

Technical report breeding birds in BioScore 2.0

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Colophon

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1. Introduction

This technical report describes the data collection, data handling and modelling of the bird data used in the BioScore 2.0 tool. An elaborate description of BioScore 2.0 can be found in Hinsberg et al. (2014).

2. Bird data

2.1 Data collation

In order to calculate distribution ranges, habitat preferences and dose-response functions information was gathered from various sources. Occurrence data is available on different scales. From atlas data with a resolution of 50 km to transects, point counts and casual observations. Table 1 shows the various sources of the used data.

In the context of this report the EBCC-data are referred to as ‘atlas data’, while all other data sources are for simplicity referred to as ‘point data’.

Table 2.1. Species information used to derive distribution maps and dose-response functions in BioScore 2.0.

Species group	Database	Number of observations (between brackets: including zero-observations)
Birds	EBCC Breeding Bird Atlas 1980-1995 (www.ebcc.info)	357,000 (1,351,000)
	eBird (www.ebird.org)	1,145,000 (23,706,000)
	Global Biodiversity Information Facility (http://www.gbif.org)	28,020,000 (28,020,000)
	Observado e& waarneming.nl (www.observado.org)	1,173,000 (1,173,000)
	EU N2000 reporting distribution maps (www.eea.eu)	1,297,000 (7,848,000)
	Bulgarian bird counts (pc.trektellen.nl)	40,000 (202,000)

Description of data sources

EBCC Breeding Bird Atlas 1980-1995

Data for this atlas was gathered over a 15-year period in a 50x50km grid. For all grids presence and breeding certainty was gathered. In approx. 50% of the squares also the abundance in classes was estimated. For all squares the completeness of the survey was estimated. For all squares with good coverage (figure 2.1, ‘well surveyed’) zero-observations for non-observed species were added.

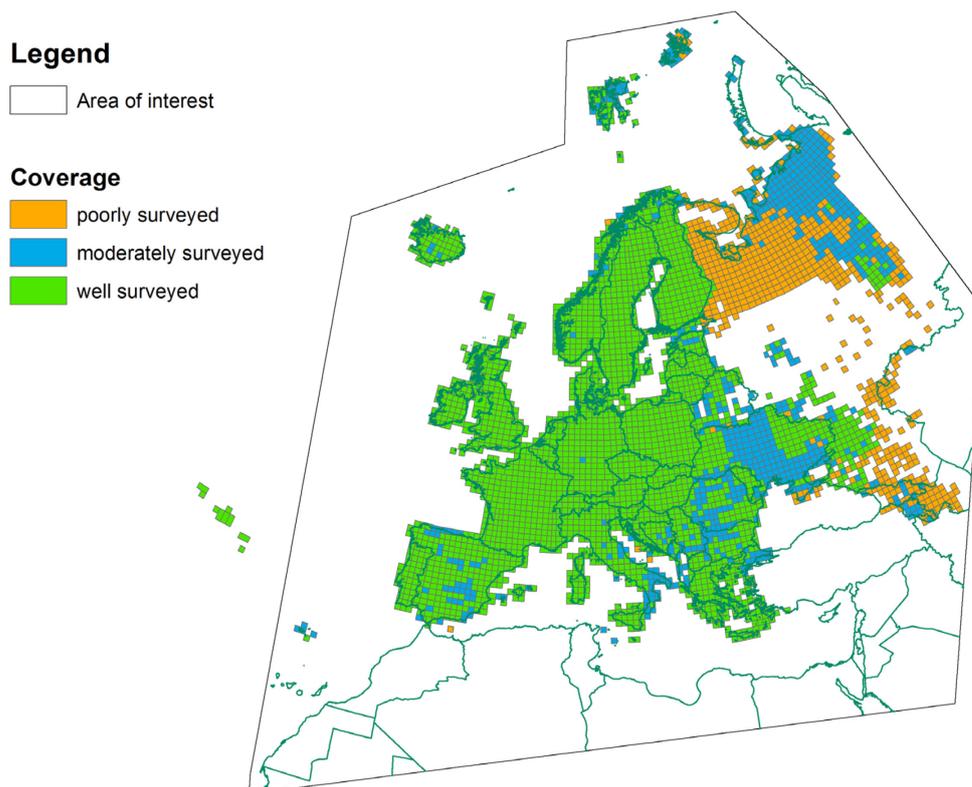


Figure 2.1. Coverage of the survey in the squares of the EBCC Breeding Bird Atlas. Only well surveyed squares were used to generate zero-observations

eBird

This datportal collects data of casual visits. The portal collects both individual observations and complete lists. The spatial detail of the information varies from exact locations to several kilometres. Nowadays more than 80 per cent of the observations stem from complete lists which make it possible to derive zero-observations.

GBIF

This datportal combines data from many other data sources. The majority of the data is stored with information on the location of the observation, but the spatial detail of the location information varies widely. All information is stored as individual casual observations. Therefore no zero-observations can be inferred from this data source.

Observado & waarneming.nl

These portals collect casual observations on a wide range of taxa. Almost information is stored as individual casual observations. Therefore no zero-observations can be inferred from this data source. All observations have detailed location information, but the spatial quality varies from meters to kilometres. From the portal waarneming.nl that collect data from the Netherlands, only observations from the last two year were used to prevent overrepresentation of The Netherlands.

EU N2000 reporting distribution maps

For the Article 12 reporting of the Birds Directive each EU-member has to provided gis-files with the distribution of all their breeding birds on a scale of 10x10 km. For the use within the BioScore2-project

these data sets were available from approx. 50 per cent of the member states. These data sets were not yet reviewed, so some additional processing was necessary. For example for some rare breeding birds in some countries only data on a 50x50m was provided or not provided at all. See appendix 1 for a complete overview of encountered issues in the data. From this data set also zero-observations could be inferred.

