

Table S1. The predictors considered for the species distribution modeling. The predictors used after accounting for multicollinearity are in bold.

Category	Predictor	Description	Units	Original Resolution	Source	Reference
Climate	mean_ann_temp	Annual Mean Temperature	°C			
	mean_diurnal_range	Mean Diurnal Range (Mean of monthly (max temp - min temp))	°C			
	isothermality	Isothermality	%			
	temp_seas	Temperature Seasonality (standard deviation *100)	%			
	max_temp_warm_mo	Maximum Temperature of Warmest Month	°C			
	min_temp_cold_mo	Minimum Temperature of Coldest Month	°C			
	temp_ann_range	Temperature Annual Range	°C			
	mean_temp_wett_quart	Mean Temperature of Wettest Quarter	°C			
	mean_temp_driest_quart	Mean Temperature of Driest Quarter	°C	2.5min	WORLDCLIM version 2.1	[1]
	mean_temp_warm_quart	Mean Temperature of Warmest Quarter	°C			
	mean_temp_cold_quart	Mean Temperature of Coldest Quarter	°C			
	ann_prec	Annual Precipitation	mm			
	prec_wett_mo	Precipitation of Wettest Month	mm			
	prec_driest_mo	Precipitation of Driest Month	mm			
Elevation	prec_seas	Precipitation Seasonality (Coefficient of Variation)	%			
	prec_wett_quart	Precipitation of Wettest Quarter	mm			
	prec_driest_quart	Precipitation of Driest Quarter	mm			
	prec_warm_quart	Precipitation of Warmest Quarter	mm			
	prec_cold_quart	Precipitation of Coldest Quarter	mm			
Water availability	dem		m	25m	EU-DEM version 1.1	[2]
	lakes	Pixel coverage	%			
	rivers	Length per pixel	km/pixel		CCM River and Catchment Database	[4]
Prey species richness	prey_sp_richness	Number of prey species per pixel				

Table 2. Spearman's rho correlation coefficients between bioclimatic variables. All correlations had significance levels $p < 0.05$.

Table S2. (Continued).

Table S3. The models used for the ensemble modeling and the associated parameter settings.

Model	Parameter settings
GLM	type = 'quadratic', interaction.level = 0, myFormula = NULL, test = 'AIC', mustart = 0.5, control = glm.control(epsilon = 1e-08, maxit = 50, trace = FALSE) algo = 'GAM_mgcv', type = 's_smoother', k = 3, interaction.level = 0, myFormula = NULL, family = binomial(link = 'logit'), method = 'GCV.Cp', optimizer = c('outer','newton'), select = FALSE, knots = NULL, paraPen = NULL, control = list(nthreads = 1, irls.reg = 0, epsilon = 1e-07, maxit = 200, trace = FALSE, mgcv.tol = 1e-07, mgcv.half = 15, rank.tol = 1.49011611938477e - 08, nlm = list(ndigit = 7, gradtol = 1e-06, stepmax = 2, steptol = 1e-04, iterlim = 200, check.analyticals = 0), optim = list(fastr=1e + 07), newton = list(conv.tol = 1e-06, maxNstep = 5, maxSstep = 2, maxHalf = 30, use.svd = 0), outerPIsteps = 0, idLinksBases = TRUE, scalePenalty = TRUE, efs.lspmax = 15, efs.tol = 0.1, keepData = FALSE, scale.est = fletcher, edge.correct = FALSE))
GAM	method = 'mars', add_args = NULL
FDA	
GBM	distribution = 'bernoulli', n.trees = 1000, interaction.depth = 7, n.minobsinnode = 5, shrinkage = 0.001, bag.fraction = 0.5, train.fraction = 1, cv.folds = 3, keep.data = FALSE, verbose = FALSE, perf.method = 'cv', n.cores = NULL

Table S4. The total number of occurrences and separately for GBIF and European atlases (Sillero, *et al.* [5] atlas for reptiles and amphibians and Mitchell-Jones, *et al.* [6] for mammals) originally in the datasets, the number of presences kept in the modeling procedure, True Skill Statistic (TSS), Area Under the Curve (AUC), sensitivity and specificity scores for the presented cut-off value used to transform continuous probability of presence (range 0–1) to binary for each prey species and the coefficient of variation of the ensemble model prediction for each species averaged over the area of prediction.

