



D4.2 Ensemble species distribution models estimated and validated for first study region

Deliverable for the Horizon Europe Project BirdWatch

Version 1.0

Legal Disclaimer

This document reflects only the views of the author(s). Neither the European Global Navigation Satellite Systems Agency (EUSPA) nor the European Commission is in any way responsible for any use that may be made of the information it contains. The information in this document is provided “as is”, and no guarantee or warranty is given that the information is fit for any particular purpose. The below referenced consortium members shall have no liability for damages of any kind including without limitation direct, special, indirect, or consequential damages that may result from the use of these materials subject to any liability which is mandatory due to applicable law.

This document and the information contained within may not be copied, used, or disclosed, entirely or partially, outside of the BirdWatch consortium without prior permission of the project partners in written form.

© 2024 by BirdWatch Consortium.

Document Information

GA Number	101082634		Type of Action	Horizon-IA
Full Title	BirdWatch - a Copernicus-based service for the improvement of habitat suitability of farmland birds via satellite-enabled monitoring, evaluation and optimisation of CAP greening measures			
Project Acronym	BirdWatch			
Start Date	February 1 st , 2023		Duration	36 Months
Project URL	https://birdwatch-europe.org/			
Deliverable	D4.2: Ensemble species distribution models estimated and validated for first study region*			
Work Package	WP 4200			
Project Month of Delivery	Contractual	M18	Actual	M18
Nature	Report	Dissemination Level		PUB
Lead Beneficiary	University of Potsdam (UP)			
Responsible Author	Levin Wiedenroth - UP			
Contributions from	Levin Wiedenroth - UP			
	Damaris Zurell - UP			
	Emma Underwood - UP			

* Please note that this deliverable was originally suggested as “D4.2: Ensemble species distribution models and joint species distribution models estimated and validated for first study region”. As detailed in deliverable D4.1, joint distribution models were discarded from the further workflow and are thus not considered here.

History of Changes

Version	Issue Date	Stage	Description	Comments	Contributor
1.0	31.07.2024	Draft	First version of D4.2		Levin Wiedenroth Damaris Zurell Emma Underwood
1.1	25.11.2024	update of excepted version	Update of D4.2	We dealt with the issue of discontinuities in our SDM output figures	Levin Wiedenroth Damaris Zurell Emma Underwood

Table of Contents

1. Introduction.....	6
2. Species distribution models.....	6
2.1 Data and methods.....	6
2.2 Results.....	11
2.2.1 European models.....	11
Model performance.....	11
Model predictions.....	12
2.2.2 Flanders models.....	13
Model performance.....	13
Model predictions.....	14
Conclusion.....	17
References.....	19
Supplementary material.....	21

1. Introduction

Here we present the second deliverable of work package 4000, which applies the workflows discussed in deliverable 4.1 “Data, algorithms, and workflows of SDM” for the first test region, Flanders. We present the results of the individual model building steps: (1) data preparation and model training, (2) model validation, and (3) model predictions. The models and final predictions of habitat suitability will then feed into the BirdWatch optimization algorithm in WP5000.

2. Species distribution models

Species distribution models (SDMs) are the most widely used modeling tool in ecology (Guisan et al., 2017). They use comparably simple data inputs such as species occurrence data and geographic information of environmental variables to understand species-environmental relationships and predict habitat suitability over space and time. For BirdWatch we use a nested SDM framework as described in deliverable 4.1 in which we combine European-wide, coarse-grained SDMs of climate suitability with fine-grained SDMs describing suitability of land use practices and intensity. For all SDMs, we built ensembles of five different model algorithms: generalized linear models (GLMs), generalized additive models (GAMs), random forest (RF), boosted regression trees (BRTs), and Maxent.

2.1 Data and methods

We use a nested species distribution model approach to account for the scale dependency in factors limiting species distribution (Adde et al., 2023; Pearson et al., 2004). Climatic factors are considered to drive a species' distribution at large scales whereas land-use factors drive a species' distribution at finer scales. To apply the nested SDM approach we constructed two sets of SDMs. The first was a set of SDMs trained at the European scale with a resolution of 50 km considering climate variables. The second was trained for the region of Flanders at a resolution of 200 m considering land-use and other habitat factors.

The EBBA2 dataset (European Breeding Bird Atlas; EBCC 2022; Keller et al., 2020) provided the occurrence data in form of presence-absence data for the European SDMs. Regions where a bird species was not detected were considered as absences. The climate data were obtained from the CHELSA dataset (Climatologies at high resolution for the earth's land surface areas; Karger et al., 2017, 2021).

Fine-scale data of bird occurrences within Flanders for the year 2018 were provided by Natuurpunt (<https://www.natuurpunt.be/>), a nature conservation NGO from Flanders. Data were quality-checked, and rasterized to 200 m spatial resolution as described in D4.1. As the fine-scale occurrence data for Flanders were presence-only data, we created background data in the form of pseudo-absences following recommendations by Barbet-Massin et al., (2012). Ten times as many pseudo-absences than presences were randomly selected in locations where no presences were detected. For GLM and GAM construction we assigned weights to the pseudo-absences such that the sum of weights of pseudo-absences equaled the sum of presences. For the model algorithms RF, BRT, and Maxent we split the pseudo-absences into ten equally sized groups and constructed ten replicate models with equal number of presences and pseudo-absences. These ten replicate models per algorithm were averaged resulting in one final output per algorithm (Barbet-Massin et al., 2012). As environmental predictor variables within the regional SDM we used the ensemble climate suitability derived from the European SDMs as well as habitat and land-use predictors derived from earth observation (WP3000; Table S1). To avoid having spatial artifacts in our habitat suitability predictions, caused by the difference in spatial resolution between our European and regional SDMs, we spatially interpolated the climate suitability to a resolution of 200 m using the bilinear interpolation.

All occurrence data were spatially thinned to avoid problems of spatial autocorrelation (Aiello-Lammens et al., 2015). The thinning distance was set twice as large as the spatial resolution for each respective scale i.e., thinning distance of 100 km for the coarse-grained European data, and 400 m for the fine-grained Flanders. As a result neither the presences nor absences fell into adjacent cells. Due to the low number of occurrences, we were not able to construct models for the species Red-backed shrike and Whinchat. A summary of the final number of occurrences for Europe can be found in table 1 and for Flanders in table 2. The distribution of the final presence points for Flanders are shown in figure 1.

Table 1: European occurrence numbers after thinning. The * indicates species excluded from model construction for Flanders because of too few occurrence points.

Species	European presence	European absence
Eurasian skylark (<i>Alauda arvensis</i>)	585	298
Meadow pipit (<i>Anthus pratensis</i>)	371	506
Yellowhammer (<i>Emberiza citrinella</i>)	495	380
Red-backed shrike* (<i>Lanius collurio</i>)	537	338
Black-tailed godwit (<i>Limosa limosa</i>)	156	727
Tree sparrow (<i>Passer montanus</i>)	602	272
Whinchat* (<i>Saxicola rubetra</i>)	491	387
European turtle dove (<i>Streptopelia turtur</i>)	463	421
Common starling (<i>Sturnus vulgaris</i>)	633	249
Northern lapwing (<i>Vanellus vanellus</i>)	515	370

Table 2: Flanders occurrence numbers after thinning. The * indicates species excluded from model construction for Flanders because of too few occurrence points.

Species	Flanders presence	Flanders pseudo-absence
Eurasian skylark (<i>Alauda arvensis</i>)	843	14974
Meadow pipit (<i>Anthus pratensis</i>)	298	4985
Yellowhammer (<i>Emberiza citrinella</i>)	524	8619
Red-backed shrike* (<i>Lanius collurio</i>)	7	80
Black-tailed godwit (<i>Limosa limosa</i>)	178	3114
Tree sparrow (<i>Passer montanus</i>)	57	725
Whinchat* (<i>Saxicola rubetra</i>)	1	10
European turtle dove (<i>Streptopelia turtur</i>)	68	1154
Common starling (<i>Sturnus vulgaris</i>)	527	6460
Northern lapwing (<i>Vanellus vanellus</i>)	857	11737

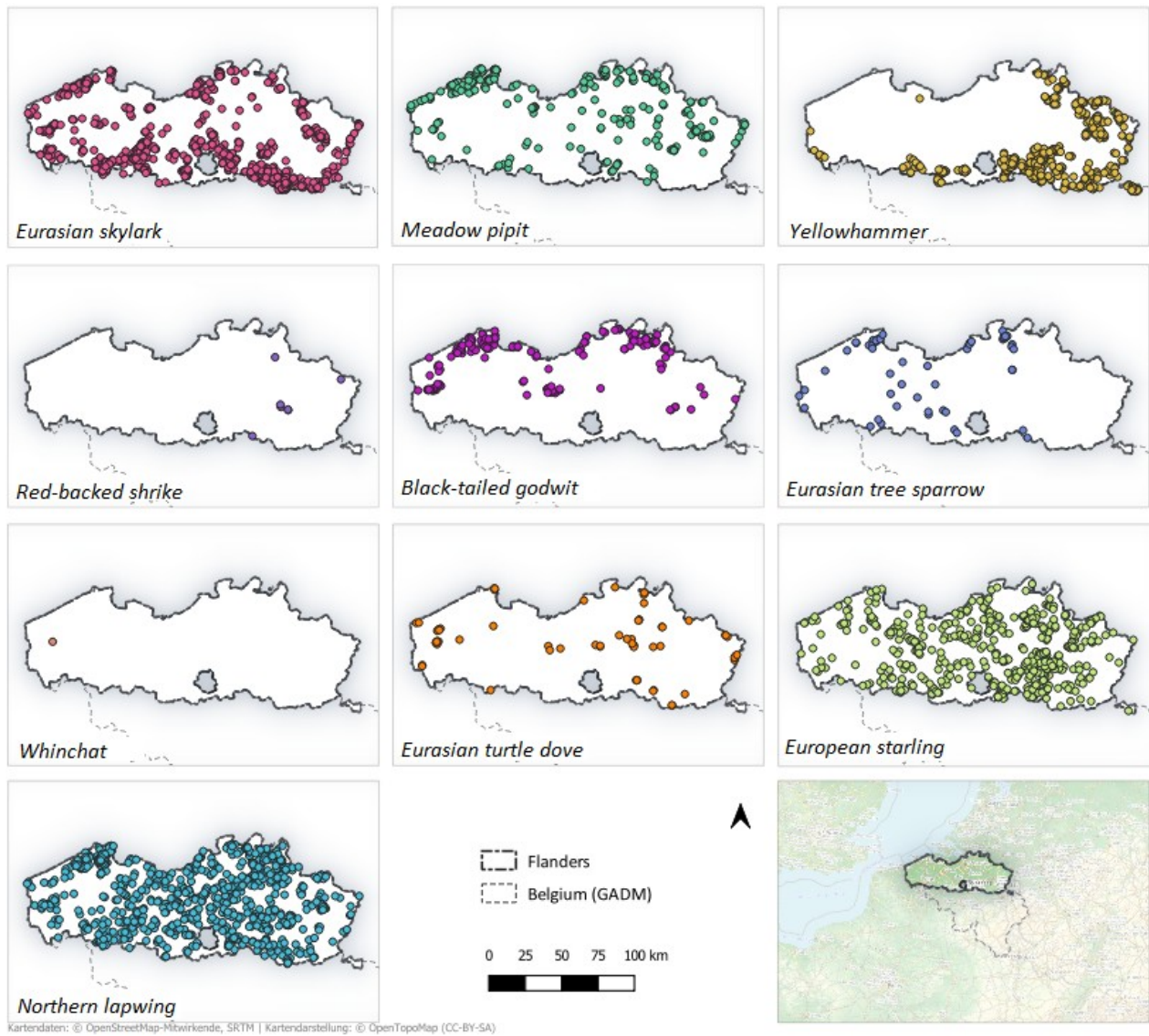


Figure 1: Final occurrence data of study species in Flanders.

At each spatial scale we tested for collinearity to identify explanatory variables strongly correlated with one another. We used the select07 method (Dormann et al., 2013) to identify pairs of highly correlated variables with an absolute correlation coefficient greater than 0.7, and out of these pairs retained the variable with higher univariate variable importance. The latter was defined as the explained deviance which was obtained by each univariate model within a five-fold spatial block cross-validation. Univariate models were fitted with binomial GAMs and four degrees of freedom if the respective predictor variable held more than four unique values. Else, the univariate models were simplified (binomial GLM with linear and quadratic terms if the predictor had three to four unique values, and binomial GLM with one linear term if the predictor had less than three unique values). The

spatial blocks for the cross-validation were determined following Valavi et al. (2019) using a hexagon shape and the block size was optimized separately for each species based on the spatial autocorrelation range of the occurrence data. Each species had a minimum of 15 blocks which were then grouped into five folds, i.e., a minimum three blocks per fold. As a consequence all folds had similar amounts of presences and absences. Further details regarding the general variable pre-selection can be found in D4.1.

We then constructed models at the European scale and at the scale of Flanders using the five algorithms GLM, GAM, RF, BRT, and Maxent. All models were validated using a five-fold spatial block cross-validation (with the same blocks as described above). The model validation metrics considered for Europe were the threshold-independent metric AUC (area under the receiver operating curve) and the threshold-dependent metrics sensitivity, and specificity, and TSS (true skill statistic). Additionally, for the fine-grained presence-only models of Flanders, we quantified the Boyce index. It indicates how well the model predicts presences and is thus especially suited for presence-only data. Its values can range from minus one to one.

To ensure good predictive performance only models with an AUC score > 0.7 were included in ensembles. Ensembles for Europe and for Flanders were built using the mean probability approach, averaging the habitat suitability predictions across the model algorithms. For Flanders, we additionally calculated the standard deviation of habitat suitability predictions across the model algorithms and the committee average. The committee average ensemble gives information on how many algorithms agree on a species being present or absent. Both serve as a measure of uncertainty for the BirdWatch optimization algorithm in WP5000. Summarized information of model building, training, and validation can also be found in our ODMAP protocol (Table S2; Zurell et al., 2020).

2.2 Results

2.2.1 European models

Model performance

All ensemble models showed very good to excellent predictive performance with AUC scores ranging 0.81 - 0.94 (Table 3; performance of individual algorithms shown in table

S3). Sensitivity values ranged from 0.77 - 0.88 and specificity ranged from 0.66 - 0.88 (Table 3). Only the Black-tailed godwit and the Tree sparrow had specificity values below 0.75 indicating slight overprediction of their European range.

Table 3: Performance metrics of the European mean probability ensemble. The ensemble includes the algorithms: GLM, GAM, RF, BRT, and Maxent. The threshold was used to binarize the continuous habitat suitability predictions and convert them into predicted presences and absences. It is the threshold that maximizes TSS (or the sum of sensitivity and specificity) in the cross-validated predictions.

Species	AUC	Sensitivity	Specificity	TSS	Threshold
Eurasian skylark (<i>Alauda arvensis</i>)	0.91	0.87	0.78	0.65	0.54
Meadow pipit (<i>Anthus pratensis</i>)	0.94	0.84	0.88	0.72	0.47
Yellowhammer (<i>Emberiza citrinella</i>)	0.90	0.87	0.78	0.65	0.28
Black-tailed godwit (<i>Limosa limosa</i>)	0.81	0.83	0.66	0.49	0.19
Tree sparrow (<i>Passer montanus</i>)	0.86	0.80	0.73	0.63	0.54
European turtle dove (<i>Streptopelia turtur</i>)	0.91	0.84	0.82	0.66	0.47
Common starling (<i>Sturnus vulgaris</i>)	0.91	0.88	0.79	0.67	0.59
Northern lapwing (<i>Vanellus vanellus</i>)	0.88	0.77	0.84	0.61	0.59

Model predictions

All species have high suitability values and large predicted ranges (Figure 2), except the Black-tailed godwit which is rarer and has overall lower predicted suitability. The Eurasian skylark, Yellowhammer, Common starling, and Northern lapwing have high suitability areas across all of central, eastern, and western parts of Europe. The Meadow pipit has a high suitability area across central and northern parts of Europe, whereas the Tree sparrow and European turtle dove have their ranges across the central, eastern, western,

and southern parts of Europe. The Black-tailed godwit has its highest suitable area in eastern Europe stretching to central Europe.

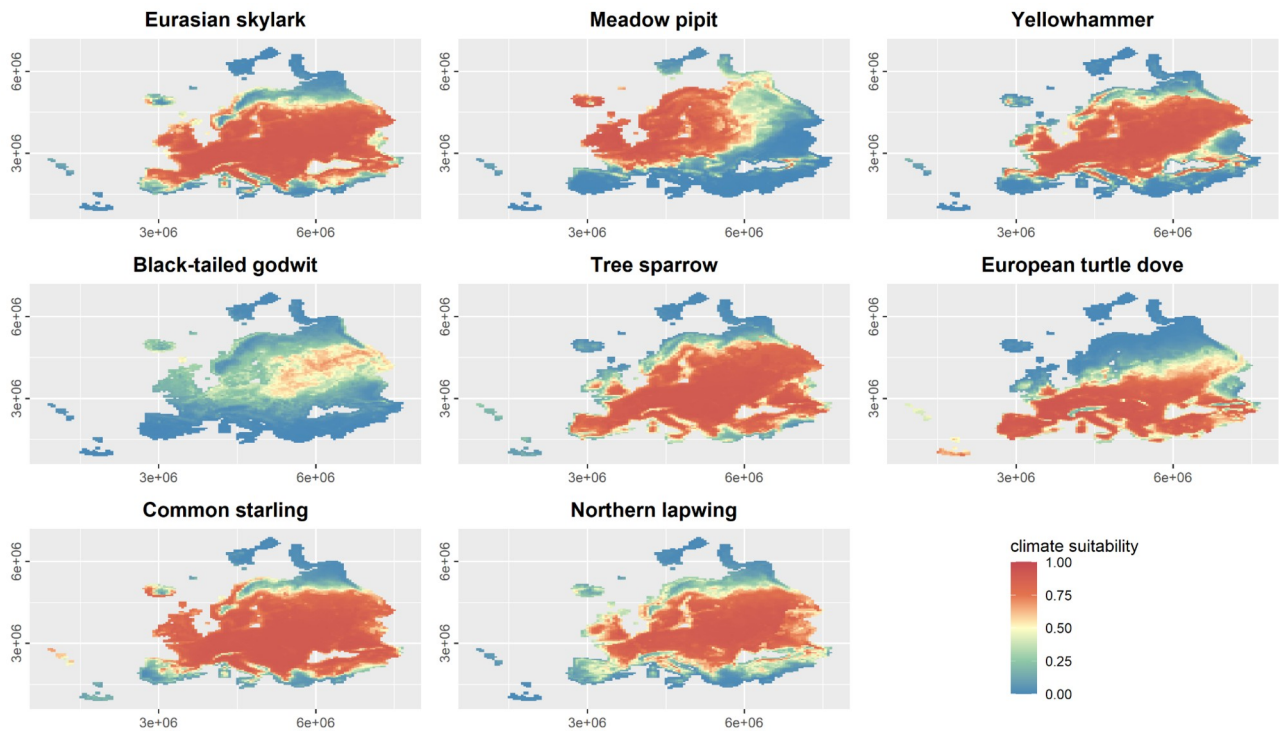


Figure 2: Climate suitability predictions for Europe based on the mean probability ensemble per species. The ensembles included the model algorithms GLM, GAM, RF, BRT, and Maxent.