Bulgarian bird counts

From Bulgaria, a country with relatively low environmental pressures, additional data was available from a project of the Habitat foundation (www.thehabitatfoundation.org) that aims to collect standardized and casual counts of complete lists of breeding birds in the Balkan. The majority of the data set consists of points counts providing complete species lists. Therefore also zero-observations can be inferred.

All bird data from the geographical range depicted in figure 2 were extracted from the data portals. This is roughly the Western Palearctic.



Figure 2.2. Geographical range of the collected bird data.

2.2 Data processing

Species names

In order to combine the various data sources first all species names had to be synchronized. Although the majority of the species have the same scientific name in the data sources, several dozen species have widely varying scientific names. Therefore a table was set up with the species name used in the various data sets. Once this table was set, a combined data set could be made. The combined data set uses the species names used in the Observado-portal, which follows most of the recent

changes in species names published by the IOC (Gill, F & D Donsker (Eds). 2014. IOC World Bird List (v 4.2).

Species selection

For BioScore2 a wide range of bird species was selected. The species list contains all the species from:

1. All the species from BioScore1, with the exception of a few species that do not breed in the geographical range of interest (mainly species breeding in the Siberian arctic)
2. Breeding birds species for which Special Protection Areas (SPA's) are designated within the Birds Directive
3. Breeding birds species selected to designate High Nature Value Farmland areas
4. Breeding bird species associated with old growth forest
5. Breeding bird species that are expected to be impacted heavily by climate change. These are mainly boreal, arctic and alpine species

In appendix 2 an overview of all selected species is shown. For each species information is presented which of the afore mentioned criteria above apply to the species.

Next to the species that scored on of the criteria mentioned above, additional species of the same family or otherwise closely related species, like all *Sylvia*-species or tits, were added to the species selection. This certifies that a wide range of ecological niches is included in the final species selection.

The species selection resulted in a list of 299 species. Compared the species list of BioScore 1 108 species were added.

Observation filtering

Apart from the data from the EBCC atlas and the Article 12-reporting the breeding bird status of the observation cannot be inferred directly from the observation. Most observations are stored in the database without explicit information on territoriality or breeding certainty. Therefore two filters were set up to distinguish observations that are likely to refer to breeding birds and observations that probably refer to migrating or straggling birds.

The first filter that was applied to the data was the known breeding ranges provided by Birdlife International. Birdlife has digitized the known range of bird species of the world (<http://www.biodiversityinfo.org/spcdownload/t6f9b4/metadata/metadata2011.pdf>) and made them available for use within this project. For some species no range maps were available for the WP: for these species range maps were made based on other species with very similar ranges (see appendix 1). Since the ranges may have changed since their publication a buffer of 50km was added to the range maps provided by Bird Life. All observations outside the buffered ranges, with the exception of data from the EBCC atlas and the Article 12-reporting were not used in the analyses.

Next to the filtering by means of the known breeding range of the species a second filtering was used. For each species a date range was defined in which the species is expected to be sedentary or non-migratory, or in short 'breeding period'. In some species that are sedentary throughout the year all observations were used, while in others only data from a 1.5 month window was used.

The result of both filters is that data used in the analyses refers as best as possible to breeding birds. Figure 2.2 gives an example of the buffered range of a bird species (yellow) and time-period filtered observations that lie within the buffered range (in blue) and observations outside the buffered range.

Figure 2.3 shows an example a species where north of the buffered range observations are filtered out that probably refer to breeding birds: in this case the range probably has shifted more than 50 km.

Although in this case some valid breeding bird observations were left out, this ensures that the analyses indeed deal with breeding bird data.

