? Do you have suggestions on increasing relevance, e.g. focus more specific on Natura 2000 habitats?

I would caution against the use of maps of species richness since this only reflect the species pool. For instance, the map of birds is quite puzzling knowing the observed distribution of species richness of breeding birds.

Figure 3.4. Care should be taken in interpreting the maps, especially for birds since they were selected as arctic/boreal and alpine species mostly. That explains the red dots.

Relative importance of change.
I am wondering whether the higher effect of climate/land-use change is not an effect of the hierarchical framework since this is the first driver included, the other ones only follow the effects. Surely climate is important, but better to double check how the statistical framework influences the results.

Which criteria can be used to determine whether a species is modelled well enough for the planned application?

Multiple tests (ROC, TSS) and Boyce index should do the trick. Better to use a combination of tests.

What type of European nature policy scenarios can the current BioScore analyse and compare?

Not sure I understand the question.

Which important policy-relevant environmental factors are missing in BioScore and do you have suggestions on their implementation? Do you have suggestions on improvement of current environmental factors?

See my response above.

On which level of spatial detail can BioScore be used? Are spatially explicit (single species) estimates representative or should results be aggregated across species and/or study area?

I think single species should be used rather than aggregation given the list of species. Perhaps reserve selection algorithms and gap analyses should then be applied to test whether those selected species are sufficiently protected and will not be threatened by climate and land-use change.

Which type of conclusions can be drawn with the model?

> Other than results specific to the list of species, I am not sure conclusion on species richness, or higher level (functional diversity) should be used. Indeed, the list of species is not complete and not representative of the overall European biodiversity. While the selection of species make sense, they do not make sense to be treated at a higher level.

Appendix IX: Correlation between climate and soil variables

The figures below show the correlations between the climate and soil variables used to calculate the species distribution range in step 1 of BioScore.

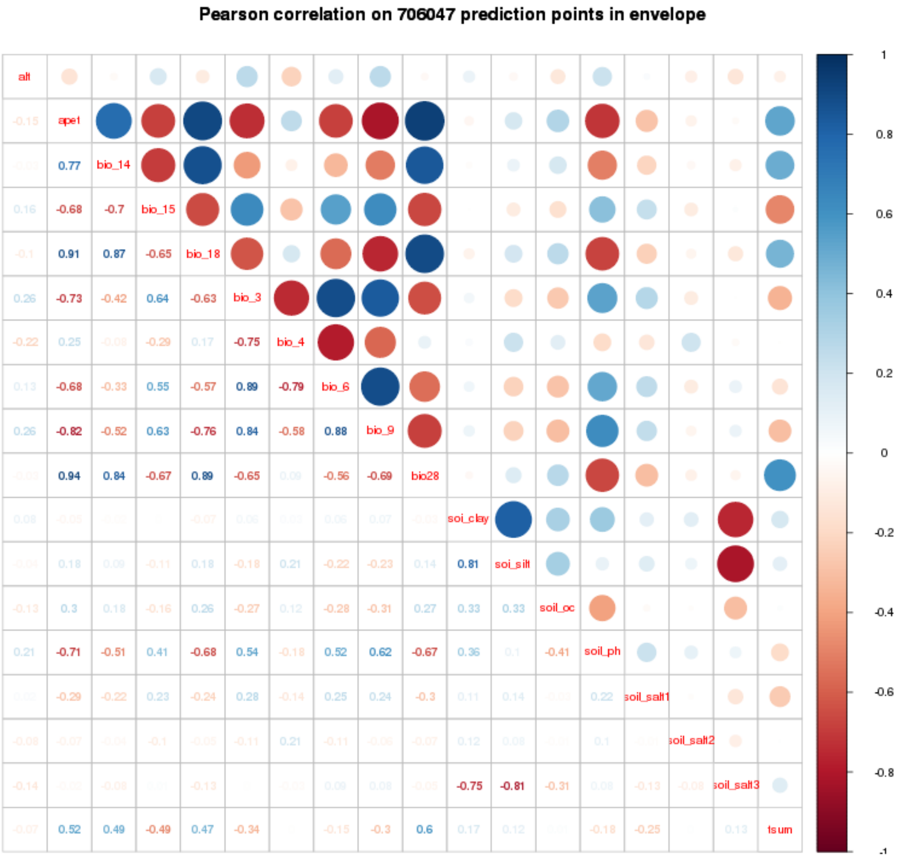

Figure 1: Pearson correlation between the climate and soil variables for all prediction locations in the EU-28 plus Switzerland

Appendix X: Correlation and interaction between pressures, and their consequences for step 4 of BioScore 2.0

On the presence of correlations between the pressure variables

The pressure variables show typically substantial correlations, as exemplified by Figure 1. As a consequence a judicious selection of these variables is recommended when constructing in step 4 of BioScore a composed model from the single pressure models, to prevent that too many correlated variables obscure and confound the results.

