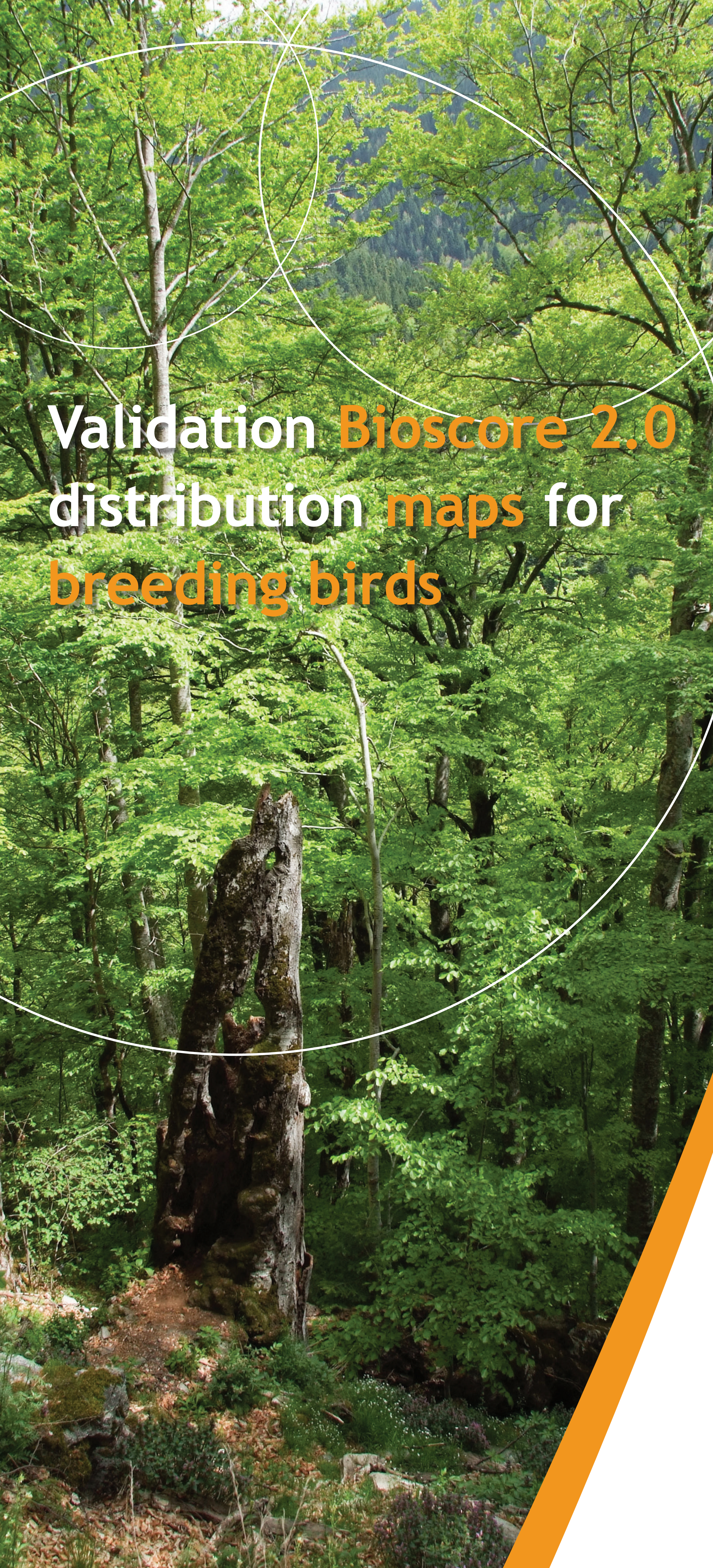


Validation Bioscore 2.0 distribution maps for breeding birds

Christian Kampichler
& Henk Sierdsema

Sovon-rapport 2016/06

Validation Bioscore 2.0 distribution maps for breeding birds

Christian Kampichler & Henk Sierdsema

This report was commisioned by
Planbureau voor de Leefomgeving

Colophon

This report was commisioned by Planbureau voor de Leefomgeving

Recommended citation: Kampichler C & Sierdsema H. 2016. Validation Bioscore 2.0 distribution maps for breeding birds. Sovon-report 2016/06. Sovon Vogelonderzoek Nederland/Sovon Dutch Centre for Field Ornithology, Nijmegen.

Illustratie omslag: Henk Sierdsema (Rila National Park, Bulgaria), Martin Mollet - Saxifraga (Nuthatch)

Opmaak: John van Betteray

ISSN-nummer: 2212 5027

Sovon Vogelonderzoek Nederland/Sovon Dutch Centre for Field Ornithology
Toernooiveld 1
6525 ED Nijmegen
e-mail: info@sovon.nl
website: www.sovon.nl

Inhoud

1. Introduction

The aim of the Bioscore 2.0 project is to design a tool for assessing the impacts of European Community policies on biodiversity in Europe (van Hinsberg *et al.* 2014).

In the course of developing BioScore 2.0 the Planbureau voor de Leefomgeving (PBL) asked for a response to the following tasks and topics:

1. Determine a full multivariate model (FMM) version for all BioScore 2.0 species, that is, with all pressure factors in one single multivariate analysis. Make a validation of the FMM's, preferably on independent data if available or by a cross-validation. Provide a possibility to examine the model for non-linearities and interactions in the relationship between predictors and predictions.
2. Describe provenance and quality of the distribution data that are used for model calibration and validation.
3. Compare the results of BioScore 2.0 of the current situation with the FMM of the current situation.
4. Compare the univariate dose-response relations that were used for BioScore 2.0 with the respective partial dependence plots of the FMM for ten sample species.
5. For each of the four ecosystem types (urban, forest, other natural and agrarian), specify which of the BioScore 2.0 species are typical and characteristic for them (may be more than one type).
6. Complement the earlier delivered univariate dose-response relationships for BioScore 2.0 for ten sample species. Display the quadratic as well as the linear relationshipes, analyse and describe the differences.
7. Determine the effect of cut-off value choice for ten sample species. Describe the effects of the different choices.

In this report we pursue these questions and present the results of the analyses.

2. Methods

2.1. Full multivariate models for all BioScore 2.0 species

2.1.1. Modelling

For 299 species (for an overview of all selected species see appendix 2 in Sierdsema 2014) a full multivariate model (FFM) was generated. The bird data are the same that were used for the BioScore 2.0 models (van Hinsberg *et al.* 2014) and were collated from eBird, Observado, waarneming.nl, the European commission and Bulgarian bird counts. The characteristics of these data sources as well as the processing of the data were described in the technical report on breeding birds in BioScore 2.0 (Sierdsema 2014). Sierdsema (2015) showed that including GBIF data to the FMMs can lead to a considerable overestimation of the the presence of species in certain parts of Europe. This is due to a heavy geographical bias in this data set. We thus omitted GBIF data from the analysis (as was done for the BioScore 2.0 models). No zeroes were generated additionally to the observed absences in the data.

The explanatory variables used in the FMMs were the same as described in the additional questions technical report (Sierdsema 2015).

The models were using a boosted regression tree approach (Friedman 2001) implemented in the custom-tailed R package TRIMmaps (Kampichler *et al.* 2015). This methodological approach was described in detail in the technical report on breeding birds in BioScore 2.0 (Sierdsema 2014). Modelling with boosted regression trees requires specification of a series of parameters. Species-specific optimisation of these parameters in order to get the optimal model for each single species was not feasible given the large amount of species that had to be modelled and the number of parameters that can be tuned. We thus ran all models with a uniform set of parameter choices, namely learning.rate = 0.01, step. size = 2 and tree.complexity = 2). This combination of parameters has proven to be robust in the case of automatized analysis of large numbers of species. Other parameter specifications might result in more accurate models but need higher computation times and are prone to failure of the modelling algorithm[1]. Even though the parameters were chosen to ease the automatized modelling process, for some species no full multivariate models could be produced, not even when the parameters were modified. Although the full multivariate models do not produce the best possible predictions for each species, we regard them to deliver reasonable benchmarks for the evaluation of the BioScore 2.0 maps.

2.1.2. Validation

The specific algorithm by Elith *et al.* (2008) that was used allows for a crossvalidation during the modelling process. This is particularly useful when a large number of species has to be modelled and saves a considerable amount of time compared to a post-hoc model evaluation. We applied a ten-fold crossvalidation and calculated the area under the receiver-operator curve (AUC) for the respective ten set-aside datasets that were not used for model training in the crossvalidation iterations. The mean of the ten AUC values and the deviance explained by the full model were used to evaluate the quality of each FMM.

2.1.3. Provenance and quality of the distribution data

An extended description of the bird data sources can be found in Sierdsema 2014 and Sierdsema 2015. The most important data sources used for the spatial modelling of the FMM's were eBird checklists, 10x10 km N2000 Article 12-reporting data sets for a number of countries and observado.org (currently called observation.org). The GBIF-dataset is heavily biased towards the Fennoscandinavian countries and had a profound influence on the distribution maps of European species that are also common in the north of Europe. The comparison of models with and without GBIF-data showed that the GBIF-data had limited influence on the distribution outside Fennoscandinavia and were therefore omitted from the dataset used to create the FMM-models. The general experience was that it is better to use a limited dataset with zero-observations than a large dataset with few zero-observations.

2.2. Comparison between BioScore 2.0 and full multivariate models

The predictions of BioScore 2.0 models and FMMs cannot be compared directly due to the fact that they are generated in completely different ways:

- The output of a BioScore 2.0 model is the combined result of a distribution map based on a soil-climate model, an overlay with suitable land cover

---

[1] A typical error message is “Error in .gbm.step : restart model with a smaller learning rate or smaller step size”.

classes in the Corine Land Cover map and the stacked predictions of presence probability based on a number of univariate logistic models, each one for a determined environmental pressure variable (Sierdsema 2014). The combined score of a BioScore 2.0 is scaled between 0 and 10,000.
- An FMM processes all explanatory variables (soil, climate, land use, pressure factors) simultaneously and predicts the probability of presence in the range of (0, 1).

To tackle this problem we binarised both FMM probabilities and BioScore 2.0 score, that is, we transformed them to predictions of presence and absence.

2.2.1 Production and evaluation of binary maps

Probability maps—that is, each cell in the grid contains a value in the interval (0, 1)—can easily made binary (only absences and presences shown instead of probabilities of presences) by applying a cut-off and setting all values below the cutoff to zero (absence) and all values larger than the cut-off to one (presence). Among all approaches to find an optimal cut-off, the true skill statistic (TSS) has been shown to be one of the best for ecological data (Allouche *et al.* 2006). It is frequently used in ecological studies (e.g. Zimmermann *et al.* 2009, Barbet-Massin *et al.* 2012) and implemented in ecological distribution modelling software, for example BIOMOD (Thuiller *et al.* 2009). The TSS compares the number of correct predictions minus those attributable to random guessing to that of a hypothetical set of perfect forecasts. It is defined as

$(ad - bc)/(a + c)(b + d) = \text{sensitivity} + \text{specificity} - 1$

where

a = correctly predicted presences,
b = incorrectly predicted presences,
c = incorrectly predicted absences,
d = correctly predicted absences,
sensitivity = proportion of correctly predicted presences a / (a + c), and
specificity = proportion of correctly predicted absences d / (b + d) (Table 2.1).

Table 2.1. Matrix of observed and predicted values for calculating the true skill statistic.

		Observed	
		Presence	Absence
Predicted	Presence	a	b
	Absence	c	d

For finding the optimal cut-off value, the TSS must be maximised. This method was already applied earlier to regression models within the BioScore 2.0 project (Sierdsema 2014). At the same time, the maximised TSS serves a statistic for the quality of the binary maps. It ranges from −1 to +1, where +1 indicates perfect agreement between observation and prediction and 0 indicates random model performance. Values close to −1 indicate “perverse” modelling performance; by exchanging presences and absences the maps can be converted into maps of high quality.

For both the FMM and the BioScore 2.0 predictions the observations used for the FMMs were used for maximising the TSS. We thus a priori expect the TSS of FMM maps to be higher than that of the BioScore 2.0 maps. This is justified since the FMM predictions serve as benchmark for the BioScore 2.0 models and we evaluate the BioScore 2.0 binary maps by observing how close their TSS comes to the TSS of the FMM maps.

2.2.2. Estimation of correspondence between binary maps

The difference between binary maps based on FMMs and BioScore 2.0 models is visualised as a difference map. For each 5x5 km cell we subtract the presence value (0 for absence, 1 for presence) of the FMM map from the the presence value of the BioScore 2.0 map. Cells in the difference map with value 1 thus indicate that the BioScore 2.0 model predicted presence, whereas the FMM predicted absence; cells with value -1 indicte the BioScore 2.0 predicted absence, whereas the FMM predicted presence.

The correspondence between two binary predictions can be done by analysing their confusion matrix (Table 2.2) where the predictions of one map are in the columns, those of the other in the rows (Table 2.2). The positions in the matrix count the cells where the models agree and disagree, respectively:

a = both models predict presence
b = BioScore 2.0 predicts presence, FMM predicts absence
c = BioScore 2.0 predicts absence, FMM predicts presence
d = both models predict absence

Table 2.2. Sample confusion matrix for analysing the predictions of FMM and BioScore 2.0 models.

		FMM	
		Presence	Absence
BioScore 2.0	Presence	a	b
	Absence	c	d

A simple measure of correspondence is the proportion of cells where both models agree. It is called overall accuracy and is calculated as (a + d) / (a + b + c + d). It must taken into account, however, that overall accuracy is dependent on prevalence. High accuracies will thus be observed for rare species with large shares of absences as well as for wide-spread species with large shares of presences. If, for example, FMM predicts presence in 10 % of the cells and BioScore 2.0 predicts presence in 15 %, then the expected proportion of cells with agreement is 0.78 (0.1 * 0.15 + 0.9 * 0.85) even when the predictions are randomly distributed (Reineking & Schröder 2004). Other measures that take the success as a result of random guessing into account (for example, the TSS) are not symmetric and depend on which model is represented in the column (usually the true values, see Table 2.2) and which in the rows (usually the estimated values) of the confusion matrix. Since here the FMM maps are used as a benchmark, their predictions are shown in the columns, BioScore 2.0 in the rows, and we calculated the corresponding TSS. Both overall accuracy and TSS are reported.

2.2.3. Final evaluation and expert judgement

If BioScore 2.0 can model a species satisfactorily was evaluated by combining information on model quality of FMMs and BioScore 2.0 models (as measured by their TSS, in the following called TSS.FMM and TSS.BioScore, respectively) and the concordance of FMM and BioScore 2.0 maps (also measured by the TSS. in the following called TSS.map_correspondence) according to the following reasoning:

1) If FMM quality is high and BioScore 2.0 model quality comes close to that of the FMM and if at the same time map correspondence is also high, then BioScore 2.0 is suitable for modelling the respective species.
2) There can, however, arise the situation that FMM quality is only intermediate, BioScore 2.0 model quality comes close to that of the FMM (and is thus at best intermediate as well) and map correspondence is good. In this unclear case the maps should be subjected to the visual evaluation by an expert.
3) When a species cannot be modelled satisfactorily by the FMM, it is also not suitable for modelling by BioScore 2.0. This is the logical consequence of the fact that all TSS.BioScore values were smaller than their TSS.FMM counterpart (see Results section).
4) In the cases when BioScore 2.0 quality did not come close to that of the FMM or map correspondence was low, again an expert should judge the maps by eye.

Using threshold values 0.75 and 0.5 for the separation between good/intermediate and intermediate/poor TSS.FMM and TSS.map_correspondence values, respectively, and a multiplication factor of 0.8 for TSS.FMM to define a TSS.BioScore that is "close to" the TSS.FMM yields the following rules:

1)
IF TSS.FMM ≥ 0.75 (= FMM quality is good)
AND TSS.BioScore ≥ 0.8 * TSS.FMM (= BioScore comes close to FMM)
AND TSS.map_correspondence ≥ 0.75 (= correspondence is high)
THEN Species is well modelled by BioScore 2.0

2)
IF 0.5 <= TSS.FMM < 0.75 (= *FMM quality is intermediate*)
AND TSS.BioScore ≥ 0.8 * TSS.FMM (= *BioScore comes close to FMM*)
AND TSS.map_correspondence ≥ 0.75 (= *correspondence is high*)
THEN Situation unclear, an expert should visually check and evaluate the maps

3)
IF TSS.FMM < 0.5 (= *FMM quality is low*)
THEN Species cannot be modelled

4)
IF 0.5 <= TSS.BioScore < 0.8 * TSS.FMM (= *BioScore does not come close to FMM*)
OR TSS.map_correspondence < 0.5 (= *correspondence is low*)
THEN Doubtful if the species should be used for BioScore 2.0, but an expert should visually check and evaluate the maps

Next to formal interpretation of the results, all distribution maps were also evaluated by a species expert (Ruud Foppen). The combined results of the two evaluation approaches can be found in Appendix 7.

2.3. Comparison between dose-response relations and partial dependence plots

Multivariate models are not as transparent as univariate models and visualisation is difficult due to the high dimensionality of the relationships between explanatory and response variables. Partial dependence plots can give an impression of how a given explanatory variable is related to the response by varying its value across its entire range and observing the resulting value of the response variable while keeping all other explanatory variables constant at their mean values. Interactions can only be shown in three-dimensional plots, but even in this case only two explanatory variables can be displayed at a time. Direct comparisons of the effects of single explanatory variables between FMMs and BioScore 2.0 models must thus be viewed with caution and must not be over-interpreted.

The dose-response curves come from univariate models and relate the respective explanatory variable to the probability of presence between 0 (certain absence) and 1 (certain presence). In contrast, the partial dependence plots stem from multivariate models that simultaneously take all explanatory variables into account. When all other variables are held constant at their mean values and the variable under scrutiny is varied over its range, the corresponding probabilities of presence are within a much smaller range. The less important a variable in the multivariate model is, the smaller gets this range, ending up in a horizontal line at a single value for probability of presence when the variable has no effect at all. Only when a single variable would be important in a multivariate model, the probability of presence in its partial dependence plot could range from 0 to 1. To be able to compare the shape of the curves, the y-axis of the partial dependence plots thus are not limited by 0 and 1 like in the dose-response curves but they zoom to the range of variation of the probability of presence.

Only explanatory variables with an AUC of at least 0.6 in the univariate BioScore 2.0 models were considered for comparison.

The ten following species were chosen to make the comparison:

- Great reed warbler *Acrocephalus arundinaceus*
- Aquatic warbler *Acrocephalus paludicola*
- Eurasian skylark *Alauda arvensis* (common, not very sensitive)
- European roller *Coracias garrulus* (rare, very sensitive)
- White-backed woodpecker *Dendrocopos leucotos*
- Woodlark *Lullula arborea*
- Corn bunting *Emberiza calandra*
- Red-backed shrike *Lanius collurio* (common, sensitive)
- Lesser grey shrike *Lanius minor*
- Grey partridge *Perdix perdix* (fairly common, not very sensitive)

2.4. Specification of typical and characteristic BioScore 2.0 species

For the Bioscore 2.0 output species are combined that occur in the same major habitat types. For this purpose species have to be assigned to one the four following habitat classes: Urban, Farmland, Forest and Nature. For some species, like the Coal tit, this classification is straightforward as is occurs almost only in one of those types. But for others this is much more complicated when they occur regularly in two or more types. In those cases we selected the habitat type where we expect that the largest past of European population occurs. As basis for this judgement we used the overlays that we made between the observations and the Corine Land Cover classes, showing the proportions of the observations in the various CLC-classes.

2.5. BioScore 2.0 models with only linear model relationships

The original BioScore 2.0 models were generated as univariate logistic models including a linear and a quadratic model term. The final model was determined by skipping the quadratic term and choosing the model with the lower AIC. This approach assumed that in the majority of cases the dose-response relationship would be a unimodal curve, in some cases—when the quadratic term is not significant—attaining the shape of a sigmoidal (or even linear) curve (van Hinsberg *et al.* 2014).

Here, we compare the original BioScore 2.0 models with models containing only the linear term, thus assuming a sigmoidal relationship between explanatory and response variable. Like in the original analysis (Sierdsema 2014), we determine the robustness of the AUC of a given model by a ten-fold crossvalidation and used 20 bootstrap iterations—each with a random subset of 50% of the data—to determine the reliability of the dose-response relationship.

We did this analysis for the same set of ten sample species as listed in section 2.5 and thus compared 210 (10 species x the 21 pressure factors “desic_mean_5km”, “div3_1_20_mean_5km” “div3_1_50_mean_5km”, “div3_2_20_mean_5km”, “div3_2_50_mean_5km”, “div3_3_20_mean_5km”, “div3_3_50_mean_5km”, “div4_1_20_mean_5km”, “div4_1_50_mean_5km”, “div4_2_20_mean_5km”, “div4_2_50_mean_5km”, “div5_1_20_mean_5km”, “div5_1_50_mean_5km” “fma_f1_5km”, “fma_f2_5km”, “fma_f3_5km”, “fma_f4_5km”, “fma_f5_5km”, “napplication_5km”, “ndep_mean_5km” and “sdep_mean_5km”) pairs of unimodal and sigmoid dose-response relationships.

2.6. Effect of cut-off values on binary distribution maps

For the sample species listed in section 2.5 we determined the effect of the cut-off value used for transforming maps with presence probability into binary maps: all values larger than the cut-off are converted into ‘presence’, all values smaller into ‘absence’.

We used three different approaches for choosing the cut-off:

1. **Fixed cut-off**
   This is the most basic way of transforming probabilities of occurrence into presence-absence data. Using a threshold of 0.5 has been used widely used in ecology, but comparative studies showed that is the least reliable among all methods (LIU *et al.* 2005).
2. **True skill statistic (TSS)**
   This statistics has been explained in section 2.2.1. We added another feature to the TSS, namely a weighing factor that modifies the importance of specificity compared to the importance of sensitivity. For example, when we aim to minimize the risk of displaying cells as ‘present’ although the species is absent, we can decrease the weight of specificity in the calculation of TSS and the distribution area will be enlarged compared to the application of TSS without weighing factor. In contrast, when we aim to minimize the risk of displaying cells as ‘absence’ although the species is present, we can increase the weight of specificity and the resulting distributional area will be smaller. In our analyses, we varied the weighing factor λ in the weighted TSS (= λ*sensitivity + specificity – 1) between 0.5 and 1.5.
3. **Prevalence as cut-off**
   Prevalence is the proportion of presences in the data and this proportion can be used as cut-off. Despite its simplicity, this approach has been shown to be almost as good as the TSS (Allouche *et al.* 2006).

3. Results

3.1. Full multivariate models for all BioScore 2.0 species

For 16 species (*Chlamydotis undulata, Cursorius cursor, Cygnus bewickii, Emberiza caesia, Emberiza cineracea, Falco biarmicus, Falco eleonorae, Francolinus francolinus, Gavia immer, Lyrurus mlokosiewiczi, Melanocorypha bimaculata, Polysticta stelleri, Sitta krueperi, Sylvia rueppelli, Vanellus spinosus, Xenus cinereus*) a FMM could not be fitted with the standard parameter settings. These species typically have a small distribution area and/or a low number of records. Reducing the number of absences in the observations and decreasing the learning rate to 0.001 resulted in successful modelling of *Cygnus bewickii* and *Falco eleonorae* but for the remaining 14 species still no FMMs could be achieved.

We combined the mean crossvalidation AUC and explained deviance to evaluate FMM quality in the following way:

Explained deviance (ED) and mean crossvalidation AUC (AUC)	Model quality
ED ≥ 50 % and AUC ≥ 0.95	Very good
(ED between 40 and 50 % and AUC ≥ 0.90) or (AUC between 0.90 and 0.95 and ED ≥ 40 %)	Good
(ED between 30 and 40 % and AUC ≥ 0.85) or (AUC between 0.85 and 0.90 and ED ≥ 30 %)	Moderate
(ED between 20 and 30 % and AUC ≥ 0.80) or (AUC between 0.80 and 0.85 and ED ≥ 20 %)	Poor
ED < 20 % and AUC < 0.80	Very poor

According to this classification, the FMMs for 126 species could be regarded as *very good*, for 78 species as *good*, for 42 species as *moderate*, for 26 species as *poor*, and only for 13 species as *very poor* (Figure 3.1 and Appendix 1).
For the ten sample species, Figure 3.2 to 3.4 show the thirty most important explanatory variables in the respective FMMs.