	TSS	AUC	Cut-off	Sensitivity	Specificity	Mean coefficient of variation	Presences	Total occurrences	GBIF occurrences	European atlas occurrences
Mammals										
<i>Apodemus sylvaticus</i>	0.73	0.94	0.46	93.28	79.58	50.68 ± 45.55	1698.00	37314.00	37314.00	1780.00
<i>Mus musculus</i>	0.69	0.92	0.42	86.88	82.39	33.29 ± 25.62	1236.00	34979.00	34979.00	965.00
<i>Rattus rattus</i>	0.75	0.94	0.50	93.16	81.78	46.26 ± 33.41	864.00	14787.00	14787.00	909.00
Amphibians										
<i>Bufo bufo</i>	0.616	0.90	0.63	72.31	89.28	2.15 ± 2.09	2417.00	101013.00	98759.00	2254.00
<i>Lissotriton vulgaris</i>	0.66	0.90	0.40	86.11	79.73	43.28 ± 38.04	1750.00	56205.00	54514.00	1691.00
<i>Pelophylax ridibundus</i>	0.71	0.94	0.51	88.42	82.11	40.38 ± 38.43	1409.00	19575.00	18170.00	1405.00
<i>Pseudoepeidalea viridis</i>	0.77	0.96	0.50	90.77	86.23	47.41 ± 34.40	337.00	8266.00	7515.00	751.00
<i>Rana temporaria</i>	0.63	0.91	0.55	77.27	85.38	21.03±37.34	2183.00	12207.00	10228.00	1979.00
Reptiles										
<i>Podarcis muralis</i>	0.83	0.97	0.41	96.41	86.97	76.65 ± 38.96	726.00	49042.00	48340.00	702.00

Table S5. Variable importance (%) for the prediction of each prey species probability of presence in the abiotic ensemble species distribution model rescaled to sum up to 100. The three most important variables are highlighted with bold.

	Mean annual temperature	Mean diurnal range	Isothermality	Mean temperature of wettest quarter	Precipitation seasonality	Precipitation of warmest quarter	Precipitation of coldest quarter	Elevation	Coverage (%) of lakes	Length of rivers
Mammals										
<i>Apodemus sylvaticus</i>	9.58	3.84	79.47	2.70	2.62	0.08	0.11	0.99	0.03	0.57
<i>Mus musculus</i>	21.82	4.64	59.37	1.64	2.08	2.06	1.06	6.77	0.45	0.12
<i>Rattus rattus</i>	61.14	3.10	14.64	11.34	2.30	1.10	0.60	2.75	0.51	2.52
Amphibians										
<i>Bufo bufo</i>	46.27	1.37	6.94	30.52	1.01	0.86	5.79	1.27	0.84	5.12
<i>Lissotriton vulgaris</i>	55.63	9.98	8.99	8.16	0.24	3.17	2.04	6.88	2.24	2.67
<i>Pelophylax ridibundus</i>	57.45	11.18	14.75	5.69	1.26	3.01	2.52	0.31	1.65	2.17
<i>Pseudoepeidalea viridis</i>	52.67	13.44	22.46	2.08	2.21	3.74	2.31	0.63	0.31	0.14
<i>Rana temporaria</i>	8.91	12.27	6.42	14.77	3.43	43.44	0.76	1.73	2.61	5.66
Reptiles										
<i>Podarcis muralis</i>	23.77	5.23	49.85	0.65	6.83	2.69	2.95	7.60	0.23	0.21