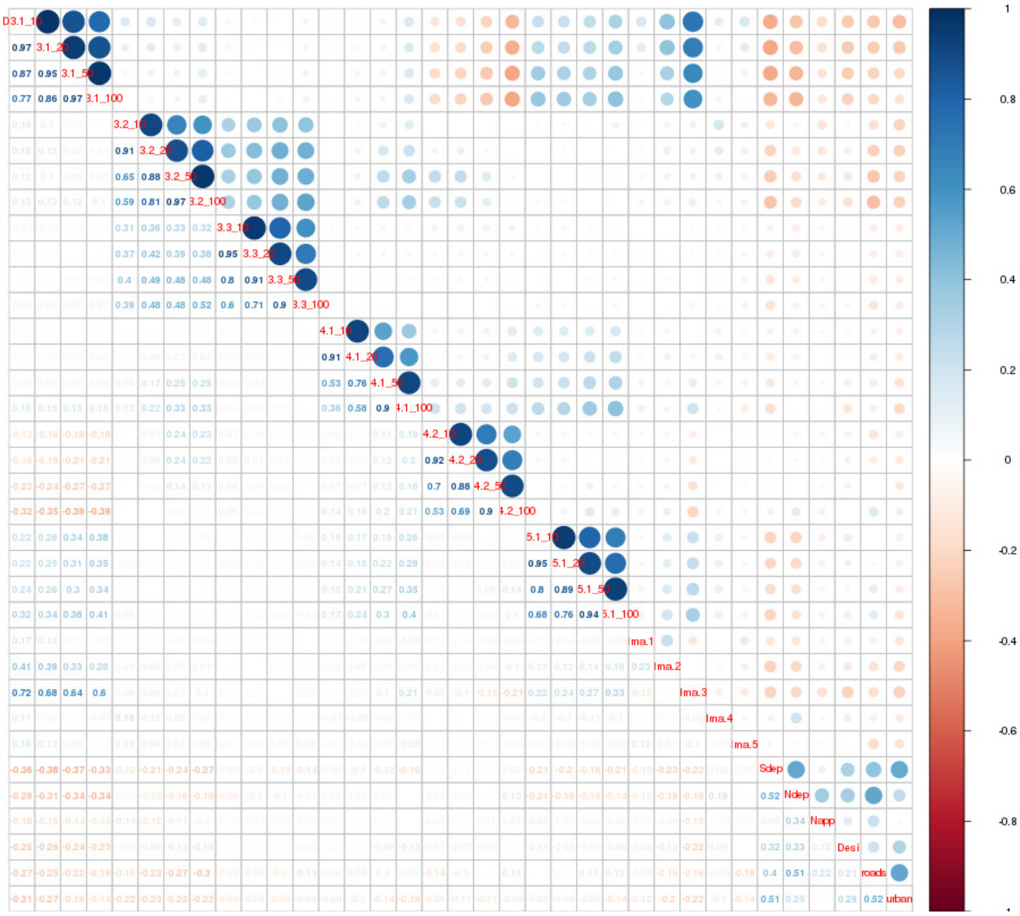

Figure 1: Pearson correlation between all pressure variables, for the observation data used in step 3 for the butterfly species Aglais io. The unit of the variables of forest management approach is the area covered.

As Figure 1 shows, especially the fragmentation-related variables – i.e. the first 24 variables which are grouped in 6 ecosystem type/land-cover classes, each being subdivided into 4 dispersion distance-related fragmentation classes – exhibit strong correlations. As expected the fragmentation values of the 4 dispersion classes within each ecosystem/land-cover type are highly correlated. Moreover there appear also to be some weaker correlations between the fragmentation values of different ecosystem types, e.g. 3.2 (shrub vegetation) and 3.3 (open vegetation), or 4.2, 5.1 (maritime wetlands and inland waters) and 3.1 (forests). Also the third forest management approach (even aged forestry) shows strong positive correlations with the fragmentation for the forest ecosystem type. Whilst S and N deposition show weak negative correlations with forest fragmentation. The data show some weak positive correlations between S deposition and N deposition, and also between the road density and urbanisation.

Due to these correlations we severely restricted the number of considered pressure variables in composing a model from the single pressure models in step 4 of BioScore. This was established by selecting only one fragmentation-related factor per species and by discarding pressures that don’t correspond to the land-cover type of interest (see Table 2.3 in this report). This definitely doesn’t remove all correlations as displayed by the correlation plot in Figure 2, for the set of remaining pressures for butterfly species Aglais io.

Figure 2: Pearson correlation between the selected pressure variables, for the observation data used in step 3 for the butterfly species Aglais io

Comparing the BioScore step 4 model with a multivariable benchmark model

As a consequence, the underlying assumptions for the approach that was used to build the composed model in step 4 of BioScore (see Appendix VI) are only partly[1] fulfilled in practice. To study the effect that this can have on the established results, we compared the results of the BioScore aggregation of pressure–response models in step 4, with a multivariable benchmark model of the pressures.

The benchmark model consists of all species-specific, selected pressure variables and was established by building a Boosted Regression Tree (BRT) model on the same data set (see Figure 3) as used in calibrating the single pressure– response relationships in step 3 of BioScore. To construct the BRT model TRIMmaps was run in a tenfold cross validation mode, with learning rate = 0.01, bag.fraction=0.75 and tree complexity = 2. Table 1 and Figure 4 show

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[1] Also the assumptions regarding absence of interaction effects and appropriateness of the simple logistic curve are not fully met, as will be shown later in this section.

the results for a selection of 11 butterfly species, and illustrate that the benchmark model performs better for all analysed species.