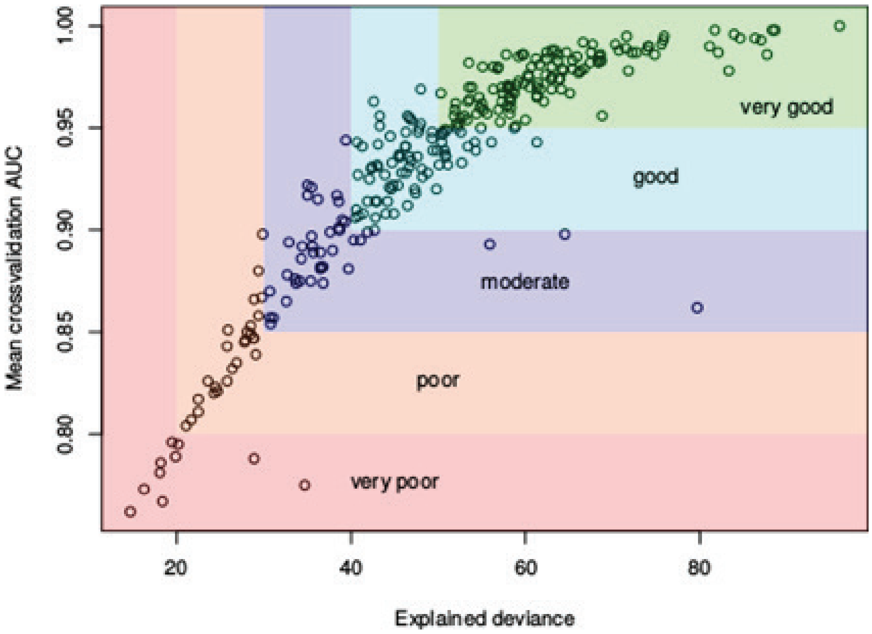


Figure 3.1. Evaluation of FMM quality based on the mean AUC determined by a ten-fold cross-validation and the explained deviance of the full model. Three “very poor” outlier species are not shown: Anser erythropus *(explained deviance = 48.8, mean AUC = 0.66),* Falco eleonorae *(explained deviance = 47.3, mean AUC = 0.71) and* Cygnus berwickii *(explained deviance = -12.3, mean AUC = 0.64).*

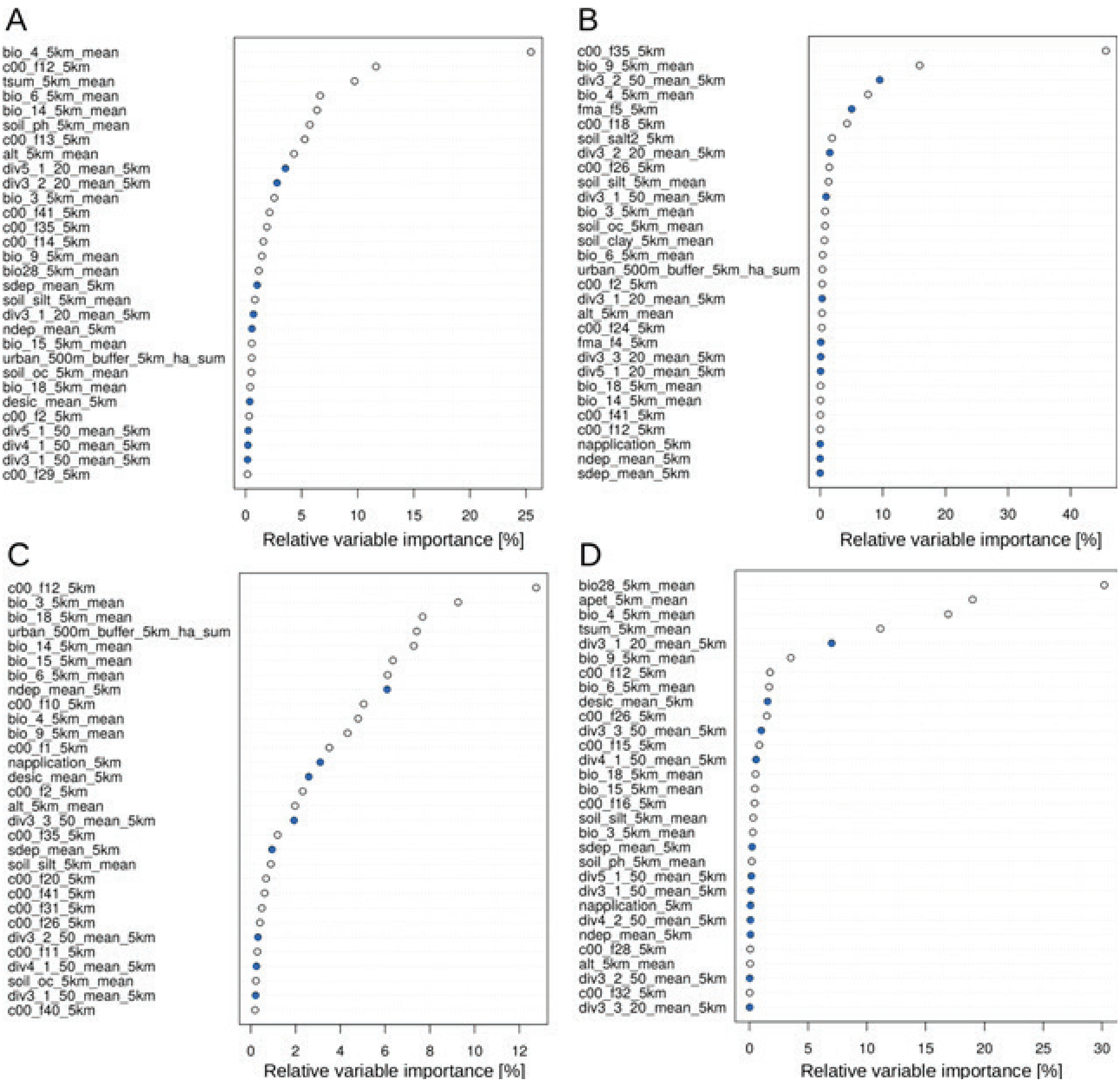


Figure 3.2. The thirty most important explanatory variables in the FMMs for the Great reed warbler Acrocephalus arundinaceus *(A), the Aquatic warbler* Acrocephalus paludicola *(B), the Eurasian skylark* Alauda arvensis *(C) and the European roller* Coracias garrulus *(D). Pressure variables are shown as blue symbols.*

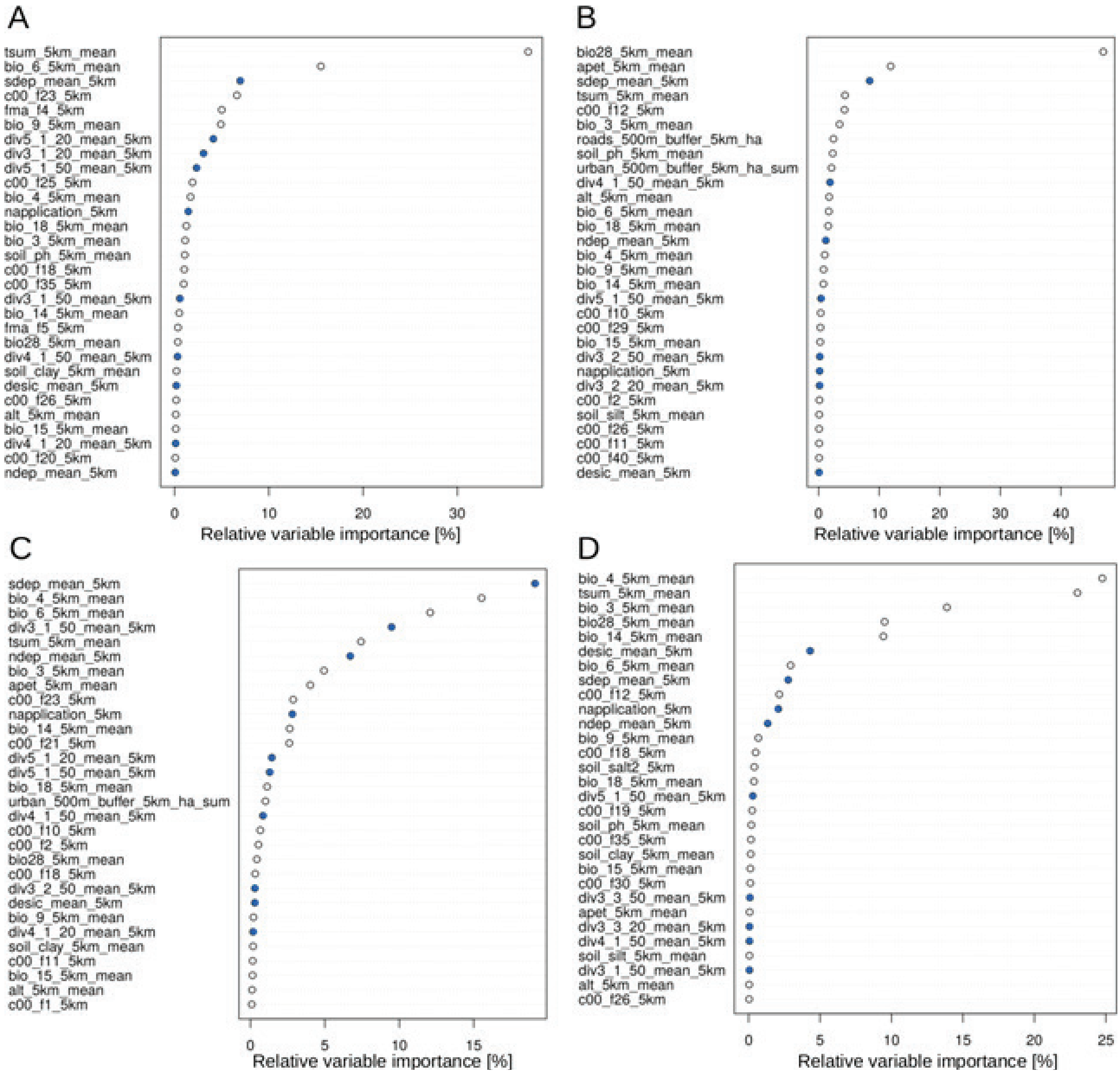


Figure 3.3. The thirty most important explanatory variables in the FMMs for the White-backed woodpecker Dendrocopos leucotos *(A), the Woodlark* Lullula arborea *(B), the Corn bunting* Emberiza calandra *(C) and the Red-backed shrike* Lanius collurio *(D). Pressure variables are shown as blue symbols.*

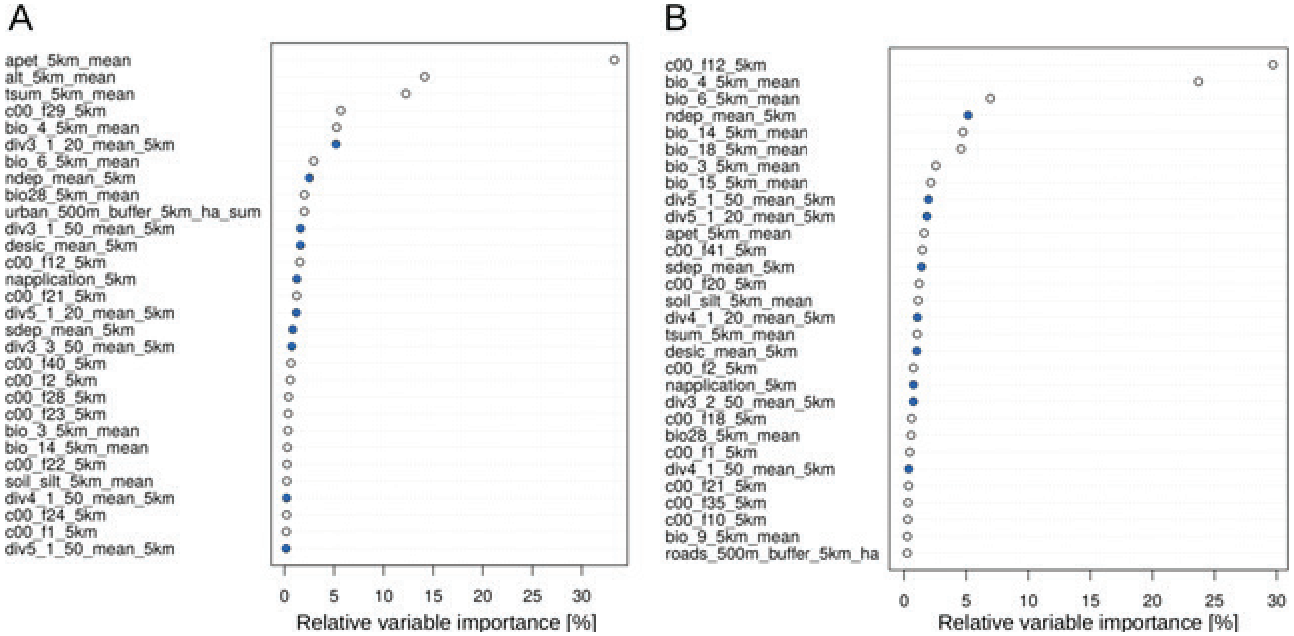


Figure 3.4. The thirty most important explanatory variables in the FMMs for the Lesser grey shrike Lanius minor *(A) and the Grey partridge* Perdix perdix *(B). Pressure variables are shown as blue symbols.*

3.2. Comparison between BioScore 2.0 and full multivariate models

3.2.1. Evaluation of binary maps with the maximised TSS[2]

The evaluation of binary maps based on BioScore 2.0 models and FMMs produced heterogeneous results. For a few species as well BioScore 2.0 as FMM maps had high TSS values (upper right corner in Figure 3.5), for example the grey-headed chickadee *Poecile cinctus* (TSS.BioScore = 0.859, TSS.FMM = 0.975) (Figure 3.6), the rustic bunting *Emberiza rustica* (TSS.BioScore = 0.855, TSS.FMM = 0.896), the rough-legged hawk *Buteo lagopus* (TSS.BioScore = 0.852, TSS.FMM = 0.904) and the Siberian jay *Perisoreus infaustus* (TSS.BioScore = 0.844, TSS.FMM = 0.945). Conspicously, all these species have a Scandinavian breeding range.

Various species showed moderate modelling success for both models (points close to the dashed diagonal in Figure 3.5), for example the boreal owl *Aegolius funereus* (TSS.BioScore = 0.735, TSS.FMM = 0.779), the black woodpecker *Dryocopus martius* (TSS.BioScore = 0.644, TSS.FMM = 0.711) and the golden eagle *Aquila chrysaetos* (TSS.BioScore = 0.635, TSS.FMM = 0.705). In both former cases the BioScore 2.0 models came close to the benchmark established by the FMMs. For some other species TSS.FMM attained very high values close to one, indicating almost perfect agreement with the observations, while the corresponding TSS.BioScore values were nearly zero, indicating random relationship between observations and binary predictions (upper left corner in Figure 3.5), for example the pallid harrier *Circus macrourus* (TSS.BioScore = -0.009, TSS.FMM = 0.9997), western rock nuthatch *Sitta neumayer* (TSS.BioScore = 0.002, TSS.FMM = 0.959), the Barbary partridge *Alectoris barbara* (TSS.BioScore = 0.051, TSS.FMM = 0.999) and the pygmy cormorant *Microcarbo pygmeus* (TSS.BioScore = 0.004, TSS.FMM = 0.904). Noticeable, these are South or South-East European breeding species.

The wide scatter of data points in Figure 3.5 stands in vivid contrast to the results of the butterfly models where the TSS.FMM and TSS.BioScore values show a close linear relationship and the majority of BioScore 2.0 models comes very close to the FMMs (van Swaay 2016).

Tables showing the maximised TSS for each species per model type can be found in Appendix 2.

---

[2] Careful: the TSS is used as a quality measure for the evaluation of binary maps as well as a measure of correspondence between BioScore and FMM binary maps! In order not to mix them up, we use subscripts to make clear to which application a TSS refers: TSS.BioScore and TSS.FMM refer to the evaluation of binary BioScore 2.0 and FMM maps, respectively; TSS.map_correspondence refers to the correspondence of binary BioScore 2.0 and FMM maps for a given species.

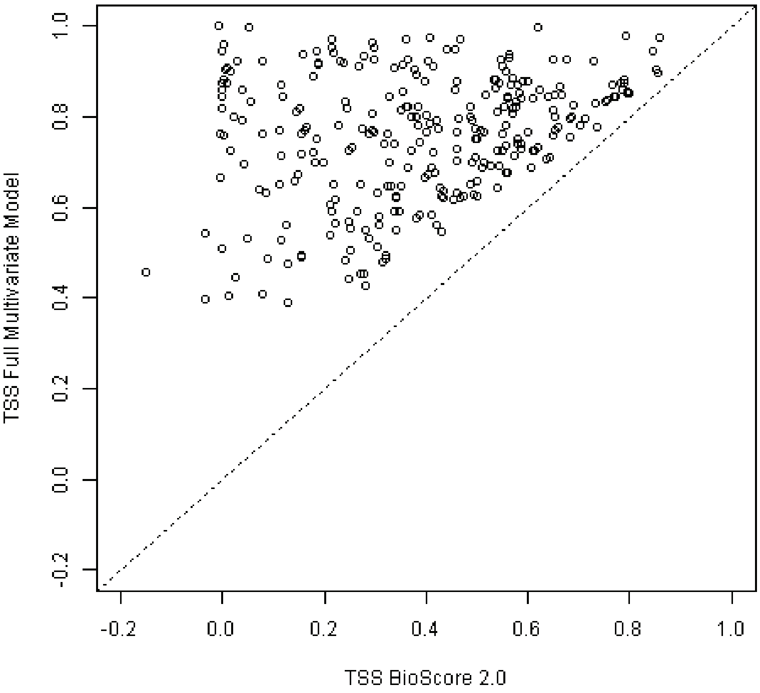


Figure 3.5. Scatterplot of the true skill statistic (TSS) of binary maps of BioScore 2.0 models and full multivariate models.

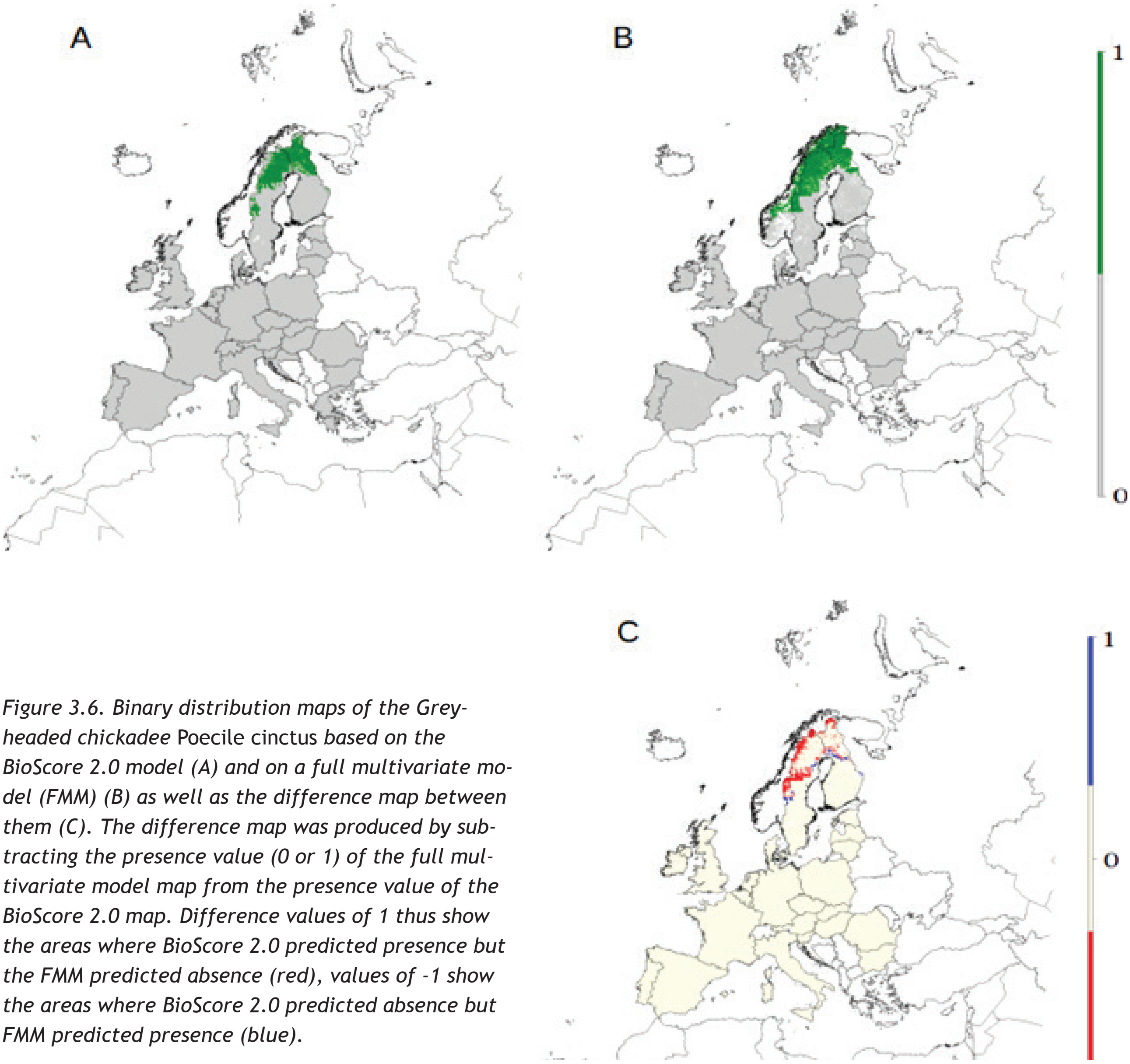


Figure 3.6. Binary distribution maps of the Grey-headed chickadee Poecile cinctus *based on the BioScore 2.0 model (A) and on a full multivariate model (FMM) (B) as well as the difference map between them (C). The difference map was produced by subtracting the presence value (0 or 1) of the full multivariate model map from the presence value of the BioScore 2.0 map. Difference values of 1 thus show the areas where BioScore 2.0 predicted presence but the FMM predicted absence (red), values of -1 show the areas where BioScore 2.0 predicted absence but FMM predicted presence (blue).*

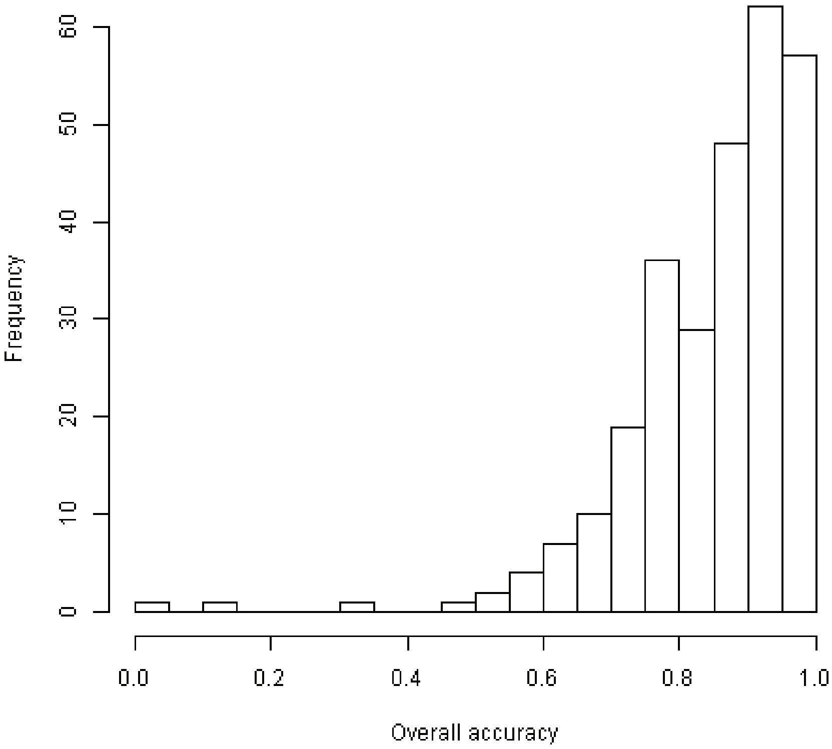


Figure 3.7. Frequency distribution of concordance between 273 binary breeding bird distribution maps based on full multivariate models and BioScore 2.0 models as evaluated by overall accuracy.

3.2.2. Correspondence between binary maps

Overall accuracy showed a negatively skewed distribution with a mode higher than 0.9, indicating good correspondence between BioScore 2.0 and FMM binary maps for most of the species (Figure 3.7). For some species, however, overall accuracy is smaller than 0.7.

Not surprisingly, the species with both high TSS. FMM and TSS.BioScore values score high when the species are ordered according to decreasing overall accuracy: the above-mentioned species rough-legged hawk, grey-headed chickadee, rustic bunting and Siberian jay are 15th, 17th, 29th and 39th, respectively, in a list of 273 species (see Table App3.1 in Appendix 3 for the full list). As pointed out in section 2.2.2, overall accuracy is dependent on the prevalence of the dominant class (*presence* or *absence*). This can distinctly be seen for the species that have been mentioned as examples for the case "TSS.FMM is

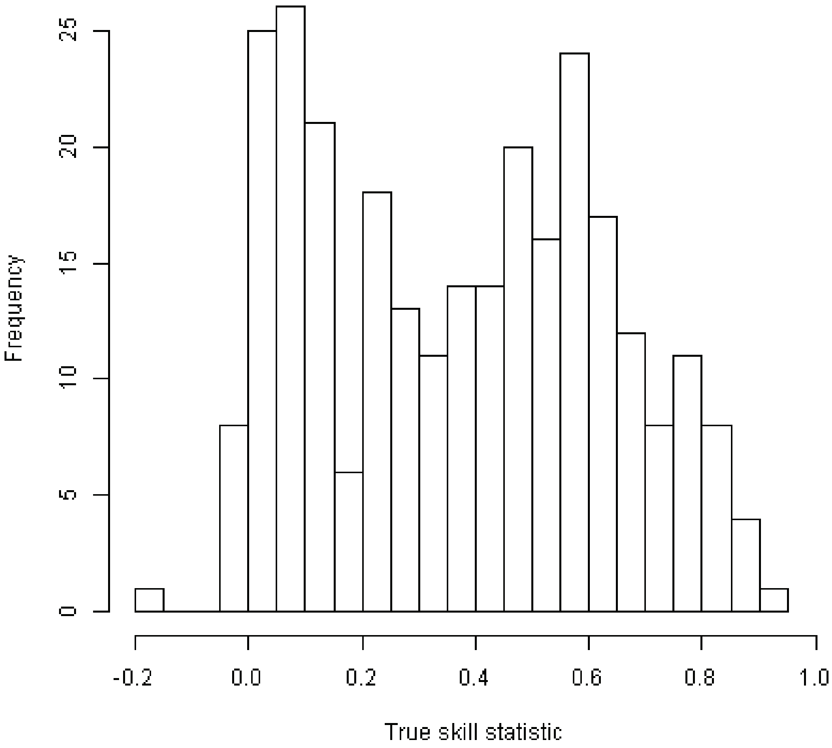


Figure 3.8. Frequency distribution of concordance between 273 binary breeding bird distribution maps based on full multivariate models and BioScore 2.0 models as evaluated by the true skill statistic.

high and TSS.BioScore is close to zero", or in other words, "FMM binary map is good and BioScore 2.0 binary map is poor": the pygmy cormorant ranks 55th, the western rock nuthatch ranks 14th, the pallid harrier ranks 8th, and the Barbary partridge even is on 4th place! For these species with a restricted breeding area, the large numbers of 'correctly' predicted absences cause a huge overall accuracy, even if the few predicted presences are completely misplaced.

The TSS as a measure of binary map correspondence better reflects the information attained during map evaluation. It is less optimistic than overall accuracy and its frequency distribution is not biased towards higher values (Figure 3.8). The species with both high TSS.FMM and TSS.BioScore values generally scored even higher in a list with species ordered according to decreasing TSS.map_correspondence (rough-legged hawk 6th, rustic bunting 8th, Siberian jay 24th, grey-headed chickadee 37th) (see Table App3.2 in Appendix 3 for the full list) than in the list ordered according to decreasing overall accuracy. In contrast to the evaluation based on overall accuracy, the species with high TSS.FMM and a TSS.BioScore close to zero are only 215th (pygmy cormorant), 236th (pallid harrier), 268th (western rock nuthatch) and 270th (Barbary partridge), confirming their difference in map quality between FMMs and BioScore 2.0 models.

TSS, however, not always performs in an optimal way. The red-throated pipit *Anthus cervinus*, for example, is predicted for the north of Sweden and Finland by both modelling approaches. Inspecting the distribution maps (Figure 3.9) by eye would lead to the conclusion that, apart from some distribution details, both draw a good picture of the real situation and that they show a high degree of concordance. Overall accuracy for the species is 0.987, ranked on 6th place (Table App3.1 in Appendix 3), but TSS.map_correspondence is only 0.593, ranked on 66th place (Table App3.2 in Appendix 3), and thus overemphasizing the differences in distribution details.