2.2.2 Flanders models

Model performance

For Flanders all ensemble models had very good to excellent predictive performance with AUC ranging 0.83 - 0.94 (Table 4; performance of single algorithms shown in table S4). The TSS and sensitivity scores also indicated fair to excellent predictive accuracy ranging from 0.53 - 0.76 and 0.79 - 0.98, respectively (Table 4).

Table 4: Performance metrics of the Flanders mean probability ensemble. The ensemble includes the algorithms: GLM, GAM, RF, BRT, and Maxent. The threshold was used to binarize the continuous habitat suitability predictions and convert them into predicted presences and absences. It is the threshold that maximizes TSS (or the sum of sensitivity and specificity) in the cross-validated predictions.

Species	AUC	TSS	Sensitivity	Boyce	Threshold
Eurasian skylark (<i>Alauda arvensis</i>)	0.9	0.65	0.86	0.92	0.27
Meadow pipit (<i>Anthus pratensis</i>)	0.91	0.68	0.93	0.98	0.21
Yellowhammer (<i>Emberiza citrinella</i>)	0.94	0.76	0.96	0.98	0.20
Black-tailed godwit (<i>Limosa limosa</i>)	0.92	0.72	0.98	0.88	0.15
Tree sparrow (<i>Passer montanus</i>)	0.83	0.54	0.88	0.89	0.29
European turtle dove (<i>Streptopelia turtur</i>)	0.86	0.56	0.85	0.87	0.23
Common starling (<i>Sturnus vulgaris</i>)	0.84	0.53	0.83	0.91	0.32
Northern lapwing (<i>Vanellus vanellus</i>)	0.87	0.59	0.79	0.93	0.35

Model predictions

For each species, we predicted the ensemble mean habitat suitability for the entire Flanders region (Figure 3; predictions for each species per algorithm Figure S1 - 8). The Northern lapwing has high habitat suitability across all parts of Flanders but especially in the north western and eastern parts. The Black-tailed godwit also has its most suitable areas in the north western parts with an additional small suitable area in the north east. The Common starling has its highest suitability across the eastern parts of Flanders whereas the Tree sparrow is predicted to be most suited to the western parts. The Yellowhammer has its highest suitability in the southern and far eastern parts. For the other species no clear spatial patterns can be recognized. From the maps of predicted suitability, the difference in habitat preference becomes apparent leading to trade-offs for

managing those species relevant for the BirdWatch optimization algorithm (WP5000). These different habitat preferences are also visible in the species-specific response curves. These curves describe the fitted species-environment relationships for the different predictor variables (Figure. 4; Figures. S9 - S34). For example, figure 4 shows habitat suitability predicted for the different species in relation to permanent grassland. While Common starling and Northern lapwing peak at intermediate levels of permanent grasslands, Eurasian skylark, Meadow pipit, Black-tailed godwit, and European turtle dove find suitable habitat under higher levels of permanent grassland.

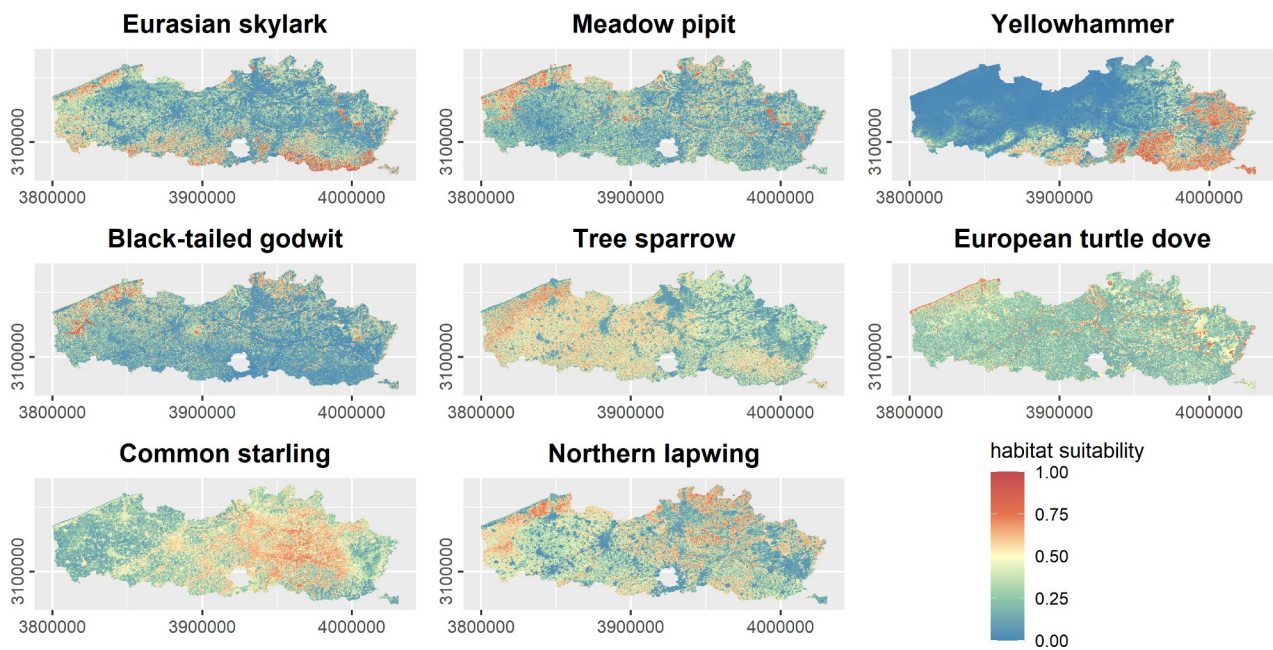


Figure 3: Habitat suitability predictions for Flanders based on the mean probability ensemble per species. The ensembles included the model algorithms GLM, GAM, RF, BRT, and Maxent.

The committee average predictions (Figure 5) and maps of standard deviation in predicted habitat suitability (Figure 6) provide more nuanced measures of uncertainty as potential input to WP5000.

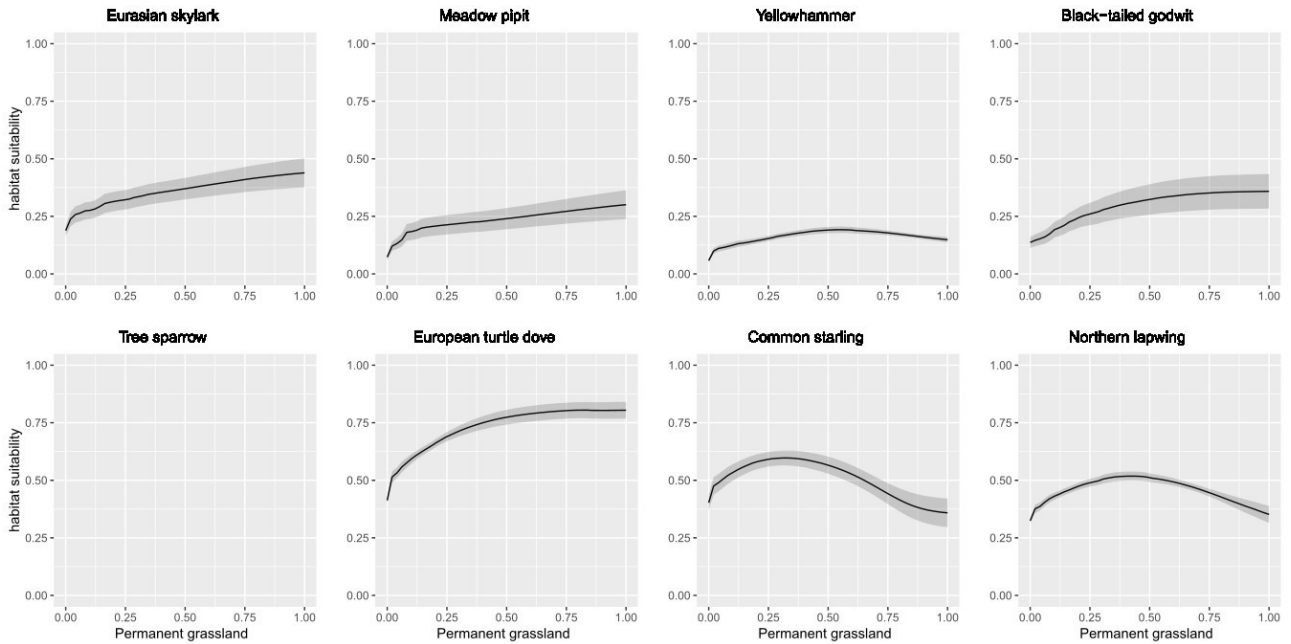


Figure 4: Partial response curves per species and Flanders for the environmental parameter “Permanent grassland” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

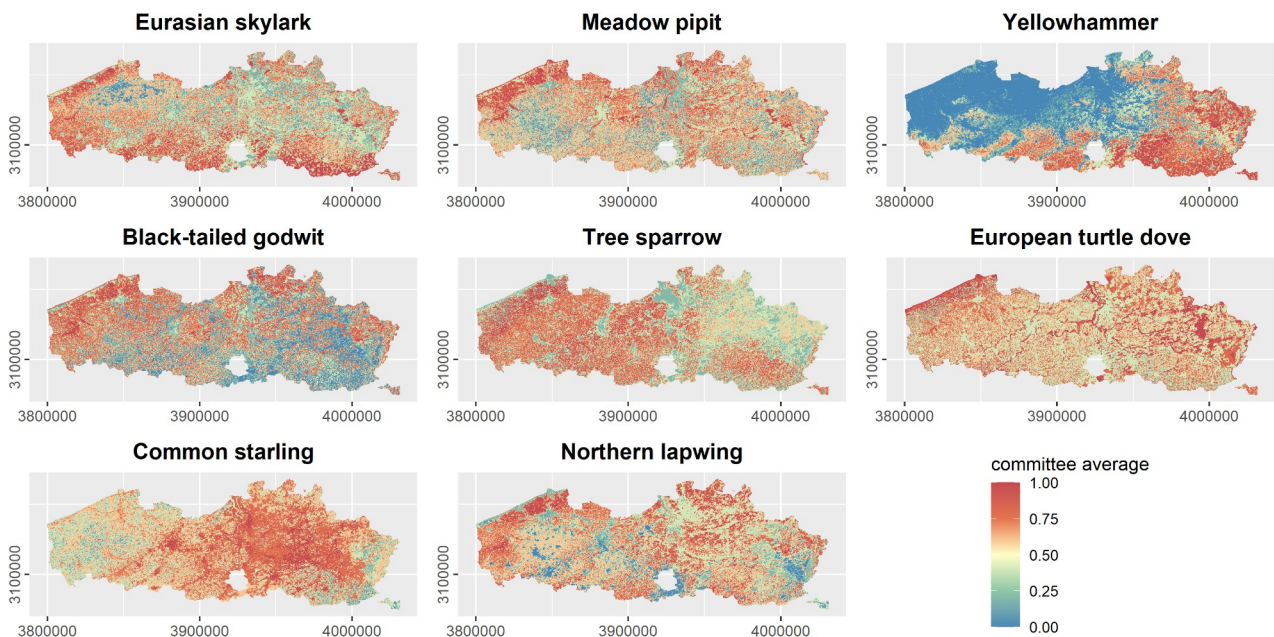


Figure 5: Committee averaged predictions for Flanders per species. Committee averages indicate the proportion of algorithms agreeing on a species being present or absent. One stands for all models agree on the species being present and 0 stands for all models agreeing on the species being absent. The model algorithms GLM, GAM, RF, BRT, and Maxent went into the ensembles.

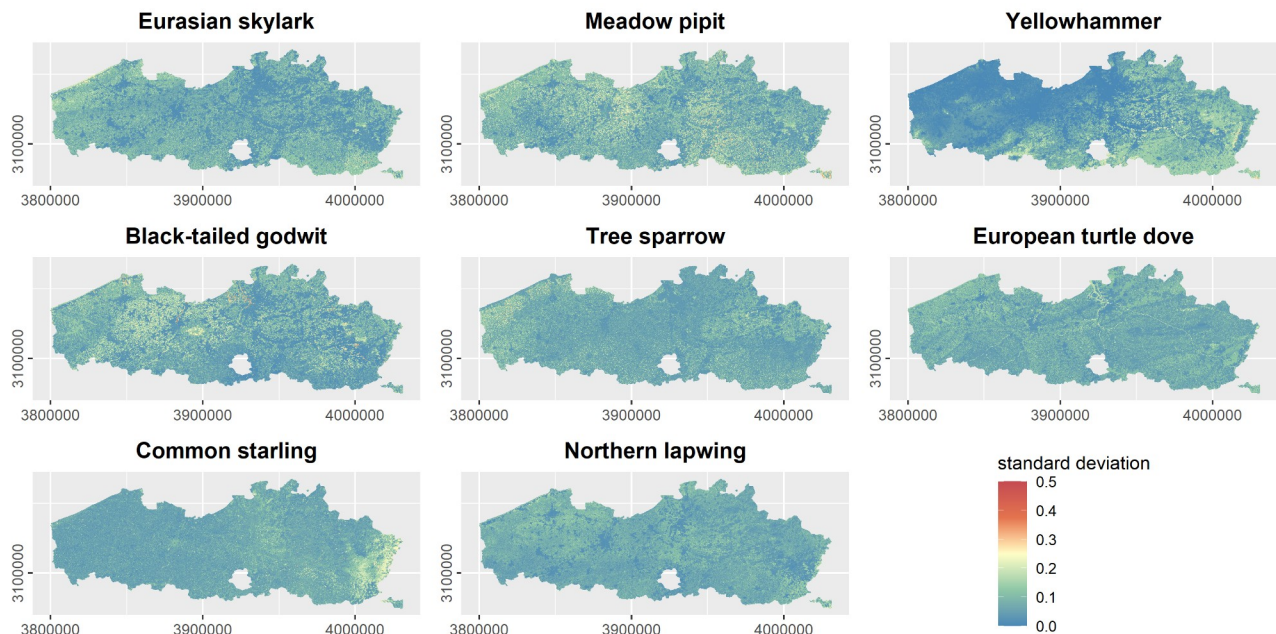


Figure 6: Standard deviation calculated from the habitat suitability predictions for Flanders by the model algorithms (GLM, GAM, RF, BRT, and Maxent).

Conclusion

We successfully applied the nested SDM approach to the first test region of Flanders. The coarse-grained climate suitability models at European scale showed very good to excellent predictive performance. Due to low data coverage of two species in Flanders, we were only able to construct fine-grained land use suitability models for eight of the ten study species. The trade-offs in habitat suitability between species indicated by the Flanders SDMs will be relevant for the BirdWatch optimization algorithm in WP5000.

Final input to WP5000

The BirdWatch optimization algorithm will require predictions of potential habitat suitability across the entire environmental space defined by the different land use features and management intensities. This allows the optimization algorithm to test different scenarios with combinations of land use features and management intensities not currently represented in the training data. Such scenarios can include, for example, promotion of Ecological Focus Areas and optimizing the placement of ecologically beneficial elements as defined by the European Commission. Thus, as input to WP5000 we will derive

species-specific predictions of habitat suitability (and their associated uncertainty measures in form of standard deviation and committee average) across all combinations of environmental input data. Reasonable bin sizes defining the step sizes for each environmental predictor (e.g. 5 percent steps vs. 1 percent steps) will be closely coordinated with the WP5000 leads and the wider BirdWatch consortium.