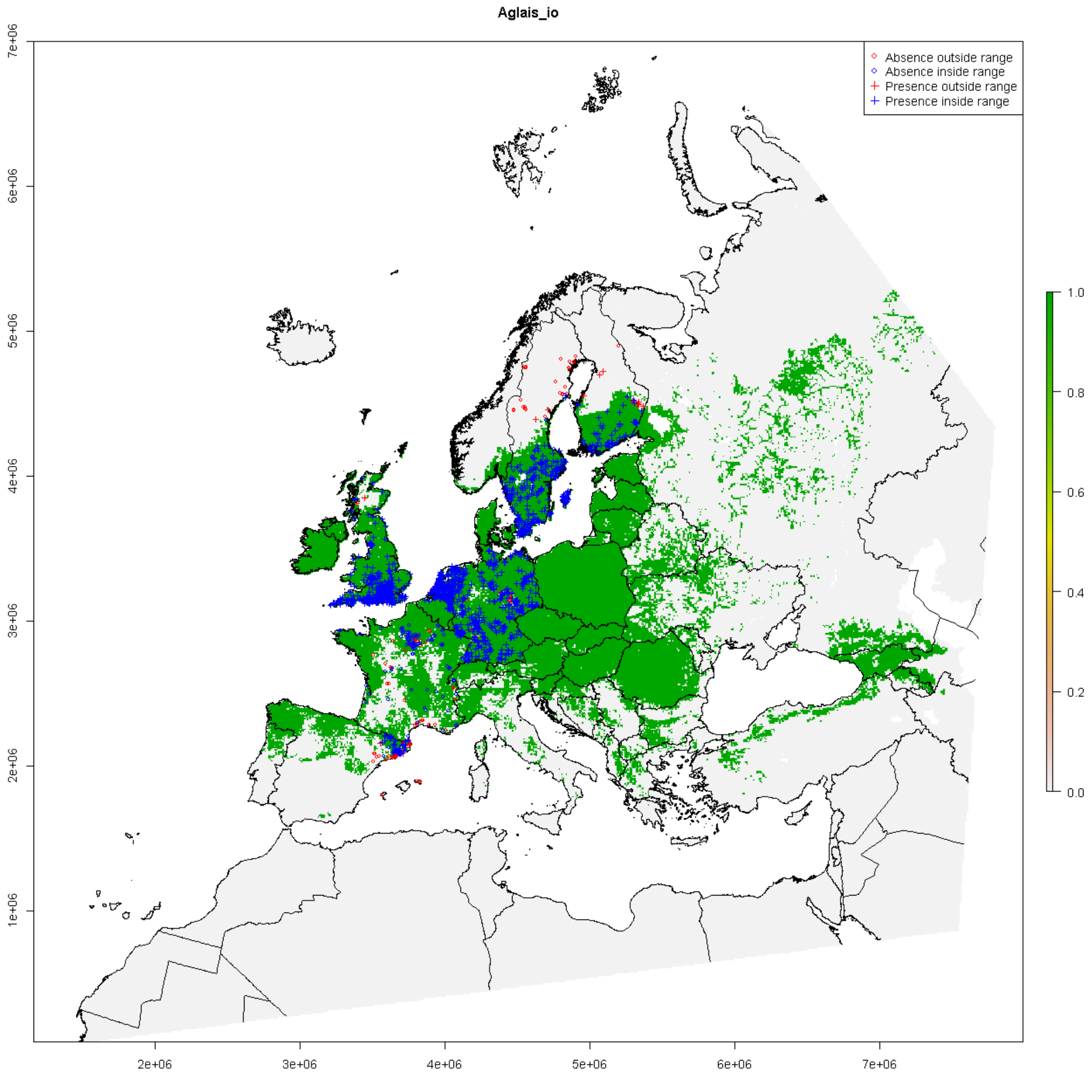

Figure 3: Locations for monitoring data for the butterfly species Aglais io. Monitoring data within the species climate envelope (green) are used for the BioScore models in step 3 and 4.

Table 1: Area Under Curve (AUC) and True scale statistics (TSS) for the results of the BioScore aggregation of pressures (step 4) and a multivariable benchmark model of the pressures for 11 butterfly species. Statistics are evaluated in cross-validation mode.

Species	AUC BioScore	AUC Multivariable model	TSS BioScore	TSS multivariable model
Aglais io	0.60	0.76	0.21	0.35
Anthocharis euphenoides	0.73	0.85	0.36	0.57
Boloria euphrosyne	0.81	0.85	0.43	0.52
Brintesia circe	0.77	0.81	0.43	0.51
Euphydryas maturna	0.60	0.80	0.12	0.39
Lasiommata megera	0.69	0.81	0.28	0.47
Limenitis camilla	0.76	0.78	0.39	0.40
Melitaea cinxia	0.78	0.84	0.44	0.53
Plebejus optilete	0.75	0.78	0.32	0.51
Polyommatus bellargus	0.67	0.74	0.23	0.34
Polyommatus coridon	0.71	0.77	0.30	0.39

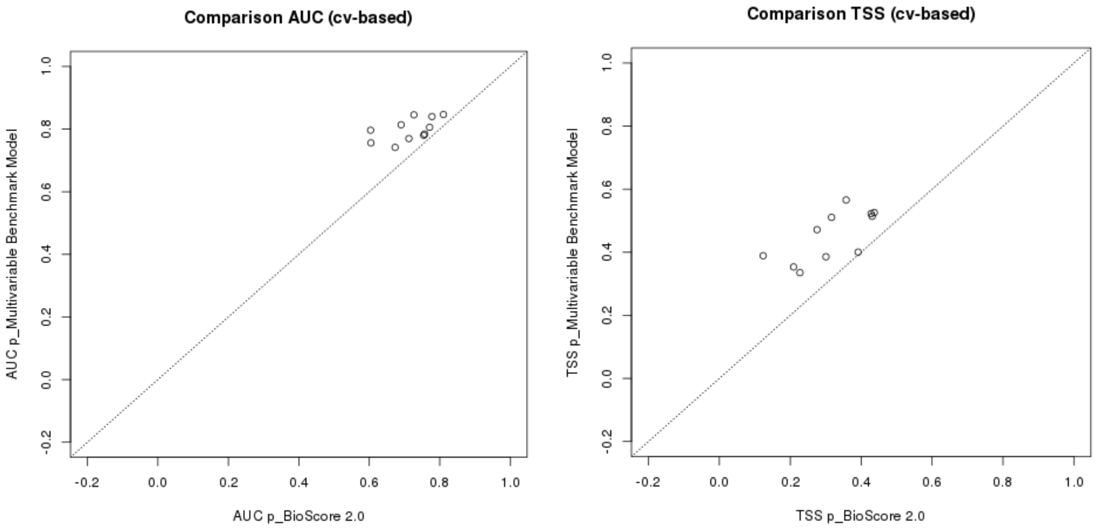

Figure 4: Comparison of AUC scores and TSS scores for the BioScore aggregation of pressures and the multivariable benchmark model for a selection of 11 butterfly species from Table 1. Statistics are evaluated in cross-validation mode (cv-based).