Lanius collurio - Red-backed Shrike

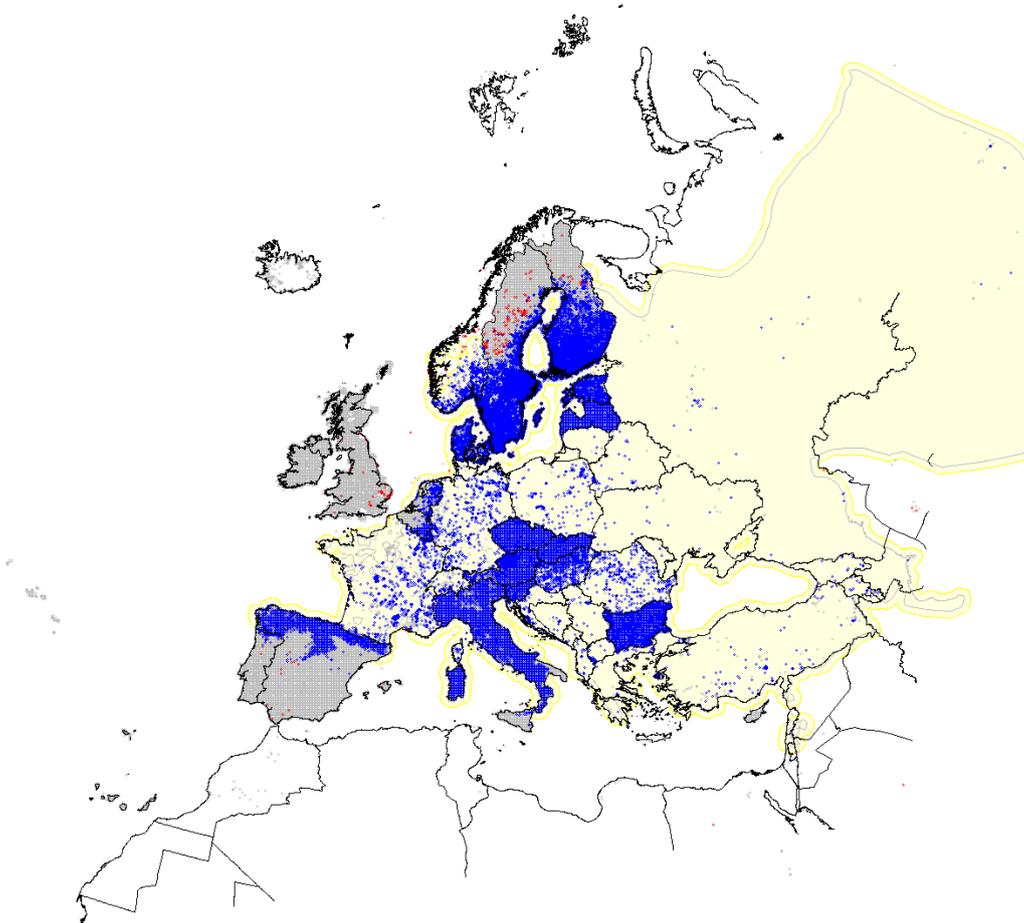


Figure 2.2. Observations used in the 'recent' model and univariate models (right) of *Lanius collurio*. The range is depicted in yellow, positive observations within the range in blue, positive observations outside the range in red and zero-observations in grey. Although all birds outside the range were seen in the breeding season, they were not used in the modelling as they are likely to be non-breeding stragglers. This may in some cases result in the discard of valid observations of breeding birds, but ensures that migrating birds and stragglers only have a minor influence on the models.

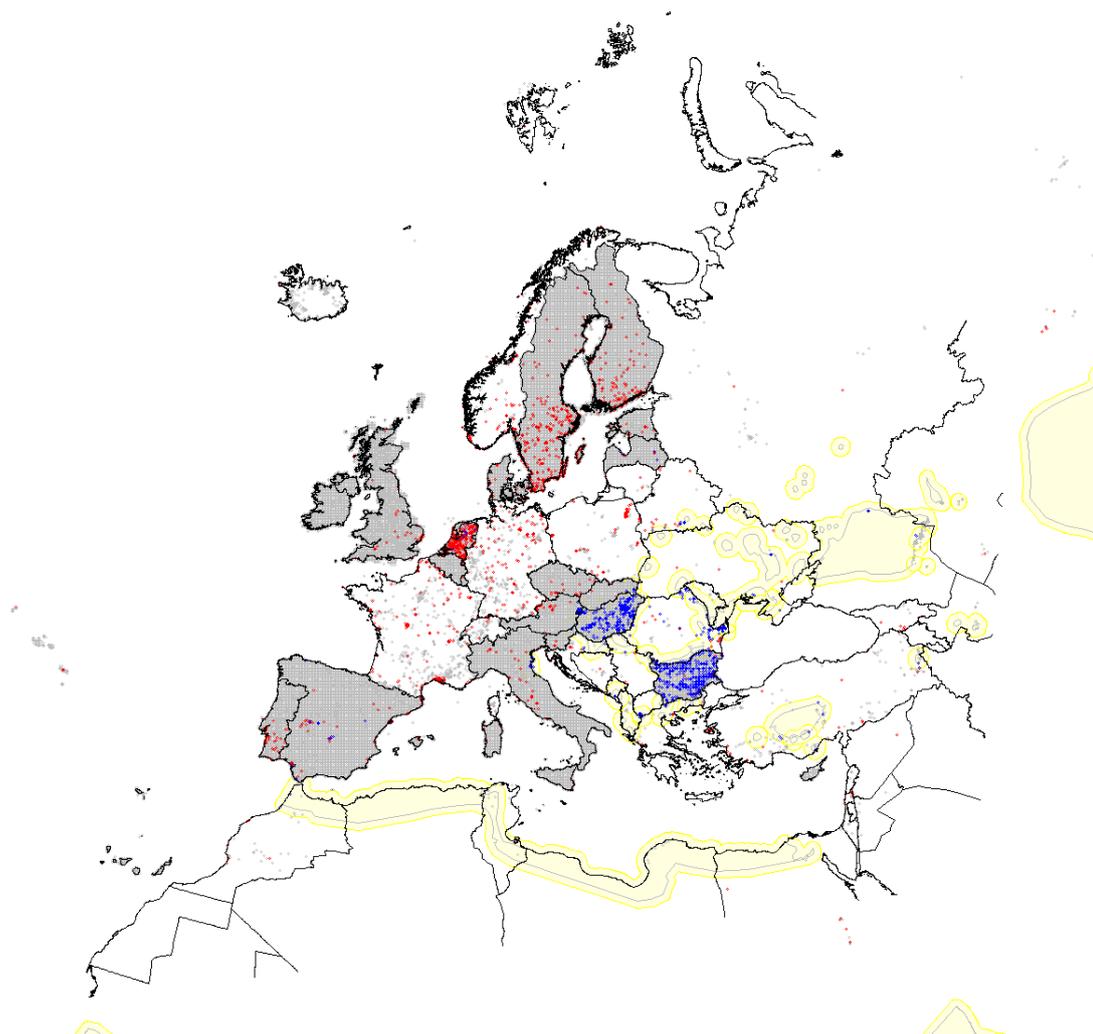
Ardea alba - Great Egret

Figure 2.3. Example of a species, *Ardea alba*, where the current breeding range probably extends beyond the buffered range maps made by Bird Life. Although observations in The Netherland and southern France refer to breeding birds, they were not used in the analysis.

Spatial overlay of observations and land cover classes

In order to determine the habitat preferences a spatial overlay was made between the filtered bird observations and the adjusted CLC-map of 2006, 100m-grid version. This CLC-map is the CLC-map 2006 combined with data from Norway and Switzerland and the 2000-data of Greece. For the spatial overlays all data sources except the EBCC Atlas data were used.

For each species the number of observations per CLC-class was calculated. Consequently all CLC-classes with more than three per cent of the observed of the observations were flagged as habitat. After this automated habitat-assignment an expert-check on the results was performed to exclude habitats that were flagged as such due to erroneous observation locations. Also CLC-classes were added as

habitat that had a small amount of observations but were considered to be suitable habitat for the species. This happened mainly with rare CLC-classes.