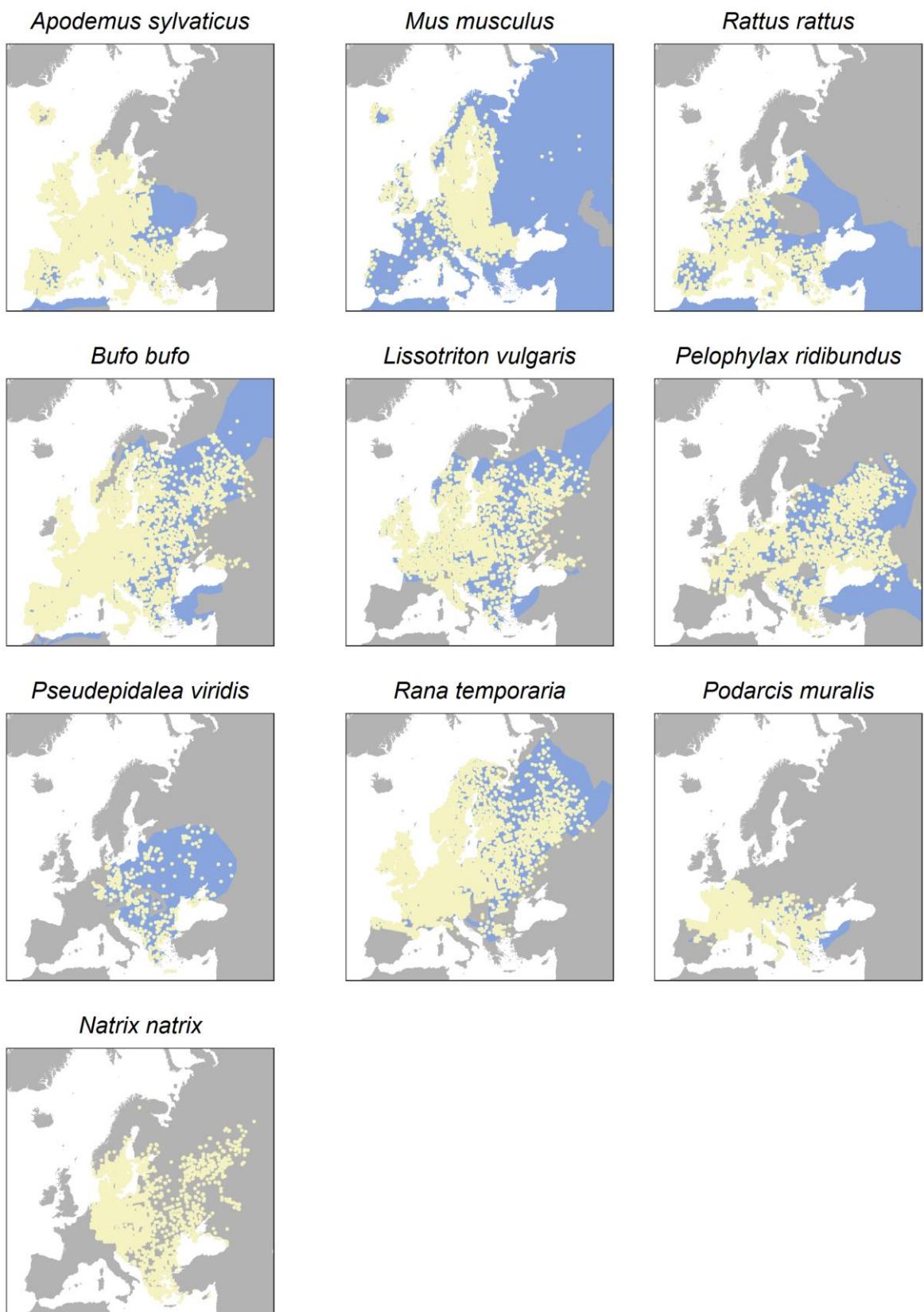


Figure S1. Presences used in the modeling process for each species after removal of invalid records and multiple observations per grid cell. The blue polygons depict the range of each species as obtained by IUCN [7], except for *Natrix natrix* for which there are no available distributional data by IUCN [7]. Scale: 1: 110,000,000.