Also, the difference maps for the calculated probabilities can be shown and these render information on the differences between the outcomes of the two model approaches on a grid scale (cf. Figure 5). The blue (red) colour in this figure refers to grids where the composed single pressure model of BioScore gives higher (lower) probabilities than the benchmark model when evaluated for the pressure variables of concern.

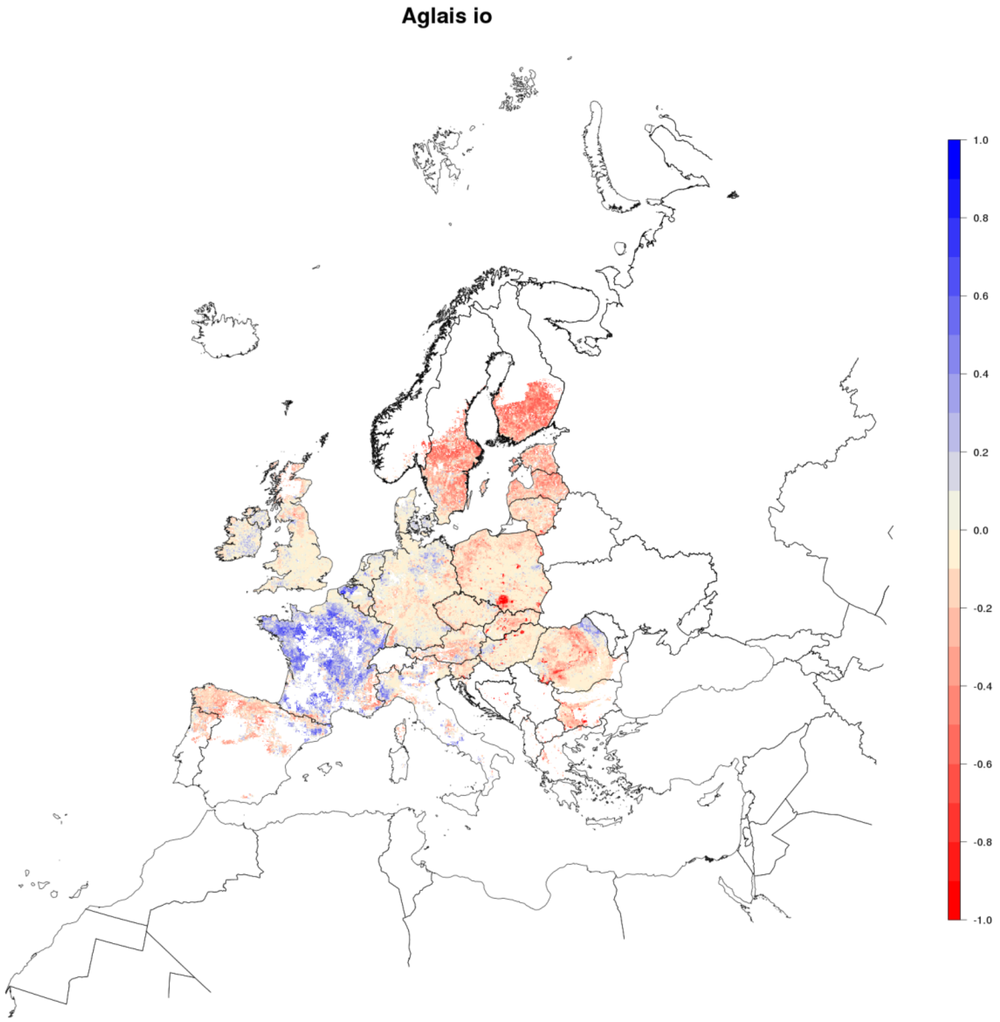

Figure 5: Difference in outcomes (probabilities) for the BioScore aggregation of pressures and the multivariable benchmark model, for the species Aglais io in the EU-28 countries within the confines of its climate envelope (as calculated in step 1 of BioScore).

Correlating these difference maps with the set of selected pressure variables for the various species, renders the correlation plot in Figure 6, which sheds some light on the question whether the differences can be attributed to certain pressures. One should however be cautious with drawing definite conclusions from this, since correlation analysis only renders information on linear relationships in this difference and overlooks other, non-linear or interaction, effects which can certainly also account for the difference in the results of the BioScore model and the benchmark model.