Spatial overlay of observations with pressures

For the modelling of the univariate models a spatial overlay was made with the observations and the 5km-grid versions of the pressure maps.

3. Spatial modelling

Two different spatial distribution models were made: one with the EBCC-atlas data and another with the other data sources.

3.1 Data preparation spatial models

EBCC Atlas data

For the spatial modelling of the EBCC-atlas data covariate values for all the spatial data sets were calculated per 50x50km atlas square. Since not all atlas-squares are squared due to corrections for the earth's sphere, covariate values were calculated based on spatial summaries for the grid polygons.

Although for the main interest of BioScore2 only are climate and soil variables are relevant, also for all the other spatial covariates summarized covariate values of the EBCC atlas squares were calculated. This allows the use all covariates in a full multivariate approach next to the three-step modelling approach in BioScore2.

The EBCC Atlas data set contains zero-observations for all the 50x50 km squares that were well surveyed (figure 2.1). Most of the squares in the EU-28 were surveyed well. Therefore the EBCC-data set provides a good quality data set for the climate-soil models within the EU-28. Outside the EU-28 data quality is much lower: therefore spatial predictions outside the EU-28 should be handled with caution.

Point Data

For simplicity all data sources except the EBCC-atlas are here referred to as point data. The data preparation for the point data was performed within the TRIMmaps spatial modelling package. Here all centroids of the observations were combined with the covariate data from a 5km-grid.

3.2 Statistical models

For the regression modelling we considered both Maxent and Boosted Regression Trees (BRT), a version of Generalized Boosting Models (GBMs). Both MaxEnt and BRT are machine-learning techniques, able to handle nonlinear relationships and to take into account synergistic effects between the different factors affecting a species' distribution (Couce et al. 2013). MaxEnt (Phillips et al. 2006) is widely used in ecological studies, including the prediction of climate change impacts on a species or ecosystem's potential distribution. To date, BRT is used less widely, despite having comparable predictive capabilities (Elith et al. 2006, Elith et al. 2008) (2008). Although Maxent has some possibilities to include absence data, BRTs are better equipped to deal with presence-absence data sets. We tested this also for the dataset of a plant species, where the predictions resulting from the BRT showed a wider range in predictions, and performed better in areas where the species was expected to be absent. Next to the better inclusion of known absences in the modelling, BRTs also have the advantage that the model description can be saved for later projections used in BioScore.

For the modelling we used a suite of R-scripts, called TRIMmaps. TRIMmaps is also available as R-package (Hallmann et al. 2014). TRIMmaps can be used for both the spatial modelling of both presence-only, presence-absence and count data and features a wide range of regression techniques amongst which GLM, GAM, MARS, BRT and Random Forest. Within TRIMmaps Maxent can be used to generate pseudo-absences on locations with a low habitat suitability.

In order to be used within BioScore the predicted probabilities of occurrence had to be transformed to predicted presences and absences. There is wide range of methods available to transform probabilities into presence-absence maps. See

http://www.cawcr.gov.au/projects/verification/#Methods_for_dichotomous_forecasts for an overview. Here we used Hanssen and Kuipers discriminant (true skill statistic, Peirce's skill score):

$$HK = \frac{\text{hits}}{\text{hits} + \text{misses}} - \frac{\text{false alarms}}{\text{false alarms} + \text{correct negatives}}$$

A cutoff was chosen, so that the proportion of correctly predicted occurrences (sensitivity) is comparable to the proportion of correctly predicted absences (specificity). We adapted the R-code that is used in BIOMOD (Thuiller et al. 2009) to calculate the cutoff-value.

The proportion of type 1-errors and type-2 errors governs the sensitivity and specificity of the predictions. A proportion higher than 1 focusses more on correctly predicted occurrences, while a proportion smaller than focusses more on correctly predicted absences.

4. Habitat masks

In order to determine the suitable land cover classes (CLC) in de Corine Land Cover map (2006), for each species an overlay was made with the observations and CLC map. From these the proportion of observations in each CLC-class was determined. CLC-classes with more than three per cent of the observations were considered to be (major) habitats for the species. This automated habitat-classification was then edited by a species-expert to include known habitats, but with few observations.

5. Univariate models

5.1 Data preparation

For the univariate models only observed zeroes were used, so no additional zeroes were generated with TRIMmaps. Zero-observations were available from the following data-sources: eBird, EU N2000-reporting and Bulgarian bird counts (table 2.1).

In order to combine the observations with the variables of interest a spatial overlay was made with the 5km-grid maps of the pressure variables.

5.2 Dose response functions

The dose response functions are derived with univariate regression within the distribution range (step 1). Since the breeding bird range maps based on the EBCC-atlas data describe the range in de eighties, a different approach was used in birds to select the observations for the univariate models. Here we used for the determination of the recent range of the breeding birds, range maps composed by Birdlife International (<http://www.biodiversityinfo.org/spcdownload/t6f9b4/metadata/metadata2011.pdf>) . To the range maps an additional buffer of 50 km was added to the ranges to account for recent range changes.

All modelling was performed with R (R Core Team, 2014). Stepwise model selection was used to select significant variables. This model selection uses the Akaike information Criterion (AIC), where the best models have the lowest AIC-values.

In order to assess model performance the AUC-values for ten cross-validations, with 10 per cent independent observations, were calculated.

Although AUC-values provide information in the global performance of the regression model, they do not give insight in the local model performance. Especially in ranges of the x-variable with low numbers of observations, the apparent relationship may be biased due to a low number of observations. In order to test local model quality or robustness, a bootstrap-procedure was developed. In this procedure a random subset of 50% of the percent of the observations is selected and a model is made with this subset. This is done 20 times, resulting in 20 different relationship between de observations and the covariate. Figure 8 shows these 20 relationships for the occurrences of two bird species, Red-backed Shrike and Roller, and nitrogen-deposition. This shows that the relationship of the occurrence of Red-backed Shrikes and nitrogen-deposition is robust throughout the range of the covariate, but that shape of the relationship largely fluctuates in Rollers above the value of 1000 and is therefore considered to be unreliable at large levels of deposition.