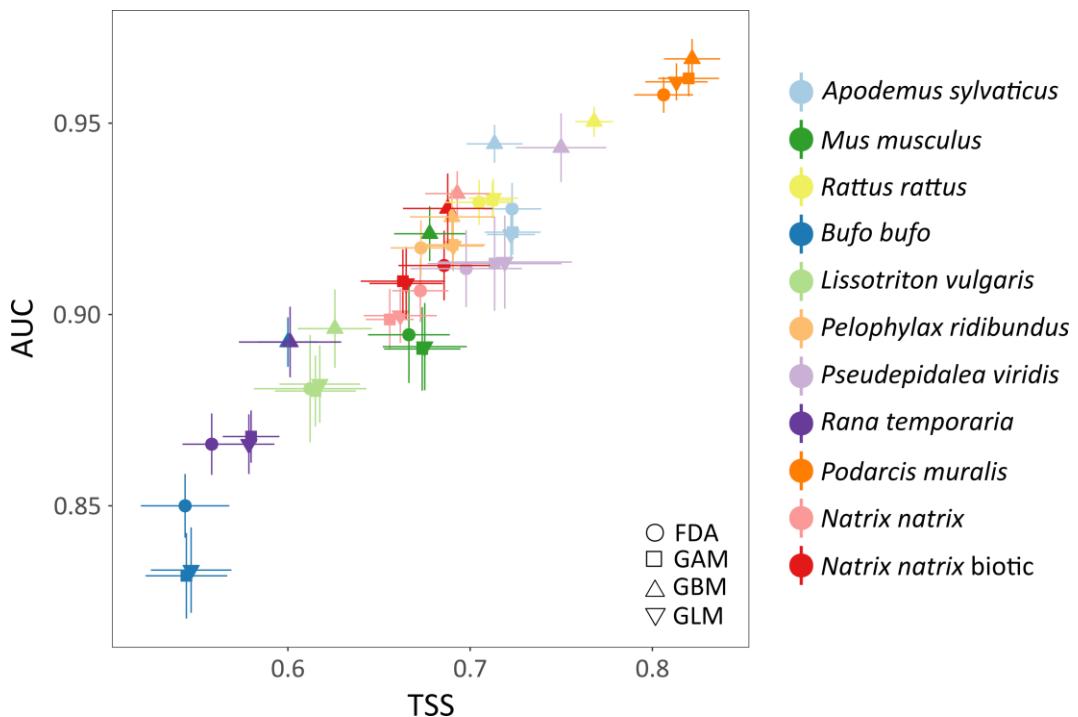


Figure S2. Scores of True Skill Statistic (TSS) and Area Under the Curve (AUC) for each individual model, prey species and model type (abiotic and biotic) for *Natrix natrix*. Different shapes represent different modeling methods and different colors correspond to different species. Horizontal and vertical lines indicate standard deviations for TSS and AUC respectively.