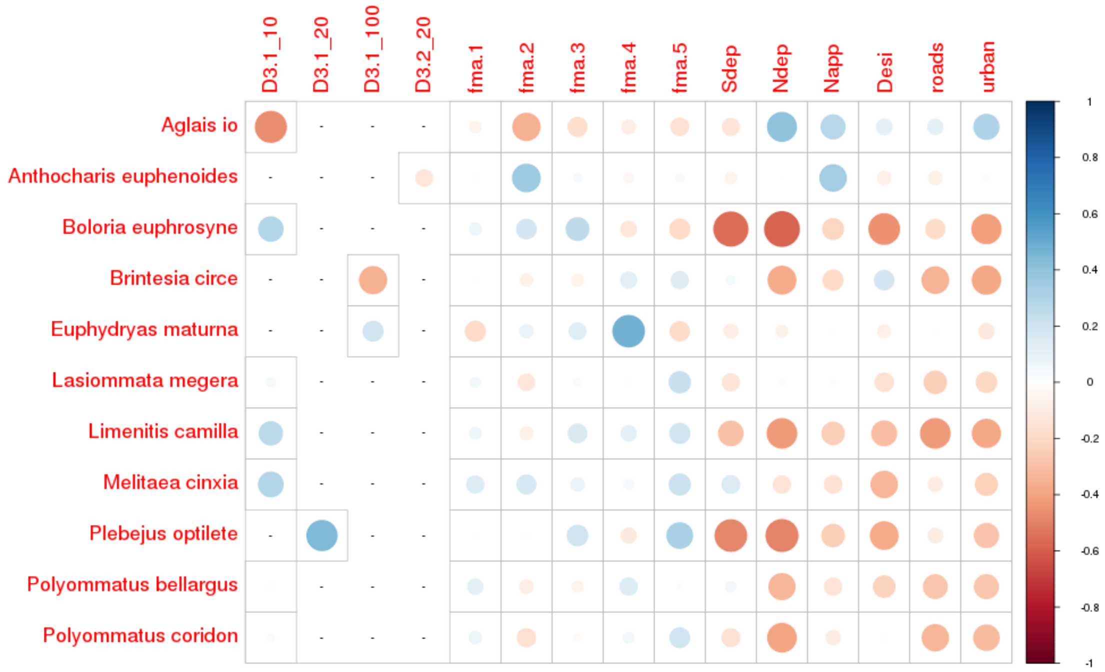

Figure 6: Correlation plot, showing the correlations between the difference in outcomes of BioScore aggregation of pressures and the multivariable benchmark model, and the various selected pressure variables (indicated in the columns), for the various butterfly species (indicated in the rows). The correlations are evaluated for the grid cells covering the EU-28 countries, within the confines of the climate envelopes for the various butterfly species

Notice namely that – in addition to the issue of correlatedness of the covariates – also the other assumptions which underlie the approach for the construction of the aggregated single pressure–response models are only partly met. This concerns the potential existence of interaction effects, and the limited appropriateness of the simple pressure–response curves. The following results highlight that these effects are indeed present in the data, and should therefore be studied for a more definite evaluation of the approach than is presented here.

On the presence of interaction effects

Figure 7 illustrates the existence of interaction effects. It renders a three dimensional plot, displaying the probability values as a function of two pressure variables, where the other variables have been set on their mean value. The plot is constructed on basis of a multivariable benchmark model, estimated by the package 'dismo', and evaluated by means of the function 'gbm.perspec' in this package. The package offers the possibility to evaluate interaction effects, by means of the function 'gbm.interactions', reporting their relative strength. This leads for Aglais io to the top 5 scores shown in Table 2, while the perspective plot in Figure 7, displays the first two pairs.

Variable 1	***Variable 2***	***Interaction size***
N-deposition	Desiccation	49.4
FMA 4	Urbanisation	48.9
Urbanisation	Impact of roads	23.6
S-deposition	FMA 3	12.8
N-deposition	FMA 3	11.5

Table 2: The 5 most important pairwise interactions in the multivariable benchmark model of butterfly species Aglais io, as estimated by gbm.interactions in package ‘dismo’

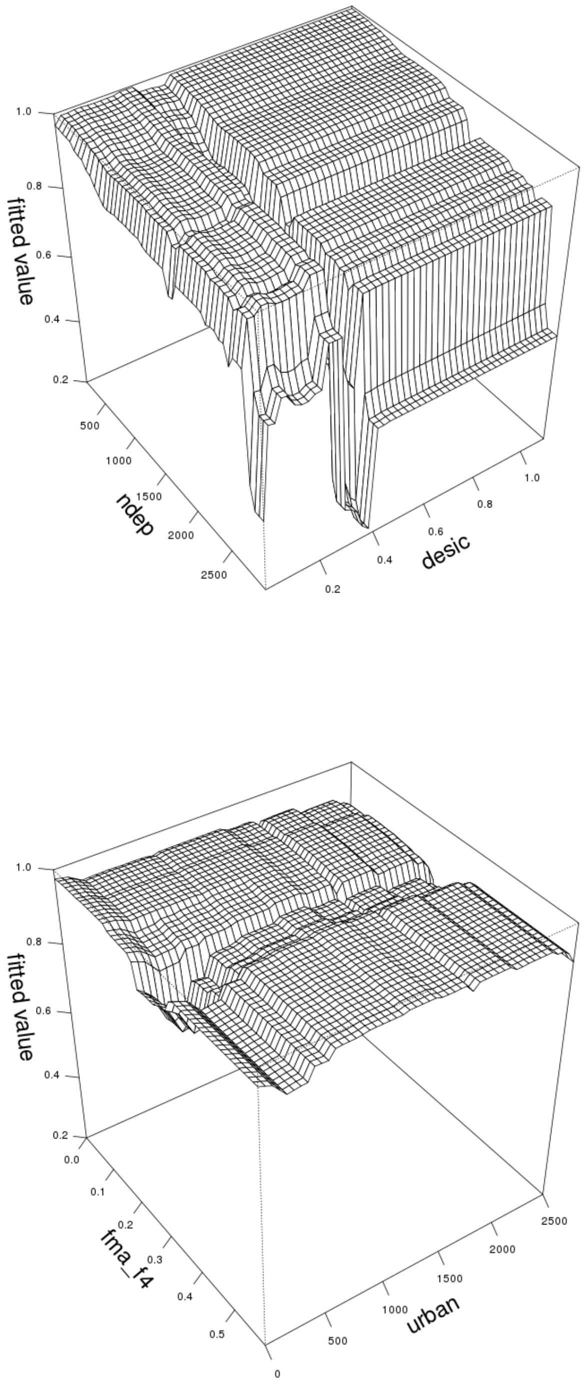

Figure 7: Perspective plots for the two most important pairwise interactions in the multivariable benchmark model of butterfly species Aglais io (see Table 2).