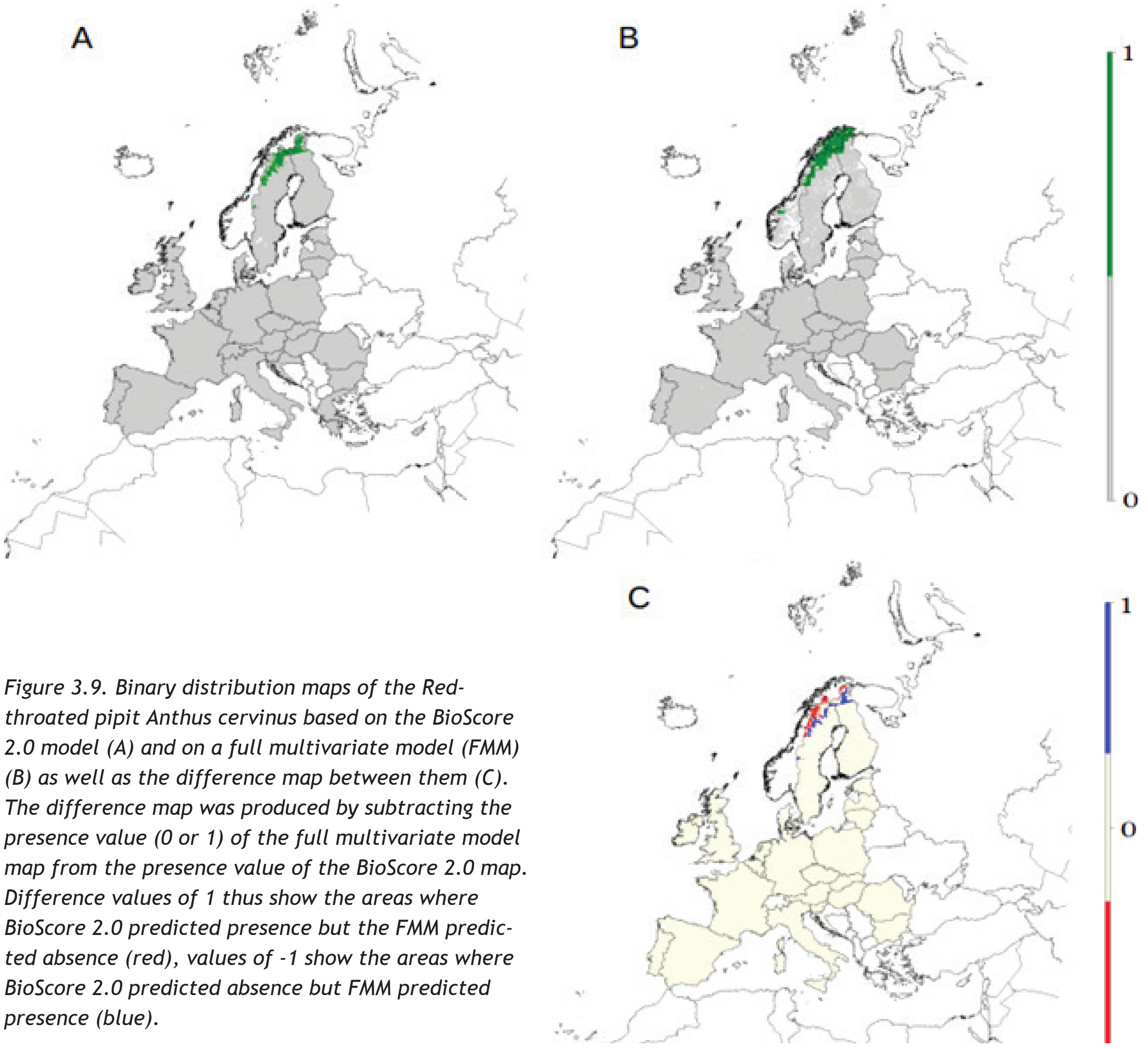


Figure 3.9. Binary distribution maps of the Red-throated pipit Anthus cervinus based on the BioScore 2.0 model (A) and on a full multivariate model (FMM) (B) as well as the difference map between them (C). The difference map was produced by subtracting the presence value (0 or 1) of the full multivariate model map from the presence value of the BioScore 2.0 map. Difference values of 1 thus show the areas where BioScore 2.0 predicted presence but the FMM predicted absence (red), values of -1 show the areas where BioScore 2.0 predicted absence but FMM predicted presence (blue).

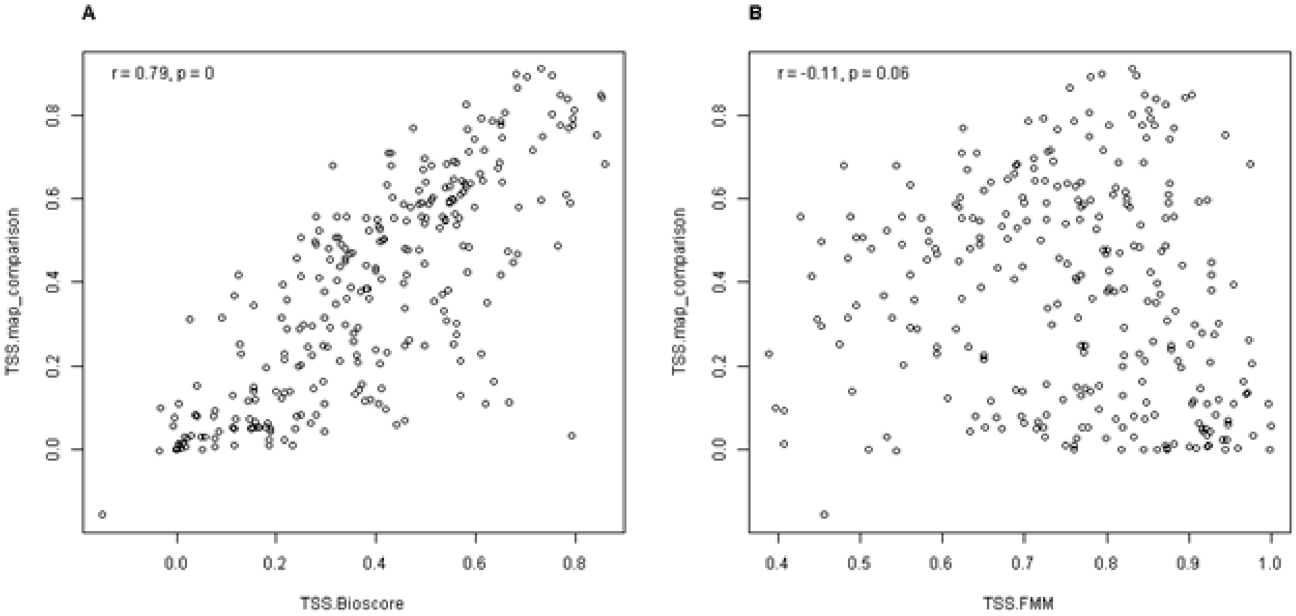


Figure 3.10. Scatterplots of map correspondence (TSS.map_correspondence) versus quality of binary maps based on full multivariate models (TSS.FMM) (A) and of binary maps based on BioScore 2.0 model (TSS.BioScore) (B).

TSS.BioScore and TSS.map_correspondence are highly correlated (r = 0.79, p < 0.001) whereas TSS.map_correspondence shows no relationship with TSS.FMM (r = -0.11, p = 0.06) (Figure 3.10). We conclude that the correspondence between FMM and BioScore 2.0 maps depends only on the quality of the BioScore 2.0 maps: the better the BioScore 2.0 models, the better their correspondence with the FMM maps. An evaluation of which species are appropriate for being modelled according to the BioScore 2.0 approach can thus simply be based on the TSS.BioScore (Table App2.2 in Appendix 2).

3.2.3. Final evaluation and expert judgement

Evaluating the maps based on the TSS of binary FMM and BioScore 2.0 maps and on the TSS of map correspondence according to the scheme presented in section 2.2.3, resulted in only 20 species that are satisfactorily modelled by BioScore 2.0 (Table 3.1). The vast majority of the species (86 %) fall in the category “doubtful is species should be used for BioScore 2.0” and called for an inspection of the maps by an expert.

Due to the high share of doubtful species, the expert made advantage of the opportunity and evaluated *all* species and, at the same time, not only judged the BioScore 2.0 maps but also the FMM maps. This led to some unexpected results.

For 29 species (10 %) the expert judged FMM as well as BioScore 2.0 to deliver good maps (Table 3.2). While according to TSS the FMM maps exceptionless outperformed their BioScore 2.0 counterparts (Figure 3.5), the expert evaluated 83 (32 %) BioScore 2.0 maps as good, while only 63 (24 %) FMM maps received this score. 97 (37 %) BioScore 2.0 maps were regarded as being poor or bad, but 121 (47 %) FMM maps scored evenly bad. In summary, according to expert judgement BioScore 2.0 delivered better maps than the FMMs.
It should however be stressed that the expert evaluated the binary Bioscore maps and the continuous FMM-maps. Unexpected differences in probability resulted often in a ‘poor’ or ‘bad’ score, despite the fact that the range was predicted quite well. This

*Table 3.1. Verdict over BioScore 2.0 maps based on TSS.FMM, TSS.BioScore and TSS.map_correspondence. Strict, the desired TSS.BioScore was calculated as 0.9 * TSS.FMM (see Introduction, section 2.2.3); Gentle, for the same calculation 0.8 was used instead of 0.9.*

Verdict	Frequency
Species satisfactorily modelled by BioScore 2.0	20
Situation unclear, expert should have a look	2
Species cannot be modelled	18
Doubtful if species should be used for BioScore 2.0, but expert should have a look	238

Table 3.2. Expert evaluation of FMM binary maps and BioScore 2.0 binary maps. Frequency per modelling approach and quality class is presented, along with the marginal sums.

		FMM				
		Good	**Reasonable**	**Poor**	**Bad**	
BioScore 2.0	**Good**	29	29	19	6	83
	Reasonable	16	22	30	11	79
	Poor	12	9	19	5	45
	Bad	6	15	9	22	52
		63	75	77	44	

may also be the basis for the observed differences between the formal evaluation and the experts' evaluation: the formal evaluation tends to look more to general quality, while the expert tends to too give focus on the local deviations.

All TSS values along with expert evaluation and comments for each species are presented in Table App3.3 in Appendix 34.

3.3. Comparison between dose-response relations and partial dependence plots

3.3.1. Effect of zooming-in

As described in the methods section, dose-response curves will be displayed by zooming in to the range of variation of the probability of presence. The effect of zooming-in and the shape of a partial dependence plot for a given variable when the y-axis ranges from 0 to 1 are shown in Figure 3.11.

3.3.2. Concordance between dose-response curves and partial dependence plots

Generally, the dose-response curves and partial dependence plots showed a low degree of concurrence. Among the many examples are the curves of div5_1_20_5km for the great reed warbler *Acrocephalus arundinaceus* (Figure 3.12): the dose-response curve is unimodal with its mode at 0.2 while the partial dependence plots shows a marked increase at very low levels and a horizontal line for the rest of the values of the explanatory variable.

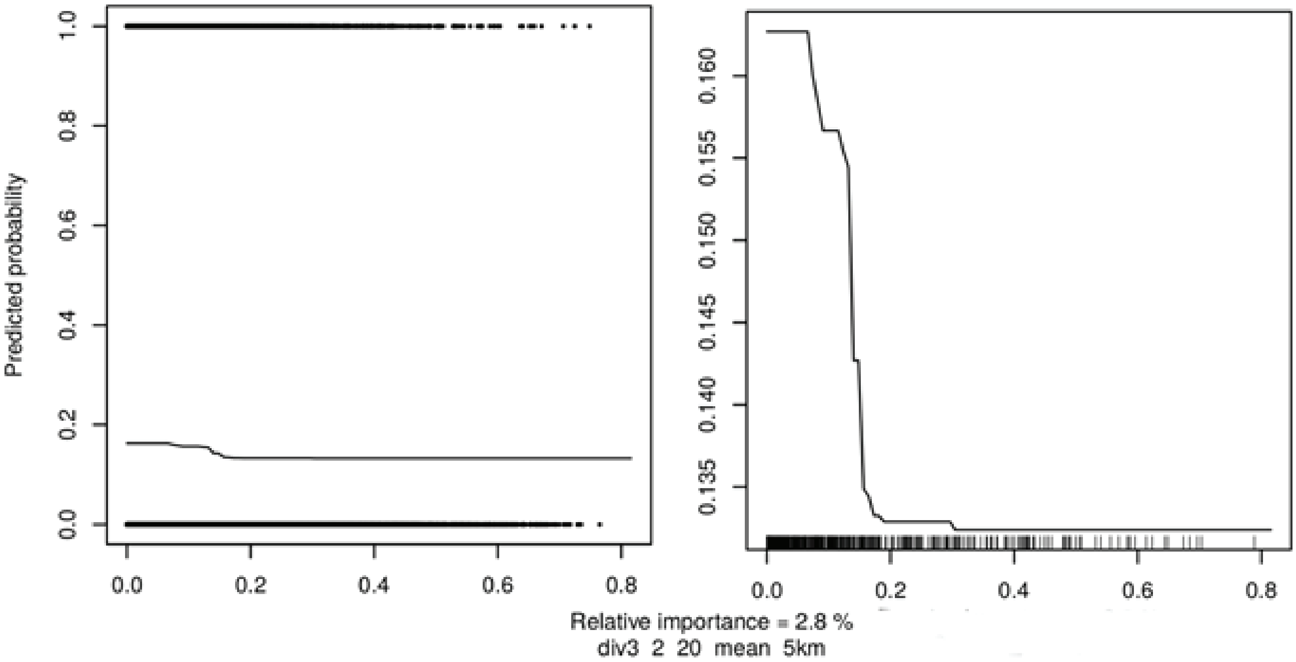


Figure 3.11. Partial dependence plots from a full multivariate model of the Great reed warbler Acrocephalus arundinaceus *for the explanatory variable div3_2_20_5km with probability of presence ranging from 0 to 1 (left) and zoomed in to the actual range of probability of presence (right). Dots at y = 0 and y = 1 in the left figure represent the observations with absences and presences, respectively, for given values of the explanatory variable. Rugs at the x-axis in the right figure represent observations for given values of the explanatory variable, not distinguishing between presences and absences.*

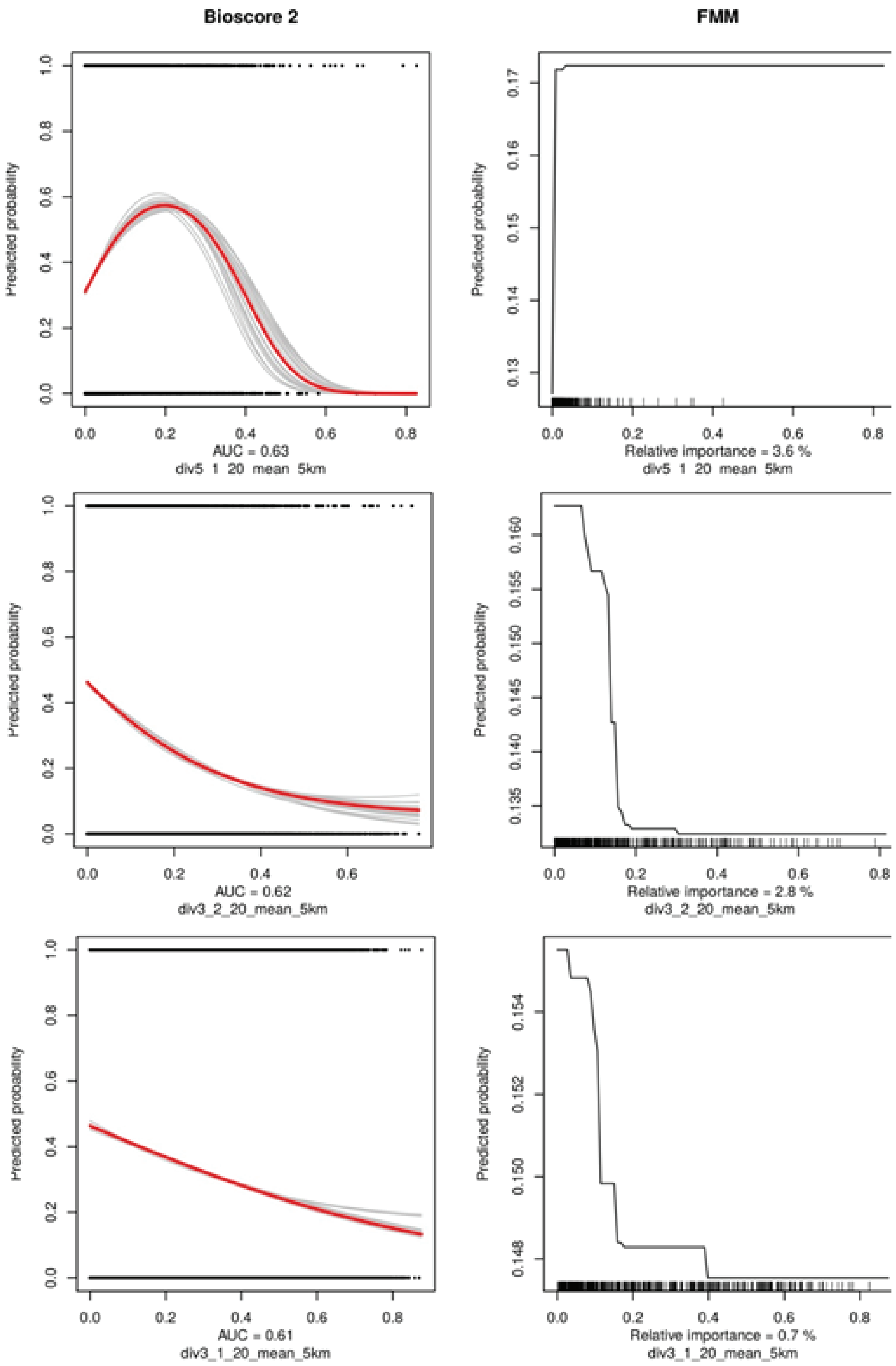


Figure 3.12. Dose effect relations based on BioScore 2.0 univariate binomial models (left panels) and partial dependence plots from a full multivariate model (right panels) of the Great reed warbler Acrocephalus arundinaceus *for the variables div5_1_20_5km (upper panels), div3_2_20_5km (middle panels) and dive_1_20_5km (lower panels) to div4_1_20_mean_5km. The AUC (area under the receiver operating characteristic curve) for the BioScore 2.0 models and the relative variable importance for the FMM are reported. Dots at y = 0 and y = 1 in the dose-response curve panels represent the observations with absences and presences, respectively, for given values of the explanatory variable. Rugs at the x-axis in the partial dependence plot panels represent observations for given values of the explanatory variable, not distinguishing between presences and absences.*

In some cases some correspondence can be observed. The presence probability of the great reed warbler decreases with increasing values of div3_2_20_5km and div3_1_20_5km and also the corresponding partial dependence plots show the same pattern (Figure 3.12). The gradual decrease in the dose-response curves, however, is accompanied by a very steep decrease in the partial dependence plots. Tree-based models such as the boosted regression trees that have been used for making the full multivariate models are known for their capability of identifying thresholds, while the dose-response curves of binomial GLMs are forced into a smooth unimodal or sigmoidal shape. Varying div3_2_20_5km and div3_1_20_5km while averaging out all other explanatory variables, as is done in the partial dependence plots, results in only slight changes in the probability of presence which is visible on the y-axis. This is not surprising since the relative importance of these variables is only 2.8 and 0.7 %, respectively. Notice that the change in the probability of presence for the univariate dose-response relations is considerably larger when these pressure-variable vary over their range.

3.3.3. Comparison of the most important explanatory variable per species

In Figures 3.13 to 3.16 we show a selected subset of dose-response curves and partial dependence plots. We chose those pressure variables that were identified as the most important ones in the FMMs and at the same time had an AUC > 0.6 in the unimodal models used for BioScore 2.0. For the European roller (Figure 3.14A), the corn bunting *Emberiza calandra* (Figure 3.15A) and the red-backed shrike *Lanius collurio* (Figure 3.15B) some resemblance can be perceived, but for the others the shapes of dose-response curves and partial dependence plots do not show much concordance. Moreover, some of the most important pressure variables as identified by the FMMs had an AUC < 0.6 and thus had no explanatory power in the univariate models. This was the case for sdep_mean_5km for the white-backed woodpecker *Dendrocopos leucotos* and the corn bunting *Emberiza calandra* and for desic_mean_5km for the lesser grey shrike *Lanius minor*. In the case of the grey partridge *Perdix perdix* even the three most important pressure variables (ndep_mean_5km, div5_1_50_mean_5km, div5_1_20_mean_5km) had no explanatory power in the univariate models.

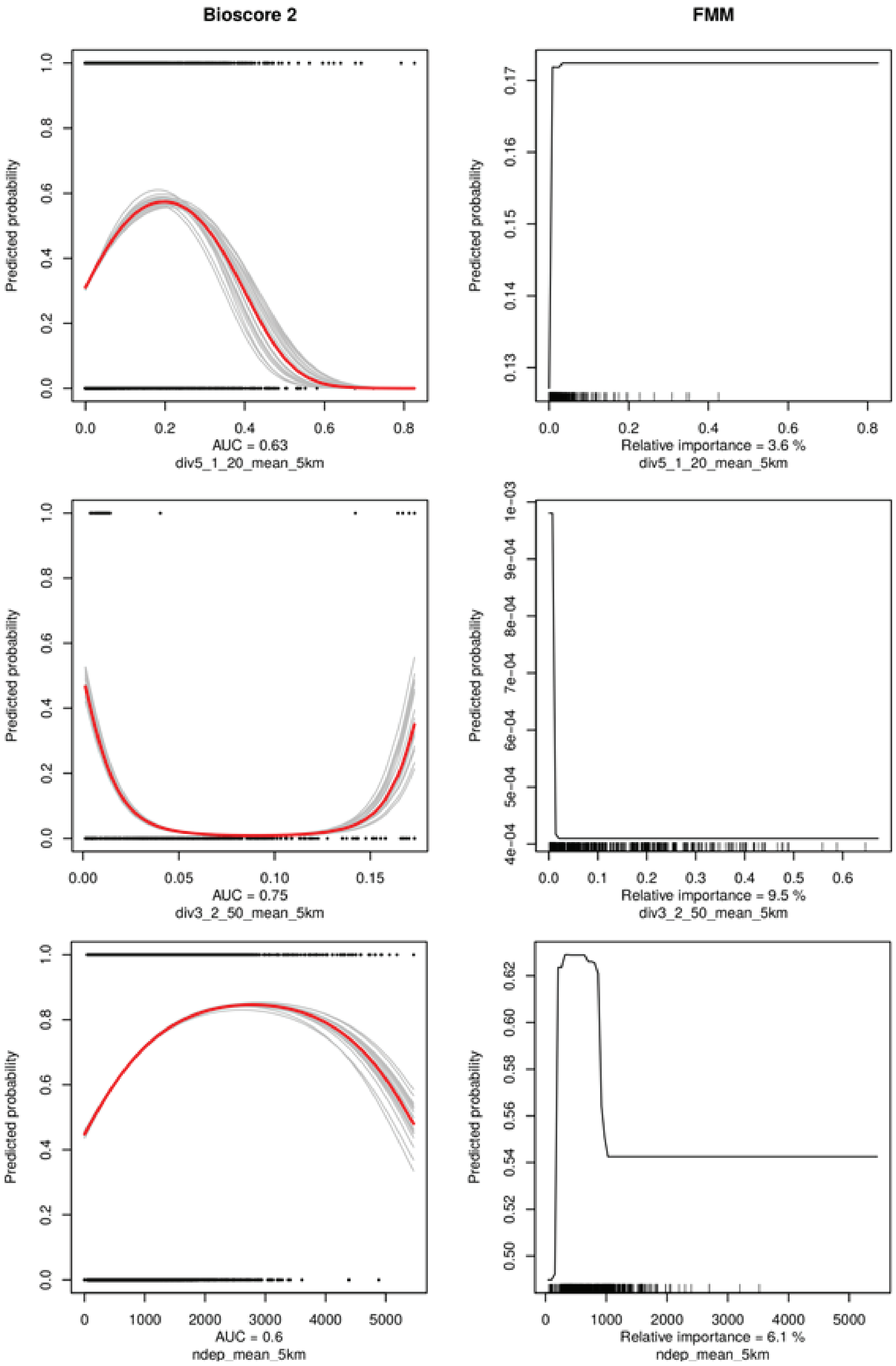


Figure 3.13. Dose effect relations based on BioScore 2.0 univariate binomial models (left) and partial dependence plots from a full multivariate model (right panels) of the Great reed warbler Acrocephalus arundinaceus*, the Aquatic warbler* Acrocephalus paludicola *and the Eurasian skylark* Alauda arvensis *for the most important pressure variable according to the FMMs among those with an AUC > 0.6 in the unimodal models for BioScore 2.0.*

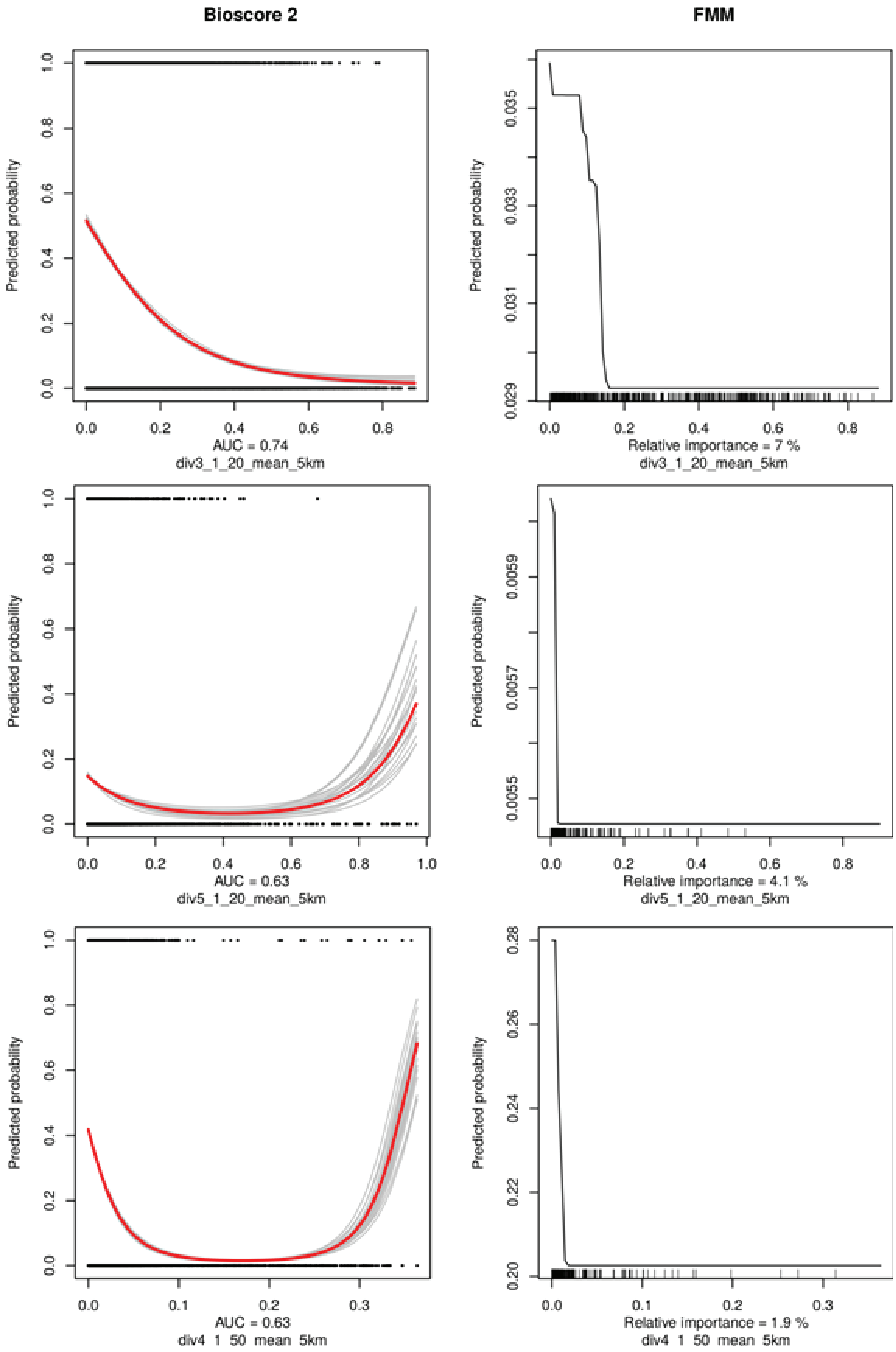


Figure 3.14. Dose effect relations based on BioScore 2.0 univariate binomial models (left) and partial dependence plots from a full multivariate model (right panels) of the European roller Coracias garrulus *(A), the White-backed woodpecker* Dendrocopos leucotos *(B) and the Woodlark* Lullula arborea *(C) for the most important pressure variable according to the FMMs among those with an AUC > 0.6 in the unimodal models for BioScore 2.0.*