References

- Adde, A., Rey, P.-L., Brun, P., Külling, N., Fopp, F., Altermatt, F., Broennimann, O., Lehmann, A., Petitpierre, B., Zimmermann, N. E., Pellissier, L., & Guisan, A. (2023). N-SDM: A high-performance computing pipeline for Nested Species Distribution Modelling. *Ecography*, 2023(6), e06540. <https://doi.org/10.1111/ecog.06540>
- Aiello-Lammens, M. E., Boria, R. A., Radosavljevic, A., Vilela, B., & Anderson, R. P. (2015). spThin: An R package for spatial thinning of species occurrence records for use in ecological niche models. *Ecography*, 38(5), 541–545. <https://doi.org/10.1111/ecog.01132>
- Barbet-Massin, M., Jiguet, F., Albert, C. H., & Thuiller, W. (2012). Selecting pseudo-absences for species distribution models: How, where and how many? *Methods in Ecology and Evolution*, 3(2), 327–338. <https://doi.org/10.1111/j.2041-210X.2011.00172.x>
- Dormann, C. F., Elith, J., Bacher, S., Buchmann, C., Carl, G., Carré, G., Marquéz, J. R. G., Gruber, B., Lafourcade, B., Leitão, P. J., Münkemüller, T., McClean, C., Osborne, P. E., Reineking, B., Schröder, B., Skidmore, A. K., Zurell, D., & Lautenbach, S. (2013). Collinearity: A review of methods to deal with it and a simulation study evaluating their performance. *Ecography*, 36(1), 27–46. <https://doi.org/10.1111/j.1600-0587.2012.07348.x>
- EBCC (2022). *European Breeding Bird Atlas 2 website*. European Bird Census Council. Accessed from: <http://ebba2.info> (22/01/2024).
- Guisan, A., Thuiller, W., & Zimmermann, N. E. (2017). *Habitat Suitability and Distribution Models: With Applications in R* (1st ed.). Cambridge University Press. <https://doi.org/10.1017/9781139028271>
- Karger, D. N., Conrad, O., Böhner, J., Kawohl, T., Kreft, H., Soria-Auza, R. W., Zimmermann, N. E., Linder, H. P., & Kessler, M. (2017). Climatologies at high resolution for the earth's land surface areas. *Scientific Data*, 4(1), 170122.

<https://doi.org/10.1038/sdata.2017.122>

Karger, D. N., Conrad, O., Böhner, J., Kawohl, T., Kreft, H., Soria-Auza, R. W., Zimmermann, N. E., Linder, H. P., & Kessler, M. (2021). *Climatologies at high resolution for the earth's land surface areas*.

<https://doi.org/10.16904/envdat.228.v2.1>

Keller, V., Herrando, S., Voříšek, P., Franch, M., Kipson, M., Milanese, P., Martí, D., Anton, M., Klvaňová, A., Kalyakin, M.V., Bauer, H.-G. & Foppen, R.P.B. (2020). *European Breeding Bird Atlas 2: Distribution, Abundance and Change*. European Bird Census Council & Lynx Edicions, Barcelona.

Pearson, R. G., Dawson, T. P., & Liu, C. (2004). Modelling species distributions in Britain: A hierarchical integration of climate and land-cover data. *Ecography*, 27(3), 285–298. <https://doi.org/10.1111/j.0906-7590.2004.03740.x>

Valavi, R., Elith, J., Lahoz-Monfort, J. J., & Guillerá-Arroita, G. (2019). blockCV: An R package for generating spatially or environmentally separated folds for k-fold cross-validation of species distribution models. *Methods in Ecology and Evolution*, 10(2), 225–232. <https://doi.org/10.1111/2041-210X.13107>

Zurell, D., Franklin, J., König, C., Bouchet, P. J., Dormann, C. F., Elith, J., Fandos, G., Feng, X., Guillerá-Arroita, G., Guisan, A., Lahoz-Monfort, J. J., Leitão, P. J., Park, D. S., Peterson, A. T., Rapacciuolo, G., Schmatz, D. R., Schröder, B., Serra-Diaz, J. M., Thuiller, W., Merow, C. (2020). A standard protocol for reporting species distribution models. *Ecography*, 43(9), 1261–1277.

<https://doi.org/10.1111/ecog.04960>

Supplementary material

Table S1: Environmental parameters used in each model algorithm for each species.

Env. Parameter	Eurasian skylark	Meadow pipit	Yellowhammer	Black-tailed godwit	Tree sparrow	European turtle dove	Common starling	Northern lapwing
Elevation	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Solar radiation	-	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	-
Slope	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	-	-	-	-	glm, gam, rf, brt, maxent
Soil moisture early breeding season	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	-	-	-
Soil moisture full breeding season	-	-	-	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Built-up land	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Tree cover	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Water cover	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent

Cultivated grassland	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Fallow	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Grapevine	gam, rf, brt, maxent	glm, gam, rf, brt	glm, gam, rf, brt, maxent	-	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Hedges	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Hops	glm, gam, rf, brt	-	glm, rf, brt	-	-	-	glm, rf, brt	glm, rf, brt
Legumes	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Maize	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Orchards and Berries	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Other cereals	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Permanent grasslands	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Rapeseed	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent

Root crops	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Summer cereals	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Sunflower	-	-	-	-	-	-	-	-
Vegetables	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	-	-	-	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
Winter cereals	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent
European climate suitability	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent	glm, gam, rf, brt, maxent

Table S2: ODMAP protocol describing the main steps of model construction.

ODMAP section	ODMAP subsection	ODMAP elements
Overview	Authorship	Authors: Levin Wiedenroth, Damaris Zurell, Emma Underwood Contact email: wiedenroth@uni-potsdam.de Title: SDM Ensemble Flanders
	Model objective	Mapping Interpolation, creating maps of relative probability of presence
	Taxon	European farmland birds
	Location	Flanders, Belgium
	Scale	Spatial extent: (minX, minY, maxX, maxY, EPSG: 3035): 3799800, 3074600, 4031200, 3168000 (lat,lon): 50.5470558°, 2.6326917°, 51.5479145°, 5.8196204° Spatial resolution: 50 km / 200m Temporal extent/resolution: 2018 (year) Boundary: political
	Biodiversity data	Observation type: Presence-absence data at European scale. Presence-only data at Flanders scale.
	Type of predictors	Climatic, topographic, land cover, land-use intensity
	Conceptual model	Hypotheses about species-environment relationships: We used a nested ensemble method that utilised European scale climate and localised land cover data including crop types, to predict habitat suitability of ten species of farmland birds across the region of Flanders.

	Assumptions	Our assumptions were that: 1. species are at equilibrium within their environment; 2. any biases in sampling and surveying has been reduced; 3. the most relevant ecological drivers are included as proxies in the model variables.
	SDM algorithms	Model algorithms: Generalized linear model (GLM), Generalized Additive Model (GAM), Random Forest (RF), Boosted Regression Trees (BRT), and MaxEnt. Justification of model complexity: We chose to utilise an ensemble of different statistical (GLM, GAM) and supervised learning algorithms (RF, BRT, MaxEnt) to get the best overall mean response. Model averaging/ensemble modelling used?: Yes
	Model workflow	Conceptual description of modelling steps including model fitting, assessment and prediction: 01 - European climate data pre-preparations: reprojecting the raw climate layers before stacking and calculating month-wise means. 02 - SDM Europe - transforming the EBBA bird data to match the climatic data, extraction of climate data for each occurrence cell, spatial thinning, spatial blocking, collinearity testing, SDM modelling and ensemble building. 03 - occurrence data prep Flanders: filtering bird occurrences based on breeding season, removing duplicates (from within the same 200m cell), spatial thinning using buffer method, creation of pseudo absences. 04 - Ensemble SDM: create a nested SDM for Flanders using mean climatic suitability extracted from European SDM and localised environmental and land cover variables (check for collinearity between all predictors), model building and testing, assessment, prediction.
	Software, codes and data	We used R version 4.4.1. With packages: terra, dplyr, sfheaders, corrplot, mecofun, randomForest, gbm, dismo, mgcv, maxnet, sf, blockCV, ecospat Availability of codes and data: currently for

		internal circulation within project
Data	Biodiversity data	Taxon names: Alauda arvensis, Anthus pratensis, Emberiza citrinella, Lanius collurio, Limosa limosa, Passer montanus, Saxicola rubetra, Streptopelia turtur, Sturnus vulgaris, Vanellus vanellus Biodiversity data source: EBBA2 (Europe); Natuurpunt (11.09.2023 - Flanders) Sampling design:: EBBA2 data are non-standardised monitoring data collected between 2013-2018 across entire Europe. EBBA2 provide presence-absence data at 50 km spatial resolution. Natuurpunt is a citizen science organisation (also non-standardised) with specialised validation, post-processing and data cleaning. They provide spatially-explicit presence-only data. Sample size per taxon: See deliverable D4.1. Details on scaling: all non raster data were converted to raster type at 200 m cell resolution to match environmental data from the rest of the project. Occurrences were spatially thinned to account for spatial autocorrelation. Data cleaning/filtering steps: Occurrences were filtered to only include the specific breeding period for each species. For full details on this process, see D4.1 including accuracy of observation, validation by an expert, and type of behaviours observed. Background data derivation: random background points were generated to serve as pseudo-absences in the Flanders models. We generated 10 times as many background data as presences were available. Potential errors and biases: misidentification was accounted for by expert validation, georeferencing errors minimized based on scale of modelling, and sampling bias accounted for by our pre-processing steps including removing duplicate occurrences per cell and spatial thinning.
	Data partitioning	Training data: The final models were trained on all data. For several model building steps (collinearity checks, threshold optimization) and for validation, a 5-fold spatial block cross-validation was used. Selection of validation data: hexagonal spatial

		blocks were generated using the cv_spatial_block_autocor function.
	Predictor variables	<u>Climatic</u>: 19 bioclimatic variables; <u>Topographic</u>: DEM, slope, solar radiation; <u>Habitat</u>: built-up cover, tree cover, water cover, soil moisture entire breeding season, soil moisture early breeding season; <u>Crop types</u>: cultivated grassland, orchards and berries, other cereals, permanent grassland, rapeseed, root crops, summer cereals, sunflower, vegetables, winter cereals, fallow, grapevine, hedges, hops, legumes, maize, miscellaneous, and rapeseed. Details on data sources: CHELSA v2.1 (2022) https://chelsa-climate.org/wp-admin/download-page/CHELSA_tech_specification_V2.pdf Spatial resolution: CHELSA (~1km) global extent. Map projection: EPSG: 3035 or WGS 84 transformed to EPSG: 3035. Temporal resolution: 2018 Details on data processing and on spatial, temporal and thematic scaling: CHELSA data (at ~1km resolution) were upscaled to 50km to match the EBBA2 occurrence grid using bilinear interpolation.
Model	Multicollinearity	We used the select07 method from Dormann et al. (2013) to check for and reduce multicollinearity. We calculated Spearman's rank correlation for each pair of variables and from pairs with $ \rho > 0.7$ we removed the less important variable in terms of cross-validated univariate importance. The climate suitability predicted from European SDM was always included in the fine-scale models.
	Model settings	GLM: linear and quadratic terms, AIC-based step-wise variable selection. binomial link. GAM: cubic smoothing splines with 4 degrees of freedom. binomial link. RF: nodesize= 5, number of trees = 1000. BRT: learning rate = model specific to end up between 1000 and 5000 trees, bag fraction = 0.75, tree complexity = 2. binomial link. Maxent: features = lh.

	Model estimates	Assessment of coefficients: not applicable. Uncertainties: not applicable. Variable importance: estimated for RF and BRT.
	Model selection / averaging / ensemble	Model selection strategy: models with AUC < 0.7 were not used in the nested ensemble. Model averaging: for the fine-scale, we ran 10 replicate BRT, RF and Maxent and averaged their predictions. Nesting method: we used the covariate method (Adde et al., 2023) Ensemble method: Ensemble predictions were derived by calculating the mean habitat suitability across the different SDM algorithms.
	Threshold selection	transforming continuous predictions into binary predictions: We use the maxTSS approach to find the optimal threshold for binarizing continuous habitat suitability predictions and deriving predicted presences and absences. The threshold was optimized using cross-validated predictions.
Assessment	Performance statistics	Performance statistics estimated on validation data: model performance was assessed with a 5-fold spatial block cross-validation. The following model performance metrics were used: "AUC", "TSS", "Sens", "Spec", Boyce
Prediction	Prediction output	Prediction unit: All models from all algorithms were combined into a single df, then thresholded for presence-absence predictions, and the mean of the probabilities was calculated.
	Uncertainty quantification	Algorithmic uncertainty: we assessed uncertainty in predictions by deriving the standard deviation across model predictions from the different SDM algorithms, and the committee average

Table S3: Performance measures for all European SDMs per species

Species	Performance metric	GLM	GAM	RF	BRT	Maxent
<i>Alauda arvensis</i>	AUC	0.90	0.88	0.90	0.91	0.91
<i>Alauda arvensis</i>	Sensitivity	0.80	0.87	0.87	0.90	0.90
<i>Alauda arvensis</i>	Specificity	0.84	0.71	0.77	0.75	0.74
<i>Alauda arvensis</i>	Explained deviance	0.50	0.53	0.85	0.72	0.13
<i>Alauda arvensis</i>	Threshold	0.71	0.52	0.52	0.48	0.38
<i>Anthus pratensis</i>	AUC	0.92	0.91	0.93	0.93	0.93
<i>Anthus pratensis</i>	Sensitivity	0.91	0.84	0.83	0.85	0.88
<i>Anthus pratensis</i>	Specificity	0.79	0.83	0.87	0.87	0.82
<i>Anthus pratensis</i>	Explained deviance	0.55	0.57	0.86	0.72	0.41
<i>Anthus pratensis</i>	Threshold	0.43	0.49	0.44	0.41	0.39
<i>Emberiza citrinella</i>	AUC	0.88	0.88	0.91	0.90	0.87
<i>Emberiza citrinella</i>	Sensitivity	0.71	0.88	0.91	0.84	0.75
<i>Emberiza citrinella</i>	Specificity	0.87	0.76	0.79	0.84	0.85
<i>Emberiza citrinella</i>	Explained deviance	0.58	0.61	0.87	0.77	0.31
<i>Emberiza citrinella</i>	Threshold	0.56	0.25	0.38	0.32	0.31
<i>Limosa limosa</i>	AUC	0.79	0.77	0.83	0.79	0.78
<i>Limosa limosa</i>	Sensitivity	0.85	0.85	0.76	0.71	0.82
<i>Limosa limosa</i>	Specificity	0.63	0.59	0.79	0.73	0.63
<i>Limosa limosa</i>	Explained deviance	0.25	0.25	0.77	0.54	0.18
<i>Limosa limosa</i>	Threshold	0.16	0.13	0.22	0.13	0.31
<i>Passer montanus</i>	AUC	0.82	0.87	0.87	0.86	0.82
<i>Passer montanus</i>	Sensitivity	0.74	0.81	0.84	0.81	0.73
<i>Passer montanus</i>	Specificity	0.76	0.74	0.75	0.74	0.77
<i>Passer montanus</i>	Explained deviance	0.46	0.50	0.83	0.62	0.06
<i>Passer montanus</i>	Threshold	0.64	0.63	0.58	0.63	0.44
<i>Streptopelia turtur</i>	AUC	0.90	0.89	0.91	0.91	0.91

<i>Streptopelia turtur</i>	Sensitivity	0.82	0.85	0.83	0.84	0.85
<i>Streptopelia turtur</i>	Specificity	0.82	0.77	0.83	0.84	0.80
<i>Streptopelia turtur</i>	Explained deviance	0.51	0.52	0.84	0.64	0.30
<i>Streptopelia turtur</i>	Threshold	0.48	0.50	0.53	0.52	0.39
<i>Sturnus vulgaris</i>	AUC	0.91	0.90	0.90	0.90	0.89
<i>Sturnus vulgaris</i>	Sensitivity	0.85	0.85	0.88	0.91	0.84
<i>Sturnus vulgaris</i>	Specificity	0.84	0.84	0.76	0.76	0.82
<i>Sturnus vulgaris</i>	Explained deviance	0.52	0.54	0.83	0.65	0.01
<i>Sturnus vulgaris</i>	Threshold	0.75	0.73	0.59	0.58	0.43
<i>Vanellus vanellus</i>	AUC	0.87	0.85	0.88	0.86	0.85
<i>Vanellus vanellus</i>	Sensitivity	0.80	0.71	0.78	0.84	0.73
<i>Vanellus vanellus</i>	Specificity	0.82	0.86	0.86	0.76	0.81
<i>Vanellus vanellus</i>	Explained deviance	0.41	0.44	0.81	0.64	0.20
<i>Vanellus vanellus</i>	Threshold	0.65	0.74	0.56	0.52	0.44

Table S4: Performance measures for all SDMs of Flanders per species

Species	performance metric	GLM	GAM	RF	BRT	Maxent
<i>Alauda arvensis</i>	AUC	0.83	0.83	0.98	0.81	0.83
<i>Alauda arvensis</i>	TSS	0.5	0.5	0.9	0.48	0.51
<i>Alauda arvensis</i>	Sensitivity	0.77	0.8	0.99	0.84	0.85
<i>Alauda arvensis</i>	Explained deviance	0.69	0.7	0.77	0.49	0.28
<i>Alauda arvensis</i>	Boyce index	0.59	0.97	1	0.59	0.95
<i>Alauda arvensis</i>	Threshold	0.05	0.42	0.54	0.03	0.21
<i>Anthus pratensis</i>	AUC	0.81	0.8	0.99	0.81	0.84
<i>Anthus pratensis</i>	TSS	0.45	0.48	0.92	0.48	0.54
<i>Anthus pratensis</i>	Sensitivity	0.73	0.75	0.99	0.75	0.83
<i>Anthus pratensis</i>	Explained deviance	0.68	0.71	0.79	0.6	0.33
<i>Anthus pratensis</i>	Boyce index	0.73	0.91	0.99	0.82	0.91