On the adequacy of the single pressure response models

In fitting the single pressure models in step 3 of BioScore only simple logistic models were used, with linear and/or quadratic terms for the covariates. The question in using these simple single pressure models within the approach of step 4, is whether these ‘simple’ functional forms appropriately describe the relation between the pressure and the response, and thus can be used as an adequate basis for building the composed model in step 4.

To shed light on this we compared the response curves of the single pressure models of step 3 with the partial dependence plots of the multivariable benchmark model. The partial dependence plots display the marginal effect of the selected variable(s), by ‘integrating’ out the other variables, see (Friedman, 2001). The comparison was established for the three most important variables in the multivariable benchmark model (Figure 7) and resulted in the plots of Figure 8, where in the left panel the single pressure-response curves are shown in red (in grey alternative curves, obtained by 10 fold cross-validation) while in the right panel the result of the partial dependence plots are shown, together with their smoothed version.

This comparison suggests that the employed simple model forms in step 3 are possibly not fully adequate in mimicking the more complex behaviour.

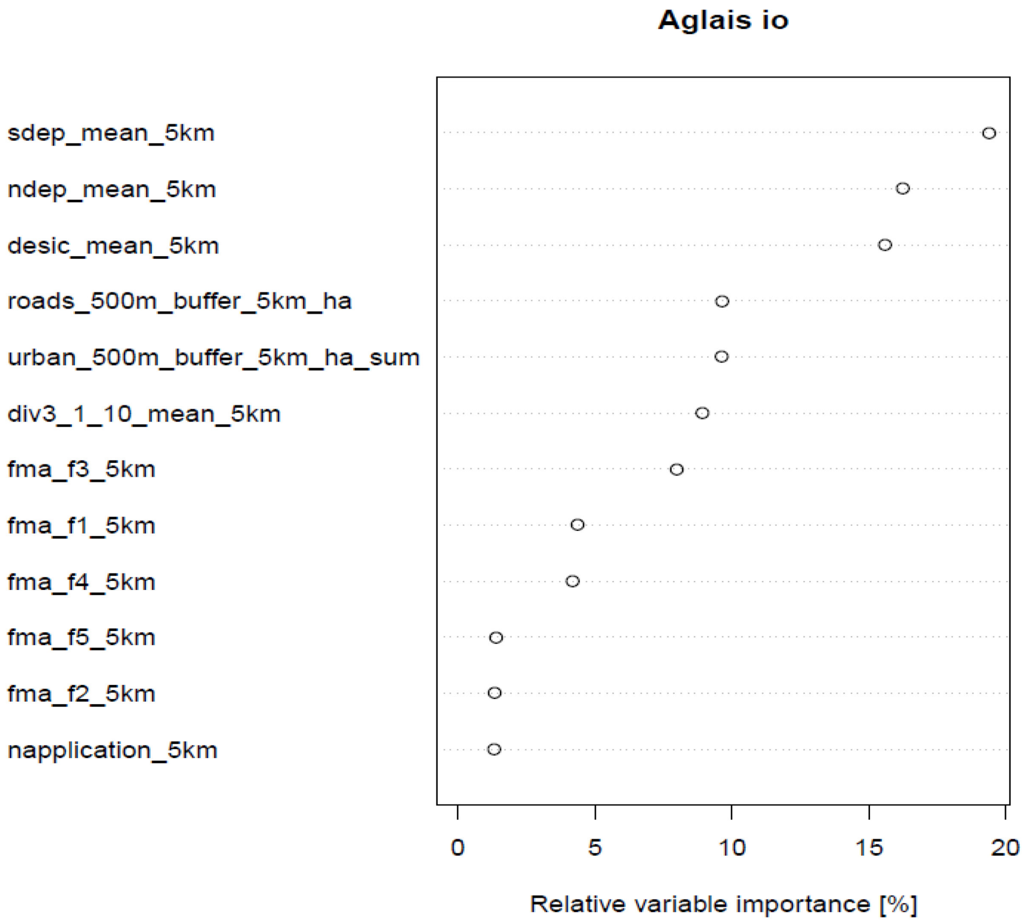

Figure 7: The relative importance of the pressure variables in the multivariable benchmark model for butterfly species Aglais io.