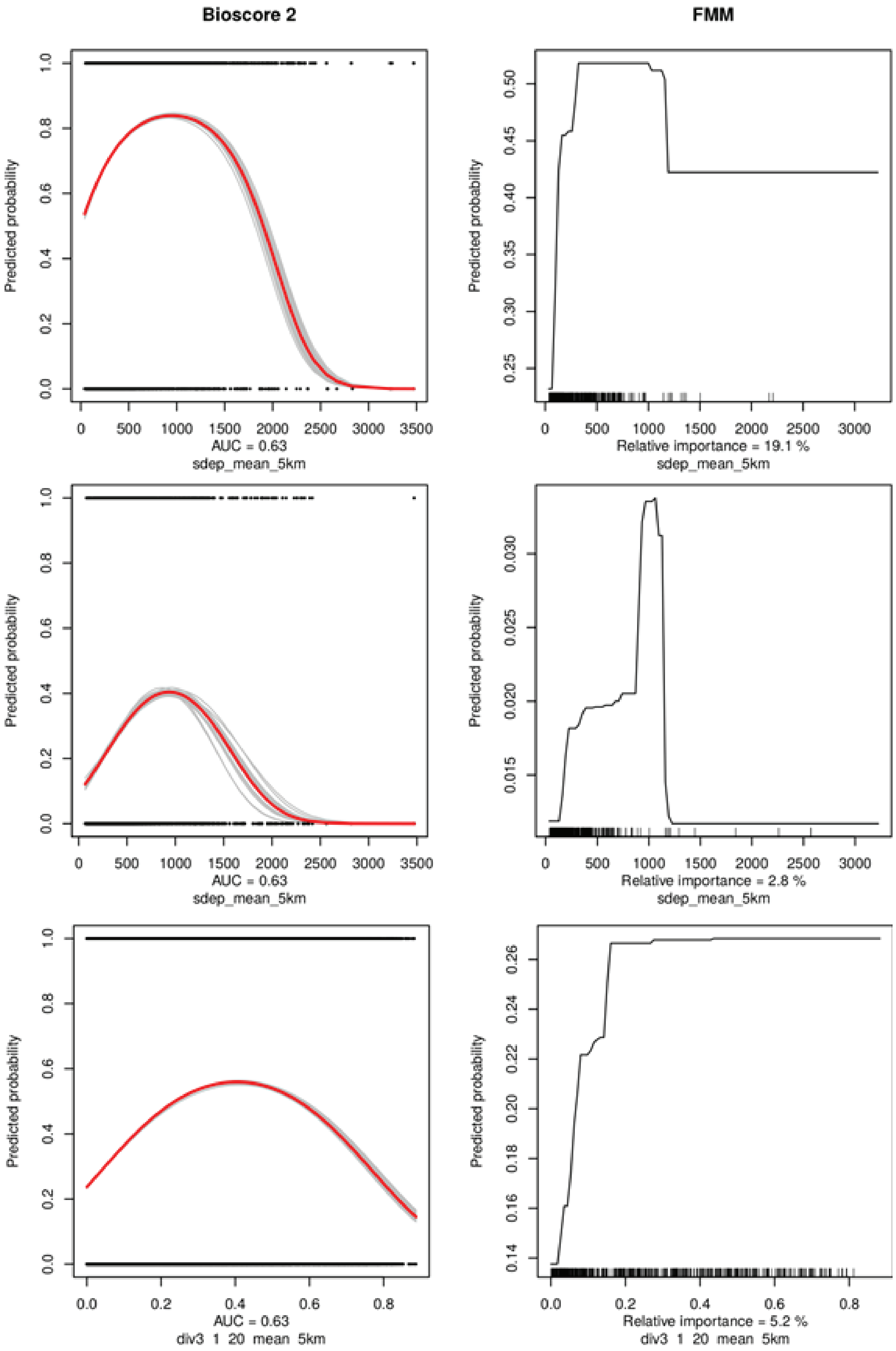


Figure 3.15. Dose effect relations based on BioScore 2.0 univariate binomial models (left) and partial dependence plots from a full multivariate model (right panels) of the Corn bunting Emberiza calandra *(A), the Red-backed shrike* Lanius collurio *(B) and the Lesser grey shrike* Lanius minor *(C) for the most important pressure variable according to the FMMs among those with an AUC > 0.6 in the unimodal models for BioScore 2.0.*

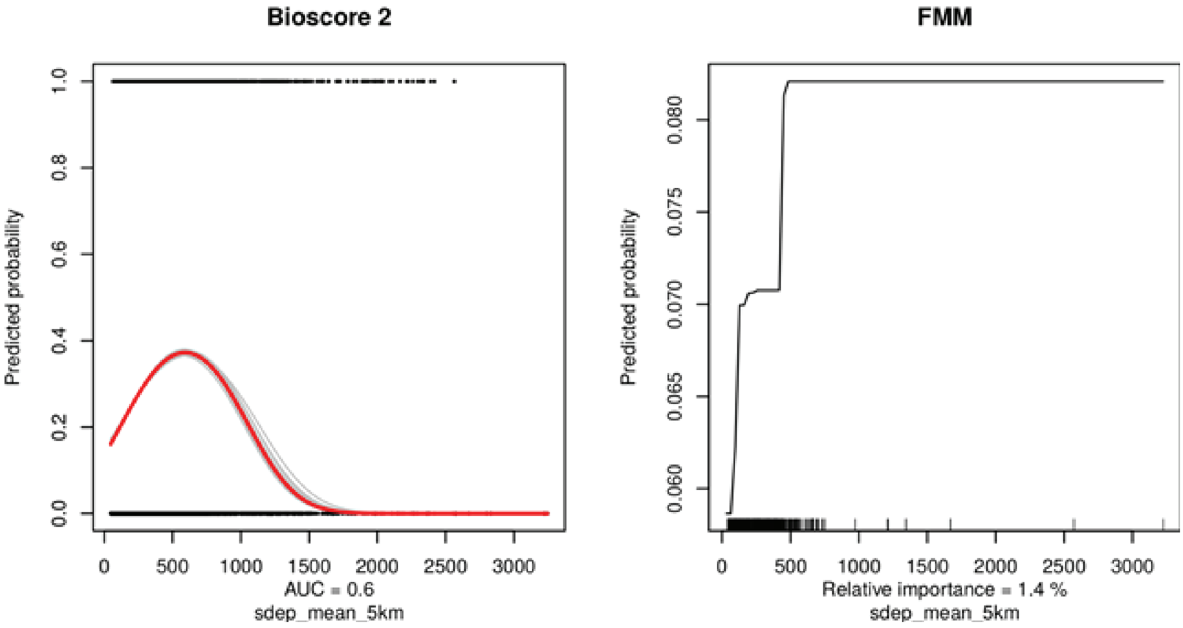


Figure 3.16. Dose effect relations based on BioScore 2.0 univariate binomial models (left) and partial dependence plots from a full multivariate model (right panel) of the grey partridge Perdix perdix *for the most important pressure variable according to the FMMs among those with an AUC > 0.6 in the unimodal models for BioScore 2.0.*

3.4. Specification of typical and characteristic BioScore 2.0 species

Appendix 7 shows the assignment of the Bioscore 2.0 bird species into the four main land use classes urban, farmland, forest and natural habitats. The assignment shows the land use type where we expect that the largest part of the European population will occur. It should be mentioned that this proportion, especially for species of open habitats, is not the same across their range: many species, like the Meadow pipit *Anthis pratensis*, that are abundant in moors and treeless open natural areas in northern Europe and mountain ranges, occur mostly in farmlands in the southern parts of their range.

3.5. BioScore 2.0 models with only linear model relationships

Sixty-one of the 210 unimodal dose-response relationships (10 sample species x 21 pressure factors, see Methods, section 2.5) had AUC-values of at least 0.6 (variables with AUC < 0.6 were regarded as having no effect on presence probability). Among the comparisons of the unimodal and sigmoid dose-response curves of these 61 variables, 33 had identical AUC for the Bioscore2 models and the models with only a linear term, 15 had a higher AUC in the Bisocore2 model and 13 higher AUC in the models with only a linear term (Appendix 5). These values are variable themselves due to the stochasticity in the 10-fold crossvalidation and can vary by values of ±0.01. They show, however, the negligible differences in terms of predictive power.

In various cases it could be observed that the right-side part of the unimodal dose-effect curves are rather unstable. As an example, we look at the variable div4_1_20_mean_5km for the Great reed warbler *Acrocephalus arundinaceus* (Figure 3.17). Due to the low number of data points with div4_1_20_mean_5km larger than 0.2, the curves based on bootstrapped subsample from the data show a considerable variability. This effect has already been described by SIERDSEMA (2014). The unimodal shape of the dose-effect relation is enforced by the quadratic term although there are no absences reported for large values of div4_1_20_mean_5km. When only a linear term is used for modelling, the dose-effect relation is represented by the right-side half of a sigmoid curve and and its variability is much lower (Figure 3.17). The AUC (the area under the receiver operating characteristic curve) of the models are almost identical because the few data points left to div4_1_20_mean_5km = 0.2 have low impact on overall sensitivity and specificity. Remarkably, the Akaike information Criterion (AIC) suggested to keep the quadratic term in the model in the Bioscore modelling run although almost no difference in model performance is visible between the models with and without it.

The enforcement of a unimodal shape of the dose-effect curve can repeatedly be seen, for example also for div5_1_50_mean_5km for the Great reed

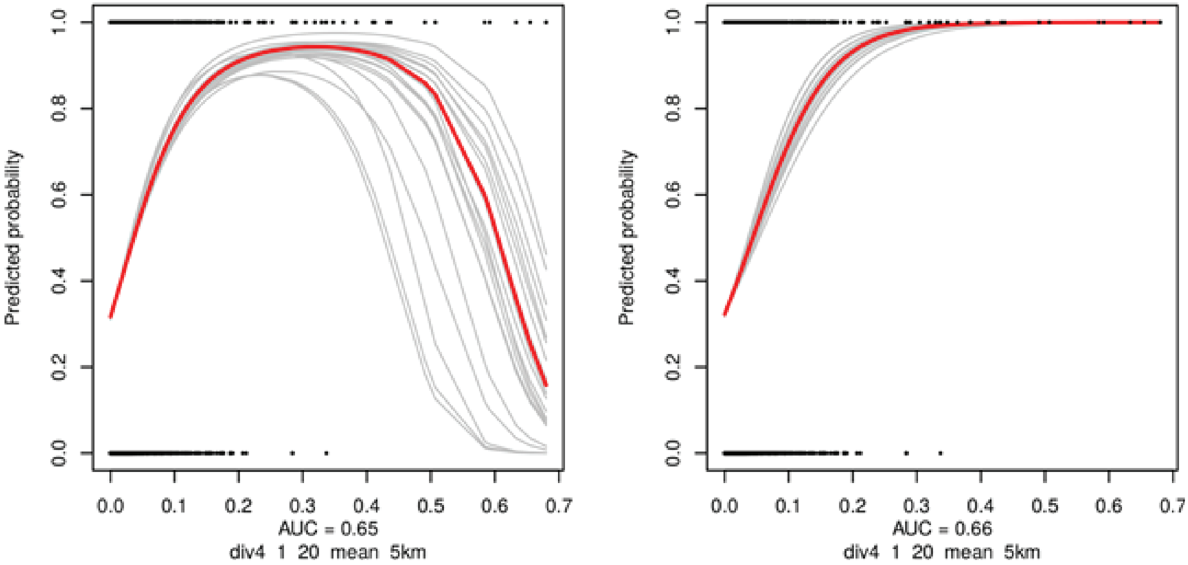


Figure 3.17. Dose effect relations based on a univariate binomial model relating the probability of presence of the Great reed warbler Acrocephalus arundinaceus *to div4_1_20_mean_5km, including a linear and a quadratic term as used in Bioscore2 (left) and including only the linear term (right). The AUC (area under the receiver operating characteristic curve) for both models are reported. Dots at y = 0 and y = 1 represent the observations with absences and presences, respectively, for given values of the explanatory variable.*

warbler (Figure 3.18). Again, above a certain value of the explanatory variable (here: 0.35) no absences were observed but the curve still bends downward. The alternative model with only the linear term is represented by the central, almost linear part of a very flat sigmoidal curve. It has an even higher AUC than the original Bioscore2 model, which makes even more visible that the model-selection based on the AIC depends to a large extent on the stochasticity of the 10-fold crossvalidation, or in plain words: if the quadratic term is kept in the model or not seems to be coincidental.
Appendix 5 summarises the effects of keeping only the linear term for ten sample species.

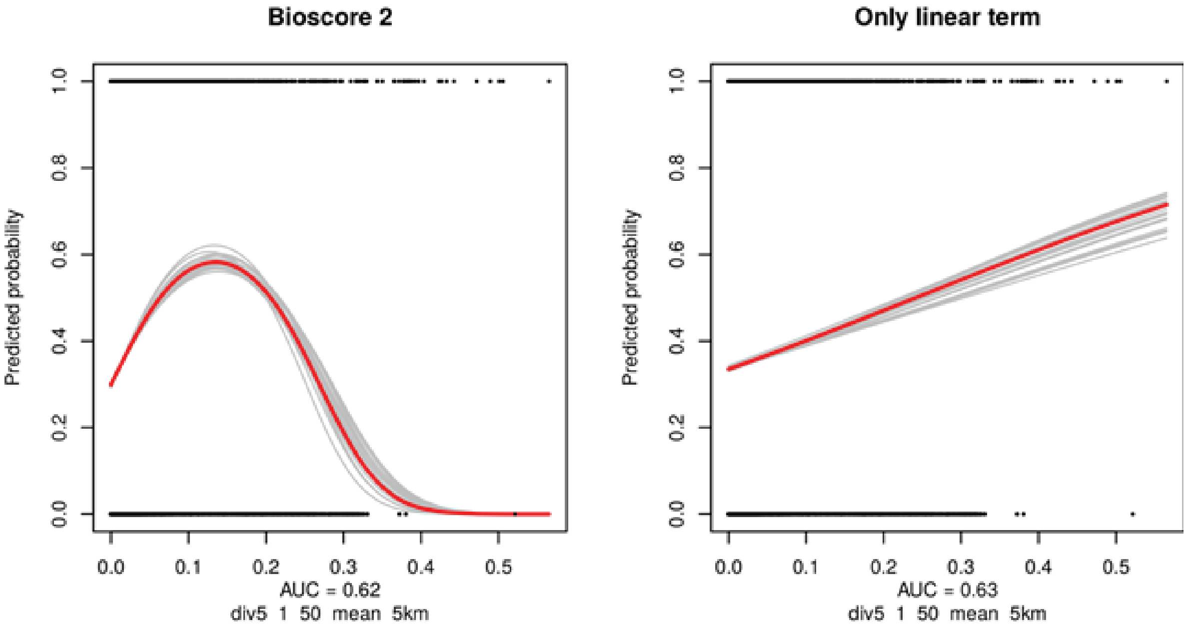


Figure 3.18. Dose effect relations based on a univariate binomial model relating the probability of presence of the Great reed warbler Acrocephalus arundinaceus *to div5_1_50_mean_5km, including a linear and a quadratic term as used in Bioscore2 (left) and including only the linear term (right). The AUC (area under the receiver operating characteristic curve) for both models are reported. Dots at y = 0 and y = 1 represent the observations with absences and presences, respectively, for given values of the explanatory variable.*

3.6. Effect of cutoff values on binary distribution maps

3.6.1. Calculation of the cutoff value with the true skill statistics (TSS)

We demonstrate the effect of cutoff choice on sensitivity, specificity and distributional area for the Great reed warbler *Acrocephalus arundinaceus* when calculated by the TSS (Table 3.3, Figure 3.20). Varying the weighing factor for specificity from 0.5 to 1.5 produces cutoffs ranging from 0.06 to 0.67. The change of sensitivity and specificity for different cutoffs can clearly be seen. For example, for a weighing factor of 0.5 99.41 % of the presences are correctly classified, whereas only 49.85 % of the absences are correctly predicted. Consequently, the predicted distribution area is very large and only very few presences are not covered by this area. On the contrary, if a high weighing factor of 1.5 is chosen, almost all absences (96.54 %) are correctly predicted, but sensitivity is low (64.36 %) and a large proportion of the presences are missed. The corresponding distribution area is very small.

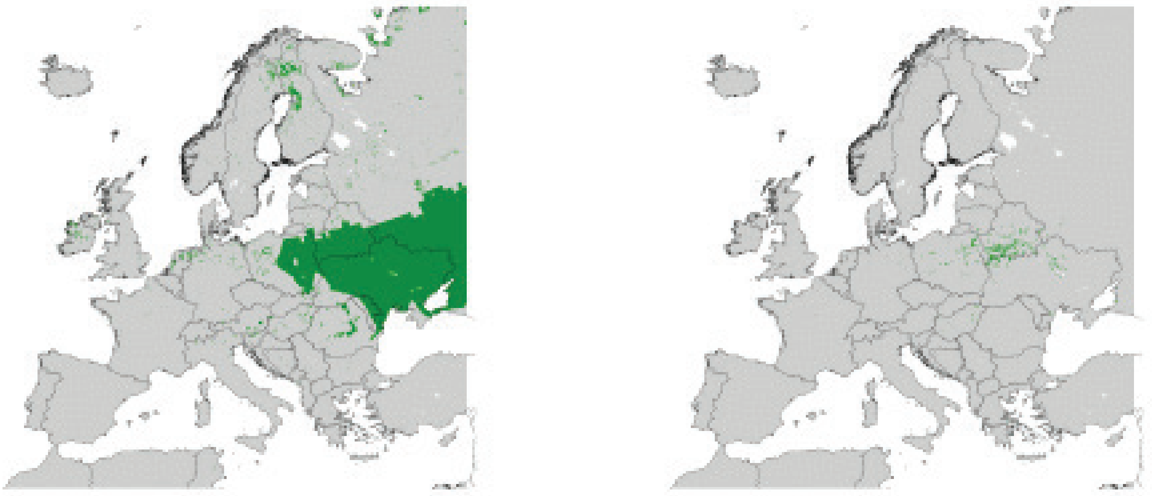
Table 3.3. The effect of the weighing factor for the true skill statistic on cutoff, sensitivity and specificity for the Great reed warbler Acrocephalus arundinaceus, based on the probabilities of presence predicted by the soil-climate distribution model.

Factor	Cutoff	Sensitivity	Specificity
0.5	0.06	99.41	49.85
0.6	0.11	98.75	59.35
0.7	0.15	96.77	67.64
0.8	0.18	93.64	74.84
0.9	0.25	90.21	81.07
1.0	0.32	86.27	86.27
1.1	0.39	81.85	90.05
1.2	0.48	77.24	92.66
1.3	0.57	72.82	94.64
1.4	0.63	68.27	95.58
1.5	0.67	64.36	96.54

In practice, such extreme factor values would not be chosen. It might for many species be desirable, however, to fine-tune the cutoff, setting the weighing factor to values close to but not identical with 1.0, as shows the example of the Aquatic warbler *Acrocephalus paludicola*. This is one of the rarest passerine species in Europe, being restricted to wetlands in Poland, Belarus en Ukraine (apart from some very small populations in Hungary en Western Siberia). The cutoff based on the standard TSS (weighing factor 1.0, cutoff 0.001) leads to a considerable overestimation of the distribution area of the species and predicts it for a large contiguous region far into Southern Russia and even for Northern Scandinavia. Increasing the weighing factor to 1.1 raises the cutoff value to 0.036 and causes the distribution area to shrink to a realistic extent (Figure 3.19).

3.6.2 Comparison with fixed and prevalence-based cutoff

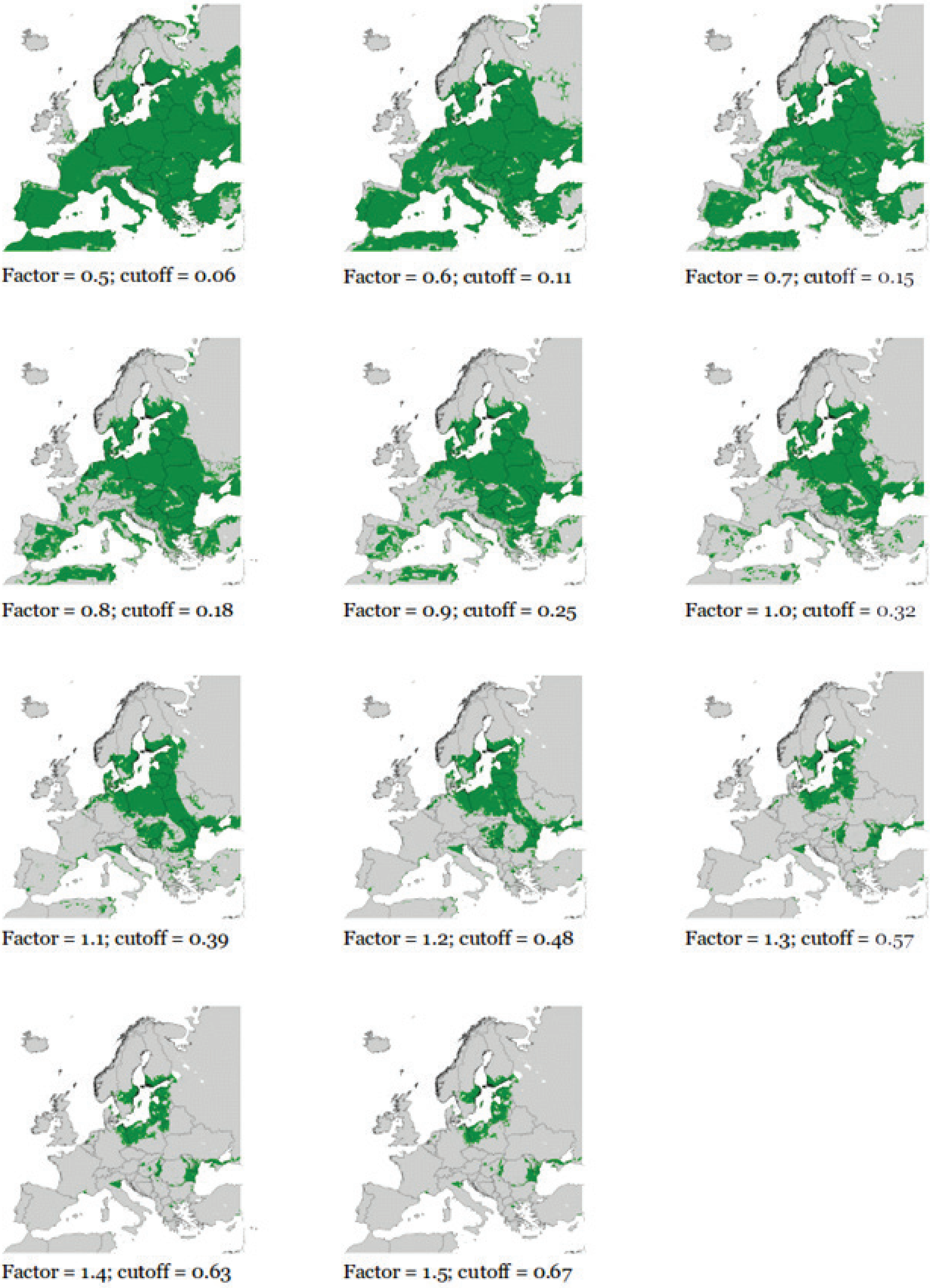
A fixed cutoff value of 0.5 does not take the relative importance of sensitivity and specificity into consideration. In the case of the Great reed warbler, a



Factor = 1.0; cutoff = 0.001

Factor = 1.1; cutoff = 0.036

Figure 3.19. The effect of the weighing factor for the true skill statistic on the predicted distribution area of the Aquatic warbler Acrocephalus paludicola*, based on the probabilities of presence predicted by the soil-climate distribution model.*



Factor = 0.5; cutoff = 0.06

Factor = 0.6; cutoff = 0.11

Factor = 0.7; cutoff = 0.15

Factor = 0.8; cutoff = 0.18

Factor = 0.9; cutoff = 0.25

Factor = 1.0; cutoff = 0.32

Factor = 1.1; cutoff = 0.39

Factor = 1.2; cutoff = 0.48

Factor = 1.3; cutoff = 0.57

Factor = 1.4; cutoff = 0.63

Factor = 1.5; cutoff = 0.67

Figure 3.20. The effect of the weighing factor for the true skill statistic on the cutoff value and the predicted distribution area of the Great reed warbler Acrocephalus arundinaceus*, based on the probabilities of presence predicted by the soil-climate distribution model.*

Fixed cutoff = 0.5 TSS cutoff = 0.32 Prevalence cutoff = 0.33

Figure 3.21. Comparison of binary distribution maps of the Great reed warbler Acrocephalus arundinaceus produced with a fixed cutoff at 0.5 (left), the cutoff as calculated by the TSS (centre) and prevalence used as cutoff (right), based on the probabilities of presence predicted by the soil-climate distribution model.

cutoff of 0.5 would be attained with the TSS with the weighing factor set between 1.2 and 1.3. For this species, the fixed value implicitly gives high weight to the correct prediction of absences, resulting in a comparably small distribution area (Figure 3.21). Prevalence as a cutoff (0.33), on the other hand, is very close to the standard TSS cutoff with even weight for sensitivity and specificity (0.32) and yields an almost identical distribution map.