<i>Anthus pratensis</i>	Threshold	0.05	0.45	0.54	0.04	0.18
<i>Emberiza citrinella</i>	AUC	0.87	0.9	0.99	0.9	0.91
<i>Emberiza citrinella</i>	TSS	0.63	0.66	0.9	0.64	0.68
<i>Emberiza citrinella</i>	Sensitivity	0.83	0.87	0.97	0.85	0.89
<i>Emberiza citrinella</i>	Explained deviance	0.75	0.77	0.83	0.63	0.41
<i>Emberiza citrinella</i>	Boyce index	0.62	0.96	0.97	0.88	0.95
<i>Emberiza citrinella</i>	Threshold	0.06	0.39	0.66	0.04	0.16
<i>Limosa limosa</i>	AUC	0.85	0.83	0.98	0.82	0.85
<i>Limosa limosa</i>	TSS	0.54	0.51	0.93	0.48	0.54
<i>Limosa limosa</i>	Sensitivity	0.79	0.84	0.99	0.61	0.76
<i>Limosa limosa</i>	Explained deviance	0.73	0.74	0.79	0.62	0.36
<i>Limosa limosa</i>	Boyce index	0.56	0.69	0.96	0.45	0.9
<i>Limosa limosa</i>	Threshold	0.04	0.24	0.55	0.05	0.13
<i>Passer montanus</i>	AUC	0.73	0.74	0.94	0.71	0.74
<i>Passer montanus</i>	TSS	0.33	0.42	0.77	0.3	0.39
<i>Passer montanus</i>	Sensitivity	0.68	0.84	0.9	0.7	0.75
<i>Passer montanus</i>	Explained deviance	0.58	0.59	0.61	0.31	0.2
<i>Passer montanus</i>	Boyce index	0.74	0.73	0.9	0.55	0.56
<i>Passer montanus</i>	Threshold	0.07	0.43	0.62	0.06	0.39
<i>Streptopelia turtur</i>	AUC	0.76	0.75	0.95	0.78	0.78
<i>Streptopelia turtur</i>	TSS	0.41	0.4	0.8	0.46	0.45
<i>Streptopelia turtur</i>	Sensitivity	0.71	0.77	0.96	0.56	0.74
<i>Streptopelia turtur</i>	Explained deviance	0.64	0.64	0.6	0.37	0.2
<i>Streptopelia turtur</i>	Boyce index	0.48	0.76	0.77	0.45	0.84
<i>Streptopelia turtur</i>	Threshold	0.06	0.43	0.42	0.05	0.29
<i>Sturnus vulgaris</i>	AUC	0.71	0.71	0.97	0.73	0.74
<i>Sturnus vulgaris</i>	TSS	0.31	0.32	0.84	0.33	0.35
<i>Sturnus vulgaris</i>	Sensitivity	0.81	0.73	0.94	0.69	0.84

<i>Sturnus vulgaris</i>	Explained deviance	0.55	0.56	0.69	0.27	0.14
<i>Sturnus vulgaris</i>	Boyce index	0.61	0.93	1	0.55	0.95
<i>Sturnus vulgaris</i>	Threshold	0.06	0.48	0.63	0.07	0.32
<i>Vanellus vanellus</i>	AUC	0.77	0.78	0.98	0.8	0.8
<i>Vanellus vanellus</i>	TSS	0.41	0.43	0.87	0.43	0.44
<i>Vanellus vanellus</i>	Sensitivity	0.78	0.74	0.97	0.68	0.81
<i>Vanellus vanellus</i>	Explained deviance	0.59	0.61	0.72	0.32	0.19
<i>Vanellus vanellus</i>	Boyce index	0.6	0.94	1	0.78	0.97
<i>Vanellus vanellus</i>	Threshold	0.07	0.53	0.61	0.08	0.33

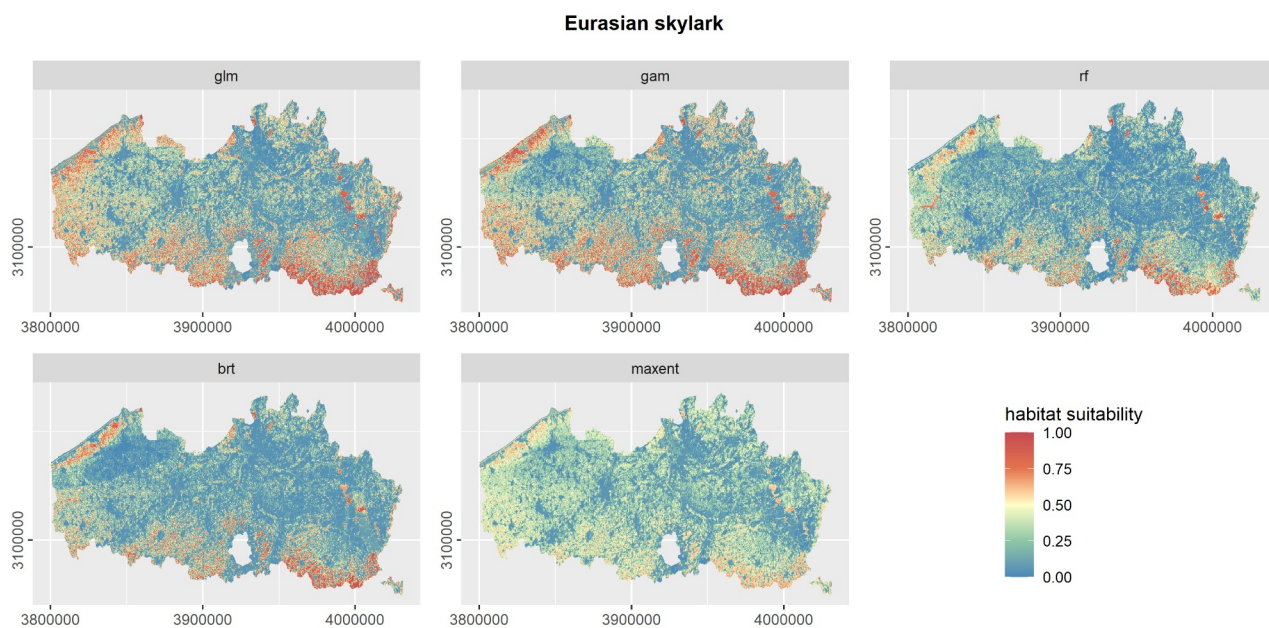


Figure S1: Habitat suitability predictions for the Eurasian skylark and Flanders by model algorithm.

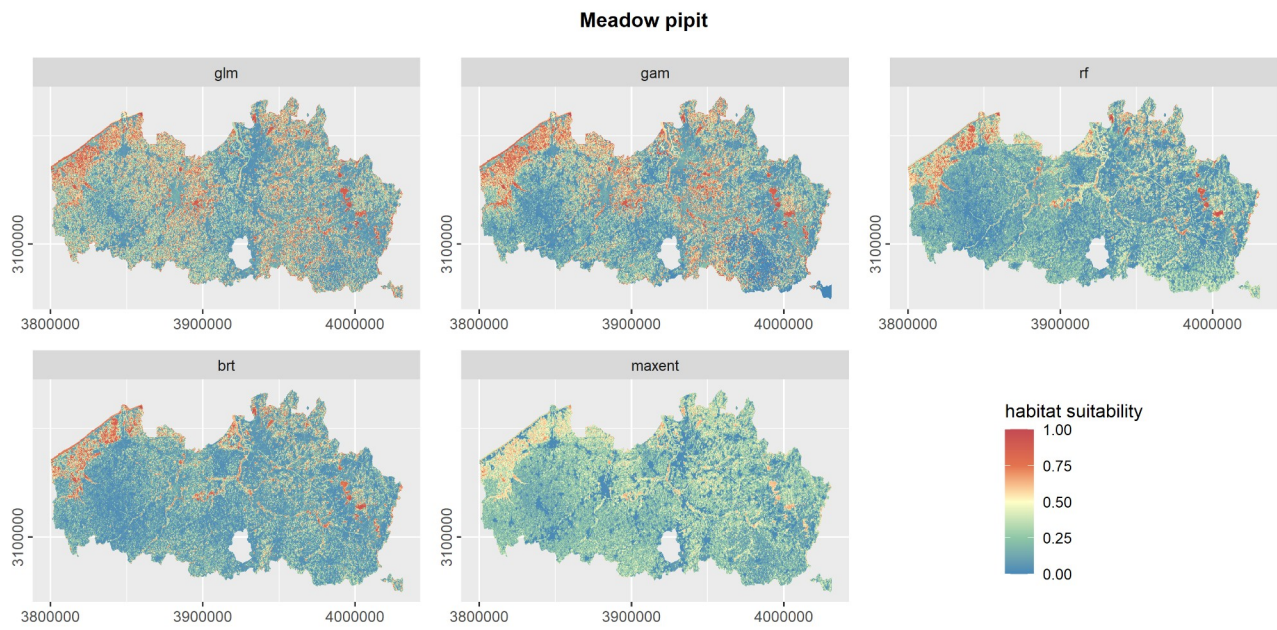


Figure S2: Habitat suitability predictions for the Meadow pipit and Flanders by model algorithm.

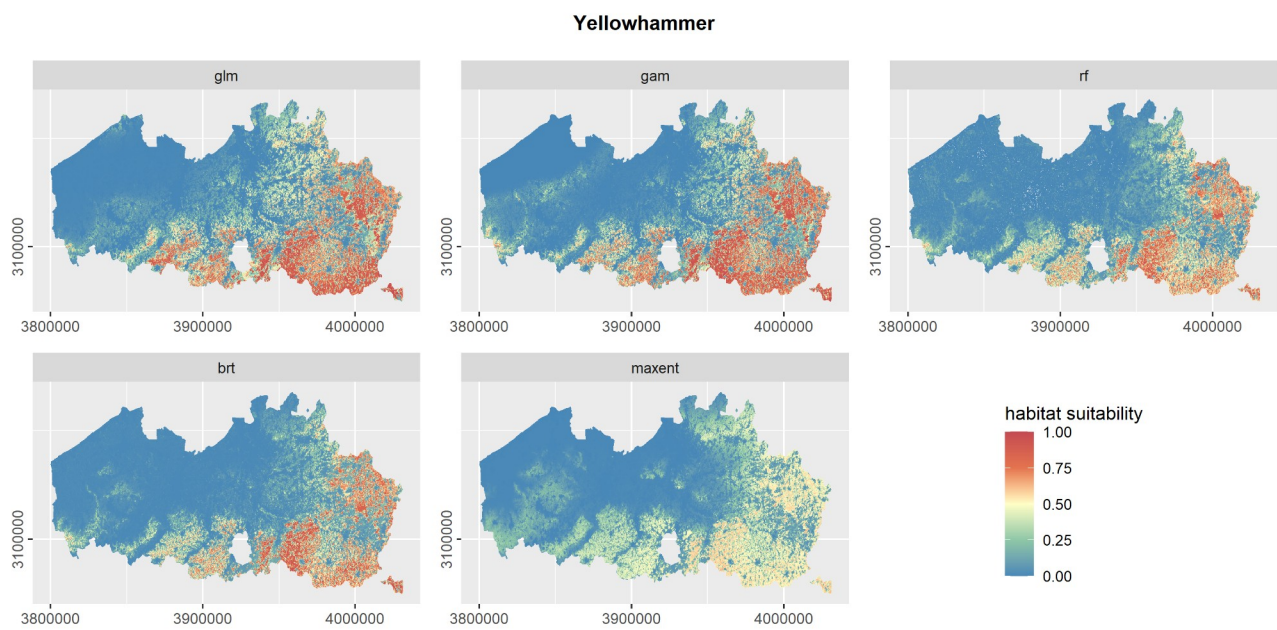


Figure S3: Habitat suitability predictions for the Yellowhammer and Flanders by model algorithm.

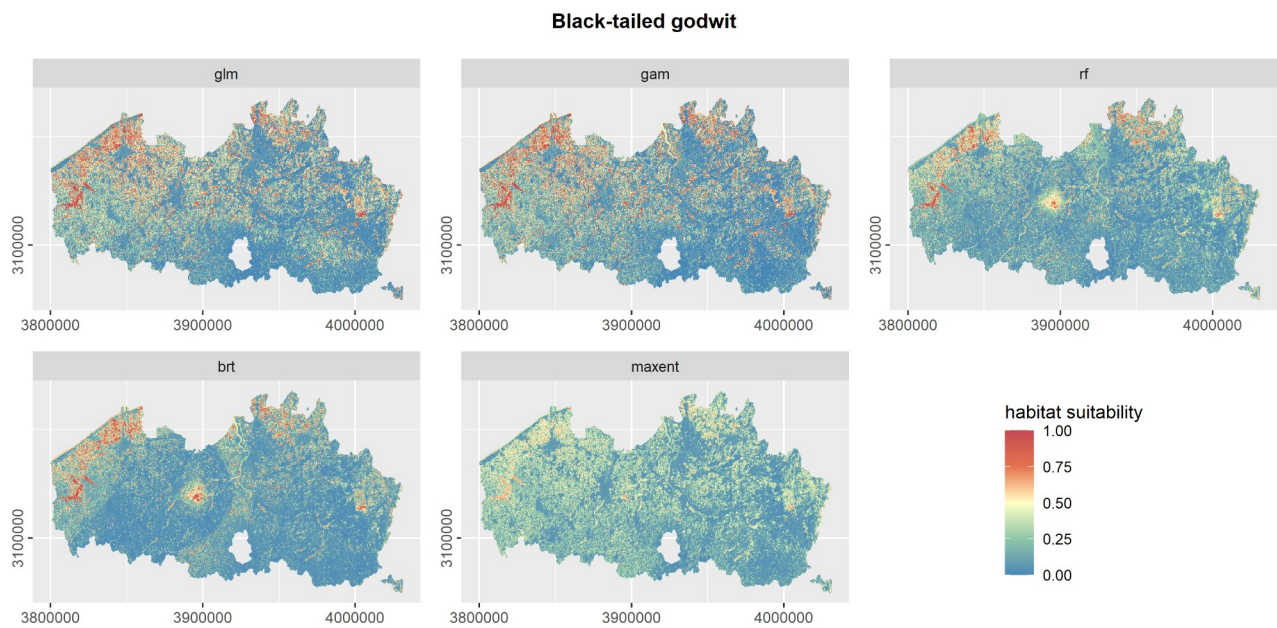


Figure S4: Habitat suitability predictions for the Black-tailed godwit and Flanders by model algorithm.

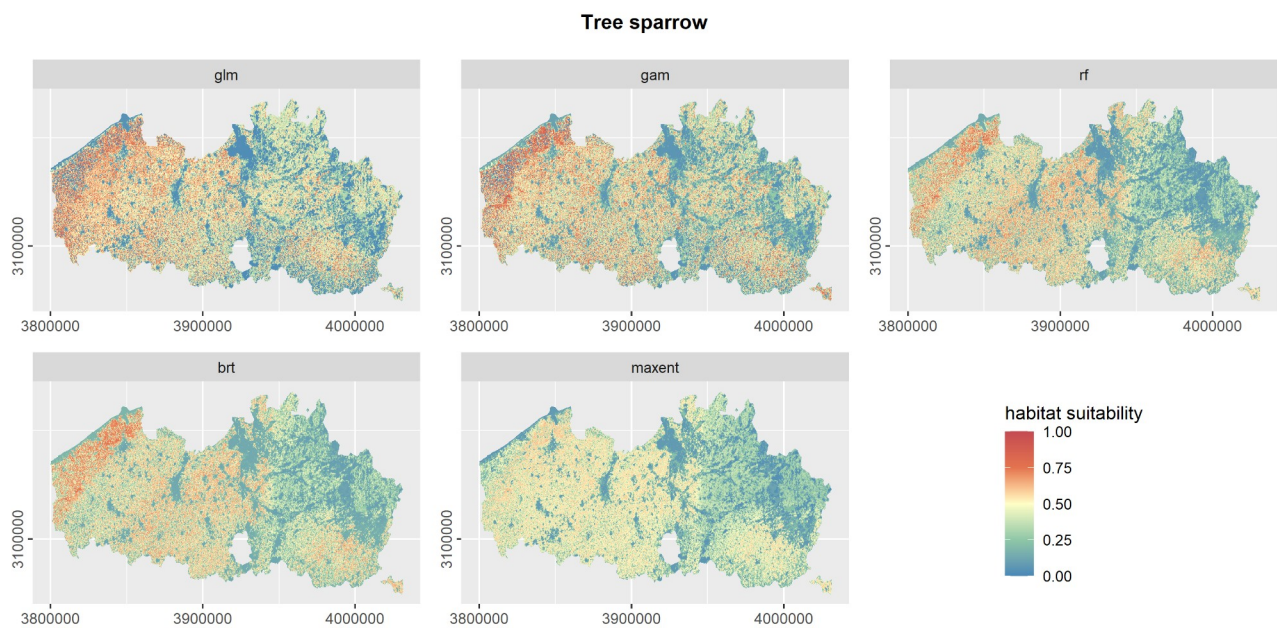


Figure S5: Habitat suitability predictions for the Tree sparrow and Flanders by model algorithm.

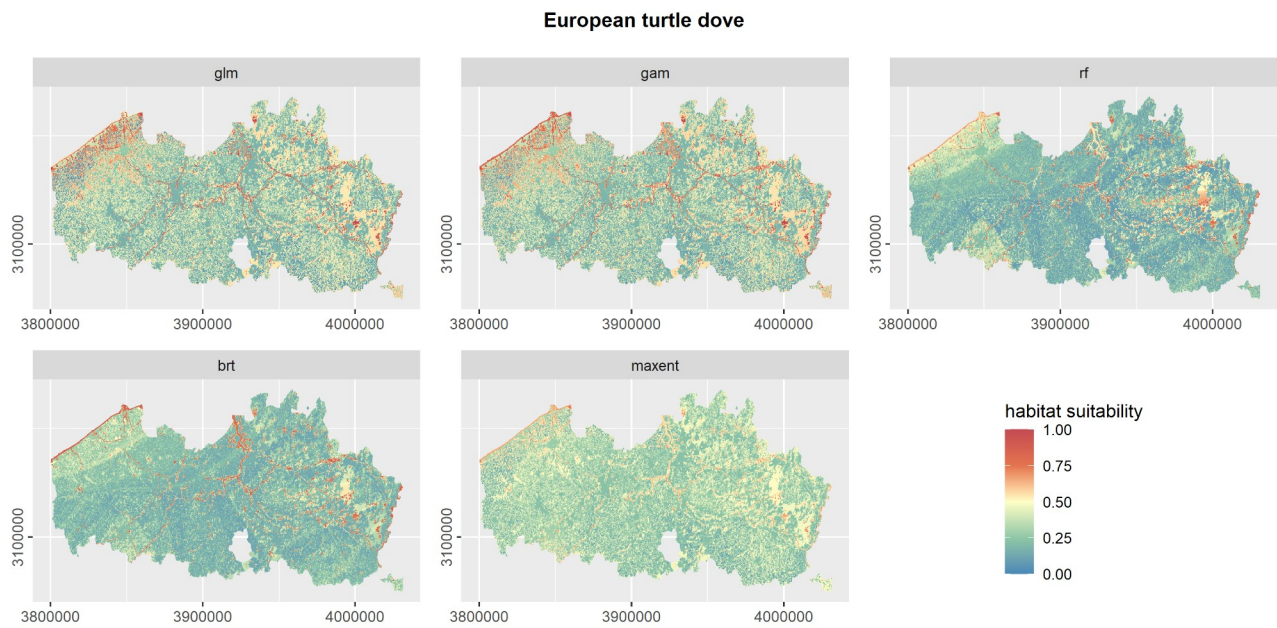


Figure S6: Habitat suitability predictions for the European turtle dove and Flanders by model algorithm.