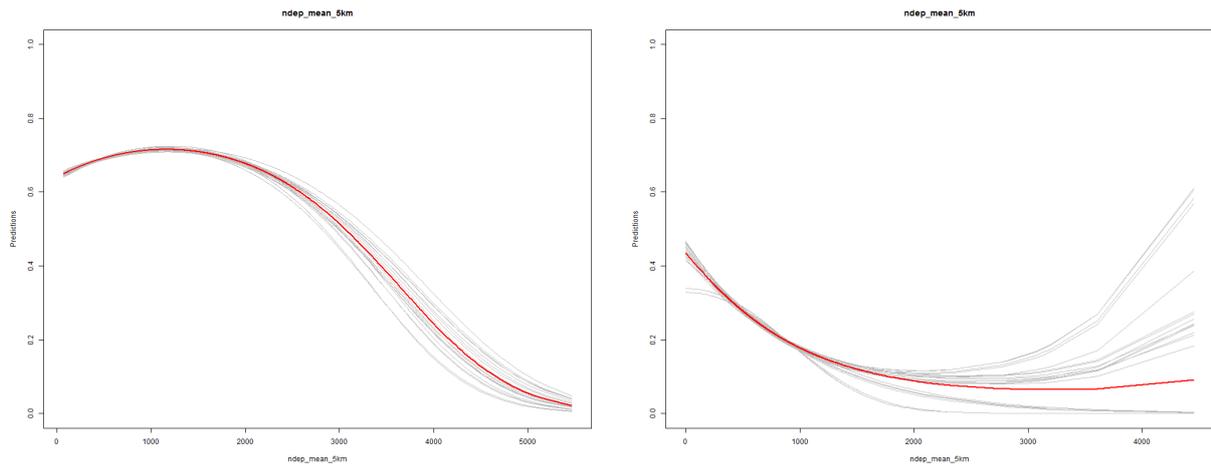


Figure 3.1. Results of 20 bootstraps on 50% of the data (grey lines) for Red-backed Shrike (left) and Roller (right) and nitrogen-deposition. The red lines shows the full model.

6. Results

6.1. Climate-soil maps

EBCC data

For 283 species climate-soil models and predicted distribution maps were made with the EBCC-atlas data.

Point data

For 282 species climate-soil models and predicted distribution maps were made with the point data.

The list of species with EBCC-maps differs slightly from the list of species of the point data maps. This is due differences in species names and data availability. Some EBCC-species were split in one or more new species, while on the other hand for some EBCC-species there was not enough data to construct a model.

6.2. Habitat masks

Appendix 3 shows the result of the overlay of the observations and the CLC-land cover classes. For each land cover class the number of observations ('Freq') and its percentage ('Prec') is shown for each species. The column 'Habitat' shows the automated habitat classification. The column 'Habitat-edt' shows the edited version of the habitat classification for each species; this column will be used to make the habitat masks.

6.3. Univariate models

For all selected 299 species univariate models were made.

6.4. Example on *Lanius Collurio*

Here an example of the output for one species, *Lanius collurio*, is shown.

Background information



The red-backed shrike (*Lanius collurio*) is a carnivorous passerine bird and member of the shrike family Laniidae. This 16–18 cm (approx. 6.3–7.1 inches) long migratory bird eats large insects, small birds, frogs, rodents and lizards. Like other shrikes it hunts from prominent perches, and impales corpses on thorns or barbed wire as a "larder." This practice has earned it the nickname of "butcher bird." The bird is listed as a "least concern" (LC) species on a global scale, but some parts of its range have seen a steep decline in numbers, so locally its status can be less secure. In Europe, trends since 1980 show that populations have undergone a moderate increase ($p < 0.05$), based on provisional data for 21 countries from the Pan-European Common Bird Monitoring Scheme (EBCC/RSPB/BirdLife/Statistics Netherlands; P. Vorisek in litt. 2008). In Europe the bird is widely distributed. In central Europe it is still a characteristic bird of farmlands, while in

north-western Europe the species is more confined to heathlands (Tryjanowski, et al., 2006).

Calculated distributions

Current' distributions of Red-backed Shrikes were calculated with three different models: a climate-soil model based on the EBCC-atlas data (50x50km grid) from the eighties ('EBCC'), a climate-soil model based on recent observations ('recent') and a full model based on recent observations ('recent full'). The predictions of 'recent-full' model are limited to those countries/region for which data are available for all variables, the other two models cover the entire range of the species. The cross-validated AUC values for the 'EBCC' model and the 'recent' model were comparable: 0.968 and 0.9555. The EBCC-model shows little variation in the core of the range since all 50x50 squares are all occupied in this region. The 'recent' models show more variation within the core of the species range. Both 'recent' models however, may suffer from the bias in the data set towards the northern countries. The EBCC-model was used to predict the range of the species. A cutoff of 0.82 was chosen to transform the maps with occurrence probabilities into a presence-absence map.