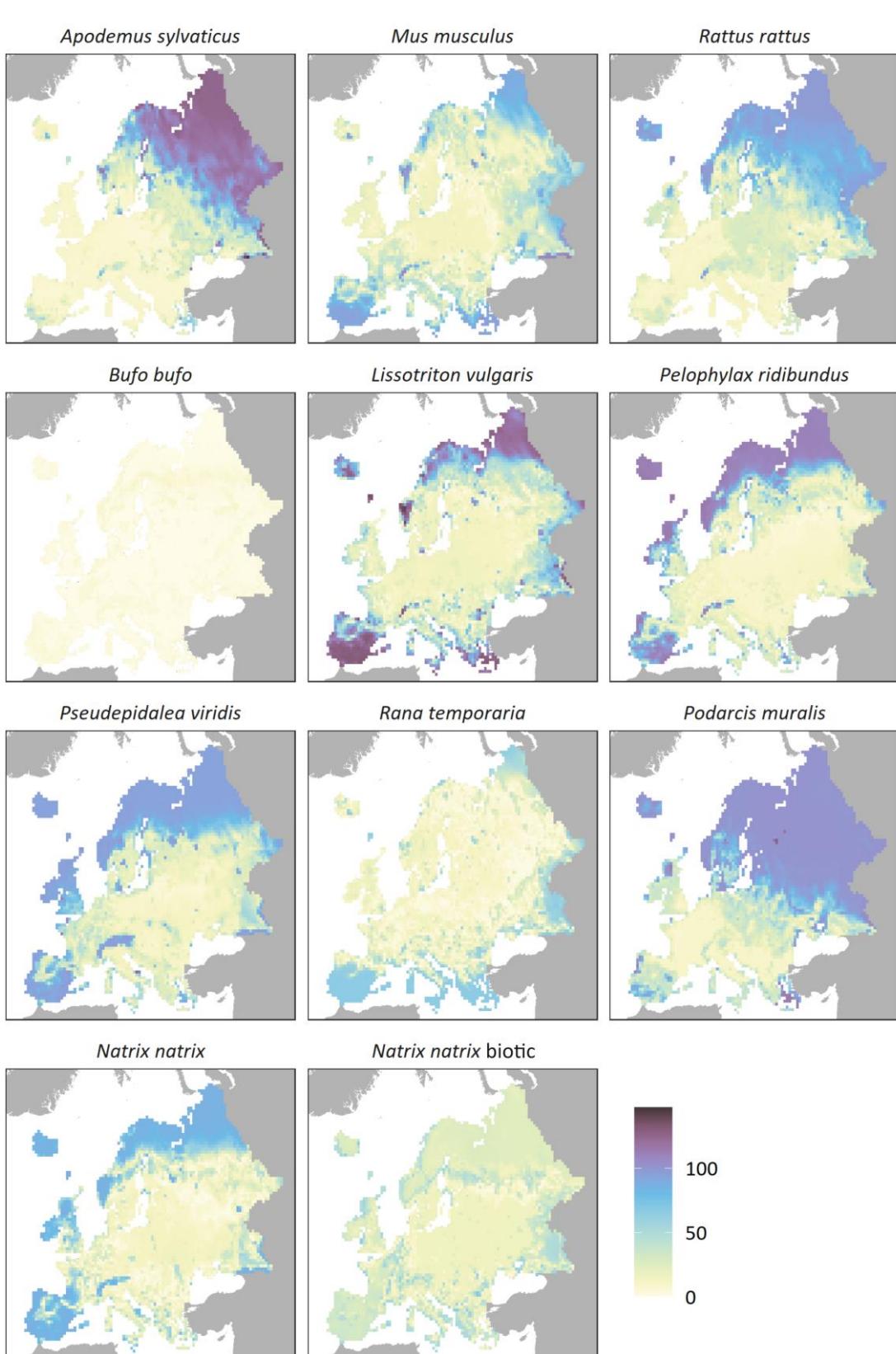


Figure S3. Coefficients of variation (standard deviation/mean) of the predictions for the ensemble species distribution model of each species and model type (abiotic and biotic) for *Natrix natrix*. Darker colors represent higher coefficient of variation and uncertainty of prediction. Scale: 1:110,000,000.

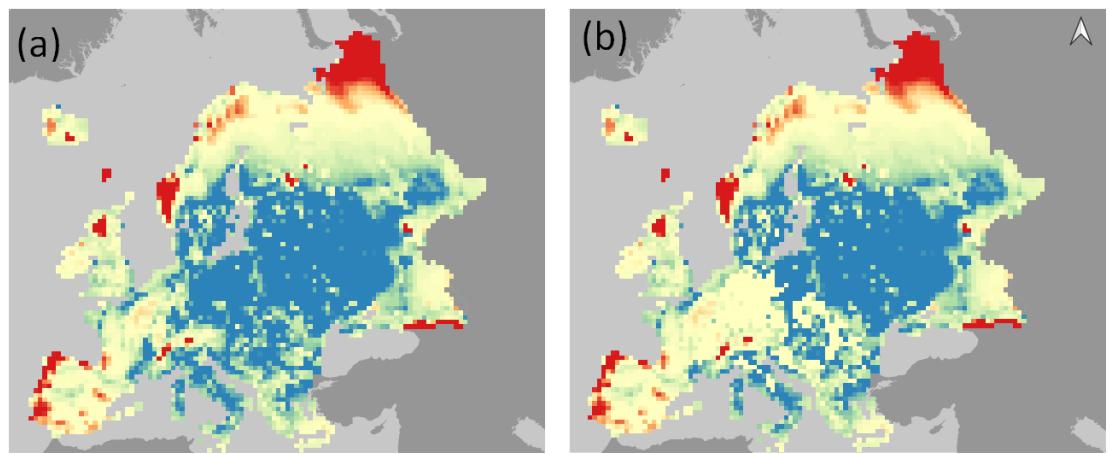


Figure S4. Multivariate environmental suitability surface maps (MESS) of the predictors included in: **(a)** the abiotic; and **(b)** the biotic model for current environmental conditions for *Natrix natrix*. Beige, red and blue colors represent marginal, common and uncommon conditions. Scale: 1:110,000,000.