Generally, cutoffs based on the prevalence lie closely to the TSS cutoffs with weighing factors set at 0.9, 1.0 or 1.1 (see Appendix 6 for a complete table of cutoff values for 10 sample species).

References

Allouche O., Tsoar A. & Kadmon R. 2006. Assessing the accuracy of species distribution models: prevalence, kappa and the true skill statistic (TSS). Journal of Applied Ecology 43:1223-1232.

Barbet-Massin M., Thuiller W. & Jiguet F. 2012. The fate of European breeding birds under climate, land-use and dispersal scenarios. Global Change Biology 18:881-890.

Elith J., Leathwick J.r. & Hastie T. 2008. A working guide to boosted regression trees. Journal of Animal Ecology 77:802-813.

Friedman J.h. 2001. Greedy Function Approximation: A Gradient Boosting Machine. Annals of Statistics 29:1189-1232.

Kampichler C., Hallmann C. & Sierdsema H. 2015. TRIMmaps: an R package for the analysis of species abundance and distribution data – Extended manual. Sovon Vogelonderzoek Nederland, Nijmegen.

Legendre P. 2005. Species Associations: The Kendall Coefficient of Concordance Revisited. Journal of Agricultural, Biological and Environmental Statistics 10:226–245.

Liu C., Berry P. M., Dawson T. P. & Pearson R.G. 2005. Selecting thresholds of occurrence in the prediction of species distributions. Ecography 28:385-393.

Reineking R. & Schröder B. 2004. Gütemaße für Habitatmodelle. *In:* Dormann C. F., Blaschke T., Lausch A., Schröder B. & Söndgerath D. (*Eds.*) Habitatmodelle – Methodik, Anwendung, utzen. UFZ-Berichte 9/2004.

Sierdsema H. 2014. Technical report breeding birds in BioScore 2.0. Sovon-report 2014/52. Sovon Vogelonderzoek Nederland, Nijmegen.

Sierdsema H. 2015. Technical report breeding birds in BioScore 2.0: additional questions. Sovon-report 2015/34. Sovon Vogelonderzoek Nederland, Nijmegen.

Thuiller W., Lafourcade B., Engler R. & Araújo M.B. 2009. BIOMOD – a platform for ensemble forecasting of species distributions . Ecography 32:369-373

van Hinsberg A., Hendriks M., Hennekens S., Sierdsema H., van Swaay C., Rondinini C., Santini L., Delbaere B., Knol O., Wiertz J. 2014. BioScore 2.0 – A tool to assess the impacts of European Community policies on Europe's biodiversity. First Draft.

Zimmermann N. E., Yoccoz N. G., Edwards T. C. Jr., Meier E.S., Thuiller W., Guisan A., Schmatz D.R. & Pearman P.B. 2009. Climatic extremes improve predictions of spatial patterns of tree species. PNAS 106, Suppl. 2:10723-19728.

Appendices

Appendix 1: Evaluation of full multivariate models

Species with very good FMM quality (126):

Accipiter brevipes
Acrocephalus paludicola
Aegypius monachus
Alectoris barbara
Alectoris chukar
Alectoris graeca
Anthus cervinus
Apus caffer
Aquila adalberti
Aquila heliaca
Ardea purpurea
Ardeola ralloides
Aythya nyroca
Buteo lagopus
Buteo rufinus
Calandrella rufescens
Calcarius lapponicus
Calidris maritima
Calidris minuta
Caprimulgus ruficollis
Cecropis daurica
Charadrius alexandrinus
Charadrius morinellus
Chersophilus duponti
Chlidonias hybrida
Ciconia ciconia
Ciconia nigra
Clanga clanga
Clanga pomarina
Clangula hyemalis
Cygnus cygnus
Dendrocopos leucotos
Dendrocopos syriacus
Elanus caeruleus
Emberiza melanocephala
Emberiza pusilla
Emberiza rustica
Eremophila alpestris
Falco cherrug
Falco naumanni
Falco rusticolus
Falco vespertinus
Ficedula albicollis
Ficedula parva
Ficedula semitorquata
Fulica cristata
Galerida cristata
Galerida theklae
Gallinago media
Gavia arctica
Gelochelidon nilotica
Glareola pratincola
Glaucidium passerinum
Grus grus
Gypaetus barbatus
Gyps fulvus
Haliaeetus albicilla
Hieraaetus pennatus
Himantopus himantopus
Hippolais icterina
Hippolais olivetorum
Hydrobates pelagicus
Ichthyaetus audouinii
Lagopus lagopus
Lagopus muta
Lanius meridionalis
Lanius minor
Lanius nubicus
Lanius senator
Larus canus
Locustella fluviatilis
Loxia leucoptera
Loxia pytyopsittacus
Loxia scotica
Luscinia luscinia
Lyrurus tetrix
Marmaronetta angustirostris
Melanitta fusca
Melanitta nigra
Melanocorypha calandra
Merops apiaster
Microcarbo pygmeus
Monticola solitarius
Motacilla citreola
Neophron percnopterus
Nucifraga caryocatactes
Numenius phaeopus
Oenanthe hispanica
Oenanthe isabellina
Oenanthe leucura
Oenanthe pleschanka
Otis tarda
Oxyura leucocephala
Passer hispaniolensis
Pelecanus crispus
Pelecanus onocrotalus
Perisoreus infaustus
Phoenicopterus roseus
Phylloscopus borealis
Platalea leucorodia
Plectrophenax nivalis
Plegadis falcinellus
Poecile cinctus
Poecile lugubris
Porphyrio porphyrio
Prunella collaris
Pterocles alchata
Pterocles orientalis
Pyrrhocorax graculus
Pyrrhocorax pyrrhocorax
Recurvirostra avosetta
Sitta neumayer
Stercorarius longicaudus
Strix nebulosa
Strix uralensis
Sturnus unicolor
Sylvia cantillans
Sylvia crassirostris
Sylvia melanocephala
Sylvia nisoria
Sylvia sarda
Sylvia undata
Tetrao urogallus
Tetrastes bonasia
Tetrax tetrax
Tringa glareola

Species with good FMM quality (78):
Acrocephalus melanopogon
Aegolius funereus
Alectoris rufa
Anas penelope
Anthus campestris
Anthus pratensis
Anthus trivialis
Aquila chrysaetos
Aquila fasciata
Ardea alba
Botaurus stellaris
Branta leucopsis
Burhinus oedicnemus
Calandrella brachydactyla
Calidris alpina
Chlidonias niger
Chroicocephalus genei
Circaetus gallicus
Clamator glandarius
Coracias garrulus
Corvus frugilegus
Crex crex
Dendrocopos medius
Dryocopus martius

Egretta garzetta
Emberiza calandra
Emberiza cia
Emberiza cirlus
Emberiza citrinella
Emberiza hortulana
Gallinago gallinago
Gavia stellata
Haematopus ostralegus
Hippolais polyglotta
Hydrocoloeus minutus
Hydroprogne caspia
Ichthyaetus melanocephalus
Lanius collurio
Lanius excubitor
Limosa lapponica
Limosa limosa
Locustella luscinioides
Locustella naevia
Lophophanes cristatus
Luscinia megarhynchos
Luscinia svecica
Mergellus albellus
Mergus merganser
Milvus migrans
Monticola saxatilis
Numenius arquata
Nycticorax nycticorax
Oriolus oriolus
Otus scops
Pandion haliaetus
Phalaropus lobatus
Phylloscopus bonelli
Phylloscopus sibilatrix
Phylloscopus trochilus
Picoides tridactylus
Picus canus
Pluvialis apricaria
Podiceps auritus
Poecile montanus
Regulus ignicapilla
Regulus regulus
Saxicola rubetra
Scolopax rusticola
Sterna paradisaea
Sternula albifrons
Streptopelia turtur
Surnia ulula
Sylvia curruca
Sylvia hortensis
Tadorna ferruginea
Thalasseus sandvicensis
Upupa epops
Uria aalge

Species with moderate FMM quality (41):
Acrocephalus arundinaceus
Anas acuta
Anas querquedula
Anas strepera
Athene noctua
Aythya ferina
Aythya fuligula
Bubo bubo
Bucanetes githagineus
Circus aeruginosus
Circus macrourus
Circus pygargus
Corvus corax
Coturnix coturnix
Emberiza schoeniclus
Falco columbarius
Ixobrychus minutus
Jynx torquilla
Loxia curvirostra
Lullula arborea
Milvus milvus
Motacilla flava
Netta rufina
Oenanthe oenanthe
Panurus biarmicus
Passer montanus
Perdix perdix
Philomachus pugnax
Phoenicurus phoenicurus
Poecile palustris
Porzana parva
Porzana pusilla
Prunella modularis
Saxicola torquatus
Sitta europaea
Sterna dougallii
Sterna hirundo
Sturnus vulgaris
Sylvia borin
Tringa totanus
Vanellus vanellus

Species with poor FMM quality (26):
Accipiter gentilis
Acrocephalus scirpaceus
Alauda arvensis
Anas clypeata
Asio flammeus
Caprimulgus europaeus
Circus cyaneus
Coloeus monedula
Columba oenas
Dendrocopos major
Dendrocopos minor
Falco peregrinus
Fulica atra
Hirundo rustica
Linaria cannabina
Motacilla cinerea
Muscicapa striata
Pernis apivorus
Phylloscopus collybita
Picus viridis
Podiceps cristatus
Porzana porzana
Saxicola rubicola
Strix aluco
Sylvia communis
Tyto alba

Species with very poor FMM quality (10):
Alcedo atthis
Columba palumbus
Falco subbuteo
Falco tinnunculus
Glareola nordmanni
Motacilla alba
Sylvia atricapilla
Tachybaptus ruficollis
Turdus viscivorus
Vanellus gregarius

Appendix 2: Maximised True Skill Statistics (TSS) of binary maps

Table App2.1: TSS of binary maps based on BioScore 2.0 models ($TSS_{BioScore}$) and on full multivariate models (TSS_{FMM}), ordered according to decreasing TSS_{FMM}.

Species	$TSS_{BioScore}$	TSS_{FMM}
Circus macrourus	-0.009	1.000
Alectoris barbara	0.051	0.999
Oenanthe pleschanka	0.619	0.997
Acrocephalus paludicola	0.792	0.979

Species	$TSS_{BioScore}$	TSS_{FMM}
Stercorarius longicaudus	0.408	0.976
Poecile cinctus	0.859	0.975
Calidris maritima	0.468	0.973
Falco rusticolus	0.215	0.972

Species	$TSS_{BioScore}$	TSS_{FMM}
Sylvia sarda	0.359	0.970
Calcarius lapponicus	0.293	0.966
Sitta neumayer	0.002	0.959
Plectrophenax nivalis	0.296	0.955
Clangula hyemalis	0.213	0.954
Pelecanus crispus	0.457	0.949
Alectoris chukar	0.441	0.948
Loxia scotica	0.185	0.946
Perisoreus infaustus	0.844	0.945
Pelecanus onocrotalus	0.000	0.944
Fulica cristata	0.216	0.941
Eremophila alpestris	0.158	0.936
Emberiza melanocephala	0.562	0.936
Buteo rufinus	0.278	0.933
Poecile lugubris	0.561	0.931
Aquila heliaca	0.651	0.928
Lagopus muta	0.545	0.928
Chersophilus duponti	0.674	0.927
Phoenicopterus roseus	0.297	0.926
Accipiter brevipes	0.363	0.925
Marmaronetta angustirostris	0.233	0.924
Gypaetus barbatus	0.404	0.923
Dendrocopos syriacus	0.730	0.923
Hippolais olivetorum	0.077	0.923
Emberiza pusilla	0.029	0.922
Falco cherrug	0.237	0.920
Oenanthe isabellina	0.188	0.918
Phylloscopus borealis	0.355	0.916
Oxyura leucocephala	0.189	0.915
Ficedula semitorquata	0.412	0.914
Anthus cervinus	0.548	0.912
Lanius nubicus	0.268	0.912
Ichthyaetus audouinii	0.010	0.909
Luscinia luscinia	0.338	0.908
Plegadis falcinellus	0.376	0.905
Microcarbo pygmeus	0.004	0.904
Buteo lagopus	0.852	0.904
Gallinago media	0.557	0.902
Oenanthe leucura	0.017	0.900
Emberiza rustica	0.855	0.896
Melanitta fusca	0.381	0.892
Aquila adalberti	0.178	0.890
Pyrrhocorax graculus	0.571	0.886
Gelochelidon nilotica	0.535	0.884
Sturnus unicolor	0.533	0.882
Clanga pomarina	0.788	0.882
Apus caffer	0.003	0.881
Pterocles alchata	0.399	0.879
Lagopus lagopus	0.459	0.879
Strix nebulosa	0.588	0.878
Melanitta nigra	0.598	0.877
Strix uralensis	0.790	0.874
Prunella collaris	0.782	0.874
Motacilla citreola	0.000	0.874
Uria aalge	0.009	0.874
Chlidonias hybrida	0.543	0.873
Charadrius morinellus	0.766	0.872
Galerida theklae	0.568	0.872
Porphyrio porphyrio	0.115	0.872
Numenius phaeopus	0.581	0.871
Nucifraga caryocatactes	0.664	0.866
Calandrella rufescens	0.535	0.865
Hydrobates pelagicus	0.000	0.862
Tringa glareola	0.456	0.861
Lyrurus tetrix	0.784	0.861
Loxia leucoptera	0.624	0.860
Clanga clanga	0.038	0.858
Tetrax tetrax	0.796	0.858

Species	$\text{TSS}_{\text{BioScore}}$	TSS_{FMM}
Pterocles orientalis	0.355	0.856
Alectoris graeca	0.583	0.853
Tetrastes bonasia	0.797	0.853
Loxia pytyopsittacus	0.799	0.852
Dendrocopos leucotos	0.516	0.850
Chroicocephalus genei	0.667	0.848
Neophron percnopterus	0.653	0.847
Glareola pratincola	0.328	0.847
Otis tarda	0.770	0.847
Pyrrhocorax pyrrhocorax	0.119	0.846
Aegypius monachus	0.561	0.845
Calidris minuta	0.000	0.844
Tetrao urogallus	0.771	0.844
Aythya nyroca	0.638	0.843
Lanius minor	0.560	0.841
Ardeola ralloides	0.611	0.840
Locustella fluviatilis	0.587	0.840
Melanocorypha calandra	0.754	0.836
Ficedula albicollis	0.576	0.833
Elanus caeruleus	0.056	0.833
Haliaeetus albicilla	0.241	0.832
Surnia ulula	0.753	0.832
Falco naumanni	0.731	0.831
Glaucidium passerinum	0.687	0.828
Passer hispaniolensis	0.554	0.824
Larus canus	0.486	0.824
Hippolais icterina	0.576	0.823
Mergellus albellus	0.36	0.822
Platalea leucorodia	0.364	0.822
Caprimulgus ruficollis	0.384	0.821
Grus grus	0.244	0.820
Acrocephalus melanopogon	0.151	0.820
Charadrius alexandrinus	0.569	0.819
Falco eleonorae	0.000	0.818

Species	$\text{TSS}_{\text{BioScore}}$	TSS_{FMM}
Phalaropus lobatus	0.351	0.816
Lanius senator	0.649	0.815
Gavia arctica	0.540	0.811
Hydroprogne caspia	0.145	0.811
Gyps fulvus	0.296	0.809
Oenanthe hispanica	0.569	0.808
Sylvia undata	0.401	0.803
Sylvia nisoria	0.651	0.802
Hydrocoloeus minutus	0.380	0.802
Sylvia cantillans	0.369	0.801
Hieraaetus pennatus	0.486	0.801
Falco vespertinus	0.685	0.800
Cecropis daurica	0.021	0.799
Ciconia ciconia	0.463	0.796
Picoides tridactylus	0.714	0.796
Sylvia melanocephala	0.682	0.795
Recurvirostra avosetta	0.419	0.791
Cygnus cygnus	0.490	0.791
Limosa lapponica	0.040	0.791
Clamator glandarius	0.408	0.787
Ardea purpurea	0.385	0.782
Limosa limosa	0.226	0.781
Ciconia nigra	0.556	0.780
Merops apiaster	0.703	0.780
Aegolius funereus	0.735	0.779
Burhinus oedicnemus	0.659	0.778
Porzana parva	0.166	0.776
Sternula albifrons	0.274	0.774
Himantopus himantopus	0.497	0.774
Chlidonias niger	0.423	0.772
Anas penelope	0.507	0.772
Ardea alba	0.160	0.771
Monticola solitarius	0.113	0.769
Picus canus	0.293	0.769

Species	$TSS_{BioScore}$	TSS_{FMM}
Ficedula parva	0.653	0.769
Dendrocopos medius	0.460	0.768
Galerida cristata	0.598	0.768
Gavia stellata	0.401	0.767
Sterna paradisaea	0.297	0.766
Sylvia hortensis	0.512	0.765
Emberiza cia	0.155	0.764
Pandion haliaetus	0.323	0.764
Tadorna ferruginea	0.077	0.764
Podiceps auritus	0.286	0.762
Hippolais polyglotta	0.548	0.762
Sterna dougallii	-0.003	0.761
Coracias garrulus	0.651	0.761
Aquila fasciata	0.003	0.759
Calandrella brachydactyla	0.683	0.755
Anthus pratensis	0.498	0.752
Pluvialis apricaria	0.579	0.752
Monticola saxatilis	0.497	0.750
Thalasseus sandvicensis	0.186	0.750
Ichthyaetus melanocephalus	0.387	0.746
Calidris alpina	0.339	0.742
Phylloscopus trochilus	0.580	0.740
Mergus merganser	0.318	0.740
Haematopus ostralegus	0.585	0.739
Crex crex	0.557	0.736
Gallinago gallinago	0.255	0.733
Phylloscopus bonelli	0.618	0.732
Lanius excubitor	0.460	0.729
Poecile montanus	0.587	0.729
Lanius collurio	0.539	0.727
Luscinia svecica	0.249	0.727
Nycticorax nycticorax	0.371	0.727
Upupa epops	0.549	0.726
Branta leucopsis	0.014	0.726
Anthus campestris	0.614	0.725
Emberiza cirlus	0.611	0.724
Locustella luscinioides	0.179	0.723
Philomachus pugnax	0.413	0.720
Botaurus stellaris	0.156	0.717
Porzana pusilla	0.116	0.714
Phylloscopus sibilatrix	0.573	0.713
Sylvia curruca	0.497	0.711
Dryocopus martius	0.644	0.711
Aquila chrysaetos	0.635	0.705
Anas acuta	0.460	0.702
Falco columbarius	0.491	0.700
Panurus biarmicus	0.182	0.699
Numenius arquata	0.326	0.698
Netta rufina	0.199	0.698
Circaetus gallicus	0.513	0.698
Saxicola rubetra	0.041	0.696
Emberiza hortulana	0.527	0.692
Regulus ignicapilla	0.542	0.690
Egretta garzetta	0.365	0.690
Otus scops	0.511	0.689
Scolopax rusticola	0.608	0.688
Oriolus oriolus	0.409	0.687
Luscinia megarhynchos	0.415	0.679
Anthus trivialis	0.555	0.679
Lophophanes cristatus	0.558	0.678
Emberiza calandra	0.404	0.673
Ixobrychus minutus	0.150	0.672
Milvus migrans	0.399	0.667
Anser erythropus	-0.005	0.666
Corvus frugilegus	0.500	0.659
Porzana porzana	0.142	0.659
Circus aeruginosus	0.113	0.653
Emberiza citrinella	0.217	0.651

Species	$TSS_{BioScore}$	TSS_{FMM}
Regulus regulus	0.486	0.650
Locustella naevia	0.273	0.650
Sterna hirundo	0.349	0.647
Saxicola torquatus	0.331	0.646
Streptopelia turtur	0.325	0.646
Circus pygargus	0.539	0.645
Alectoris rufa	0.425	0.642
Emberiza schoeniclus	0.073	0.640
Poecile palustris	0.435	0.638
Bubo bubo	0.458	0.634
Acrocephalus arundinaceus	0.084	0.634
Anas querquedula	0.303	0.632
Loxia curvirostra	0.493	0.630
Asio flammeus	0.475	0.626
Lullula arborea	0.501	0.624
Tringa totanus	0.342	0.623
Perdix perdix	0.430	0.623
Vanellus vanellus	0.433	0.622
Milvus milvus	0.468	0.620
Circus cyaneus	0.339	0.620
Motacilla flava	0.222	0.618
Phoenicurus phoenicurus	0.454	0.617
Anas strepera	0.210	0.607
Oenanthe oenanthe	0.215	0.593
Athene noctua	0.346	0.593
Aythya ferina	0.263	0.592
Sylvia borin	0.337	0.592
Jynx torquilla	0.409	0.583
Prunella modularis	0.386	0.583
Corvus corax	0.306	0.581
Sturnus vulgaris	0.380	0.575
Anas clypeata	0.248	0.570
Aythya fuligula	0.22	0.567
Passer montanus	0.125	0.561

Species	$TSS_{BioScore}$	TSS_{FMM}
Accipiter gentilis	0.421	0.560
Caprimulgus europaeus	0.307	0.560
Podiceps cristatus	0.250	0.552
Pernis apivorus	0.340	0.551
Coturnix coturnix	0.280	0.551
Sitta europaea	0.429	0.545
Motacilla cinerea	-0.035	0.544
Dendrocopos minor	0.211	0.538
Columba oenas	0.286	0.533
Acrocephalus scirpaceus	0.049	0.532
Tyto alba	0.114	0.529
Phylloscopus collybita	0.305	0.514
Glareola nordmanni	0.000	0.510
Alauda arvensis	0.250	0.504
Sylvia communis	0.154	0.495
Picus viridis	0.319	0.494
Fulica atra	0.153	0.491
Strix aluco	0.322	0.489
Linaria cannabina	0.090	0.485
Muscicapa striata	0.241	0.485
Falco peregrinus	0.313	0.481
Coloeus monedula	0.127	0.475
Hirundo rustica	-0.150	0.456
Turdus viscivorus	0.272	0.454
Dendrocopos major	0.277	0.452
Motacilla alba	0.025	0.448
Sylvia atricapilla	0.249	0.441
Falco subbuteo	0.280	0.427
Tachybaptus ruficollis	0.077	0.408
Alcedo atthis	0.012	0.407
Falco tinnunculus	-0.033	0.398
Columba palumbus	0.128	0.389

Table App2.2: TSS of binary maps based on BioScore 2.0 models ($TSS_{BioScore}$) and on full multivariate models (TSS_{FMM}), ordered according to decreasing $TSS_{BioScore}$.