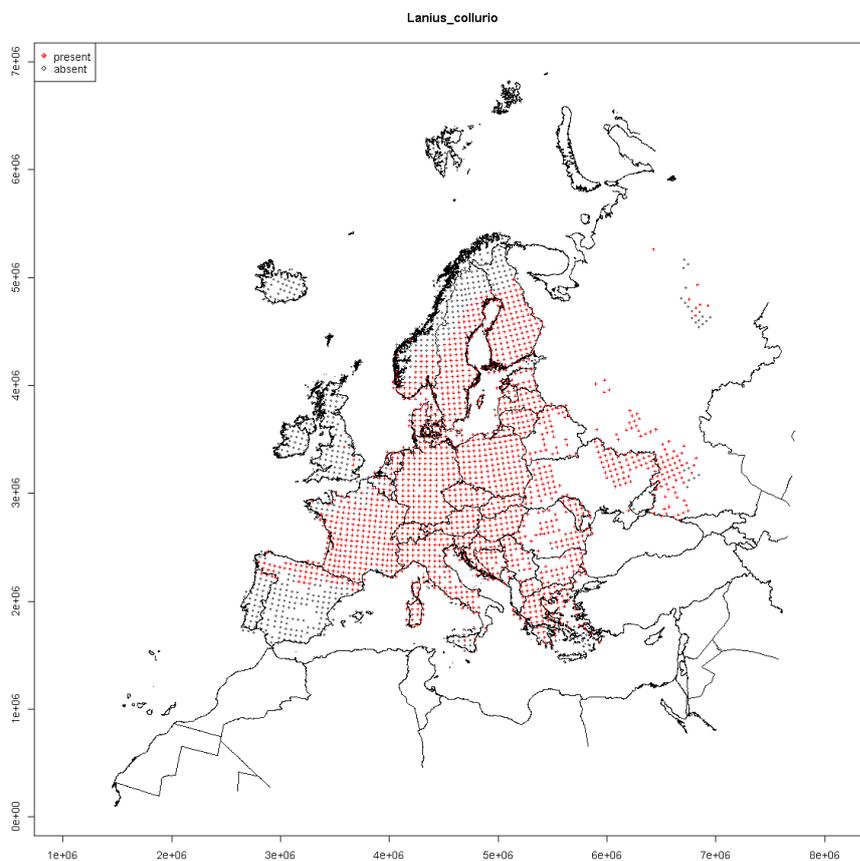


Figure 6.1 Observations used in the EBCC climate-soil model for *Lanius collurio*. Positive observations are red, while zero-observations are grey.

Lanius collurio - Red-backed Shrike

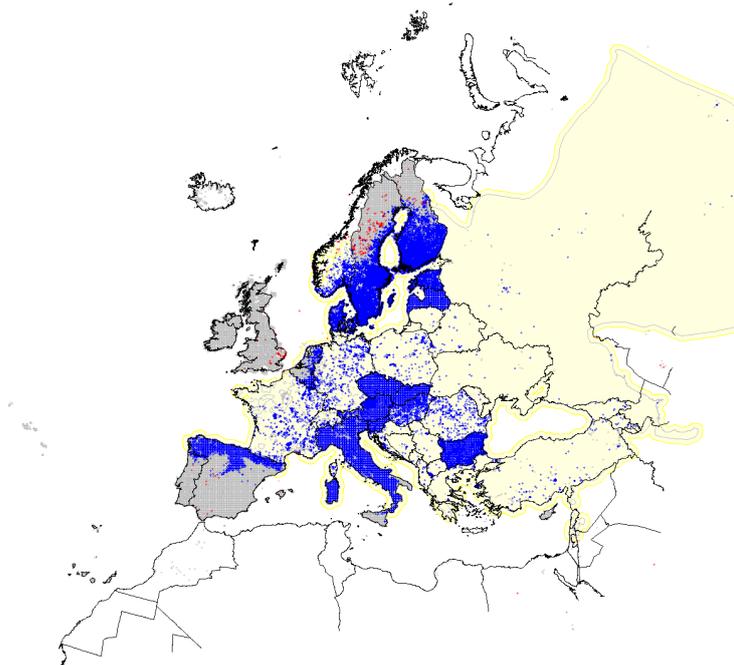


Figure 6.2 Observations used in the ‘recent’ model and univariate models (right) of *Lanius collurio*. The range is depicted in yellow, positive observations within the range in blue, positive observations outside the range in red and zero-observations in grey. Although all birds outside the range were seen in the breeding season, they were not used in the modelling as they are likely to be non-breeding stragglers. This may in some cases result in the discard of valid observations of breeding birds, but ensures that migrating birds and stragglers only have a minor influence on the models.