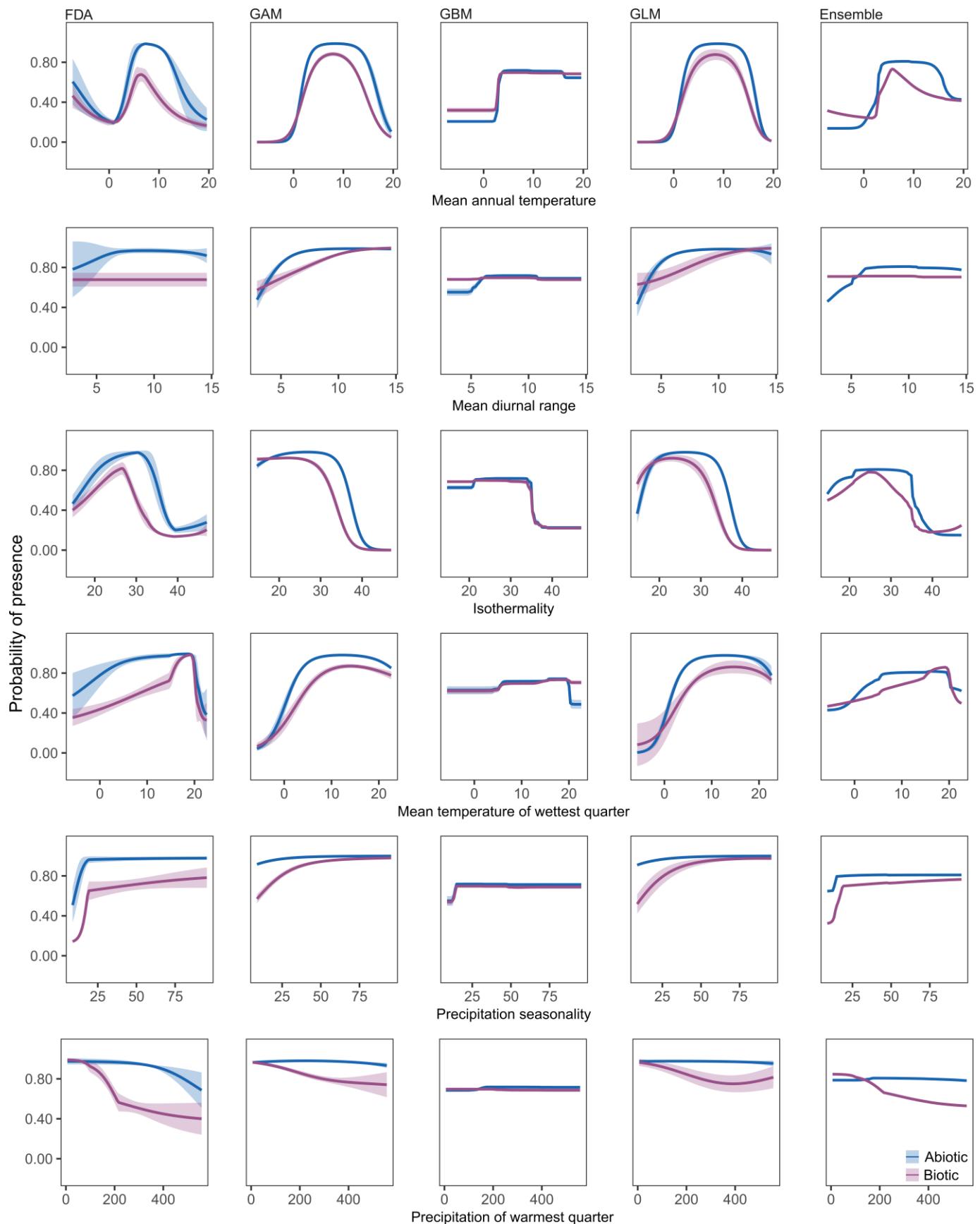


Figure S5. Predicted response curves from the different algorithms that were used in the individual and the ensemble models for *Natrix natrix* when all the other variables are set to their mean value. The lines are the average of the ten cross-validation runs for each algorithm. Colors blue and purple refer to the abiotic and biotic model respectively.