Species	$TSS_{BioScore}$	TSS_{FMM}	Species	$TSS_{BioScore}$	TSS_{FMM}
Poecile cinctus	0.859	0.975	*Neophron percnopterus*	0.653	0.847
Emberiza rustica	0.855	0.896	*Ficedula parva*	0.653	0.769
Buteo lagopus	0.852	0.904	*Sylvia nisoria*	0.651	0.802
Perisoreus infaustus	0.844	0.945	*Coracias garrulus*	0.651	0.761
Loxia pytyopsittacus	0.799	0.852	*Aquila heliaca*	0.651	0.928
Tetrastes bonasia	0.797	0.853	*Lanius senator*	0.649	0.815
Tetrax tetrax	0.796	0.858	*Dryocopus martius*	0.644	0.711
Acrocephalus paludicola	0.792	0.979	*Aythya nyroca*	0.638	0.843
Strix uralensis	0.790	0.874	*Aquila chrysaetos*	0.635	0.705
Clanga pomarina	0.788	0.882	*Loxia leucoptera*	0.624	0.860
Lyrurus tetrix	0.784	0.861	*Oenanthe pleschanka*	0.619	0.997
Prunella collaris	0.782	0.874	*Phylloscopus bonelli*	0.618	0.732
Tetrao urogallus	0.771	0.844	*Anthus campestris*	0.614	0.725
Otis tarda	0.770	0.847	*Emberiza cirlus*	0.611	0.724
Charadrius morinellus	0.766	0.872	*Ardeola ralloides*	0.611	0.840
Melanocorypha calandra	0.754	0.836	*Scolopax rusticola*	0.608	0.688
Surnia ulula	0.753	0.832	*Melanitta nigra*	0.598	0.877
Aegolius funereus	0.735	0.779	*Galerida cristata*	0.598	0.768
Falco naumanni	0.731	0.831	*Strix nebulosa*	0.588	0.878
Dendrocopos syriacus	0.730	0.923	*Poecile montanus*	0.587	0.729
Picoides tridactylus	0.714	0.796	*Locustella fluviatilis*	0.587	0.840
Merops apiaster	0.703	0.780	*Haematopus ostralegus*	0.585	0.739
Glaucidium passerinum	0.687	0.828	*Alectoris graeca*	0.583	0.853
Falco vespertinus	0.685	0.800	*Numenius phaeopus*	0.581	0.871
Calandrella brachydactyla	0.683	0.755	*Phylloscopus trochilus*	0.580	0.740
Sylvia melanocephala	0.682	0.795	*Pluvialis apricaria*	0.579	0.752
Chersophilus duponti	0.674	0.927	*Hippolais icterina*	0.576	0.823
Chroicocephalus genei	0.667	0.848	*Ficedula albicollis*	0.576	0.833
Nucifraga caryocatactes	0.664	0.866	*Phylloscopus sibilatrix*	0.573	0.713
Burhinus oedicnemus	0.659	0.778	*Pyrrhocorax graculus*	0.571	0.886

Species	TSS$_{BioScore}$	TSS$_{FMM}$
Charadrius alexandrinus	0.569	0.819
Oenanthe hispanica	0.569	0.808
Galerida theklae	0.568	0.872
Emberiza melanocephala	0.562	0.936
Poecile lugubris	0.561	0.931
Aegypius monachus	0.561	0.845
Lanius minor	0.560	0.841
Lophophanes cristatus	0.558	0.678
Crex crex	0.557	0.736
Gallinago media	0.557	0.902
Ciconia nigra	0.556	0.780
Anthus trivialis	0.555	0.679
Passer hispaniolensis	0.554	0.824
Upupa epops	0.549	0.726
Anthus cervinus	0.548	0.912
Hippolais polyglotta	0.548	0.762
Lagopus muta	0.545	0.928
Chlidonias hybrida	0.543	0.873
Regulus ignicapilla	0.542	0.690
Gavia arctica	0.540	0.811
Lanius collurio	0.539	0.727
Circus pygargus	0.539	0.645
Gelochelidon nilotica	0.535	0.884
Calandrella rufescens	0.535	0.865
Sturnus unicolor	0.533	0.882
Emberiza hortulana	0.527	0.692
Dendrocopos leucotos	0.516	0.850
Circaetus gallicus	0.513	0.698
Sylvia hortensis	0.512	0.765
Otus scops	0.511	0.689
Anas penelope	0.507	0.772
Lullula arborea	0.501	0.624
Corvus frugilegus	0.500	0.659
Anthus pratensis	0.498	0.752
Monticola saxatilis	0.497	0.750
Himantopus himantopus	0.497	0.774
Sylvia curruca	0.497	0.711
Loxia curvirostra	0.493	0.63
Falco columbarius	0.491	0.700
Cygnus cygnus	0.490	0.791
Hieraaetus pennatus	0.486	0.801
Larus canus	0.486	0.824
Regulus regulus	0.486	0.650
Asio flammeus	0.475	0.626
Milvus milvus	0.468	0.620
Calidris maritima	0.468	0.973
Ciconia ciconia	0.463	0.796
Dendrocopos medius	0.460	0.768
Anas acuta	0.460	0.702
Lanius excubitor	0.460	0.729
Lagopus lagopus	0.459	0.879
Bubo bubo	0.458	0.634
Pelecanus crispus	0.457	0.949
Tringa glareola	0.456	0.861
Phoenicurus phoenicurus	0.454	0.617
Alectoris chukar	0.441	0.948
Poecile palustris	0.435	0.638
Vanellus vanellus	0.433	0.622
Perdix perdix	0.430	0.623
Sitta europaea	0.429	0.545
Alectoris rufa	0.425	0.642
Chlidonias niger	0.423	0.772
Accipiter gentilis	0.421	0.560
Recurvirostra avosetta	0.419	0.791
Luscinia megarhynchos	0.415	0.679
Philomachus pugnax	0.413	0.720
Ficedula semitorquata	0.412	0.914
Oriolus oriolus	0.409	0.687

Species	$TSS_{BioScore}$	TSS_{FMM}
Jynx torquilla	0.409	0.583
Stercorarius longicaudus	0.408	0.976
Clamator glandarius	0.408	0.787
Emberiza calandra	0.404	0.673
Gypaetus barbatus	0.404	0.923
Gavia stellata	0.401	0.767
Sylvia undata	0.401	0.803
Pterocles alchata	0.399	0.879
Milvus migrans	0.399	0.667
Ichthyaetus melanocephalus	0.387	0.746
Prunella modularis	0.386	0.583
Ardea purpurea	0.385	0.782
Caprimulgus ruficollis	0.384	0.821
Melanitta fusca	0.381	0.892
Sturnus vulgaris	0.380	0.575
Hydrocoloeus minutus	0.380	0.802
Plegadis falcinellus	0.376	0.905
Nycticorax nycticorax	0.371	0.727
Sylvia cantillans	0.369	0.801
Egretta garzetta	0.365	0.690
Platalea leucorodia	0.364	0.822
Accipiter brevipes	0.363	0.925
Mergellus albellus	0.360	0.822
Sylvia sarda	0.359	0.970
Pterocles orientalis	0.355	0.856
Phylloscopus borealis	0.355	0.916
Phalaropus lobatus	0.351	0.816
Sterna hirundo	0.349	0.647
Athene noctua	0.346	0.593
Tringa totanus	0.342	0.623
Pernis apivorus	0.340	0.551
Circus cyaneus	0.339	0.620
Calidris alpina	0.339	0.742
Luscinia luscinia	0.338	0.908
Sylvia borin	0.337	0.592
Saxicola torquatus	0.331	0.646
Glareola pratincola	0.328	0.847
Numenius arquata	0.326	0.698
Streptopelia turtur	0.325	0.646
Pandion haliaetus	0.323	0.764
Strix aluco	0.322	0.489
Picus viridis	0.319	0.494
Mergus merganser	0.318	0.740
Falco peregrinus	0.313	0.481
Caprimulgus europaeus	0.307	0.560
Corvus corax	0.306	0.581
Phylloscopus collybita	0.305	0.514
Anas querquedula	0.303	0.632
Sterna paradisaea	0.297	0.766
Phoenicopterus roseus	0.297	0.926
Plectrophenax nivalis	0.296	0.955
Gyps fulvus	0.296	0.809
Calcarius lapponicus	0.293	0.966
Picus canus	0.293	0.769
Columba oenas	0.286	0.533
Podiceps auritus	0.286	0.762
Coturnix coturnix	0.280	0.551
Falco subbuteo	0.280	0.427
Buteo rufinus	0.278	0.933
Dendrocopos major	0.277	0.452
Sternula albifrons	0.274	0.774
Locustella naevia	0.273	0.650
Turdus viscivorus	0.272	0.454
Lanius nubicus	0.268	0.912
Aythya ferina	0.263	0.592
Gallinago gallinago	0.255	0.733
Alauda arvensis	0.250	0.504
Podiceps cristatus	0.250	0.552

Species	$\mathrm{TSS}_{\mathrm{BioScore}}$	$\mathrm{TSS}_{\mathrm{FMM}}$
Luscinia svecica	0.249	0.727
Sylvia atricapilla	0.249	0.441
Anas clypeata	0.248	0.570
Grus grus	0.244	0.820
Muscicapa striata	0.241	0.485
Haliaeetus albicilla	0.241	0.832
Falco cherrug	0.237	0.920
Marmaronetta angustirostris	0.233	0.924
Limosa limosa	0.226	0.781
Motacilla flava	0.222	0.618
Aythya fuligula	0.220	0.567
Emberiza citrinella	0.217	0.651
Fulica cristata	0.216	0.941
Falco rusticolus	0.215	0.972
Oenanthe oenanthe	0.215	0.593
Clangula hyemalis	0.213	0.954
Dendrocopos minor	0.211	0.538
Anas strepera	0.210	0.607
Netta rufina	0.199	0.698
Oxyura leucocephala	0.189	0.915
Oenanthe isabellina	0.188	0.918
Thalasseus sandvicensis	0.186	0.750
Loxia scotica	0.185	0.946
Panurus biarmicus	0.182	0.699
Locustella luscinioides	0.179	0.723
Aquila adalberti	0.178	0.890
Porzana parva	0.166	0.776
Ardea alba	0.160	0.771
Eremophila alpestris	0.158	0.936
Botaurus stellaris	0.156	0.717
Emberiza cia	0.155	0.764
Sylvia communis	0.154	0.495
Fulica atra	0.153	0.491
Acrocephalus melanopogon	0.151	0.820

Species	$\mathrm{TSS}_{\mathrm{BioScore}}$	$\mathrm{TSS}_{\mathrm{FMM}}$
Ixobrychus minutus	0.150	0.672
Hydroprogne caspia	0.145	0.811
Porzana porzana	0.142	0.659
Columba palumbus	0.128	0.389
Coloeus monedula	0.127	0.475
Passer montanus	0.125	0.561
Pyrrhocorax pyrrhocorax	0.119	0.846
Porzana pusilla	0.116	0.714
Porphyrio porphyrio	0.115	0.872
Tyto alba	0.114	0.529
Monticola solitarius	0.113	0.769
Circus aeruginosus	0.113	0.653
Linaria cannabina	0.090	0.485
Acrocephalus arundinaceus	0.084	0.634
Tadorna ferruginea	0.077	0.764
Tachybaptus ruficollis	0.077	0.408
Hippolais olivetorum	0.077	0.923
Emberiza schoeniclus	0.073	0.640
Elanus caeruleus	0.056	0.833
Alectoris barbara	0.051	0.999
Acrocephalus scirpaceus	0.049	0.532
Saxicola rubetra	0.041	0.696
Limosa lapponica	0.040	0.791
Clanga clanga	0.038	0.858
Emberiza pusilla	0.029	0.922
Motacilla alba	0.025	0.448
Cecropis daurica	0.021	0.799
Oenanthe leucura	0.017	0.900
Branta leucopsis	0.014	0.726
Alcedo atthis	0.012	0.407
Ichthyaetus audouinii	0.010	0.909
Uria aalge	0.009	0.874
Microcarbo pygmeus	0.004	0.904
Apus caffer	0.003	0.881

Species	TSS$_{\mathrm{BioScore}}$	TSS$_{\mathrm{FMM}}$
Aquila fasciata	0.003	0.759
Sitta neumayer	0.002	0.959
Glareola nordmanni	0.000	0.510
Motacilla citreola	0.000	0.874
Pelecanus onocrotalus	0.000	0.944
Hydrobates pelagicus	0.000	0.862
Calidris minuta	0.000	0.844
Falco eleonorae	0.000	0.818
Sterna dougallii	-0.003	0.761
Anser erythropus	-0.005	0.666
Circus macrourus	-0.009	1.000
Falco tinnunculus	-0.033	0.398
Motacilla cinerea	-0.035	0.544
Hirundo rustica	-0.150	0.456

Appendix 3: Correspondence of BioScore 2.0 and FMM binary maps

Table App3.1: Correspondence between binary maps based on BioScore 2.0 models and full multivariate models as measured by overall accuracy ordered, ordered according to decreasing overall accuracy.

Species	Overall accuracy
Sterna dougallii	0.997
Anser erythropus	0.994
Alectoris barbara	0.993
Oenanthe pleschanka	0.993
Loxia scotica	0.989
Anthus cervinus	0.987
Chroicocephalus genei	0.986
Circus macrourus	0.986
Sylvia sarda	0.985
Glareola nordmanni	0.984
Phoenicopterus roseus	0.984
Calidris maritima	0.983
Fulica cristata	0.983
Sitta neumayer	0.983
Buteo lagopus	0.982
Pelecanus crispus	0.977
Poecile cinctus	0.976
Stercorarius longicaudus	0.974
Clangula hyemalis	0.973
Falco rusticolus	0.973
Ichthyaetus audouinii	0.972
Melanitta nigra	0.971
Numenius phaeopus	0.971
Charadrius morinellus	0.970
Acrocephalus paludicola	0.969
Limosa lapponica	0.969
Chersophilus duponti	0.968
Marmaronetta angustirostris	0.968
Emberiza rustica	0.966
Gypaetus barbatus	0.966
Oxyura leucocephala	0.966
Apus caffer	0.965
Hippolais olivetorum	0.965
Plectrophenax nivalis	0.965
Aquila adalberti	0.964
Lanius nubicus	0.964

Species	Overall accuracy
Calcarius lapponicus	0.963
Calidris minuta	0.963
Perisoreus infaustus	0.963
Calandrella rufescens	0.961
Surnia ulula	0.961
Gelochelidon nilotica	0.960
Hydrobates pelagicus	0.960
Accipiter brevipes	0.958
Loxia pytyopsittacus	0.958
Sylvia melanocephala	0.958
Uria aalge	0.958
Ficedula semitorquata	0.956
Lagopus muta	0.956
Porphyrio porphyrio	0.956
Alectoris chukar	0.954
Oenanthe isabellina	0.954
Plegadis falcinellus	0.954
Buteo rufinus	0.953
Microcarbo pygmeus	0.953
Phalaropus lobatus	0.953
Strix nebulosa	0.953
Calidris alpina	0.950
Phylloscopus borealis	0.950
Emberiza melanocephala	0.948
Prunella collaris	0.948
Hydroprogne caspia	0.947
Melanocorypha calandra	0.947
Melanitta fusca	0.946
Galerida theklae	0.944
Passer hispaniolensis	0.944
Pterocles alchata	0.944
Ardeola ralloides	0.943
Eremophila alpestris	0.943
Pluvialis apricaria	0.943
Aegypius monachus	0.941
Calandrella brachydactyla	0.941
Elanus caeruleus	0.941
Falco naumanni	0.941
Falco eleonorae	0.941
Glareola pratincola	0.940
Alectoris graeca	0.939
Pyrrhocorax graculus	0.939
Thalasseus sandvicensis	0.939
Caprimulgus ruficollis	0.938
Pterocles orientalis	0.938
Falco columbarius	0.937
Mergellus albellus	0.936
Merops apiaster	0.935
Hydrocoloeus minutus	0.934
Charadrius alexandrinus	0.933
Gavia stellata	0.932
Gallinago media	0.930
Platalea leucorodia	0.930
Poecile lugubris	0.930
Sturnus unicolor	0.930
Haematopus ostralegus	0.929
Gavia arctica	0.927
Otis tarda	0.927
Philomachus pugnax	0.926
Gyps fulvus	0.925
Oenanthe leucura	0.923
Asio flammeus	0.922
Emberiza pusilla	0.922
Picoides tridactylus	0.922
Recurvirostra avosetta	0.922
Oenanthe hispanica	0.921
Tetrao urogallus	0.920
Cygnus cygnus	0.919

Species	Overall accuracy
Anas penelope	0.918
Clanga pomarina	0.918
Podiceps auritus	0.918
Sterna paradisaea	0.918
Aquila heliaca	0.917
Sylvia nisoria	0.917
Sylvia hortensis	0.915
Dendrocopos syriacus	0.913
Sylvia undata	0.912
Clamator glandarius	0.910
Acrocephalus melanopogon	0.909
Falco vespertinus	0.907
Monticola saxatilis	0.906
Tetrax tetrax	0.905
Anas acuta	0.902
Loxia leucoptera	0.899
Tetrastes bonasia	0.899
Aythya nyroca	0.898
Lanius minor	0.898
Strix uralensis	0.898
Sternula albifrons	0.896
Himantopus himantopus	0.895
Aquila fasciata	0.894
Emberiza cirlus	0.894
Branta leucopsis	0.893
Tringa glareola	0.893
Sylvia cantillans	0.892
Ichthyaetus melanocephalus	0.890
Larus canus	0.889
Lyrurus tetrix	0.889
Lagopus lagopus	0.887
Neophron percnopterus	0.887
Otus scops	0.887
Aquila chrysaetos	0.885

Species	Overall accuracy
Ficedula parva	0.885
Pyrrhocorax pyrrhocorax	0.884
Limosa limosa	0.882
Cecropis daurica	0.881
Aegolius funereus	0.880
Pandion haliaetus	0.880
Alectoris rufa	0.873
Falco cherrug	0.872
Hippolais polyglotta	0.872
Phylloscopus bonelli	0.872
Clanga clanga	0.871
Egretta garzetta	0.870
Monticola solitarius	0.870
Porzana pusilla	0.870
Falco peregrinus	0.868
Chlidonias hybrida	0.865
Glaucidium passerinum	0.865
Burhinus oedicnemus	0.864
Hieraaetus pennatus	0.864
Tadorna ferruginea	0.862
Netta rufina	0.860
Ardea purpurea	0.858
Ficedula albicollis	0.858
Lanius senator	0.856
Ciconia nigra	0.854
Circaetus gallicus	0.854
Perdix perdix	0.852
Poecile montanus	0.851
Sylvia curruca	0.851
Crex crex	0.849
Nycticorax nycticorax	0.849
Regulus ignicapilla	0.848
Coracias garrulus	0.847
Dendrocopos leucotos	0.847

Species	Overall accuracy
Loxia curvirostra	0.847
Chlidonias niger	0.844
Luscinia luscinia	0.844
Mergus merganser	0.843
Emberiza cia	0.838
Dryocopus martius	0.836
Locustella fluviatilis	0.832
Sitta europaea	0.830
Dendrocopos major	0.825
Nucifraga caryocatactes	0.823
Scolopax rusticola	0.823
Anthus trivialis	0.822
Hippolais icterina	0.822
Phylloscopus sibilatrix	0.821
Accipiter gentilis	0.819
Corvus frugilegus	0.815
Phylloscopus trochilus	0.814
Regulus regulus	0.813
Sturnus vulgaris	0.813
Ardea alba	0.807
Phoenicurus phoenicurus	0.805
Alauda arvensis	0.804
Milvus milvus	0.801
Vanellus vanellus	0.801
Anas clypeata	0.800
Sylvia atricapilla	0.799
Grus grus	0.797
Ixobrychus minutus	0.797
Sterna hirundo	0.797
Porzana parva	0.792
Numenius arquata	0.791
Phylloscopus collybita	0.791
Muscicapa striata	0.787
Tringa totanus	0.786

Species	Overall accuracy
Anthus campestris	0.784
Upupa epops	0.784
Panurus biarmicus	0.783
Lophophanes cristatus	0.782
Ciconia ciconia	0.780
Strix aluco	0.780
Pernis apivorus	0.779
Lullula arborea	0.777
Lanius collurio	0.776
Dendrocopos medius	0.775
Falco subbuteo	0.774
Passer montanus	0.774
Gallinago gallinago	0.768
Picus viridis	0.768
Luscinia megarhynchos	0.767
Poecile palustris	0.767
Haliaeetus albicilla	0.766
Streptopelia turtur	0.766
Circus pygargus	0.764
Aythya fuligula	0.759
Botaurus stellaris	0.757
Motacilla alba	0.757
Jynx torquilla	0.754
Porzana porzana	0.752
Anas querquedula	0.751
Prunella modularis	0.751
Sylvia borin	0.750
Coturnix coturnix	0.749
Aythya ferina	0.746
Bubo bubo	0.744
Circus cyaneus	0.744
Emberiza hortulana	0.739
Emberiza calandra	0.737
Lanius excubitor	0.735

Species	Overall accuracy
Anthus pratensis	0.733
Columba oenas	0.733
Saxicola torquatus	0.727
Galerida cristata	0.726
Locustella luscinioides	0.726
Milvus migrans	0.725
Athene noctua	0.722
Luscinia svecica	0.716
Columba palumbus	0.703
Oriolus oriolus	0.702
Picus canus	0.702
Linaria cannabina	0.697
Anas strepera	0.690
Oenanthe oenanthe	0.685
Turdus viscivorus	0.685
Falco tinnunculus	0.676
Caprimulgus europaeus	0.675
Corvus corax	0.670
Locustella naevia	0.670
Podiceps cristatus	0.670
Tyto alba	0.667
Acrocephalus arundinaceus	0.647
Circus aeruginosus	0.647
Motacilla flava	0.645
Sylvia communis	0.640
Coloeus monedula	0.618
Fulica atra	0.610
Emberiza schoeniclus	0.606
Dendrocopos minor	0.586
Saxicola rubetra	0.584
Acrocephalus scirpaceus	0.568
Tachybaptus ruficollis	0.563
Emberiza citrinella	0.541
Motacilla cinerea	0.539
Alcedo atthis	0.465
Hirundo rustica	0.322
Motacilla citreola	0.119
Pelecanus onocrotalus	0.019

Table Appendix 3.2: Correspondence between binary maps based on BioScore 2.0 models and full multivariate models as measured by the TSS, ordered according to decreasing TSS.

Species	TSS
Falco naumanni	0.910
Sylvia melanocephala	0.899
Melanocorypha calandra	0.894
Merops apiaster	0.890
Calandrella brachydactyla	0.866
Buteo lagopus	0.847
Otis tarda	0.847
Emberiza rustica	0.843
Lyrurus tetrix	0.838
Numenius phaeopus	0.825
Loxia pytyopsittacus	0.811
Burhinus oedicnemus	0.807

Species	TSS
Surnia ulula	0.801
Emberiza cirlus	0.793
Tetrastes bonasia	0.791
Coracias garrulus	0.787
Aquila chrysaetos	0.786
Sylvia nisoria	0.776
Tetrax tetrax	0.776
Tetrao urogallus	0.775
Asio flammeus	0.770
Clanga pomarina	0.770
Haematopus ostralegus	0.767
Perisoreus infaustus	0.754
Aegolius funereus	0.750
Neophron percnopterus	0.747
Melanitta nigra	0.741
Phylloscopus bonelli	0.716
Picoides tridactylus	0.715
Poecile montanus	0.712
Alectoris rufa	0.708
Perdix perdix	0.708
Sylvia curruca	0.696
Crex crex	0.688
Lanius senator	0.687
Aegypius monachus	0.685
Poecile cinctus	0.682
Regulus ignicapilla	0.682
Otus scops	0.679
Falco peregrinus	0.678
Sitta europaea	0.678
Dryocopus martius	0.673
Loxia curvirostra	0.668
Scolopax rusticola	0.658
Anthus trivialis	0.645
Anthus campestris	0.644

Species	TSS
Phylloscopus sibilatrix	0.643
Corvus frugilegus	0.639
Ficedula parva	0.639
Pluvialis apricaria	0.636
Strix nebulosa	0.636
Accipiter gentilis	0.633
Hippolais polyglotta	0.631
Phylloscopus trochilus	0.630
Gavia arctica	0.627
Regulus regulus	0.621
Hippolais icterina	0.617
Oenanthe hispanica	0.609
Prunella collaris	0.609
Vanellus vanellus	0.604
Circaetus gallicus	0.602
Passer hispaniolensis	0.600
Dendrocopos syriacus	0.597
Ciconia nigra	0.595
Sylvia hortensis	0.595
Anthus cervinus	0.593
Falco columbarius	0.591
Strix uralensis	0.591
Upupa epops	0.589
Larus canus	0.588
Phoenicurus phoenicurus	0.588
Anas penelope	0.586
Milvus milvus	0.581
Glaucidium passerinum	0.580
Galerida cristata	0.579
Lophophanes cristatus	0.564
Falco subbuteo	0.558
Cygnus cygnus	0.557
Pernis apivorus	0.556
Strix aluco	0.556

Species	TSS
Sturnus unicolor	0.556
Lullula arborea	0.555
Galerida theklae	0.554
Poecile palustris	0.554
Sturnus vulgaris	0.552
Gavia stellata	0.550
Lanius collurio	0.550
Anas acuta	0.548
Circus pygargus	0.548
Monticola saxatilis	0.540
Lanius minor	0.536
Emberiza calandra	0.534
Emberiza hortulana	0.532
Clamator glandarius	0.526
Columba oenas	0.524
Prunella modularis	0.523
Streptopelia turtur	0.508
Picus viridis	0.507
Alauda arvensis	0.506
Luscinia megarhynchos	0.503
Philomachus pugnax	0.502
Dendrocopos major	0.498
Jynx torquilla	0.498
Saxicola torquatus	0.492
Coturnix coturnix	0.489
Charadrius morinellus	0.488
Ficedula albicollis	0.486
Locustella fluviatilis	0.485
Sylvia borin	0.482
Bubo bubo	0.481
Phylloscopus collybita	0.481
Hieraaetus pennatus	0.477
Ciconia ciconia	0.476
Nucifraga caryocatactes	0.474

Species	TSS
Phalaropus lobatus	0.471
Athene noctua	0.469
Falco vespertinus	0.468
Calidris alpina	0.456
Muscicapa striata	0.456
Corvus corax	0.455
Circus cyaneus	0.452
Chersophilus duponti	0.448
Anthus pratensis	0.443
Melanitta fusca	0.442
Numenius arquata	0.437
Milvus migrans	0.434
Sylvia undata	0.428
Alectoris graeca	0.426
Passer montanus	0.419
Dendrocopos medius	0.418
Aquila heliaca	0.417
Sylvia atricapilla	0.414
Podiceps auritus	0.411
Oriolus oriolus	0.408
Pandion haliaetus	0.403
Tringa glareola	0.397
Clangula hyemalis	0.393
Sterna hirundo	0.387
Caprimulgus ruficollis	0.384
Hydrocoloeus minutus	0.383
Lagopus muta	0.380
Gyps fulvus	0.379
Sylvia cantillans	0.379
Calandrella rufescens	0.373
Tyto alba	0.367
Tringa totanus	0.362
Ardea purpurea	0.360
Aythya fuligula	0.357

Species	TSS
Dendrocopos leucotos	0.356
Loxia leucoptera	0.350
Mergus merganser	0.349
Sylvia communis	0.346
Lanius excubitor	0.337
Gelochelidon nilotica	0.330
Dendrocopos minor	0.316
Sterna paradisaea	0.316
Linaria cannabina	0.314
Motacilla alba	0.312
Chlidonias hybrida	0.310
Emberiza melanocephala	0.301
Gallinago gallinago	0.298
Luscinia luscinia	0.298
Turdus viscivorus	0.295
Platalea leucorodia	0.292
Caprimulgus europaeus	0.291
Motacilla flava	0.289
Anas clypeata	0.288
Phylloscopus borealis	0.277
Poecile lugubris	0.276
Calidris maritima	0.263
Pterocles orientalis	0.259
Coloeus monedula	0.252
Gallinago media	0.251
Lagopus lagopus	0.250
Himantopus himantopus	0.249
Picus canus	0.249
Anas querquedula	0.246
Aythya ferina	0.246
Pterocles alchata	0.239
Chlidonias niger	0.232
Ardeola ralloides	0.230
Columba palumbus	0.230

Species	TSS
Oenanthe oenanthe	0.228
Locustella naevia	0.224
Mergellus albellus	0.224
Emberiza citrinella	0.216
Glareola pratincola	0.213
Pyrrhocorax graculus	0.212
Accipiter brevipes	0.208
Stercorarius longicaudus	0.206
Podiceps cristatus	0.202
Grus grus	0.198
Aquila adalberti	0.196
Aythya nyroca	0.164
Calcarius lapponicus	0.162
Nycticorax nycticorax	0.155
Limosa lapponica	0.154
Emberiza cia	0.148
Ficedula semitorquata	0.145
Sternula albifrons	0.145
Egretta garzetta	0.143
Netta rufina	0.141
Fulica atra	0.138
Limosa limosa	0.138
Falco rusticolus	0.135
Sylvia sarda	0.133
Monticola solitarius	0.130
Charadrius alexandrinus	0.128
Anas strepera	0.124
Eremophila alpestris	0.121
Ichthyaetus melanocephalus	0.118
Plegadis falcinellus	0.117
Porzana porzana	0.116
Chroicocephalus genei	0.114
Microcarbo pygmeus	0.110
Plectrophenax nivalis	0.109

Species	TSS
Gypaetus barbatus	0.108
Oenanthe pleschanka	0.108
Falco tinnunculus	0.100
Recurvirostra avosetta	0.096
Tachybaptus ruficollis	0.092
Clanga clanga	0.084
Buteo rufinus	0.083
Luscinia svecica	0.082
Emberiza schoeniclus	0.081
Haliaeetus albicilla	0.080
Saxicola rubetra	0.080
Anser erythropus	0.075
Hydroprogne caspia	0.074
Pyrrhocorax pyrrhocorax	0.072
Pelecanus crispus	0.069
Botaurus stellaris	0.067
Panurus biarmicus	0.063
Lanius nubicus	0.062
Alectoris chukar	0.059
Circus macrourus	0.057
Ardea alba	0.054
Circus aeruginosus	0.054
Locustella luscinioides	0.054
Porzana parva	0.054
Acrocephalus melanopogon	0.053
Falco cherrug	0.051
Ixobrychus minutus	0.051
Porzana pusilla	0.051
Oxyura leucocephala	0.050
Acrocephalus arundinaceus	0.045
Oenanthe isabellina	0.045
Phoenicopterus roseus	0.043

Species	TSS
Emberiza pusilla	0.035
Acrocephalus paludicola	0.034
Acrocephalus scirpaceus	0.031
Branta leucopsis	0.029
Elanus caeruleus	0.029
Cecropis daurica	0.028
Tadorna ferruginea	0.027
Fulica cristata	0.023
Loxia scotica	0.023
Alcedo atthis	0.013
Apus caffer	0.012
Aquila fasciata	0.009
Marmaronetta angustirostris	0.009
Porphyrio porphyrio	0.009
Thalasseus sandvicensis	0.009
Hippolais olivetorum	0.007
Oenanthe leucura	0.007
Ichthyaetus audouinii	0.004
Uria aalge	0.004
Sitta neumayer	0.003
Hydrobates pelagicus	0.001
Alectoris barbara	0.000
Calidris minuta	0.000
Falco eleonorae	0.000
Glareola nordmanni	0.000
Motacilla citreola	0.000
Pelecanus onocrotalus	0.000
Sterna dougallii	0.000
Motacilla cinerea	-0.003
Hirundo rustica	-0.156

Appendix 4: Integrative table of map evaluation

Based on true skill statistics and on expert judgement. TSS FMM, true kill statistic of the binary FMM map; TSS Bioscore, true kill statistic of the binary BioScore 2.0 map; TSS comp, true skill statistic of map concordance between binary FMM and BioScore 2.0 maps; TSS Eval, evaluation based on TSS FMM, TSS Bioscore and TSS comp: 1 - „Species is well modelled by BioScore 2.0“, 2 - „Situation unclear, an expert should visually check and evaluate the maps“, 3 - „Species cannot be modelled“, 4 - „Doubtful if the species should be used for BioScore 2.0, but an expert should visually check and evaluate the maps“.