Figure S7: Habitat suitability predictions for the Common starling and Flanders by model algorithm.

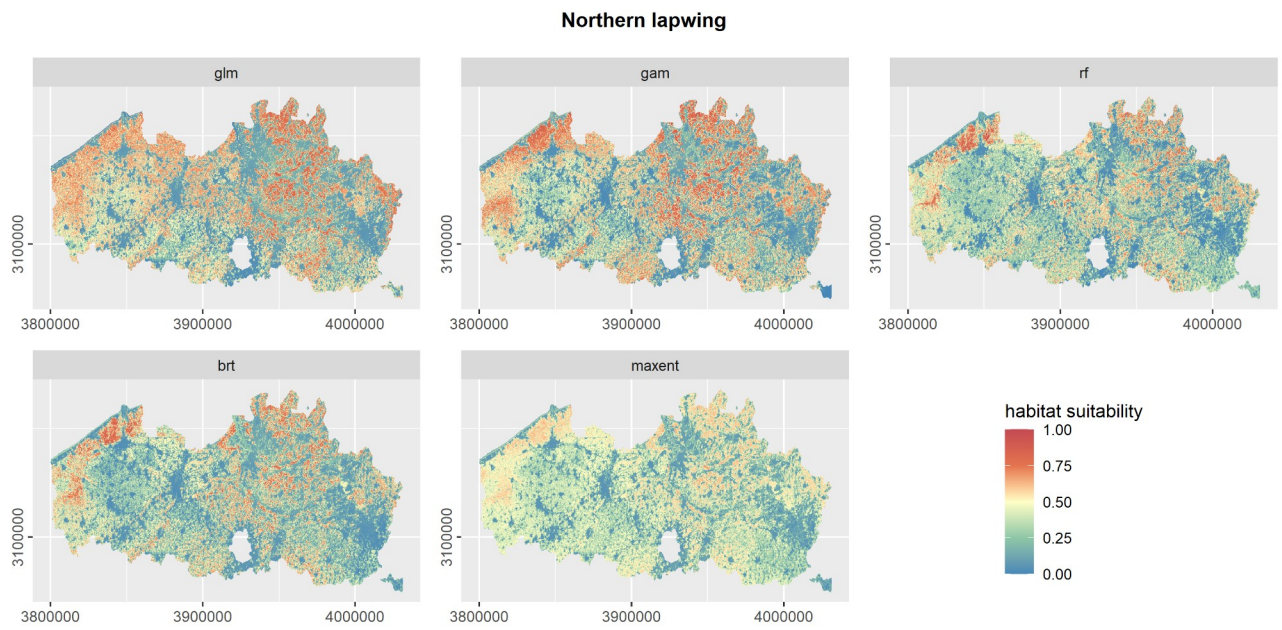


Figure S8: Habitat suitability predictions for the Northern lapwing and Flanders by model algorithm.

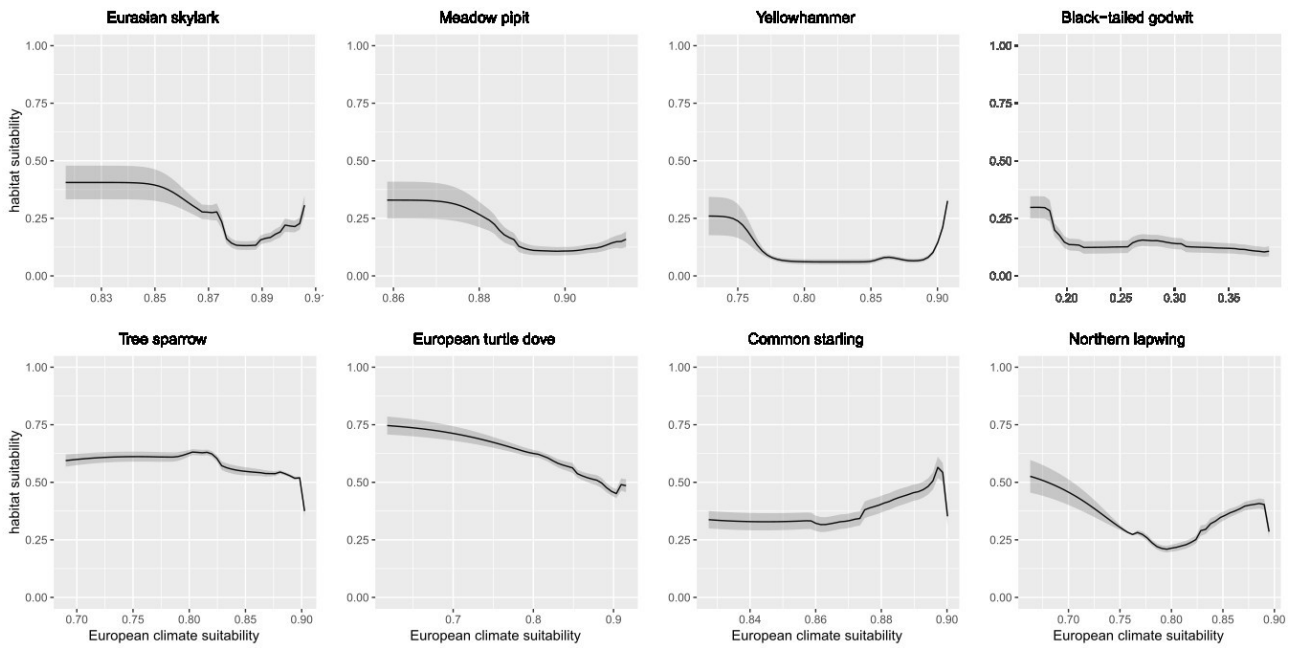


Figure S9: Partial response curves per species and Flanders for the environmental parameter "European climate suitability" ranging from zero to one. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

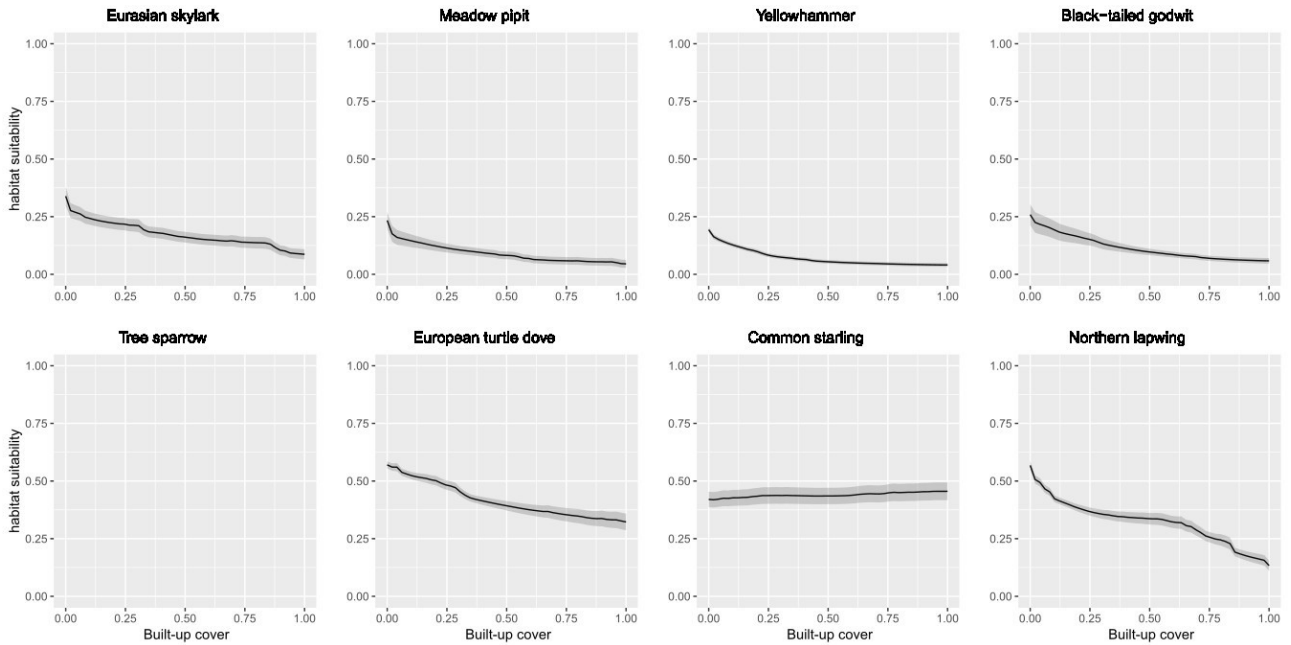


Figure S10: Partial response curves per species and Flanders for the environmental parameter "Built-up cover" given in %. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

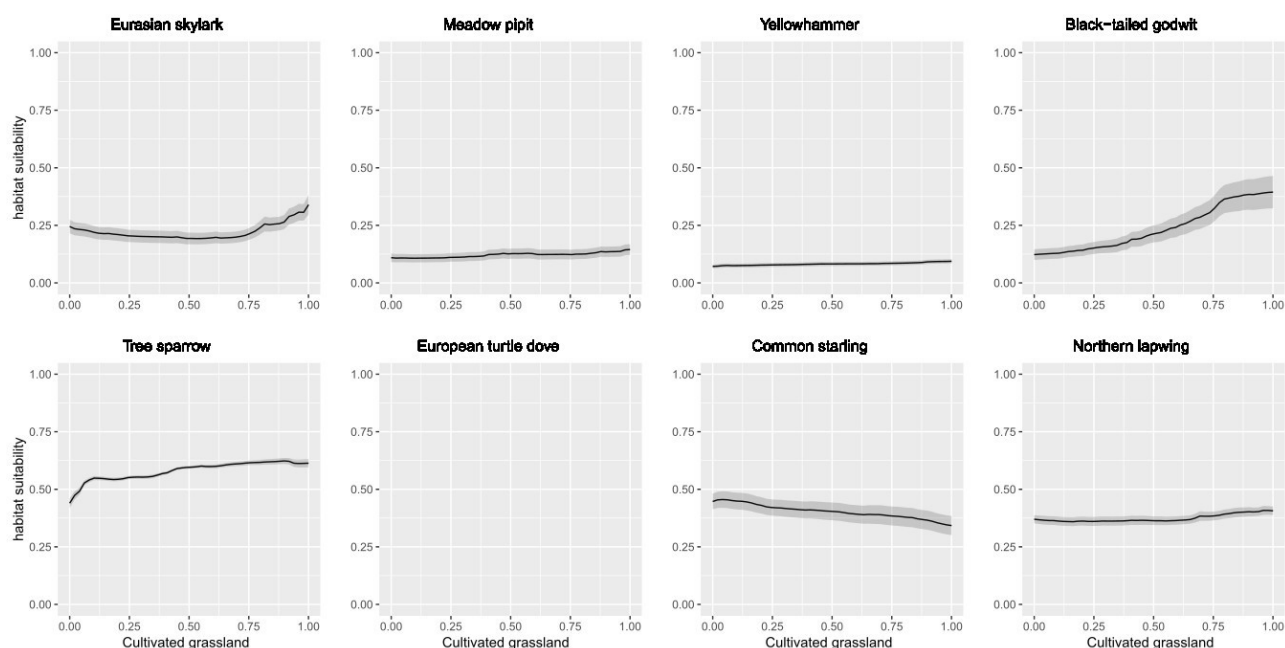


Figure S11: Partial response curves per species and Flanders for the environmental parameter “Cultivated grassland” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

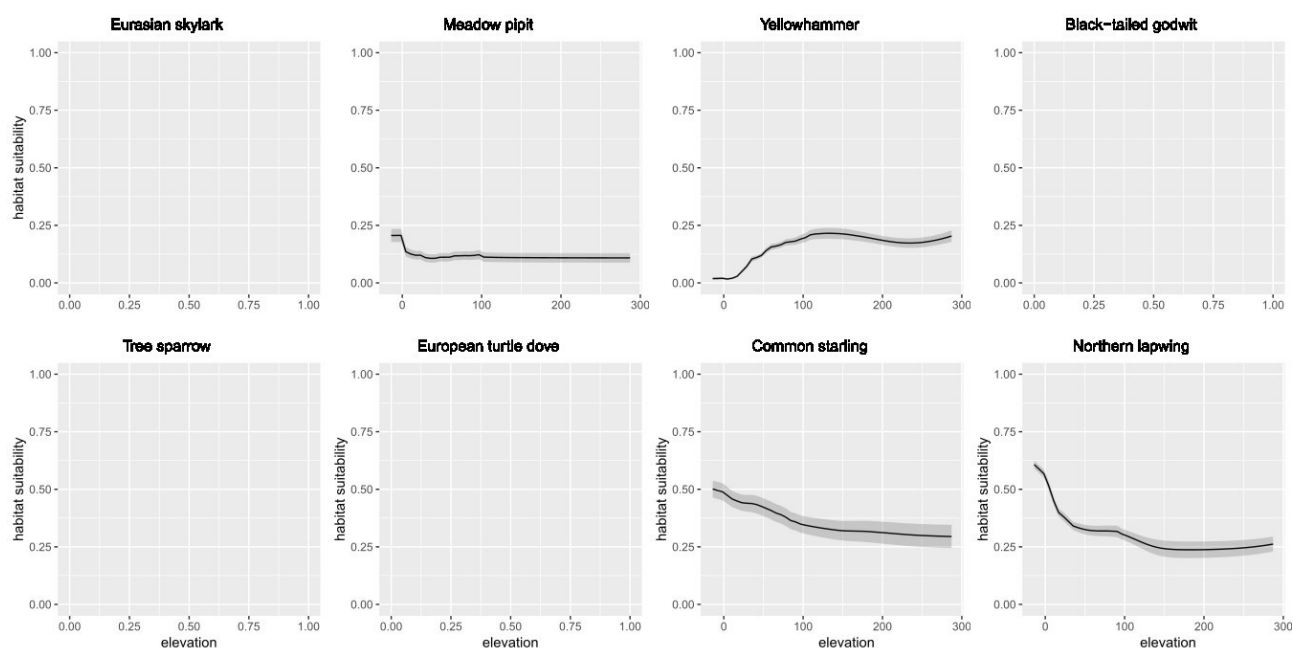


Figure S12: Partial response curves per species and Flanders for the environmental parameter “Elevation” given in meters. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

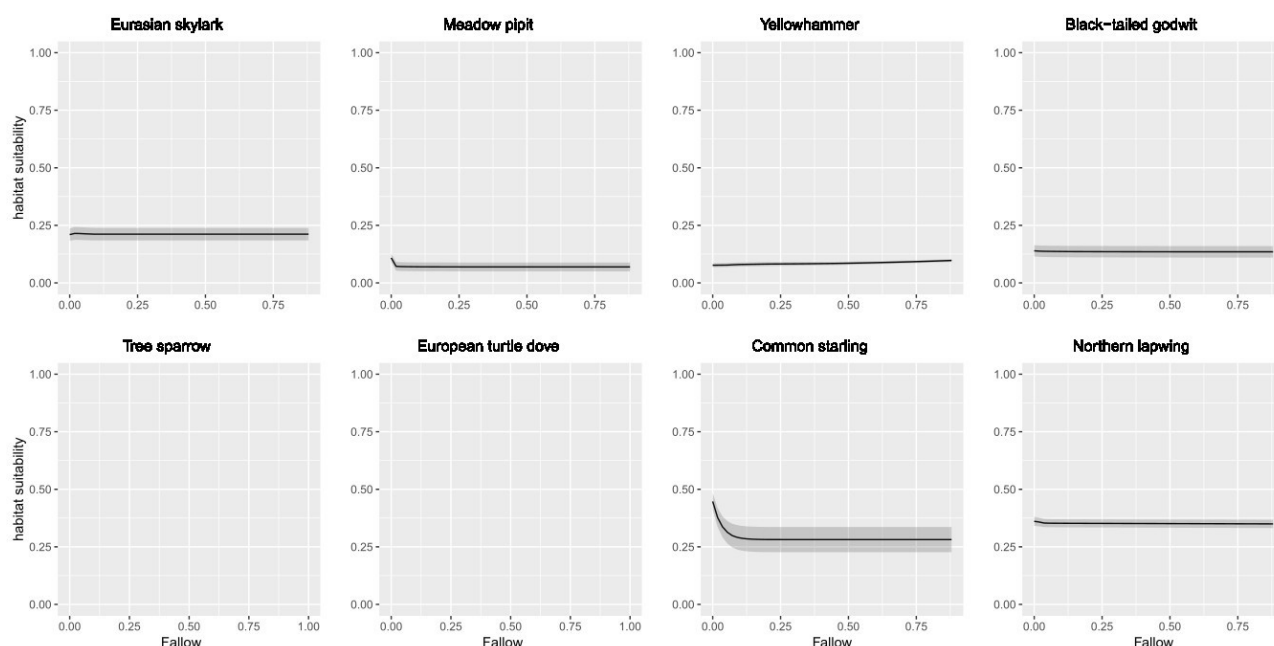


Figure S13: Partial response curves per species and Flanders for the environmental parameter “Fallow” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