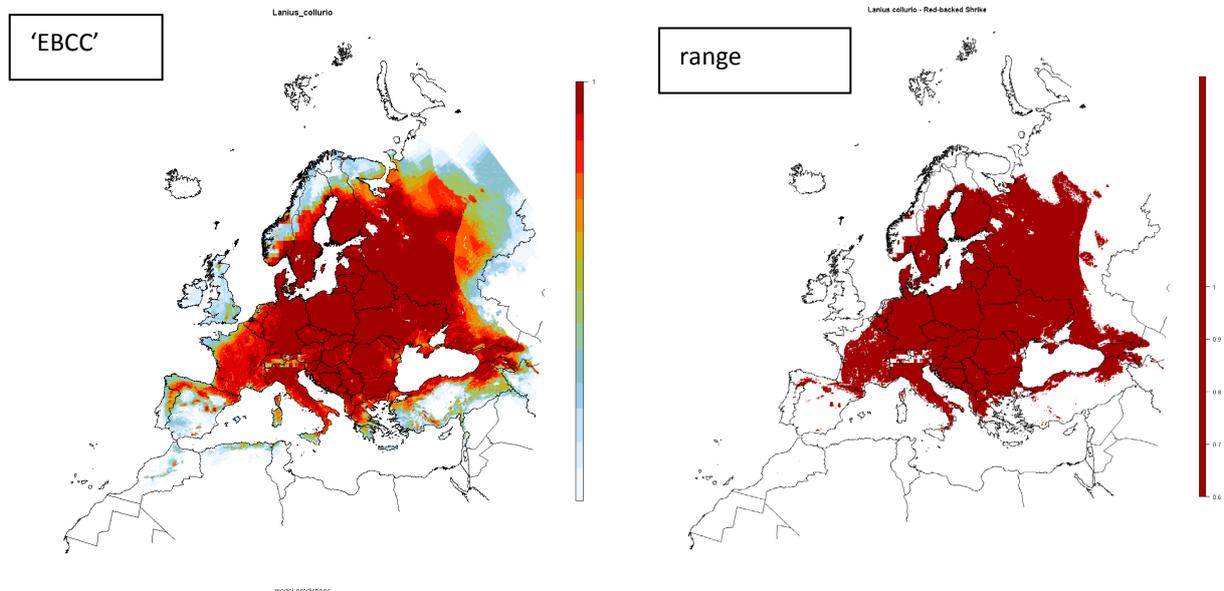


Figure 6.3 Modelled distribution of *Lanius collurio* based on data of the EBCC-breeding atlas (50x50m grid data) and corresponding range based on a cutoff-value of 0.82. Predictions in Russia are unreliable due to a lack of bird data and poor data quality in some of the covariables.

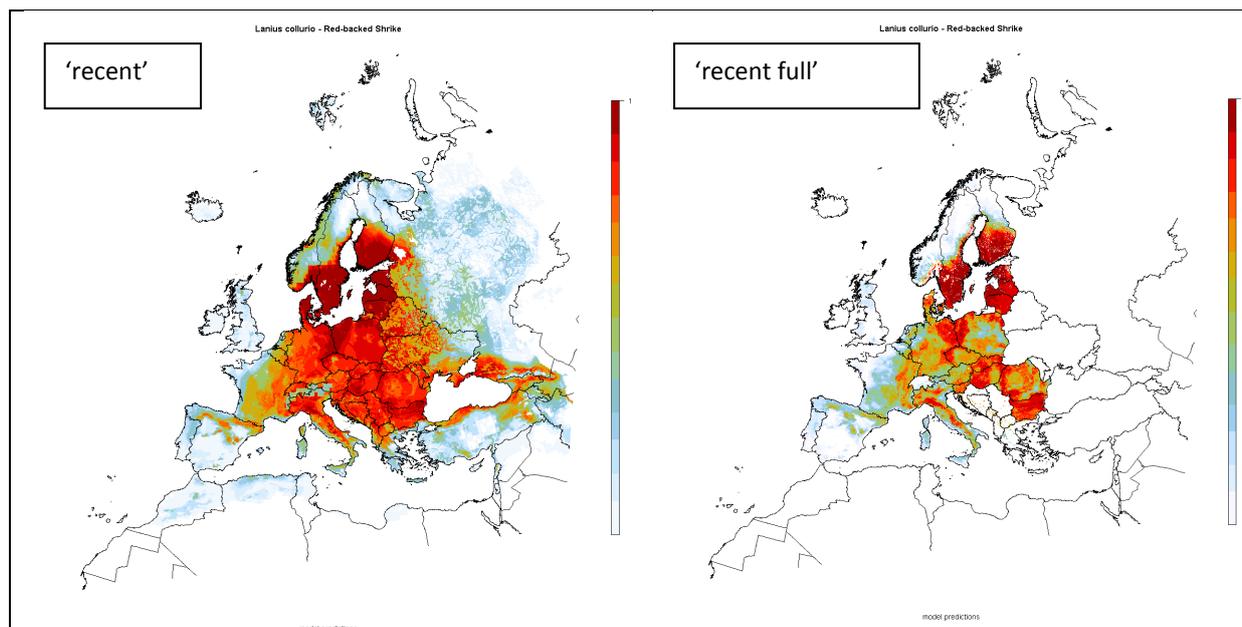


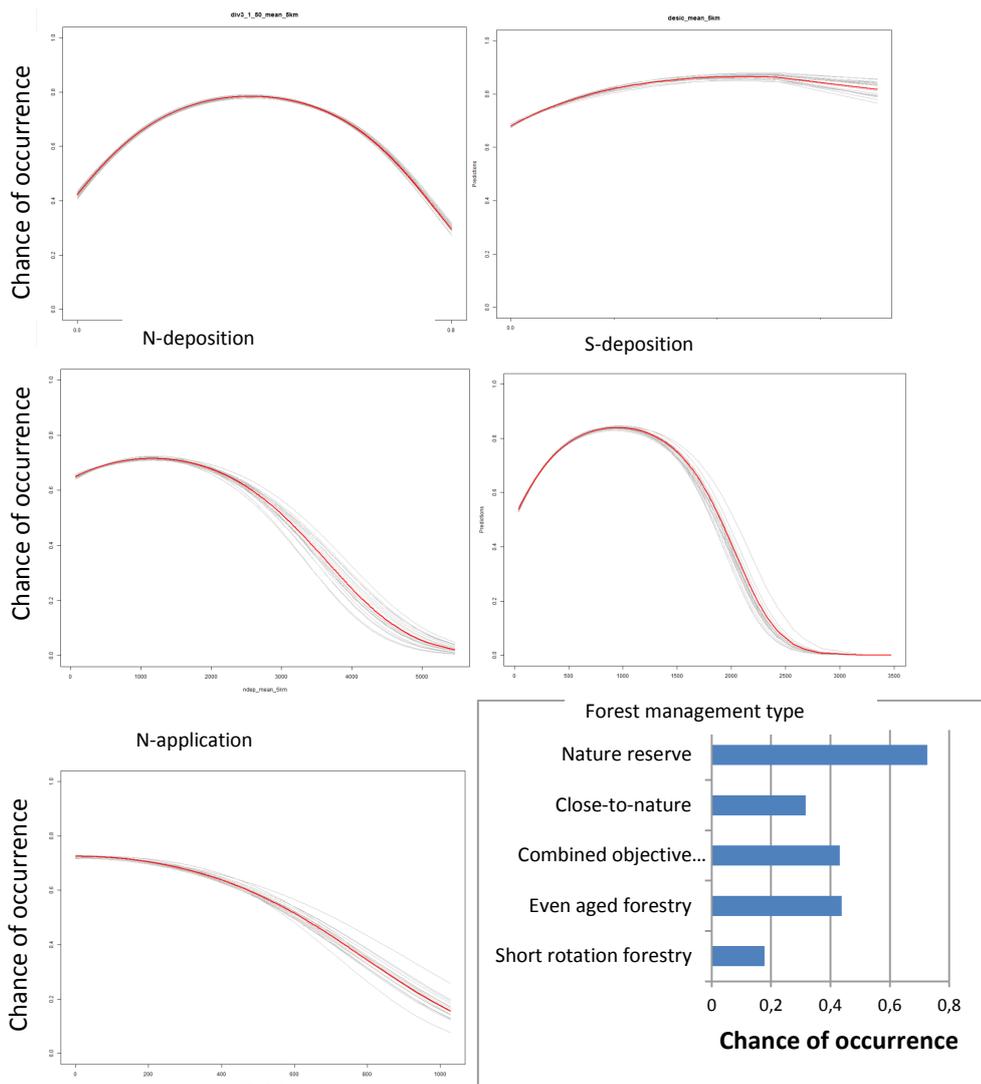
Figure 6.4 Modelled distribution of *Lanius collurio* based on a variety of recent data sets (all data sets except EBCC atlas) and two different models: (left) only climate and soil variables and (right) climate, soil, lands use and pressure variables. Predictions in Russia are unreliable due to a lack of bird data and poor data quality in some of the covariables.