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Accipiter brevipes	0.925	0.363	0.208	4	Good	presence outside know breeding range	good	
Accipiter gentilis	0.56	0.421	0.633	4	Poor		reasonable	density in Scandinavia too high; where is Switzerland?
Acrocephalus arundinaceus	0.634	0.084	0.045	4	Bad	marshland not well represented	poor	occurrence in many countries too low or even absent (Greece)
Acrocephalus melanopogon	0.82	0.151	0.053	4	Bad	marshland not well represented	bad	
Acrocephalus paludicola	0.979	0.792	0.034	4	Poor	marshland not well represented	bad	
Acrocephalus scirpaceus	0.532	0.049	0.031	4	Bad	marshland not well represented	reasonable	But where is Greece?
Aegolius funereus	0.779	0.735	0.750	1	Good		poor	Pyrenees lacking and in general too low values
Aegypius monachus	0.845	0.561	0.685	4	reasonable	is really a potential map and not actual due to i.e. persecution	poor	too restricted (even for actual)
Alauda arvensis	0.504	0.25	0.506	4	good		reasonable	SE Europe and Switzerland underestimated
Alcedo atthis	0.407	0.012	0.013	3	bad		good	SE Europe and Switzerland underestimated
Alectoris barbara	0.999	0.051	0	4	bad		good	
Alectoris chukar	0.948	0.441	0.059	4	bad	map seems not te be clipped with range (within actual range area it seems okay)	bad	Greece underestimated
Alectoris graeca	0.853	0.583	0.426	4	bad	map seems not te be clipped with range (within actual range area it seems okay)	bad	underestimated

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Alectoris rufa	0.642	0.425	0.708	4	bad	map seems not te be clipped with range (within actual range area it seems okay)	bad	Overestimated in SE
Anas acuta	0.702	0.46	0.548	4	poor	strange breeding areas in the Alps, also this map should be clipped with range map	poor	probably too restricted
Anas clypeata	0.57	0.248	0.288	4	reasonable		poor	too restricted
Anas penelope	0.772	0.507	0.586	4	good	sligthly underestimating breeding in western Europe?	reasonable	slightly too restricted
Anas querquedula	0.632	0.303	0.246	4	poor	distribution in eastern and southern Europe not well represented	poor	too restricted
Anas strepera	0.607	0.21	0.124	4	reasonable	difficult to judge	poor	Netherland i.e. too restricted
Anser erythropus	0.666	-0.005	0.075	4	reasonable	potential breeding range and actual situation is different because of reintroduced populations	bad	map is empty
Anthus campestris	0.725	0.614	0.644	4	good		poor	Northern Europe is missing
Anthus cervinus	0.912	0.548	0.593	4	good		reasonable	probably too restricted
Anthus pratensis	0.752	0.498	0.443	4	good		reasonable	Southern part range too restricted
Anthus trivialis	0.679	0.555	0.645	4	good		reasonable	SE Europe and Switzerland underestimated
Apus caffer	0.881	0.003	0.012	4	reasonable	erratic strange species, why presented?	reasonable	difficult too judge
Aquila adalberti	0.89	0.178	0.196	4	poor	breeding area is and certainly was bigger	good	
Aquila chrysaetos	0.705	0.635	0.786	2	good	distribution in UK a bit too positive	good	
Aquila fasciata	0.759	0.003	0.009	4	bad	spain has largest numbers which is not reflected in map, Corsica seems best but species does not occur here	reasonable	missing areas but Spain ok

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Aquila heliaca	0.928	0.651	0.417	4	good	probable potential breeding areas are reflected	reasonable	probably reflecting potential breeding area
Ardea alba	0.771	0.16	0.054	4	bad	inaccurate and outdated, species has recolonised many areas which are not depicted	reasonable	proably too pessimistic
Ardea purpurea	0.782	0.385	0.36	4	reasonable		poor	too restricted
Ardeola ralloides	0.84	0.611	0.23	4	reasonable		poor	difficult too model colonial species
Asio flammeus	0.626	0.475	0.77	4	poor	northern Europe okay but southern and central Europe inadequate	poor	too restricted mainly in southern Europe
Athene noctua	0.593	0.346	0.469	4	reasonable		poor	SE Europe and Switzerland underestimated
Aythya ferina	0.592	0.263	0.246	4	poor	southern Europe underrepresented	reasonable	
Aythya fuligula	0.567	0.22	0.357	4	poor	southern Europe underrepresented	reasonable	probably southern Europe underestimated
Aythya nyroca	0.843	0.638	0.164	4	reasonable	But southern Europe (Spain) underrepresented	reasonable	
Botaurus stellaris	0.717	0.156	0.067	4	reasonable	But southern Europe (Spain) underrepresented	poor	Northern Europe has too high densities France and Spain missing
Branta leucopsis	0.726	0.014	0.029	4	bad	nonsense map	bad	
Bubo bubo	0.634	0.458	0.481	4	good		poor	northern europe too low, spain too high croatia missing
Burhinus oedicnemus	0.778	0.659	0.807	1	reasonable		reasonable	SE Europe underestimated
Buteo lagopus	0.904	0.852	0.847	1	good		good	
Buteo rufinus	0.933	0.278	0.083	4	reasonable		reasonable	Greece is lacking
Calandrella brachydactyla	0.755	0.683	0.866	1	good		good	
Calandrella rufescens	0.865	0.535	0.373	4	good		good	
Calcarius lapponicus	0.966	0.293	0.162	4	good		good	
Calidris alpina	0.742	0.339	0.456	4	reasonable	Clip map with range (Alps should not be included)	poor	too restricted

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation on FMM	Expert comments FMM
Calidris maritima	0.973	0.468	0.263	4	good		good	
Calidris minuta	0.844	0	0	4	bad	map is empty	bad	no breeding occurrences
Caprimulgus europaeus	0.56	0.307	0.291	4	reasonable		good	
Caprimulgus ruficollis	0.821	0.384	0.384	4	still due	map should be clipped (Italy is outside range)	still due	map should be clipped (Italy is outside range)
Cecropis daurica	0.799	0.021	0.028	4	poor	distribution is too feable	poor	SE Europe is not correct
Charadrius alexandrinus	0.819	0.569	0.128	4	poor	strange aberrations in eastern Europe (border effects)	poor	Western Europe not correct
Charadrius morinellus	0.872	0.766	0.488	4	good		reasonable	
Chersophilus duponti	0.927	0.674	0.448	4	poor	distribution in Switzerland incorrect, clip with actual range, values too high?	good	
Chlidonias hybrida	0.873	0.543	0.31	4	poor		reasonable	
Chlidonias niger	0.772	0.423	0.232	4	reasonable		bad	underestimated
Chroicocephalus genei	0.848	0.667	0.114	4	reasonable	Sardinia is missing	bad	
Ciconia ciconia	0.796	0.463	0.476	4	good		reasonable	SE Europe and Switzerland underestimated
Ciconia nigra	0.78	0.556	0.595	4	good	But F and B are missing so possibly outdated situation	good	
Circaetus gallicus	0.698	0.513	0.602	4	good		good	but Greece underestimated
Circus aeruginosus	0.653	0.113	0.054	4	bad	probably occurrence in farmland habitat not taken in to account	good	
Circus cyaneus	0.62	0.339	0.452	4	good		bad	Sweden lacking and France too low
Circus macrourus	1	-0.009	0.057	4	bad	only predicted in Spain!!!	still due	almost absent in Europe
Circus pygargus	0.645	0.539	0.548	4	reasonable	I think too optimistic	reasonable	Romania too high
Clamator glandarius	0.787	0.408	0.526	4	good		bad	SE Europe is missing
Clanga clanga	0.858	0.038	0.084	4	poor		reasona	

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
							ble	
Clanga pomarina	0.882	0.788	0.77	1	poor	strange predictions outside range (Italy-Sweden)	poor	Occurrence in Sweden incorrect and also lacking in SE
Clangula hyemalis	0.954	0.213	0.393	4	good		good	
Coloeus monedula	0.475	0.127	0.252	3	reasonable		reasonable	SE Europe and Switzerland underestimated
Columba oenas	0.533	0.286	0.524	4	reasonable		good	but probably SE Europe underestimated
Columba palumbus	0.389	0.128	0.23	3	good		good	SE Europe and Switzerland underestimated
Coracias garrulus	0.761	0.651	0.787	1	good		good	
Corvus corax	0.581	0.306	0.455	4	poor		good	
Corvus frugilegus	0.659	0.5	0.639	4	good		good	
Coturnix coturnix	0.551	0.28	0.489	4	reasonable	There should be much higher occurrence in south than in north	reasonable	occurrence in north too high, see also CH and Greece
Crex crex	0.736	0.557	0.688	4	reasonable		poor	Western Europe not correct
Cygnus cygnus	0.791	0.49	0.557	4	good		good	
Dendrocopos leucotos	0.85	0.516	0.356	4	good		reasonable	But Pyrenees missing
Dendrocopos major	0.452	0.277	0.498	3	reasonable		reasonable	SE Europe and Switzerland underestimated
Dendrocopos medius	0.768	0.46	0.418	4	good		reasonable	densities in France too low
Dendrocopos minor	0.538	0.211	0.316	4	poor		poor	densities in North too high
Dendrocopos syriacus	0.923	0.73	0.597	4	reasonable	map seems not te be clipped with range (within actual range area it seems okay)	reasonable	Greece and SE are missing
Dryocopus martius	0.711	0.644	0.673	4	good		reasonable	SE Europe and Switzerland underestimated
Egretta garzetta	0.69	0.365	0.143	4	reasonable		poor	
Elanus caeruleus	0.833	0.056	0.029	4	poor		good	

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Emberiza calandra	0.673	0.404	0.534	4	good		good	SE Europe and Switzerland underestimated
Emberiza cia	0.764	0.155	0.148	4	poor	only high altitudes seem to be selected but species occurs also at lower altitudes	good	SE Europe and Switzerland underestimated
Emberiza cirlus	0.724	0.611	0.793	2	good		poor	large parts of SE too low
Emberiza citrinella	0.651	0.217	0.216	4	reasonable		good	SE Europe and Switzerland underestimated
Emberiza hortulana	0.692	0.527	0.532	4	reasonable	some areas like Corsica show occurrences but are outside of range	poor	
Emberiza melanocephala	0.936	0.562	0.301	4	good		poor	Greece is missing
Emberiza pusilla	0.922	0.029	0.035	4	reasonable		poor	Finland too low densities
Emberiza rustica	0.896	0.855	0.843	1	good		poor	Finland too low densities in south
Emberiza schoeniclus	0.64	0.073	0.081	4	bad	something went clearly wrong with model	reasonable	
Eremophila alpestris	0.936	0.158	0.121	4	reasonable	only reasonable when alps are removed (outside range)	reasonable	Greece is missing
Falco cherrug	0.92	0.237	0.051	4	reasonable		good	
Falco columbarius	0.7	0.491	0.591	4	reasonable		poor	densities in Uk too high compared to Scandinavia
Falco eleonorae	0.818	0	0	4	bad	no distribution modelled?	bad	no occurrences
Falco naumanni	0.831	0.731	0.91	1	reasonable	probabilities are too high (in general)	poor	SE Europe is missing
Falco peregrinus	0.481	0.313	0.678	3	reasonable	probably mimicking the old situation and not present breeding range	good	SE Europe and Switzerland underestimated
Falco rusticolus	0.972	0.215	0.135	4	good		good	
Falco subbuteo	0.427	0.28	0.558	3	reasonable	too low probs in Meditteranean	reasonable	
Falco tinnunculus	0.398	-0.033	0.1	3	good	seems okay but difficult to judge density differences	good	SE Europe and Switzerland underestimated

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Falco vespertinus	0.8	0.685	0.468	4	poor	too optimistic, for instance Poland is out of range	good	
Ficedula albicollis	0.833	0.576	0.486	4	good		reasonable	
Ficedula parva	0.769	0.653	0.639	4	reasonable	Italy is indicated as breeding area but species does not occur here	good	small mistakes (Italy)
Ficedula semitorquata	0.914	0.412	0.145	4	reasonable		poor	Greece is lacking
Fulica atra	0.491	0.153	0.138	3	bad	probs too low and Med basin missing	good	SE Europe and Switzerland underestimated
Fulica cristata	0.941	0.216	0.023	4	good	but very limited breeding range	good	but very limited breeding range
Galerida cristata	0.768	0.598	0.579	4	good		reasonable	SE Europe and Switzerland underestimated
Galerida theklae	0.872	0.568	0.554	4	reasonable	Portugal too low	poor	observations outside range
Gallinago gallinago	0.733	0.255	0.298	4	poor	mainland Europe much too low (altitude seems to be too dominant)	poor	too low
Gallinago media	0.902	0.557	0.251	4	reasonable	Alps are included which is not in breeding range	poor	breeding range too restricted
Gavia arctica	0.811	0.54	0.627	4	good		good	
Gavia stellata	0.767	0.401	0.55	4	good		good	
Gelochelidon nilotica	0.884	0.535	0.33	4	reasonable	Eastern Europe too prominent (potential areas?)	bad	
Glareola nordmanni	0.51	0	0	4	no occurences		bad	no occurrences
Glareola pratincola	0.847	0.328	0.213	4	poor	many areas missing	poor	many areas missing
Glaucidium passerinum	0.828	0.687	0.58	4	good		poor	Poland too positive, areas missing
Grus grus	0.82	0.244	0.198	4	reasonable	recent recent expansion	good	
Gypaetus barbatus	0.923	0.404	0.108	4	poor	difficult to model because of reintroductions but Alps are missing	good	difficult to model because of reintroductions but Alps are missing

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Gyps fulvus	0.809	0.296	0.379	4	reasonable	this is more of a potential map	good	
Haematopus ostralegus	0.739	0.585	0.767	4	good		reasonable	
Haliaeetus albicilla	0.832	0.241	0.08	4	poor	very incomplete map	poor	too many areas missing mainly in north
Hieraaetus pennatus	0.801	0.486	0.477	4	reasonable		poor	
Himantopus himantopus	0.774	0.497	0.249	4	reasonable		poor	Greece is lacking, Bulgaria too high
Hippolais icterina	0.823	0.576	0.617	4	good		reasonable	densities in North too high
Hippolais olivetorum	0.923	0.077	0.007	4	poor	Croatia completely missing	poor	Greece is lacking
Hippolais polyglotta	0.762	0.548	0.631	4	good		reasonable	Germany is not breeding area
Hirundo rustica	0.456	-0.15	-0.156	3	bad	what is this? Map of infrastructure?	reasonable	SE Europe and Switzerland underestimated
Hydrobates pelagicus	0.862	0	0.001	4	Bad	Difficult	bad	no occurrences
Hydrocoloeus minutus	0.802	0.38	0.383	4	good		poor	Baltic states missing
Hydroprogne caspia	0.811	0.145	0.074	4	Reasonable		bad	??
Ichthyaetus audouinii	0.909	0.01	0.004	4	bad	no occurrences	bad	no occurrences
Ichthyaetus melanocephalus	0.746	0.387	0.118	4	bad	best area Alps?	bad	totally wrong
Ixobrychus minutus	0.672	0.15	0.051	4	bad	basically all marshland bird maps are crap	bad	too low in Southwest
Jynx torquilla	0.583	0.409	0.498	4	poor		good	SE Europe and Switzerland underestimated
Lagopus lagopus	0.879	0.459	0.25	4	bad	Finland is lacking	good	
Lagopus muta	0.928	0.545	0.38	4	good		reasonable	too restricted and pyrenees missing
Lanius collurio	0.727	0.539	0.55	4	good		reasonable	SE Europe and Switzerland underestimated
Lanius excubitor	0.729	0.46	0.337	4	poor	Meditteranean shrike is now different species (L.	reasona	falsely apparent absence in Western Europe and

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
						meridionalis), densities outside Scandinavia too low	ble	France, but probabilities too low to show in map
Lanius minor	0.841	0.56	0.536	4	Good		poor	too low densities in Balkans and Greece
Lanius nubicus	0.912	0.268	0.062	4	reasonable	Doesn't occur in Spain	poor	too low densities in Balkans and Greece
Lanius senator	0.815	0.649	0.687	4	good		good	too low densities in Balkans and Greece
Larus canus	0.824	0.486	0.588	4	still due	again this irritating occurrence in Alps	good	
Limosa lapponica	0.791	0.04	0.154	4	good		reasonable	very restricted
Limosa limosa	0.781	0.226	0.138	4	poor		poor	eastern Europe too low
Linaria cannabina	0.485	0.09	0.314	3	good		good	SE Europe and Switzerland underestimated
Locustella fluviatilis	0.84	0.587	0.485	4	good		poor	Sweden is not within range
Locustella luscinioides	0.723	0.179	0.054	4	poor	marshland not well represented	poor	SW Europe is lacking
Locustella naevia	0.65	0.273	0.224	4	reasonable		reasonable	France too low
Lophophanes cristatus	0.678	0.558	0.564	4	good	only some strange occurrences in Italy	reasonable	SE Europe too high
Loxia curvirostra	0.63	0.493	0.668	4	reasonable		reasonable	SE Europe and Switzerland underestimated
Loxia leucoptera	0.86	0.624	0.35	4	good		poor	
Loxia pytyopsittacus	0.852	0.799	0.811	1	good		poor	
Loxia scotica	0.946	0.185	0.023	4	reasonable		poor	
Lullula arborea	0.624	0.501	0.555	4	good	but NW Europe to feeble	reasonable	strange occurrences in Scotland, no data in Greece
Luscinia luscinia	0.908	0.338	0.298	4	reasonable		reasonable	
Luscinia megarhynchos	0.679	0.415	0.503	4	good		good	SE Europe and Switzerland underestimated

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation on FMM	Expert comments FMM
Luscinia svecica	0.727	0.249	0.082	4	poor	too many aberrations	poor	many areas missing
Lyrurus tetrix	0.861	0.784	0.838	1	reasonable	But Pyrenees out of current range	poor	too restricted
Marmaronetta angustirostris	0.924	0.233	0.009	4	bad	most breeding sites are missing	reasonable	very rare
Melanitta fusca	0.892	0.381	0.442	4	bad	Baltic see pop is missing	bad	Baltic states missing
Melanitta nigra	0.877	0.598	0.741	4	good		reasonable	too restricted
Melanocorypha calandra	0.836	0.754	0.894	1	reasonable	Croatia is missing	good	but SE Balkan missing
Mergellus albellus	0.822	0.36	0.224	4	reasonable		bad	Sweden is missing
Mergus merganser	0.74	0.318	0.349	4	reasonable	parts of Germany are missing	good	
Merops apiaster	0.78	0.703	0.89	1	reasonable	occurrences in North are too high	reasonable	too optimistic in North
Microcarbo pygmeus	0.904	0.004	0.11	4	reasonable		poor	impossible to model
Milvus migrans	0.667	0.399	0.434	4	good		poor	distribution in East too low
Milvus milvus	0.62	0.468	0.581	4	good		good	
Monticola saxatilis	0.75	0.497	0.54	4	reasonable		poor	too few in SE Europe
Monticola solitarius	0.769	0.113	0.13	4	poor	is more common than indicated here	poor	too few in SE Europe
Motacilla alba	0.448	0.025	0.312	3	no map		good	SE Europe and Switzerland underestimated
Motacilla cinerea	0.544	-0.035	-0.003	4	bad	only main rivers indicated	reasonable	very hard to judge
Motacilla citreola	0.874	0	0	4	bad	Where is Poland	bad	Too rare
Motacilla flava	0.618	0.222	0.289	4	still due		poor	UK, CH and Greece too low
Muscicapa striata	0.485	0.241	0.456	3	reasonable	Iberian peninsula too low occurerrences	good	SE Europe and Switzerland underestimated
Neophron percnopterus	0.847	0.653	0.747	4	reasonable		poor	SE underestimated
Netta rufina	0.698	0.199	0.141	4	poor		bad	

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Nucifraga caryocatactes	0.866	0.664	0.474	4	good		bad	too high in Scandinavia
Numenius arquata	0.698	0.326	0.437	4	good		reasonable	
Numenius phaeopus	0.871	0.581	0.825	4	good		reasonable	Baltic states missing
Nycticorax nycticorax	0.727	0.371	0.155	4	bad	colonial birds are very difficult to model!!!	poor	
Oenanthe hispanica	0.808	0.569	0.609	4	good		poor	SE Europe not well represented
Oenanthe isabellina	0.918	0.188	0.045	4	good		good	
Oenanthe leucura	0.9	0.017	0.007	4	bad		good	
Oenanthe oenanthe	0.593	0.215	0.228	4	bad	only higher altitude habitat is modelled correctly	reasonable	SE Europe and Switzerland underestimated
Oenanthe pleschanka	0.997	0.619	0.108	4	good		good	
Oriolus oriolus	0.687	0.409	0.408	4	good		reasonable	SE Europe and Switzerland underestimated
Otis tarda	0.847	0.77	0.847	1	reasonable	except for France	reasonable	mistakes in Southeast
Otus scops	0.689	0.511	0.679	4	good		good	SE Europe and Switzerland underestimated
Oxyura leucocephala	0.915	0.189	0.05	4	bad		bad	
Pandion haliaetus	0.764	0.323	0.403	4	bad	i.e. UK and Mediterranean is missing	poor	
Panurus biarmicus	0.699	0.182	0.063	4	reasonable	difficult to judge	bad	
Passer hispaniolensis	0.824	0.554	0.6	4	good	only in Italy some mistakes	good	SE underestimated
Passer montanus	0.561	0.125	0.419	4	poor		good	Southeast and CH underestimated
Pelecanus crispus	0.949	0.457	0.069	4	bad	pfff too difficult	poor	Greece underestimated
Pelecanus onocrotalus	0.944	0	0	4	bad	map is empty	poor	Greece underestimated
Perdix perdix	0.623	0.43	0.708	4	good		poor	Meditteranean area too low
Perisoreus infaustus	0.945	0.844	0.754	1	good		reasona	too restricted

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation on Bioscore	Expert comments Bioscore	Expert evaluation on FMM	Expert comments FMM
							ble	
Pernis apivorus	0.551	0.34	0.556	4	good		reasonable	SE Europe and Switzerland underestimated
Phalaropus lobatus	0.816	0.351	0.471	4	good		poor	too restricted
Philomachus pugnax	0.72	0.413	0.502	4	reasonable		bad	what happened?
Phoenicopterus roseus	0.926	0.297	0.043	4	bad	lacking occurrences	reasonable	SE underestimated
Phoenicurus phoenicurus	0.617	0.454	0.588	4	poor	mountain areas too much exaggerated?	poor	Scandinavia too high
Phylloscopus bonelli	0.732	0.618	0.716	4	good		bad	many mistakes
Phylloscopus borealis	0.916	0.355	0.277	4	poor	Sweden is not right	bad	Finland missing
Phylloscopus collybita	0.514	0.305	0.481	4	good		reasonable	SE Europe and Switzerland underestimated
Phylloscopus sibilatrix	0.713	0.573	0.643	4	reasonable	Northern Europe is too high	reasonable	Northern Europe is too high and edges too restricted
Phylloscopus trochilus	0.74	0.58	0.63	4	reasonable	Northern Europe is too low	good	
Picoides tridactylus	0.796	0.714	0.715	4	reasonable		good	But Switzerland is lacking
Picus canus	0.769	0.293	0.249	4	reasonable	North is too low	poor	Western Europe not correct
Picus viridis	0.494	0.319	0.507	3	reasonable	North is too high	reasonable	SE Europe and Switzerland underestimated
Platalea leucorodia	0.822	0.364	0.292	4	poor	too many mistakes	bad	
Plectrophenax nivalis	0.955	0.296	0.109	4	good		poor	too restricted
Plegadis falcinellus	0.905	0.376	0.117	4	bad		bad	too restricted mainly in SE
Pluvialis apricaria	0.752	0.579	0.636	4	reasonable	Alps are outside breeding range	reasonable	
Podiceps auritus	0.762	0.286	0.411	4	reasonable		bad	too restricted
Podiceps cristatus	0.552	0.25	0.202	4	bad	difficult to have all potential habitat probably	reasonable	
Poecile cinctus	0.975	0.859	0.682	4	good		reasonable	Norway too positive