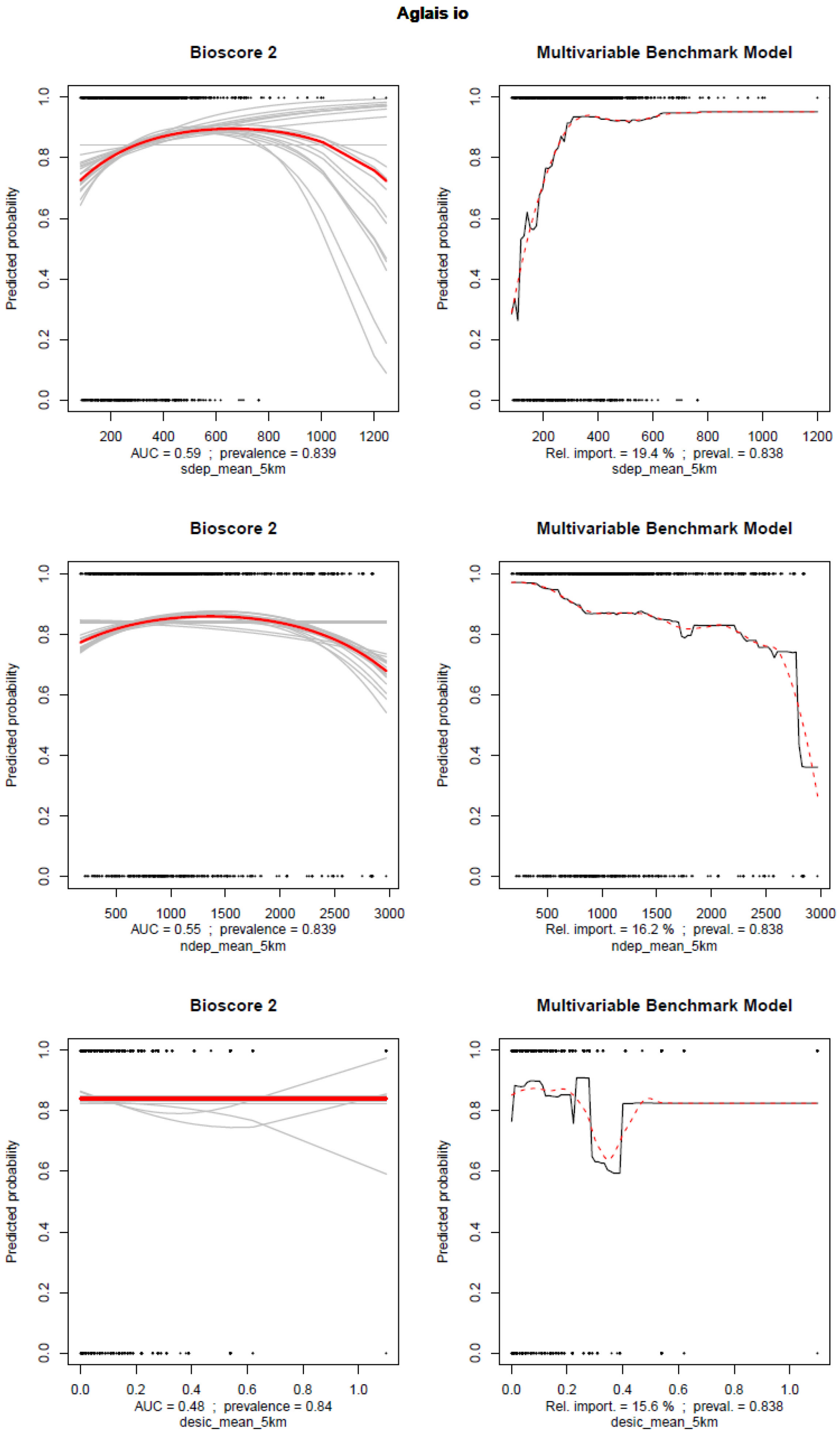

Figure 8: Comparison of single pressure-response curves of step 3 of BioScore with the partial dependence plots of the multivariable benchmark model, for butterfly species Aglais io.

Conclusion and consequence

The comparison of BioScore step 4 model with the multivariable benchmark model learns that substantial differences can occur between both approaches (see Figures 4–6), which in part can be attributed to violation of the conditions which underlie the applied odds approach in step 4.

This clearly indicates a weak point in the BioScore 2.0 model, which should be addressed in the development of BioScore 3.0. Meanwhile one should be careful with using the results of BioScore 2.0, especially concerning statements on the impact of environmental pressures on species occurrence. Thoughtful sensitivity analysis should be applied, to test whether the BioScore results are robust to other specifications of the modelling part, as illustrated e.g. in Appendix XI.

Appendix XI: On robustness analysis of BioScore 2.0

Figures 1 and 2 of this appendix illustrate the impact of climate change on species occurrence, under two different climate scenarios, as calculated by BioScore 2.0. As we indicated in the conclusions of Appendix IX one should be careful when using BioScore 2.0, especially regarding the effects that environmental pressures could have. We suggested – as a robustness analysis of the BioScore 2.0 results – to accompany its calculations with alternative calculations that use a different set-up of the environmental pressures model (in steps 3 and 4).

Since using an alternative set up, such as applying a multivariable benchmark model for the environmental pressures, as in Appendix IX, was not yet available for all species, we took a pragmatic approach for a robustness analysis, and decided to compare the BioScore results with alternative calculations where the ecological pressures impact modelling part in steps 3 and 4 was stripped, evaluating both climate scenarios, on the basis of the model of step 1 (accounting for soil/climate effects) and on the basis of the models of steps 1 and 2 (i.e. accounting for soil/climate and land-use effects).

The results of these alternative calculations are shown in Figures 1 and 2, and indicate that the general picture (on this aggregated scale level) of the full BioScore calculations as displayed in Figure 3.4 of this report, is also reflected by the alternative calculations, that don’t use the steps 3 and 4.
Needless to say, this robustness check is only partial, since it compares BioScore 2.0 with an approach where the ecological impact modelling is discarded, and not with an approach where this part of the model is improved. Whether such a comparison with an improved model still renders similar robustness results remains an interesting issue for the future development of BioScore.