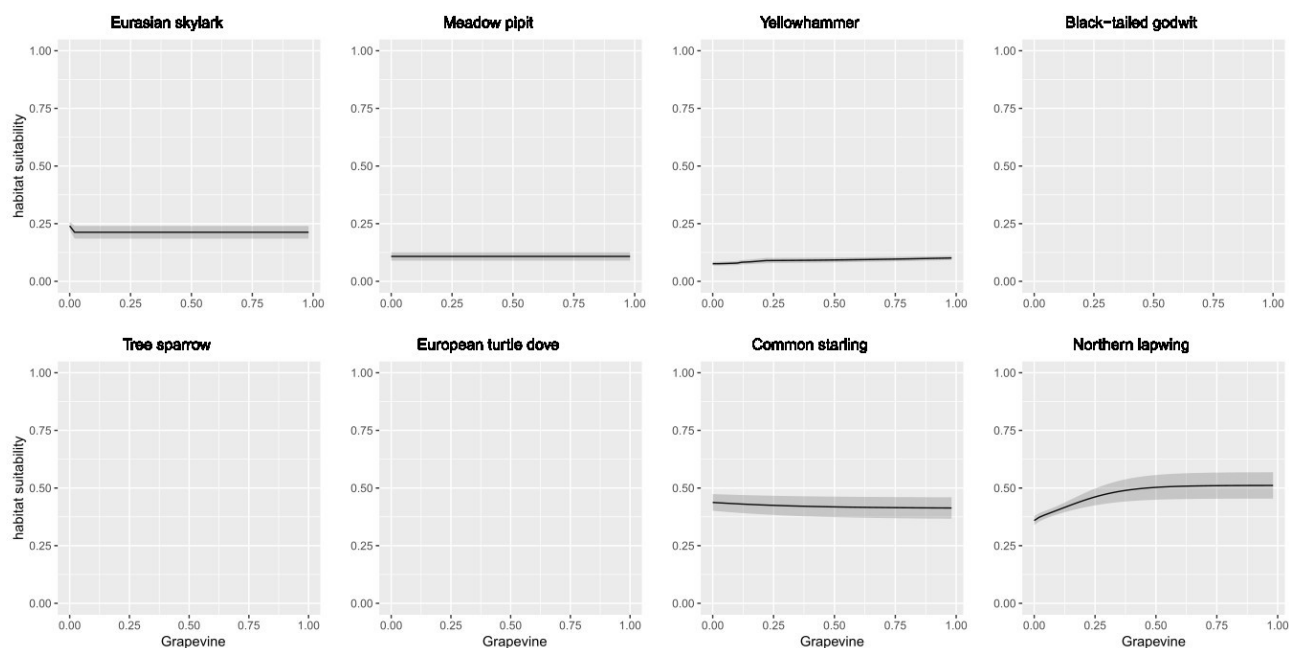


Figure S14: Partial response curves per species and Flanders for the environmental parameter “Grapevine” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

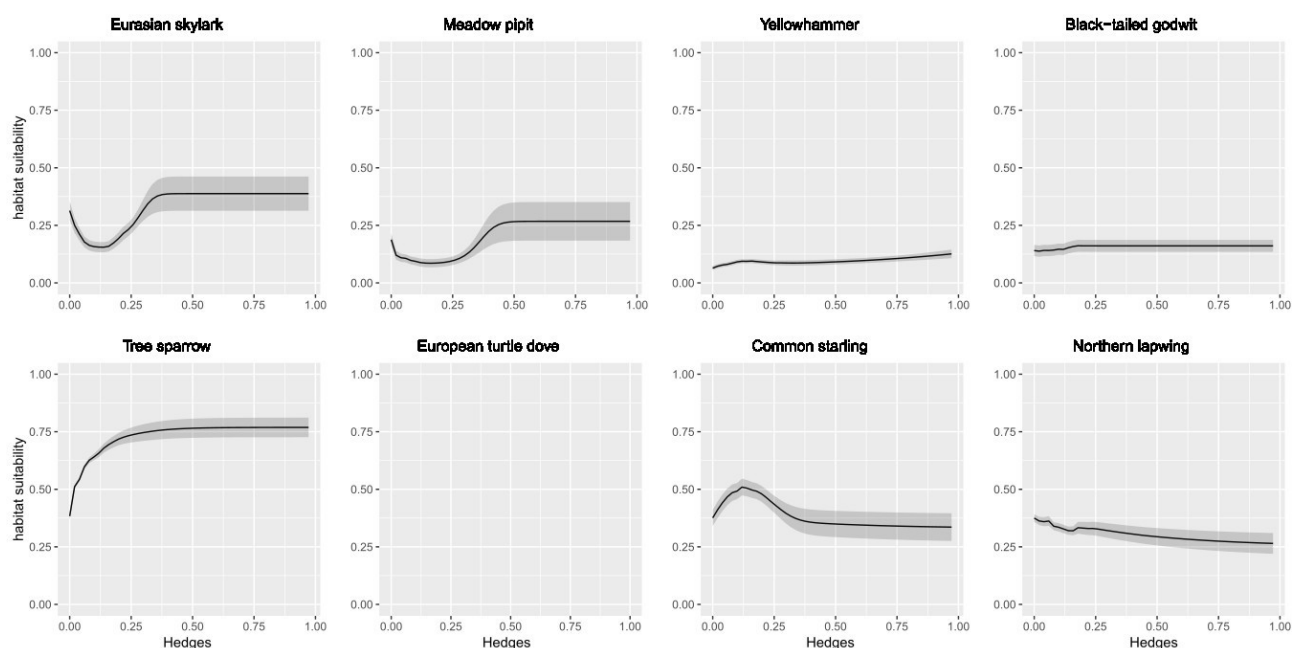


Figure S15: Partial response curves per species and Flanders for the environmental parameter "Hedges" given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

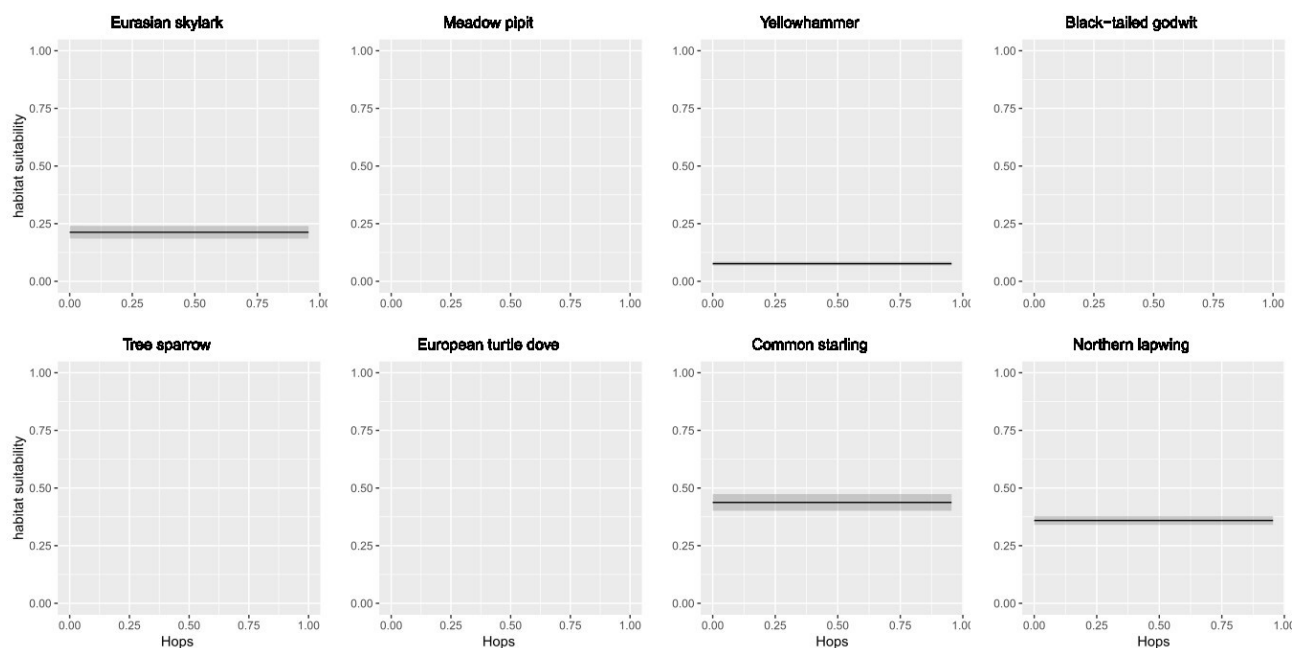


Figure S16: Partial response curves per species and Flanders for the environmental parameter "Hops" given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

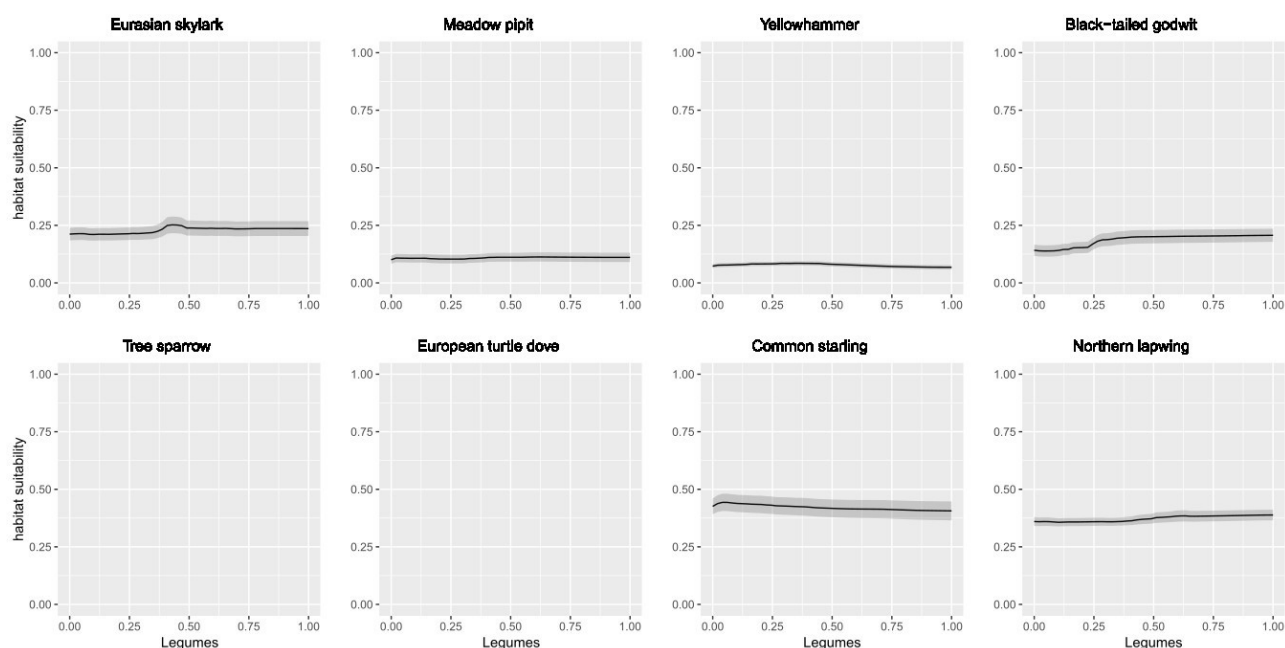


Figure S17: Partial response curves per species and Flanders for the environmental parameter “Legumes” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

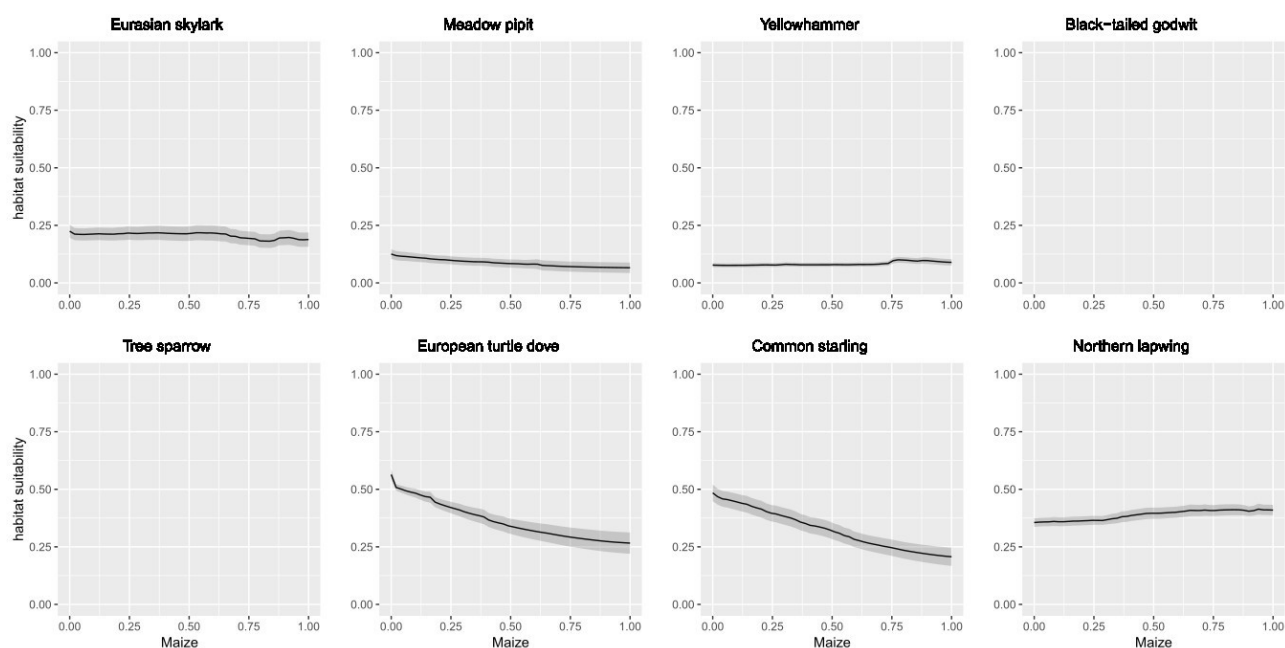


Figure S18: Partial response curves per species and Flanders for the environmental parameter “Maize” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

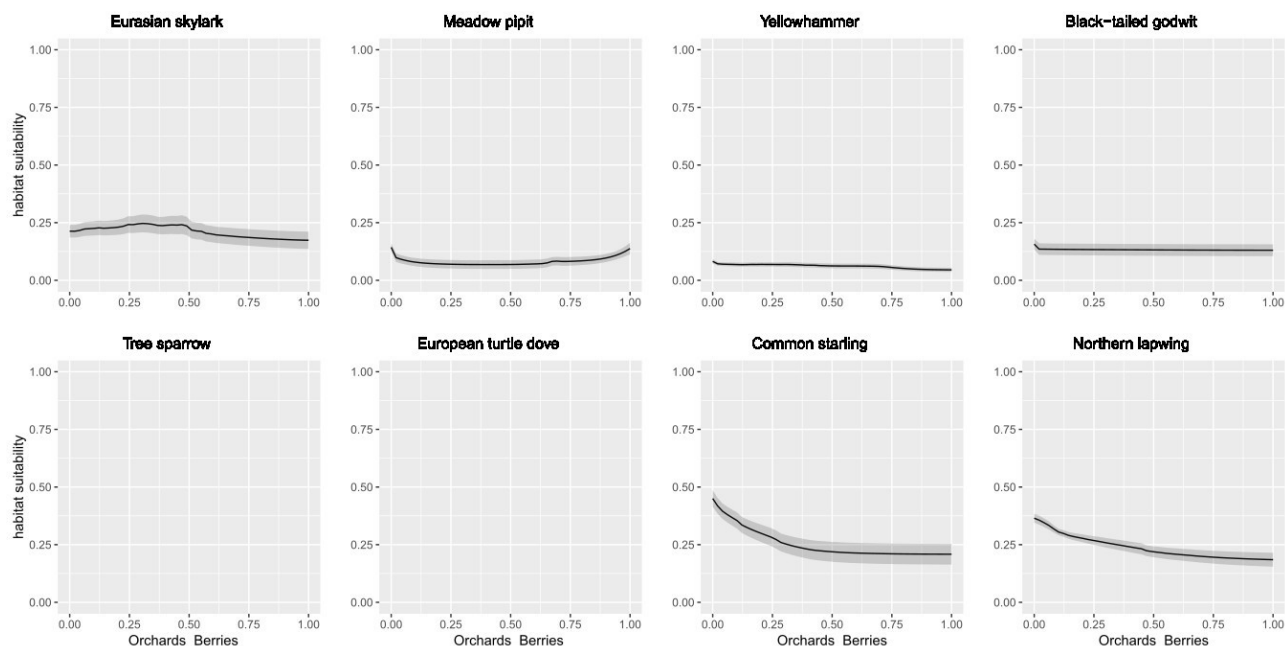


Figure S19: Partial response curves per species and Flanders for the environmental parameter "Orchards and Berries" given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