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
Poecile lugubris	0.931	0.561	0.276	4	bad	many occurrences outside range	reasonable	Balkan range is missing
Poecile montanus	0.729	0.587	0.712	4	reasonable	UK and NL wrong!	bad	UK wrong
Poecile palustris	0.638	0.435	0.554	4	reasonable		poor	Spain is not within range
Porphyrio porphyrio	0.872	0.115	0.009	4	bad		poor	Sardinia is missing
Porzana parva	0.776	0.166	0.054	4	bad		bad	
Porzana porzana	0.659	0.142	0.116	4	bad		bad	
Porzana pusilla	0.714	0.116	0.051	4	bad		bad	
Prunella collaris	0.874	0.782	0.609	4	reasonable		good	but Greece is lacking
Prunella modularis	0.583	0.386	0.523	4	reasonable		reasonable	Too high density in north too low in SE
Pterocles alchata	0.879	0.399	0.239	4	bad		reasonable	too restricted maybe and occurrences in East are false
Pterocles orientalis	0.856	0.355	0.259	4	reasonable		reasonable	too restricted maybe
Pyrrhocorax graculus	0.886	0.571	0.212	4	good		good	but see Greece
Pyrrhocorax pyrrhocorax	0.846	0.119	0.072	4	bad		poor	missing in too many areas (UK)
Recurvirostra avosetta	0.791	0.419	0.096	4	bad	too many inland sites missing	poor	too restricted
Regulus ignicapilla	0.69	0.542	0.682	4	reasonable		reasonable	
Regulus regulus	0.65	0.486	0.621	4	poor	too low occurrences in western part	good	
Saxicola rubetra	0.696	0.041	0.08	4	bad	only high latitudes modelled	reasonable	
Saxicola torquatus	0.646	0.331	0.492	4	good	Maps shows combined distribution of S. torquatus and rubicola	reasonable	Maps shows combined distribution of S. torquatus and rubicola
Scolopax rusticola	0.688	0.608	0.658	4	reasonable	values in west too low?	poor	too restricted
Sitta europaea	0.545	0.429	0.678	4	poor	too many parts with too ow occurrence probs	bad	too high probs in North
Sitta neumayer	0.959	0.002	0.003	4	bad	no occurrences	bad	unclear

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation on FMM	Expert comments FMM
Stercorarius longicaudus	0.976	0.408	0.206	4	reasonable		good	
Sterna dougallii	0.761	-0.003	0	4	bad	no occurrences	bad	no occurrences
Sterna hirundo	0.647	0.349	0.387	4	reasonable		bad	too many area lacking
Sterna paradisaea	0.766	0.297	0.316	4	bad	no occurences in west but occurrences in Alps!!	bad	too many areas lacking
Sternula albifrons	0.774	0.274	0.145	4	bad	too many mistakes	bad	only rivers
Streptopelia turtur	0.646	0.325	0.508	4	bad	clear mistakes in map	reasonable	too high occurrences in Sweden
Strix aluco	0.489	0.322	0.556	3	poor		reasonable	SE Europe and Switzerland underestimated
Strix nebulosa	0.878	0.588	0.636	4	good		bad	too restricted
Strix uralensis	0.874	0.79	0.591	4	reasonable		reasonable	But Balkan is lacking
Sturnus unicolor	0.882	0.533	0.556	4	reasonable		reasonable	France and Italy are not within range
Sturnus vulgaris	0.575	0.38	0.552	4	good	but hard to judge	reasonable	SE Europe and Switzerland underestimated
Surnia ulula	0.832	0.753	0.801	1	good		bad	too restricted
Sylvia atricapilla	0.441	0.249	0.414	3	poor	clear mistakes in map	reasonable	SE Europe and Switzerland underestimated
Sylvia borin	0.592	0.337	0.482	4	poor	clear aberrations in soouth	reasonable	SE Europe and Switzerland underestimated
Sylvia cantillans	0.801	0.369	0.379	4	poor	Italy and East underestimated	reasonable	West is good East is restricted
Sylvia communis	0.495	0.154	0.346	3	poor	Med area underestimated	good	SE Europe and Switzerland underestimated
Sylvia curruca	0.711	0.497	0.696	4	reasonable	But Pryrenees wrong	reasonable	some mistakes in the map
Sylvia hortensis	0.765	0.512	0.595	4	reasonable		poor	east Med is missing
Sylvia melanocephala	0.795	0.682	0.899	1	good		poor	too restricted in east and too extended in west
Sylvia nisoria	0.802	0.651	0.776	1	still due	Iberian peninsula is	poor	too restricted

Species	TSS FMM	TSS Bioscore	TSS comp	TSS Eval	Expert evaluation Bioscore	Expert comments Bioscore	Expert evaluation FMM	Expert comments FMM
						outside range		
Sylvia sarda	0.97	0.359	0.133	4	good		good	
Sylvia undata	0.803	0.401	0.428	4	bad	complete north is missing	poor	France is missing
Tachybaptus ruficollis	0.408	0.077	0.092	3	bad		reasonable	SE Europe and Switzerland underestimated
Tadorna ferruginea	0.764	0.077	0.027	4	reasonable		good	
Tetrao urogallus	0.844	0.771	0.775	1	reasonable		poor	too restricted ie Scotland
Tetrastes bonasia	0.853	0.797	0.791	1	reasonable		poor	too restricted
Tetrax tetrax	0.858	0.796	0.776	1	good		poor	too restricted
Thalasseus sandvicensis	0.75	0.186	0.009	4	bad		bad	no occurrences
Tringa glareola	0.861	0.456	0.397	4	reasonable		good	
Tringa totanus	0.623	0.342	0.362	4	poor	in many parts missing	poor	in many parts missing
Turdus viscivorus	0.454	0.272	0.295	3	reasonable		poor	too extended in north
Tyto alba	0.529	0.114	0.367	4	reasonable		poor	too restricted
Upupa epops	0.726	0.549	0.589	4	reasonable	but strange mistakes	reasonable	SE Europe and Switzerland underestimated
Uria aalge	0.874	0.009	0.004	4	bad	no occurrences	bad	no occurrences
Vanellus vanellus	0.622	0.433	0.604	4	poor	much commoner than indicated here	good	

Appendix 5: Comparison of AUC and dose-effect relation between univariate Bioscore2 pressure models and alternative univariate models with only a linear term

Comparison of AUC and summarizing description of dose-effect relation between univariate Bioscore2 pressure models and alternative univariate models with only a linear term. Ten sample species are analysed. Only variables where at least in one of the two models an AUC of 0.60 or higher was attained are shown. The direction of dose-effect relations is described as from the left to the right; 'ascending' thus means that presence probability increases with increasing values of the explanatory variable. Used abbreviations: AUC-B, AUC of Bioscore2 model; AUC-L, AUC of model with only linear term; DRC-B, dose-response curve of the Bisocore2 model; DCR-L, dose-response curve of the model with only linear term.

Species	Variable	AUC B	AUC L	Description
Acrocephalus arundinaceus	div3_1_20_mean_5km	0.61	0.60	already Bioscore2 model with only the linear term
	div3_2_20_mean_5km	0.62	0.61	already Bioscore2 model with only the linear term
	div3_2_50_mean_5km	0.61	0.61	already Bioscore2 model with only the linear term
	div4_1_20_mean_5km	0.65	0.66	few observations at high values of explanatory variable; DRC-B highly variable; DRC-L ascending
	div4_1_50_mean_5km	0.64	0.64	few observations at high values of explanatory variable; DRC-B highly variable; DRC-L ascending
	div5_1_20_mean_5km	0.64	0.63	few observations at high values of explanatory variable; DRC-L ascending
	div5_1_50_mean_5km	0.62	0.63	few observations at high values of explanatory variable; DRC-L ascending
Acrocephalus paludicola	desic_mean_5km	0.71	0.71	few observations at high values of explanatory variable; DRC-B highly variable; DRC-L almost horizontal
	div3_1_20_mean_5km	0.59	0.60	DRC-B highly variable; DRC-L ascending
	div3_1_50_mean_5km	0.80	0.85	DRC-L ascending
	div3_2_20_mean_5km	0.69	0.68	few observations at high values of explanatory variable; DRC-B concave; DRC-L descending
	div3_2_50_mean_5km	0.75	0.78	DRC-B concave; DRC-L descending
	div3_3_20_mean_5km	0.65	0.68	few observations at high values of explanatory variable; DRC-B concave; DRC-B highly variable; DRC-L descending
	div3_3_50_mean_5km	0.69	0.64	few observations at high values of explanatory variable; DRC-B concave; DRC-B highly variable; DRC-L descending
	div4_1_20_mean_5km	0.93	0.93	already Bioscore2 model with only the linear term
	div4_1_50_mean_5km	0.92	0.92	already Bioscore2 model with only the linear term
	div5_1_20_mean_5km	0.81	0.80	DRC-B concave; DRC-B highly variable; DRC-L descending
	div5_1_50_mean_5km	0.75	0.72	DRC-B concave; DRC-L descending
	fma_f3_5km	0.69	0.68	few observations at high values of explanatory variable; DRC-B concave; DRC-B highly variable; DRC-L descending
	fma_f5_5km	0.88	0.88	few observations at high values of explanatory variable;

Species	Variable	AUC B	AUC L	Description
				DRC-B highly variable; DRC-L ascending
	ndep_mean_5km	0.73	0.75	DRC-L ascending
	sdep_mean_5km	0.61	0.59	DRC-B highly variable; DRC-L ascending
Alauda arvensis	div3_2_20_mean_5km	0.62	0.61	DRC-B concave; DRC-L descending
	div3_2_50_mean_5km	0.61	0.61	DRC-B concave; DRC-L descending
	div3_3_20_mean_5km	0.61	0.61	DRC-B concave; DRC-L descending
	div3_3_50_mean_5km	0.60	0.60	DRC-B concave; DRC-L descending
	div4_1_50_mean_5km	0.65	0.65	DRC-L descending
	napplication_5km	0.64	0.64	DRC-L ascending
	ndep_mean_5km	0.60	0.61	DRC-L ascending
	sdep_mean_5km	0.62	0.62	few observations at high values of explanatory variable; DRC-L descending
Coracius garrulus	div3_1_20_mean_5km	0.73	0.73	already Bioscore2 model with only the linear term
	div3_1_50_mean_5km	0.72	0.72	already Bioscore2 model with only the linear term
	fma_f3_5km	0.62	0.62	DRC-B concave; DRC-L descending
Dendrocopos leucotos	div3_1_20_mean_5km	0.73	0.73	DRC-L descending
	div3_1_50_mean_5km	0.75	0.75	DRC-L descending
	div5_1_20_mean_5km	0.63	0.61	DRC-B concave; DRC-L descending
	fma_f4_5km	0.60	0.61	already Bioscore2 model with only the linear term
	fma_f5_5km	0.61	0.61	DRC-L ascending
	napplication_5km	0.62	0.61	few observations at high values of explanatory variable; DRC-B and DRC-L almost identical
	ndep_mean_5km	0.59	0.60	DRC-B and DRC-L almost identical
Lullula arborea	div3_1_20_mean_5km	0.63	0.63	DRC-L ascending
	div3_2_20_mean_5km	0.65	0.66	DRC-L ascending
	div3_2_50_mean_5km	0.62	0.62	DRC-B and DRC-L almost identical
	ndep_mean_5km	0.66	0.66	DRC-B concave; DCR-L almost horizontal
Emberiza calandra	Desic_mean_5km	0.66	0.66	few observations at high values of explanatory variable; DRC-L ascending
	div3_1_50_mean_5km	0.60	0.60	DRC-L descending
	div3_2_50_mean_5km	0.61	0.61	DRC-L ascending
	div4_1_20_mean_5km	0.61	0.61	DRC-B concave; DCR-L descending
	div4_1_50_mean_5km	0.63	0.63	DRC-B concave; DCR-L descending
	ndep_mean_5km	0.64	0.64	DRC-B and DRC-L almost identical

Species	Variable	AUC B	AUC L	Description
Lanius collorio	div3_1_20_mean_5km	0.62	0.62	DRC-L ascending
	div3_1_50_mean_5km	0.62	0.62	DRC-L ascending
	fma_f4_5km	0.61	0.61	DRC-L ascending
	sdep_mean_5km	0.64	0.63	DRC-L ascending
Lanius minor	div3_1_20_mean_5km	0.66	0.67	DRC-B and DRC-L almost identical
	div3_1_50_mean_5km	0.67	0.67	DRC-B and DRC-L almost identical
	div3_3_50_mean_5km	0.62	0.61	DRC-B concave; DCR-L descending
	div4_1_20_mean_5km	0.63	0.63	few observations at high values of explanatory variable; DRC-B highly variable; DRC-L ascending
	div4_1_50_mean_5km	0.66	0.67	few observations at high values of explanatory variable; DRC-B and DRC-L almost identical
	fma_f3_5km	0.63	0.62	already Bioscore2 model with only the linear term
	ndep_mean_5km	0.72	0.72	DRC-B concave; DRC-L descending
	sdep_mean_5km	0.63	0.63	DRC-L ascending
Perdix perdix	div4_1_50_mean_5km	0.64	0.64	DRC-L ascending
	napplication_5km	0.64	0.64	DRC-B and DRC-L very similar

Appendix 6. Effect of cutoff values on binary distribution maps

Cut-off values for transforming maps with presence probability into binary maps for ten sample species. Cut-offs were determined according to three methods: calculating cut-off with the the True Skill Statistic (TSS), using a species' prevalence as cut-off and choosing a fixed cut-off. Weighing factor, factor for weighing the relative importance of sensitivity and specificity in the calculation of the cut-off with the TSS; Cut-off, the cut-off caluclated with the TSS; Sensitivity and Specificity, the resulting sensitivity and specificity for a determined cut-off; Prevalence, the prevalence for a given species; Fixed, the fixed cut-off. The values of Prevalence and Fixed are written in the lines with the values of Cut-Off closest to Prevalence and Fixed.

Species	Weighing factor	Cut-off	Sensitivity	Specificity	Prevalence	Fixed
Acrocephalus arundinaceus	0.5	0.06	99.41	49.85		
	0.6	0.11	98.75	59.35		
	0.7	0.15	96.77	67.64		
	0.8	0.18	93.64	74.84		
	0.9	0.25	90.21	81.07		
	1.0	0.32	86.27	86.27	0.33	
	1.1	0.39	81.85	90.05		
	1.2	0.48	77.24	92.66		0.50
	1.3	0.57	72.82	94.64		
	1.4	0.63	68.27	95.58		
	1.5	0.67	64.36	96.54		
Acrocephalus paludicola	0.5	0.001	96.64	97.31		
	0.6	0.001	96.64	97.31		
	0.7	0.001	96.64	97.31		
	0.8	0.001	96.64	97.31		
	0.9	0.001	96.64	97.31		
	1.0	0.001	96.64	97.31	0.003	
	1.1	0.036	90.60	99.93		
	1.2	0.491	83.89	99.98		0.50
	1.3	0.700	77.18	99.99		
	1.4	0.786	71.14	99.99		
	1.5	0.827	66.44	99.99		
Alauda arvensis	0.5	0.25	99.35	49.83		
	0.6	0.48	97.67	58.75		0.50
	0.7	0.55	95.88	67.36		

Species	Weighing factor	Cut-off	Sensitivity	Specificity	Prevalence	Fixed
	0.8	0.63	93.62	74.77		
	0.9	0.69	90.18	81.14		
	1.0	0.77	86.93	86.91	0.79	
	1.1	0.82	83.14	91.47		
	1.2	0.87	78.31	93.88		
	1.3	0.93	73.57	95.77		
	1.4	0.94	68.89	97.03		
	1.5	0.96	64.78	97.92		
Coracius garrulus	0.5	0.01	99.25	52.49		
	0.6	0.01	98.94	61.07		
	0.7	0.02	97.80	68.23		
	0.8	0.03	96.74	77.36		
	0.9	0.09	93.64	84.26	0.08	
	1.0	0.13	88.57	88.46		
	1.1	0.17	82.89	91.10		
	1.2	0.23	77.73	93.33		
	1.3	0.28	72.78	94.50		
	1.4	0.33	68.09	95.35		
	1.5	0.36	64.49	96.09		0.50
Dendrocopos leucotos	0.5	0.00	99.43	49.70		
	0.6	0.01	98.85	62.31		
	0.7	0.01	98.44	68.35		
	0.8	0.02	97.66	77.63		
	0.9	0.04	95.77	85.99	0.05	
	1.0	0.08	92.97	92.93		
	1.1	0.16	87.74	96.50		
	1.2	0.25	81.28	97.58		
	1.3	0.31	75.54	98.12		
	1.4	0.37	70.22	98.54		
	1.5	0.42	65.65	98.99		0.50
Emberiza calandra	0.5	0.10	97.92	48.92		

Species	Weighing factor	Cut-off	Sensitivity	Specificity	Prevalence	Fixed
	0.6	0.14	96.65	58.07		
	0.7	0.18	94.55	66.22		
	0.8	0.22	91.48	73.30		
	0.9	0.27	87.71	78.87	0.29	
	1.0	0.32	83.33	83.33		
	1.1	0.38	78.87	86.76		
	1.2	0.45	74.28	89.08		
	1.3	0.49	69.88	90.71		0.50
	1.4	0.52	65.68	91.89		
	1.5	0.55	61.88	93.01		
Lanius collurio	0.5	0.08	99.89	50.03		
	0.6	0.11	99.75	59.80		
	0.7	0.21	98.98	69.31		
	0.8	0.40	97.13	77.69		0.50
	0.9	0.62	94.07	84.64	0.67	
	1.0	0.77	89.21	89.17		
	1.1	0.85	83.58	91.90		
	1.2	0.89	78.25	93.96		
	1.3	0.91	73.31	95.31		
	1.4	0.93	68.54	96.09		
	1.5	0.93	64.56	96.57		
Lanius minor	0.5	0.01	99.82	49.47		
	0.6	0.01	99.56	59.36		
	0.7	0.01	99.09	70.29		
	0.8	0.01	97.41	78.22		
	0.9	0.02	95.37	86.25		
	1.0	0.05	91.32	91.26	0.05	
	1.1	0.09	85.59	94.19		
	1.2	0.14	79.75	95.64		
	1.3	0.18	74.21	96.37		
	1.4	0.25	69.34	97.19		

Species	Weighing factor	Cut-off	Sensitivity	Specificity	Prevalence	Fixed
	1.5	0.32	65.09	97.66		0.50
Lullula arborea	0.5	0.10	99.46	49.81		
	0.6	0.15	98.74	59.10		
	0.7	0.21	96.62	67.63		
	0.8	0.31	93.67	74.95		
	0.9	0.41	90.87	81.79	0.45	
	1.0	0.52	86.46	86.44		0.50
	1.1	0.58	81.66	89.85		
	1.2	0.63	76.51	91.85		
	1.3	0.67	71.66	93.16		
	1.4	0.69	67.02	93.85		
	1.5	0.73	63.33	95.03		
Perdix perdix	0.5	0.05	99.78	49.73		
	0.6	0.08	99.01	59.59		
	0.7	0.12	97.72	68.25		
	0.8	0.17	95.22	76.13		
	0.9	0.25	92.54	83.27		
	1.0	0.33	88.70	88.71	0.33	
	1.1	0.47	83.99	92.40		0.50
	1.2	0.58	79.07	94.87		
	1.3	0.65	73.84	96.04		
	1.4	0.71	69.49	96.86		
	1.5	0.77	65.06	97.61		

Appendix 7. Assignment of species to the four main land use classes

Species	**LU1**	**LU2**	**LU3**	**LU4**
	Urban	**Farm-land**	**Forest**	**Open Natural**
Accipiter brevipes			1	
Accipiter gentilis			1	
Acrocephalus arundinaceus				1
Acrocephalus melanopogon				1
Acrocephalus paludicola				1
Acrocephalus scirpaceus				1
Aegolius funereus			1	
Aegypius monachus			1	1
Alauda arvensis		1		
Alcedo atthis				1
Alectoris barbara				1
Alectoris chukar				1
Alectoris graeca				1
Alectoris rufa		1		
Anas acuta				1
Anas clypeata				1
Anas penelope				1
Anas querquedula				1
Anas strepera				1
Anser erythropus				1
Anthus campestris				1
Anthus cervinus				1
Anthus pratensis				1
Anthus trivialis			1	
Aquila adalberti				1
Aquila chrysaetos				1
Aquila fasciata				
Aquila heliaca				
Ardea alba				1
Ardea purpurea				1
Ardeola ralloides				1
Asio flammeus				1
Athene noctua	1			
Aythya ferina				1
Aythya fuligula				1
Aythya nyroca				1
Botaurus stellaris				1
Bubo bubo			1	
Bucanetes githagineus				1
Burhinus oedicnemus		1		

Buteo lagopus				1
Buteo rufinus				1
Calandrella brachydactyla				
Calandrella rufescens				1
Calcarius lapponicus				1
Calidris alpina				1
Calidris maritima				1
Calidris minuta				1
Caprimulgus europaeus				
Caprimulgus ruficollis		1		
Charadrius alexandrinus				1
Charadrius morinellus				1
Chersophilus duponti				1
Chlidonias hybrida				1
Chlidonias niger				1
Chroicocephalus genei				1
Ciconia ciconia	1			
Ciconia nigra			1	
Circaetus gallicus			1	
Circus aeruginosus				1
Circus cyaneus		1		
Circus macrourus				
Circus pygargus		1		
Clamator glandarius		1		
Clanga clanga			1	
Clanga pomarina		1		
Clangula hyemalis				1
Coloeus monedula				
Columba oenas				
Columba palumbus		1		
Coracias garrulus		1		
Corvus corax			1	
Corvus frugilegus		1		
Coturnix coturnix		1		
Crex crex				1
Cygnus cygnus				1
Dendrocopos leucotos			1	
Dendrocopos major			1	
Dendrocopos medius			1	
Dendrocopos minor			1	
Dendrocopos syriacus		1		
Dryocopus martius			1	
Egretta garzetta				1
Elanus caeruleus		1		
Emberiza caesia				1

Emberiza calandra		1		
Emberiza cia				1
Emberiza cineracea				
Emberiza cirlus		1		
Emberiza citrinella				
Emberiza hortulana				
Emberiza melanocephala		1		
Emberiza rustica			1	
Emberiza schoeniclus				1
Eremophila alpestris				1
Falco biarmicus				1
Falco cherrug				1
Falco columbarius				1
Falco eleonorae				1
Falco naumanni				
Falco peregrinus			1	
Falco subbuteo			1	
Falco tinnunculus	1			
Falco vespertinus		1		
Ficedula albicollis			1	
Ficedula parva			1	
Ficedula semitorquata			1	
Francolinus francolinus		1		
Fulica atra				1
Fulica cristata				1
Galerida cristata		1		
Galerida theklae				1
Gallinago gallinago				1
Gallinago media				1
Gavia arctica				1
Gavia immer				1
Gavia stellata				1
Gelochelidon nilotica				1
Glareola nordmanni				1
Glareola pratincola				1
Glaucidium passerinum			1	
Grus grus				1
Gypaetus barbatus				1
Gyps fulvus				1
Haematopus ostralegus				
Haliaeetus albicilla				1
Hieraaetus pennatus			1	
Himantopus himantopus				1
Hippolais icterina		1		
Hippolais polyglotta				

Hirundo rustica	1			
Hydrocoloeus minutus				1
Hydroprogne caspia				1
Ichthyaetus audouinii				1
Ichthyaetus melanocephalus				1
Ixobrychus minutus				1
Jynx torquilla			1	
Lagopus lagopus				1
Lagopus muta				1
Lanius collurio				1
Lanius excubitor				1
Lanius minor		1		
Lanius nubicus			1	
Lanius senator				1
Larus canus				1
Limosa lapponica				1
Limosa limosa				1
Linaria cannabina				
Locustella fluviatilis		1		
Locustella luscinioides				1
Locustella naevia				1
Lophophanes cristatus			1	
Loxia curvirostra			1	
Loxia leucoptera			1	
Loxia pytyopsittacus			1	
Loxia scotica			1	
Lullula arborea				1
Luscinia luscinia			1	
Luscinia megarhynchos			1	
Luscinia svecica				1
Lyrurus mlokosiewiczi				1
Lyrurus tetrix				
Marmaronetta angustirostris				1
Melanitta fusca				1
Melanitta nigra				1
Melanocorypha calandra		1		
Mergellus albellus				1
Mergus merganser				1
Merops apiaster		1		
Microcarbo pygmeus				1
Milvus migrans				
Milvus milvus		1		
Monticola saxatilis				1
Monticola solitarius	1			

Motacilla alba		1		
Motacilla citreola				1
Motacilla flava		1		
Muscicapa striata			1	
Neophron percnopterus				1
Netta rufina				1
Nucifraga caryocatactes			1	
Numenius arquata		1		
Numenius phaeopus				1
Nycticorax nycticorax				1
Oenanthe hispanica				1
Oenanthe isabellina				1
Oenanthe leucura				1
Oenanthe oenanthe				1
Oenanthe pleschanka				1
Oriolus oriolus			1	
Otis tarda		1		
Otus scops				
Oxyura leucocephala				1
Pandion haliaetus				1
Panurus biarmicus				1
Passer hispaniolensis		1		
Passer montanus				
Pelecanus crispus				1
Pelecanus onocrotalus				1
Perdix perdix		1		
Perisoreus infaustus			1	
Pernis apivorus			1	
Phalaropus lobatus				1
Philomachus pugnax				1
Phoenicopterus roseus				1
Phoenicurus phoenicurus			1	
Phylloscopus bonelli			1	
Phylloscopus borealis			1	
Phylloscopus collybita				
Phylloscopus sibilatrix			1	
Phylloscopus trochilus		1		
Picoides tridactylus			1	
Picus canus			1	
Picus viridis			1	
Platalea leucorodia			1	1
Plectrophenax nivalis				1
Plegadis falcinellus				1
Pluvialis apricaria				1
Podiceps auritus				1

Podiceps cristatus				1
Poecile cinctus			1	
Poecile lugubris				
Poecile montanus			1	
Poecile palustris			1	
Porphyrio porphyrio				1
Porzana parva				1
Porzana porzana				1
Prunella collaris				1
Prunella modularis		1		
Pterocles alchata				1
Pterocles orientalis				1
Pyrrhocorax graculus				1
Pyrrhocorax pyrrhocorax				1
Recurvirostra avosetta				1
Regulus ignicapilla			1	
Regulus regulus			1	
Saxicola rubetra				1
Saxicola torquatus		1		
Scolopax rusticola			1	
Sitta europaea			1	
Sitta krueperi			1	
Sitta neumayer				1
Stercorarius longicaudus				1
Sterna dougallii				1
Sterna hirundo				1
Sterna paradisaea				1
Sternula albifrons				1
Streptopelia turtur		1		
Strix aluco			1	
Strix nebulosa			1	
Strix uralensis			1	
Sturnus unicolor	1			
Sturnus vulgaris	1			
Surnia ulula			1	
Sylvia atricapilla				
Sylvia borin		1		
Sylvia cantillans				1
Sylvia communis		1		
Sylvia curruca		1		
Sylvia hortensis				
Sylvia melanocephala		1		
Sylvia nisoria		1		
Sylvia rueppelli				1
Sylvia sarda				1

Sylvia undata				1
Tachybaptus ruficollis				1
Tadorna ferruginea				1
Tetrao urogallus			1	
Tetrastes bonasia			1	
Tetrax tetrax				
Thalasseus sandvicensis				1
Tringa glareola				1
Tringa totanus		1		
Turdus viscivorus			1	
Tyto alba				
Upupa epops				
Uria aalge				1
Vanellus spinosus				1
Vanellus vanellus		1		

In opdracht van:

Planbureau voor de Leefomgeving

Sovon Vogelonderzoek Nederland

Postbus 6521
6503 GA Nijmegen
Toernooiveld 1
6525 ED Nijmegen
T (024) 7 410 410

E info@sovon.nl
I www.sovon.nl

Sovon