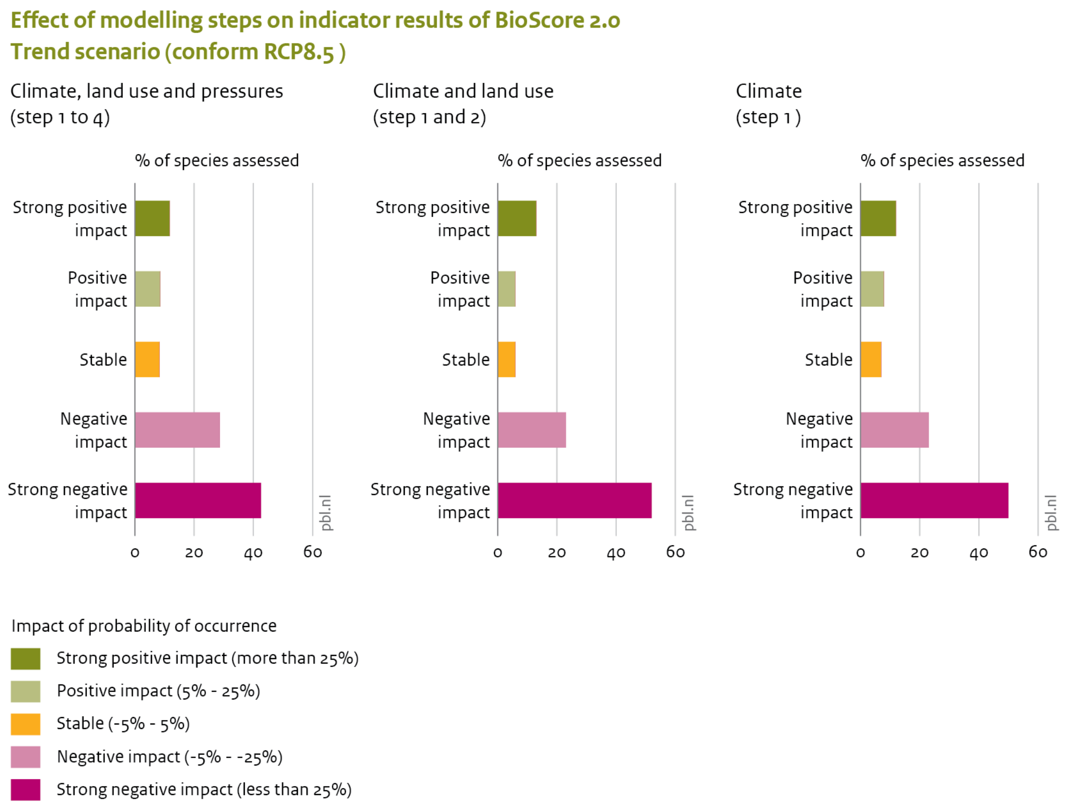

Figure 1: Results of alternative calculations of the impact of climate change on species for the Trend scenario

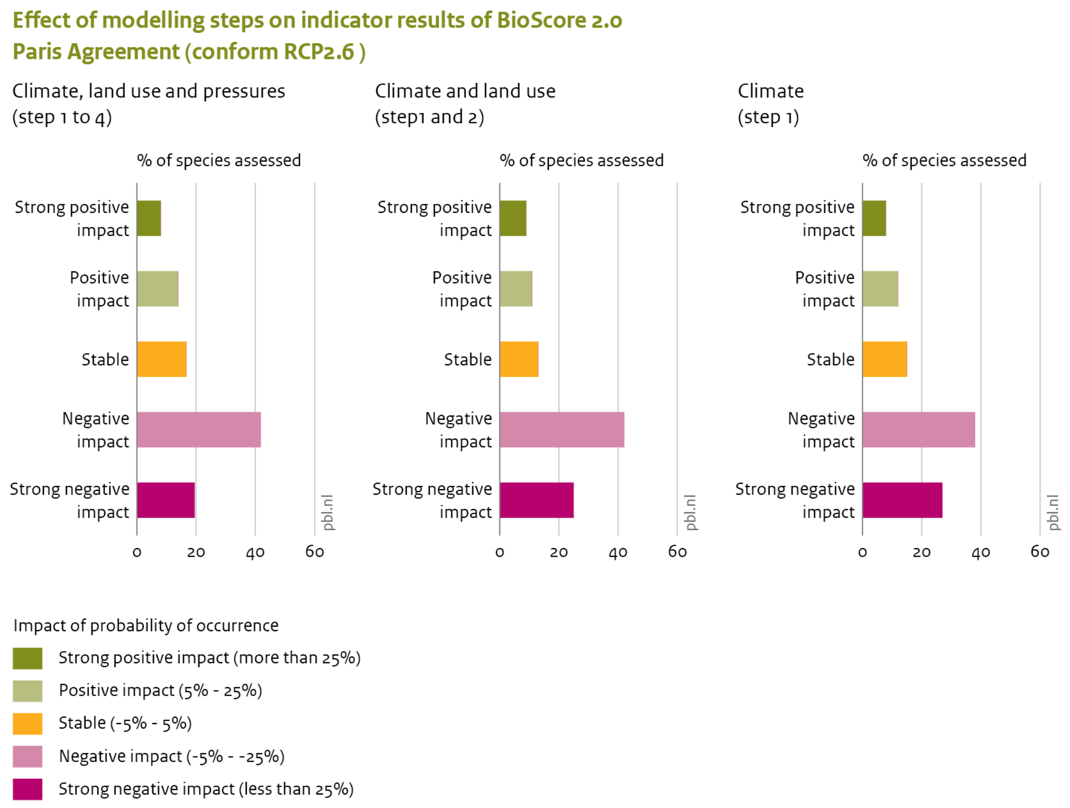

Figure 2: Results of alternative calculations of the impact of climate change on species for the Paris scenario