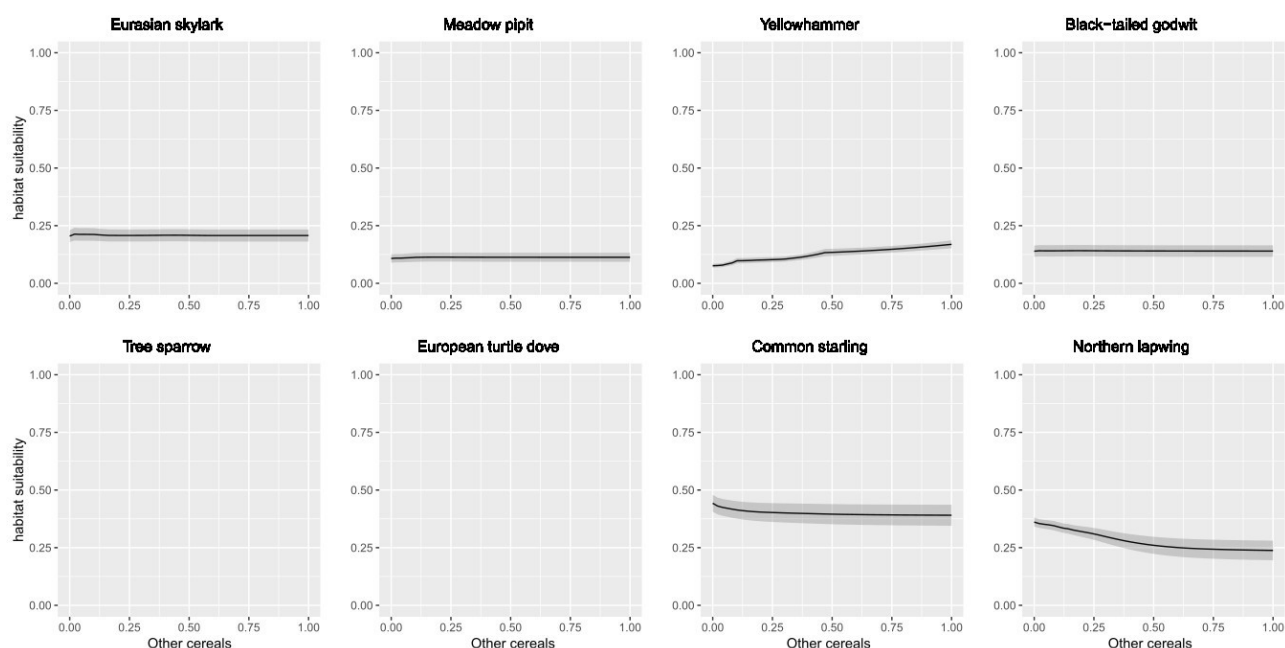


Figure S20: Partial response curves per species and Flanders for the environmental parameter "Other cereals" given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

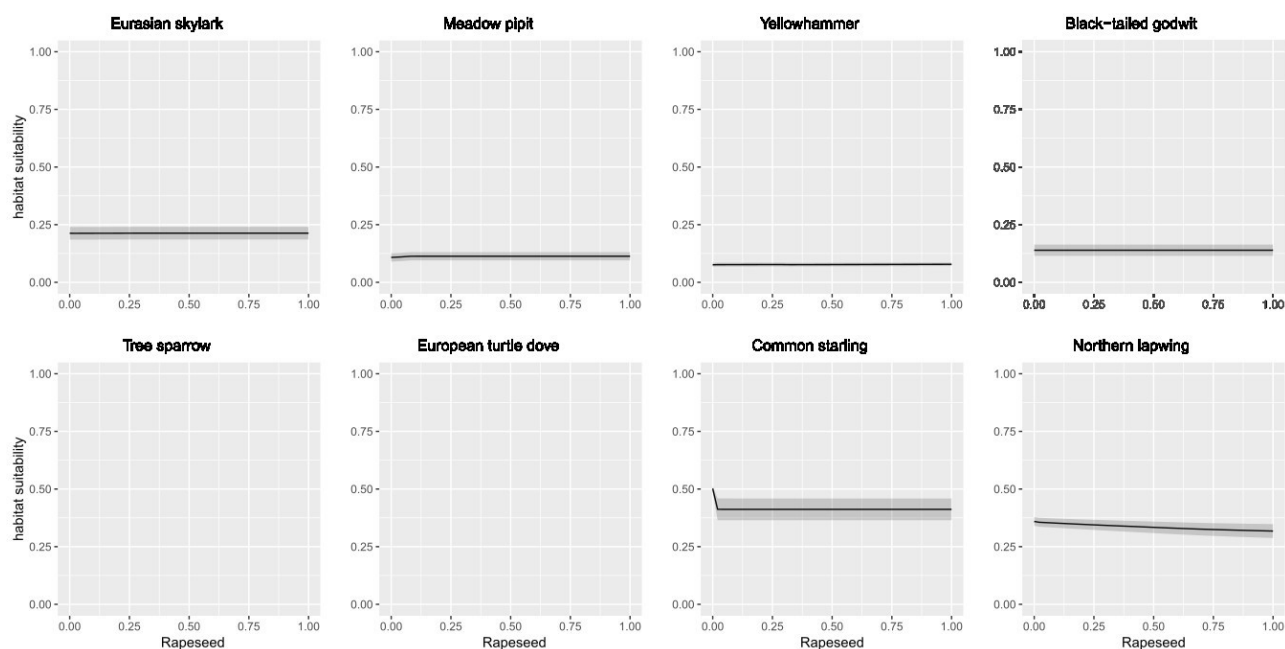


Figure S21: Partial response curves per species and Flanders for the environmental parameter "Rapeseed" given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

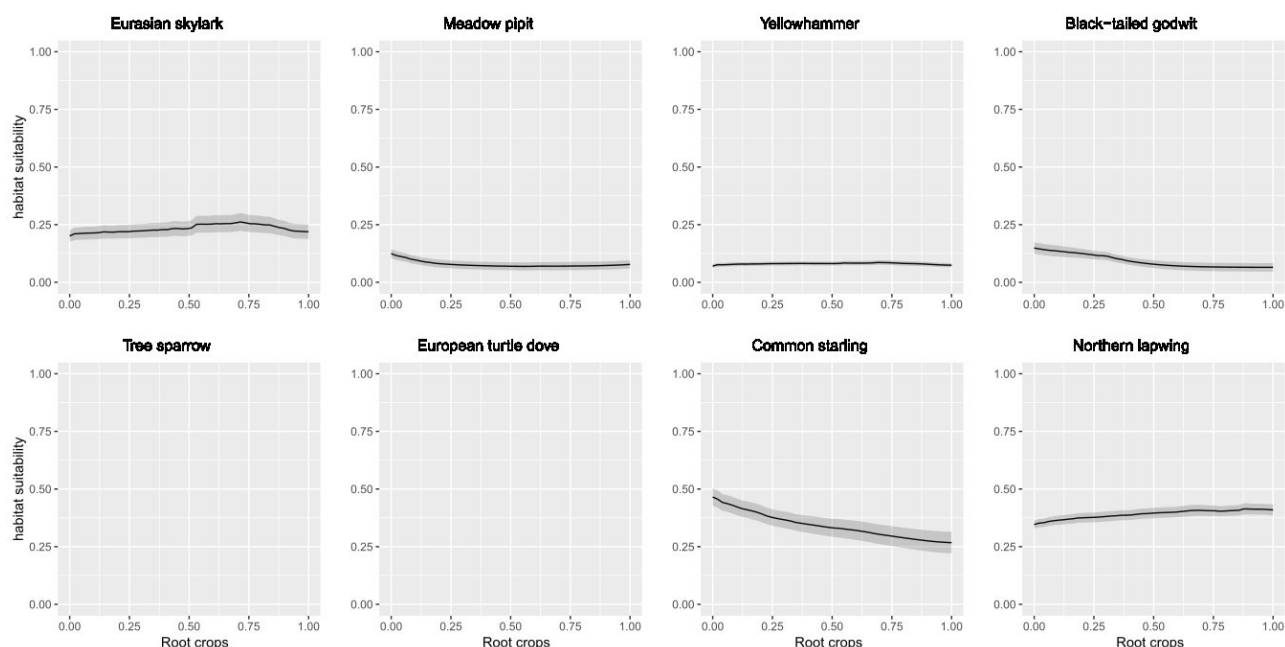


Figure S22: Partial response curves per species and Flanders for the environmental parameter "Root crops" given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

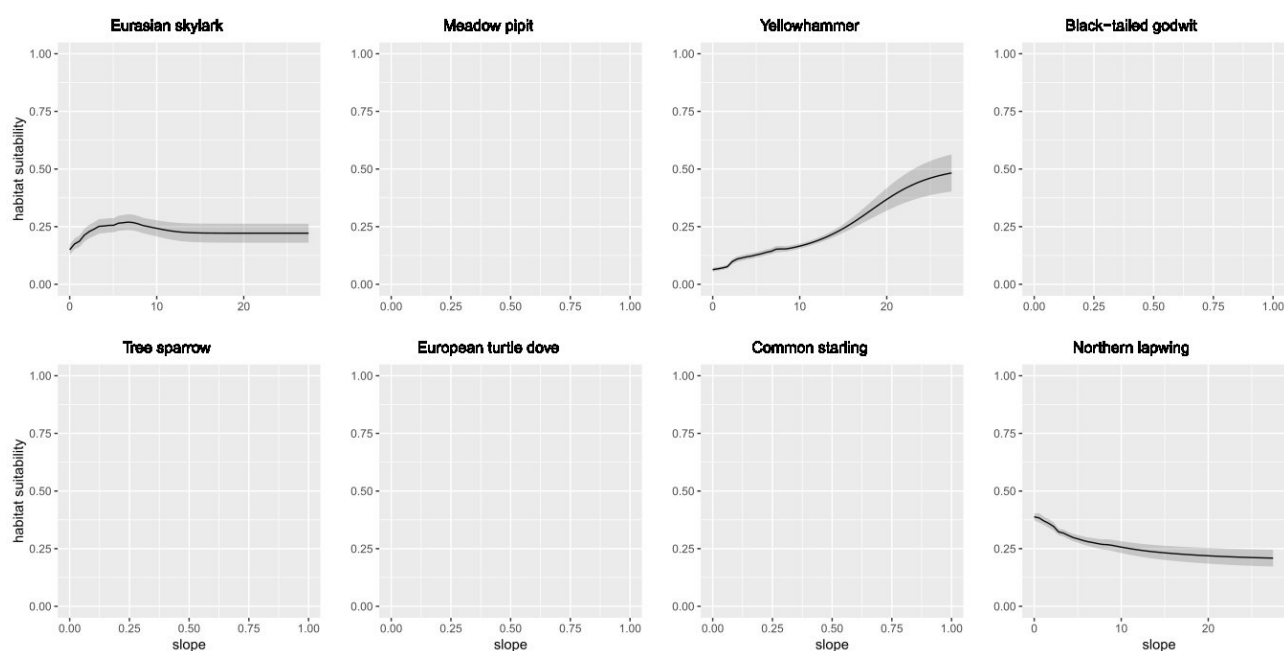


Figure S23: Partial response curves per species and Flanders for the environmental parameter “Slope” given in degree. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

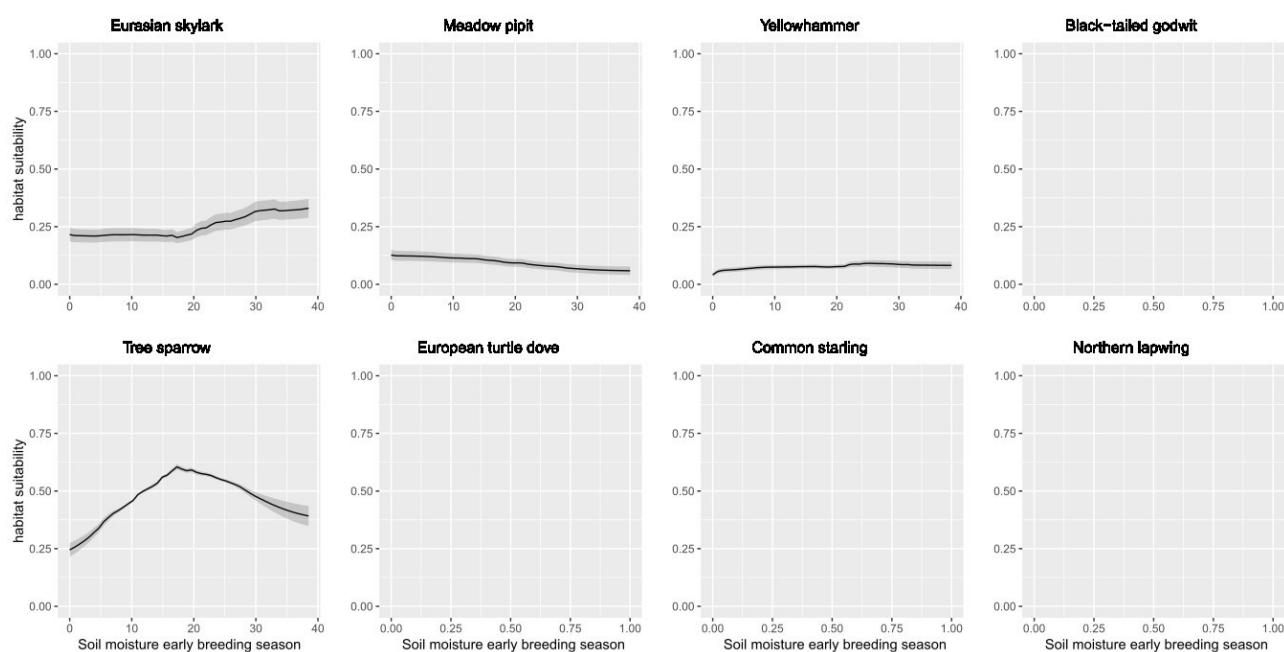


Figure S24: Partial response curves per species and Flanders for the environmental parameter “Soil moisture early breeding season” given in m^3/m^3 . A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

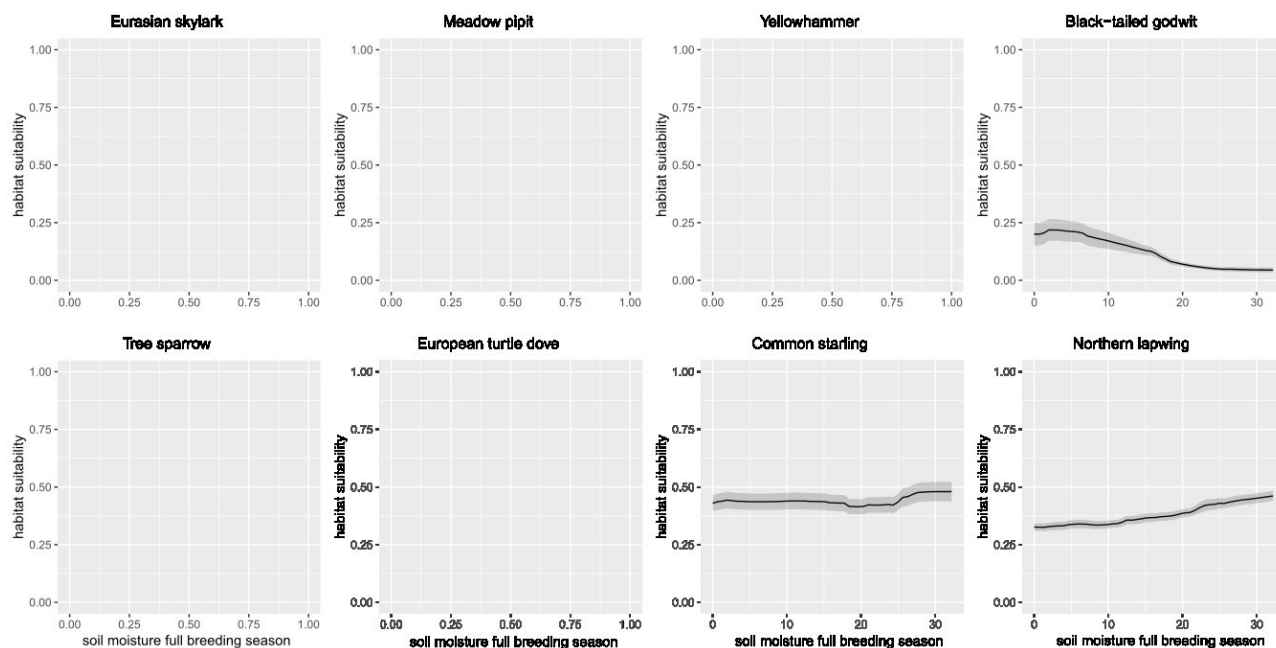


Figure S25: Partial response curves per species and Flanders for the environmental parameter "Soil moisture full breeding season" given in m^3/m^3 . A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

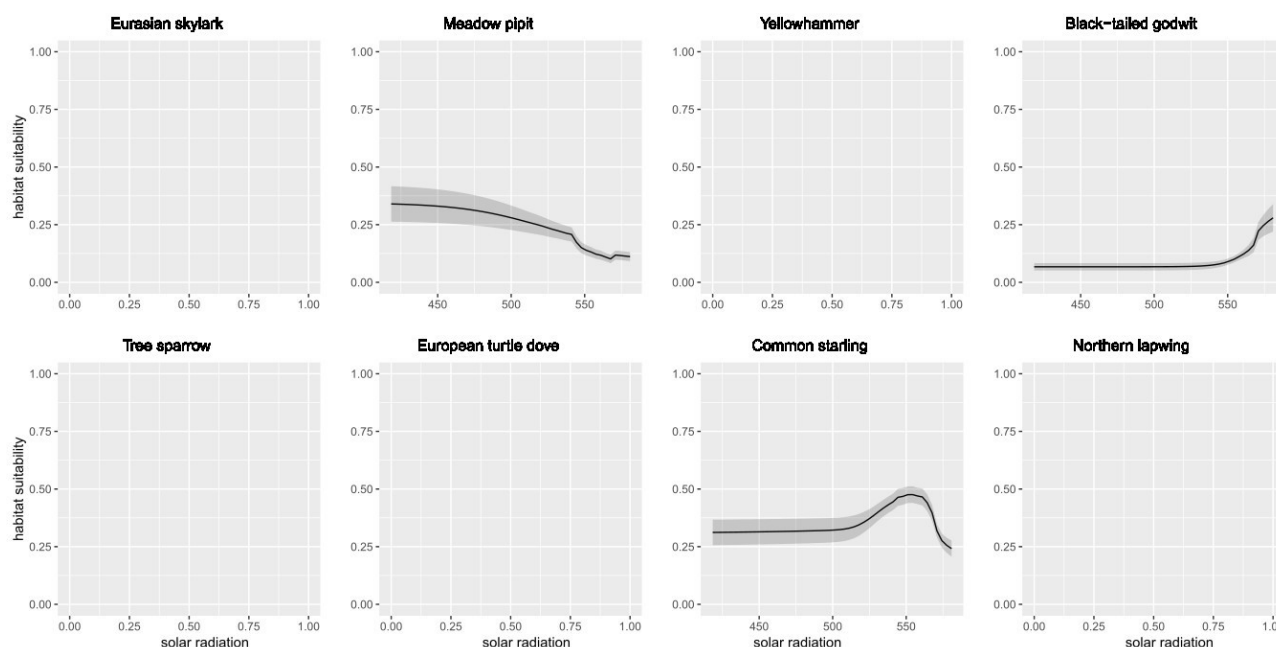


Figure S26: Partial response curves per species and Flanders for the environmental parameter "solar radiation" given in kWh/m^2 . A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