Derived dose-response functions

Factor	Dose-response function	Interpretation
Fragmentation of forests	Significant optimum curve	Sensitive for severe fragmentation. But variable landscape is important.
Nitrogen deposition	Significant optimum curve	Sensitive for high deposition levels
Sulfur deposition	Significant optimum curve	Sensitive for high deposition levels
Desiccation	Significant optimum curve	Moderate sensitive
Nitrogen application	Significant negative sigmoid	Sensitive for severe agricultural intensification
Forest management	Variation among forest types	Optimal with non-used forests

Fragmentation of forests

Desiccation



7. Discussion

Which climate-model should be used in BioScore?

Two sources of data were available to construct the climate-soil models: the EBCC atlas data and the data from all the other data sources ('point data'). With both types of data sources climate-soil distribution maps were made. The models based on the point data did not perform better than the models based on the EBCC-atlas data.

For use within BioScore 2.0 the EBCC-models are probably most suited. The bird data stem from the same period as the climate data from BIOCLIM, resulting in close concurrence between the data sets.

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Appendix 1. Review and processing distribution maps

Review and processing of EU distribution maps

No distinction between species (in bold name used in EU-dataset):

Lanius excubitor and Lanius meridionalis

Sylvia hortensis and Sylvia crassirostris

Loxia curvirostra and Loxia scotica

Oenanthe hispanica and Oenanthe melanoleuca

Saxicola rubicola only in Italy

Loxia scotica?

Distribution data incomplete:

Not all squares included where species is expected to be present:

Sweden (reasonably complete for most Annex I species)

Hungary (Red-backed Shrike)

Romania (most species)

Denmark (reasonably complete for most Annex I species)

Only data on limited of species:

Latvia (selection criteria unclear)

Czech Republic (only Annex I species)

Romania

Bulgaria: no data provided on the following (vulnerable) species

Aquila chrysaetos

Aquila fasciata

Aquila heliaca

Falco cherrug

Falco peregrinus

Gyps fulvus

Haliaeetus albicilla

Hieraaetus pennatus

Neophron percnopterus

Finland: no data provided on the following (vulnerable) species

Aquila chrysaetos

Falco peregrinus

Pandion haliaetus

Distribution data only at course scale (50x50 km):

SE Anser erythropus

SE Aquila chrysaetos

SE Bubo bubo

SE Dendrocopos leucotos

SE Falco peregrinus

SE Falco rusticolus

SE Haliaeetus albicilla

SE Strix nebulosa

SE Tringa glareola

UK Aquila chrysaetos

UK Calidris maritima

UK Charadrius morinellus

UK Circus pygargus

UK Grus grus
UK Lanius collurio
UK Pernis apivorus
UK Phalaropus lobatus
UK Podiceps auritus
UK Tringa glareola

Distribution errors in data

CZ: Grus grus is probably other species

Problems Birdlife Range maps

Anas strepera: extended range in Finland

Ardea alba: expansion to NW is missing

Botaurus stellaris: range expansion in Finland

Buteo lagopus: range expands further south in Finland

Corvus corax: expansion in Germany and England

Coturnix coturnix: occurs now all over south-Finland and Sweden

Cursorius cursor: also in SW Marocco

Emberiza calandra (Miliaria calandra): range is completely wrong, is probably different species. Used Carduelis carduelis

Locustella fluviatilis: breeds now over most of southern Sweden, also expanded in Finland

Motacilla cinerea: expansion in Sweden

Picus canus: range extends further north in Sweden

Phylloscopus collybita is now breeding bird in southern Sweden

Appendix 2. BioScore 2.0 Bird Species list

Description of contents:

OBSERVADO_NAME: Scientific name used in Observado and in the BioScore 2.0 point data set

EBIRD_NAME: Scientific name used in eBird

GBIF_NAME; Scientific name used in GBIF

ENGLISH_NAME: English name

BIOSCORE1: Species included in BioScore 1

BIOSCORE2: Species selected for BioScore 2.0

N2000: Species for which SPA's are designated

HNV: High Nature Value Farmland species

CLIMATE: Species is (very) sensitive to climate change

OLDFOREST: Species of old growth forest

MIGRATORY: Migratory species

MONTH_MIN: Start month of the non-migratory period

DAY_MIN: Start day of the non-migratory period

MONTH_MAX: End month of the non-migratory period

DAY_MAX: End day of the non-migratory period

Appendix 3. Habitat preferences