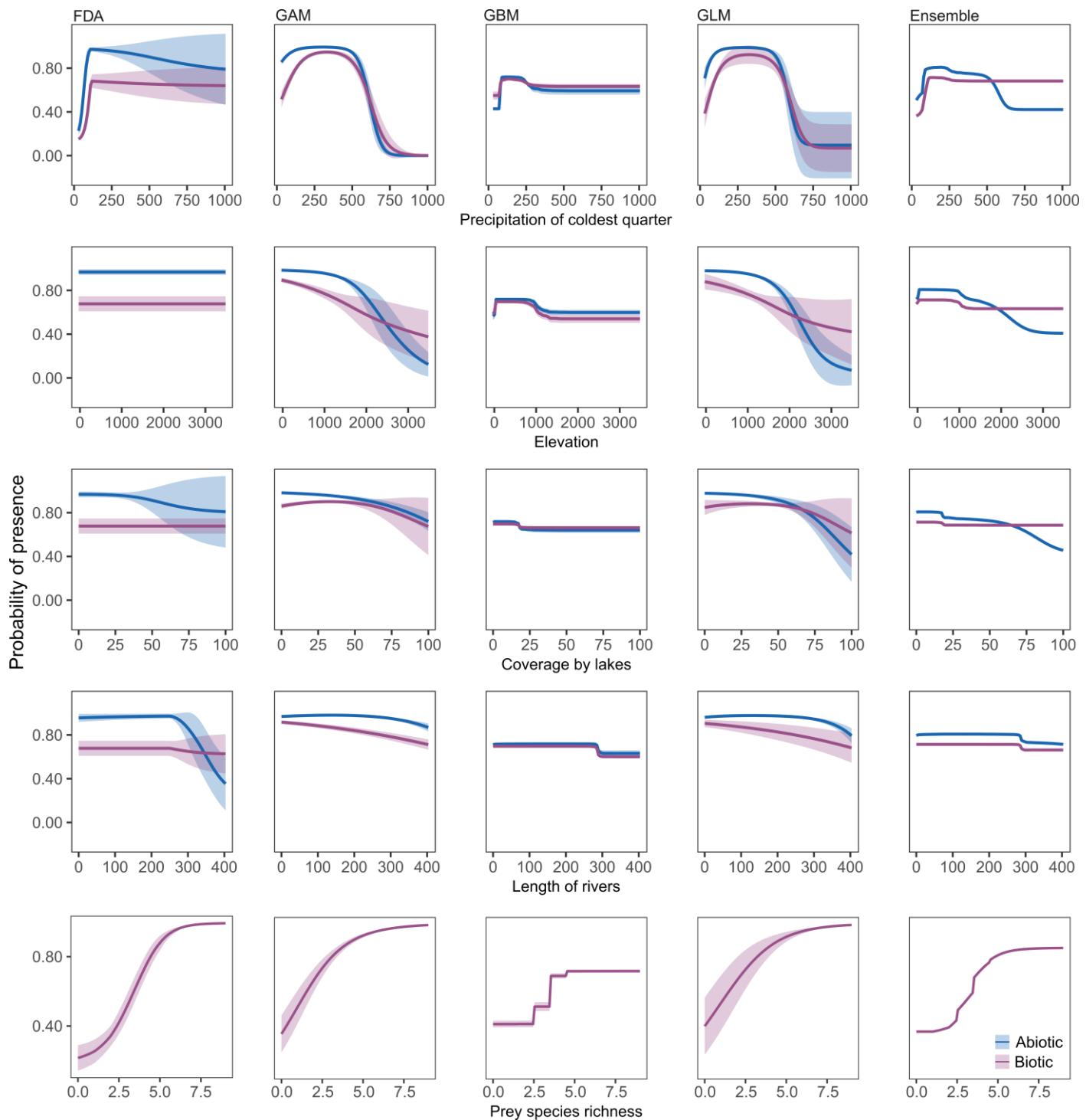


Figure S5. (Continued).

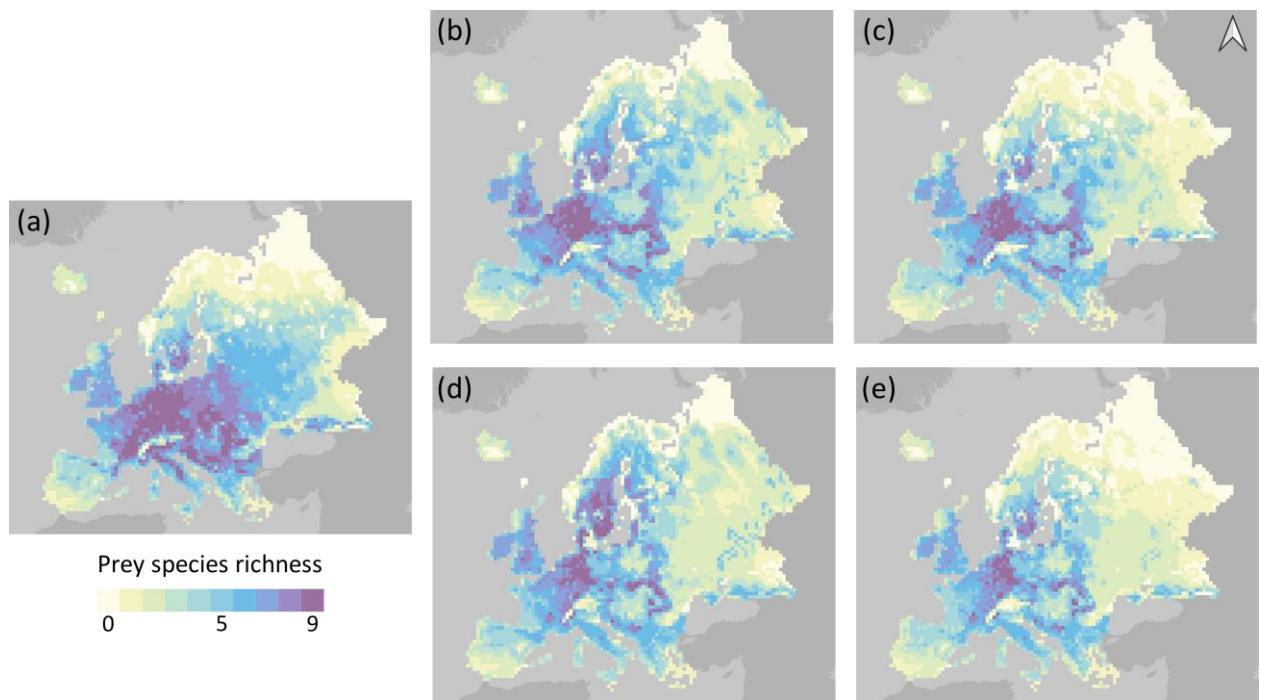


Figure S6. Predicted prey species richness: (a) under current environmental conditions; and by 2060 and 2080 respectively according to: (b,d) unhindered dispersal scenario; and (c,e) no dispersal scenario. The potential distribution of each prey species was estimated by an abiotic ensemble species distribution model. Scale: 1:110,000,000.