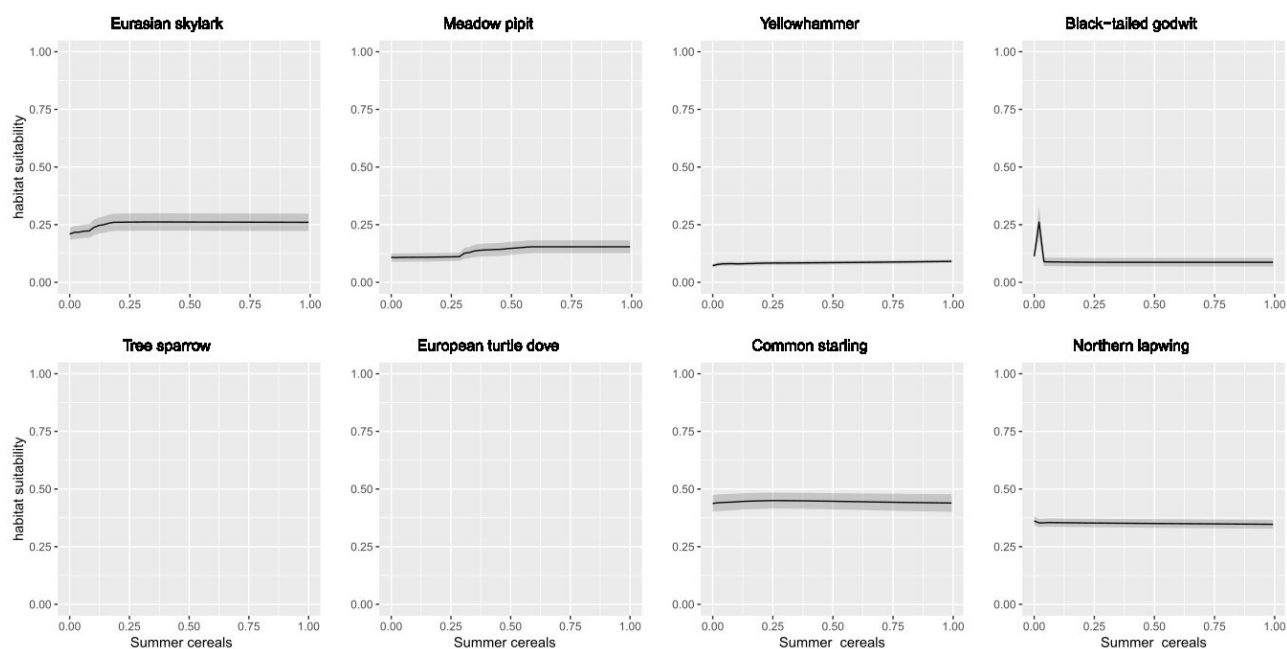


Figure S27: Partial response curves per species and Flanders for the environmental parameter “Summer cereals” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

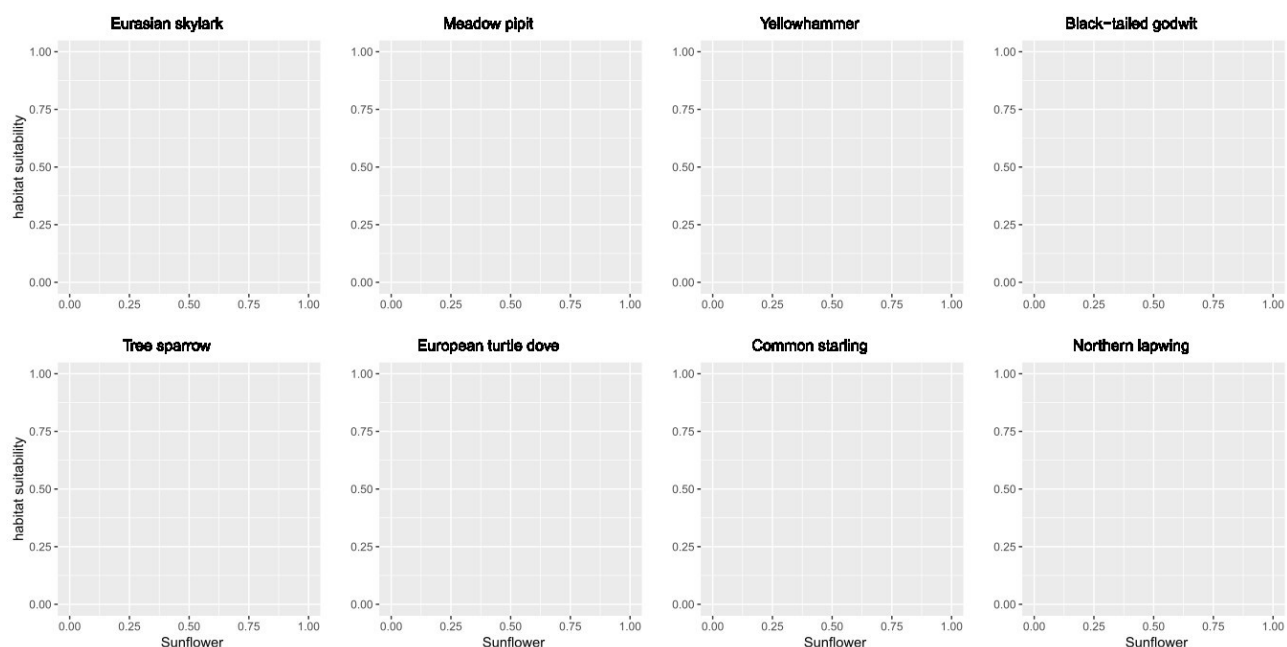


Figure S28: Partial response curves per species and Flanders for the environmental parameter “Sunflower” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

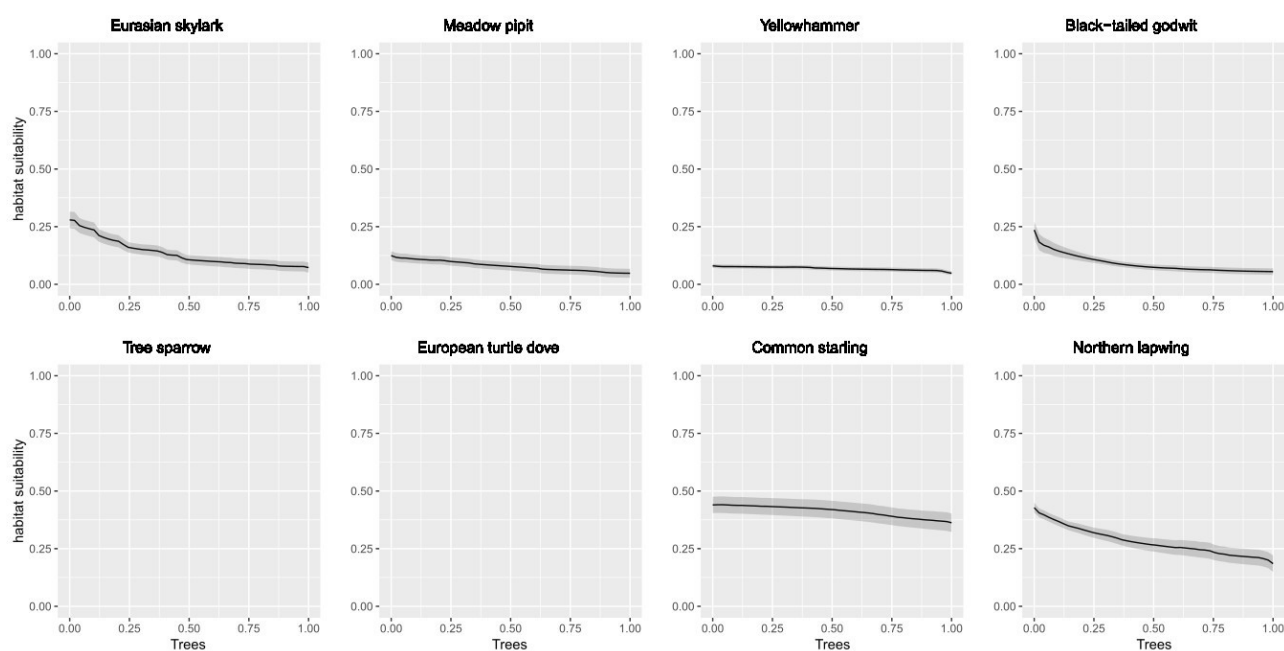


Figure S29: Partial response curves per species and Flanders for the environmental parameter “Trees” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

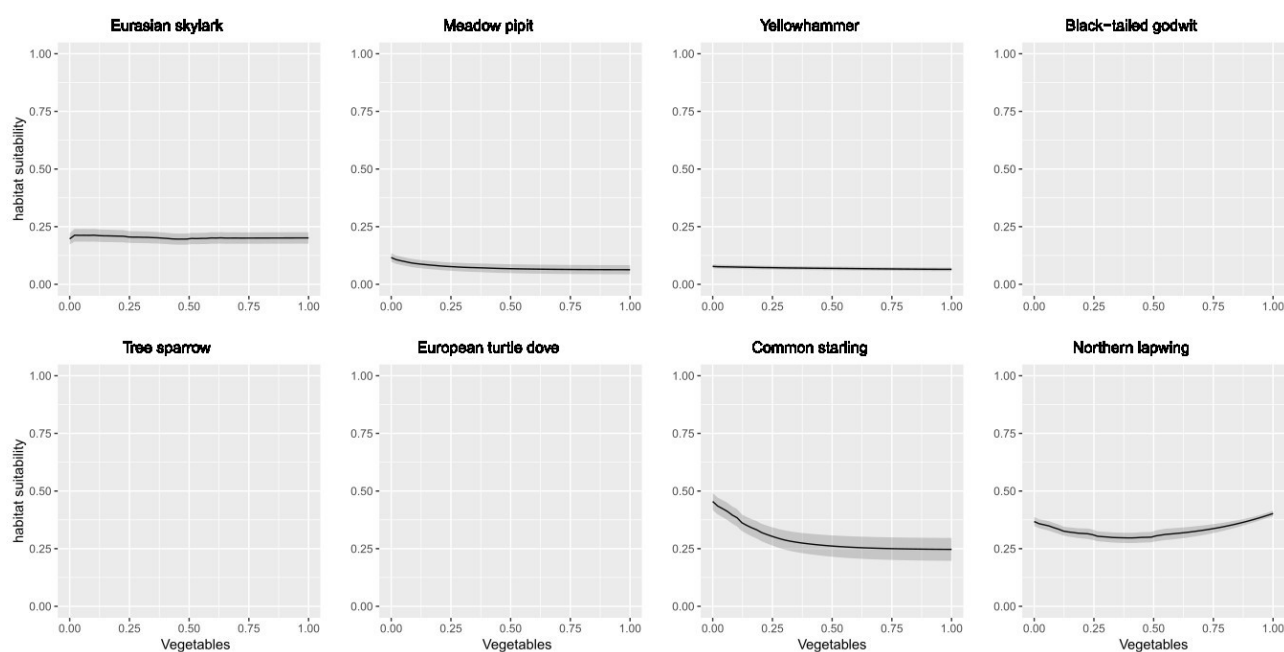


Figure S30: Partial response curves per species and Flanders for the environmental parameter “Vegetables” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

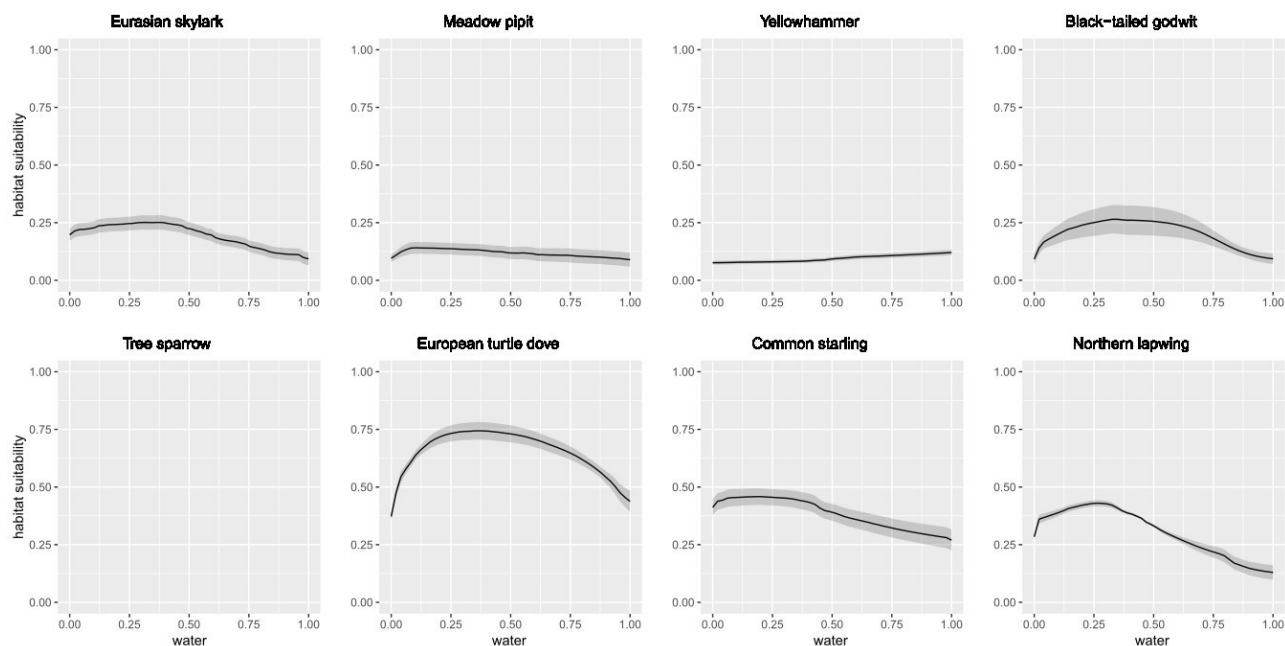


Figure S31: Partial response curves per species and Flanders for the environmental parameter “Water” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.

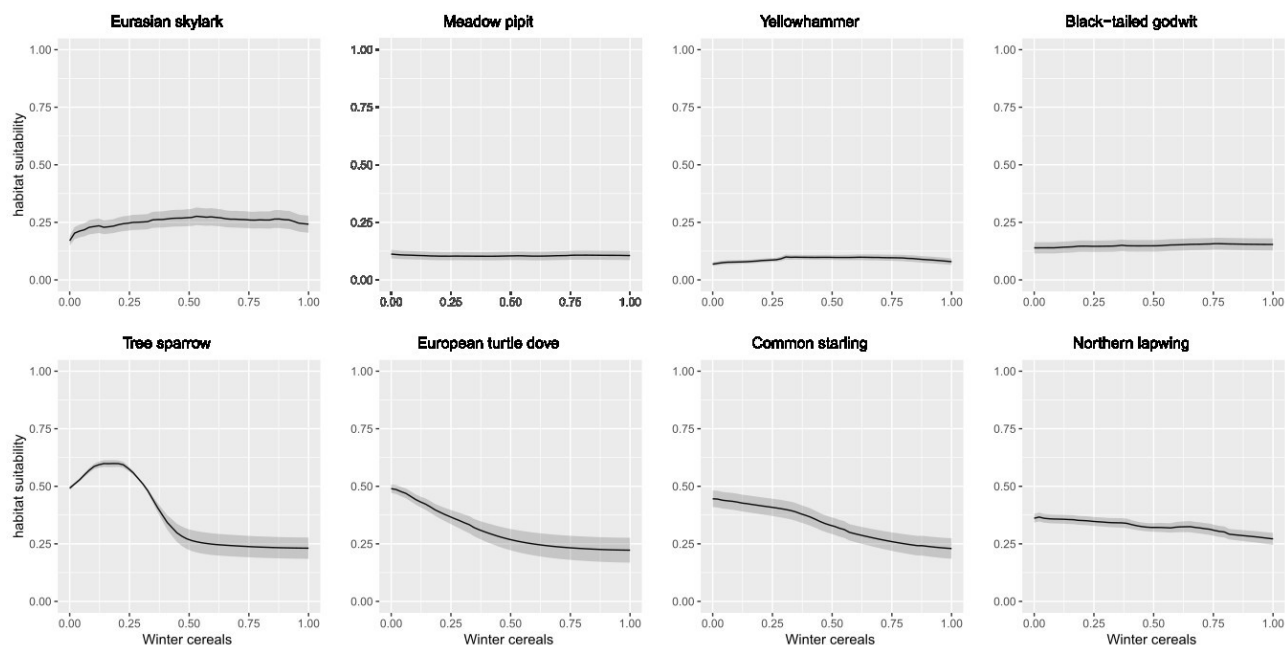


Figure S32: Partial response curves per species and Flanders for the environmental parameter “Winter cereals” given in % cover. A plot is empty if the variable was not used in the models of this species. The solid line represents the mean ensemble predictions, the gray bands around the line plot represent the standard error across the SDM algorithm.