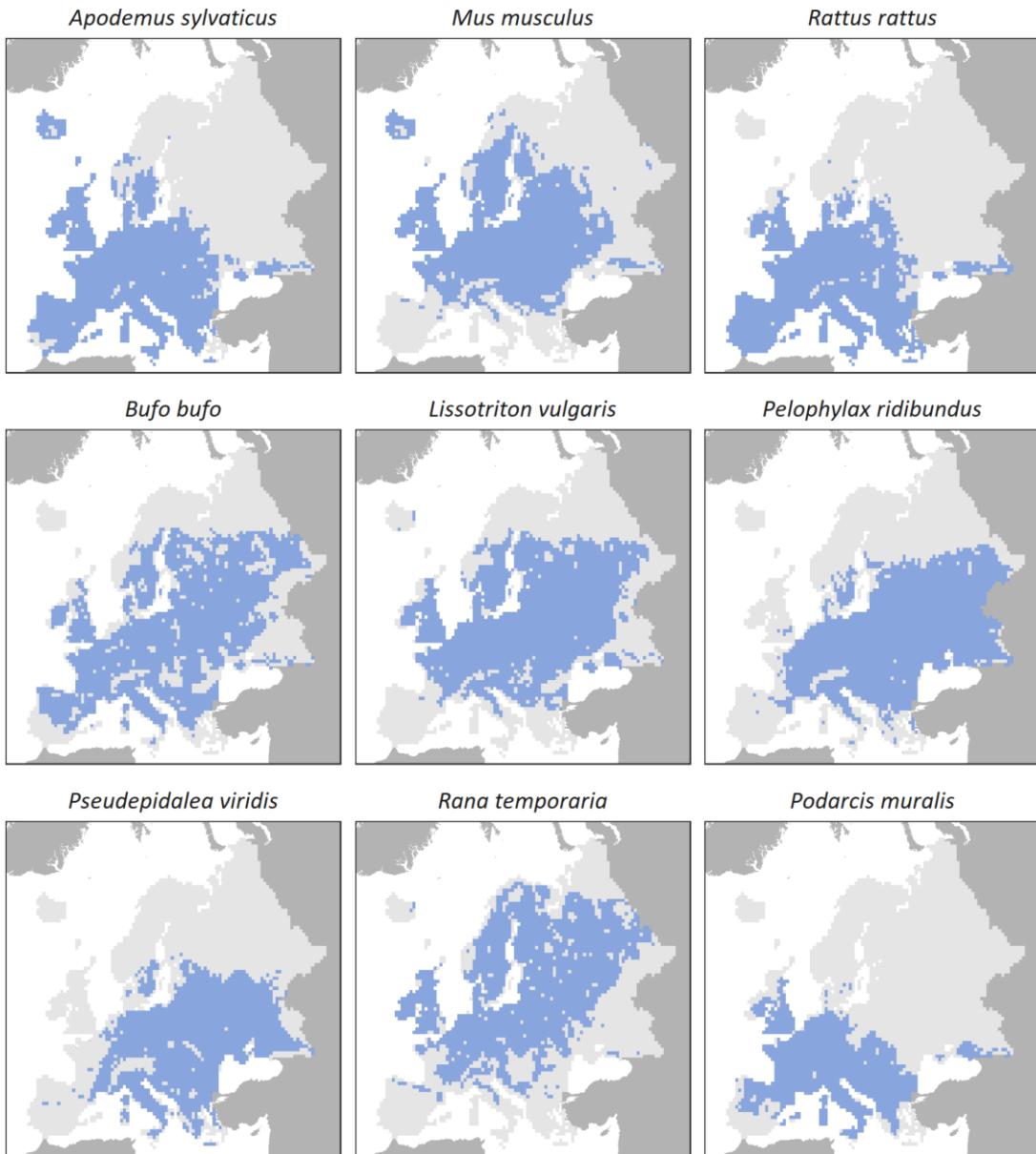


Figure S7. Predicted distribution of each prey species according to an abiotic ensemble species distribution model. Blue color represents presence and light gray absence. Scale: 1: 110,000,000.

References

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