Habitat suitability modeling test

2023-07-21

Mammalia

Functional group 1 ; Number of species: 3

Species name	Order
Canis lupus	Carnivora
Lynx lynx	Carnivora
Lutra lutra	Carnivora

In total, 4038 pixels of 1km^2 were occupied by the group within metropolitan France and 5000 pseudo-absences were randomly generated over the same territory (3 times, see figures below).

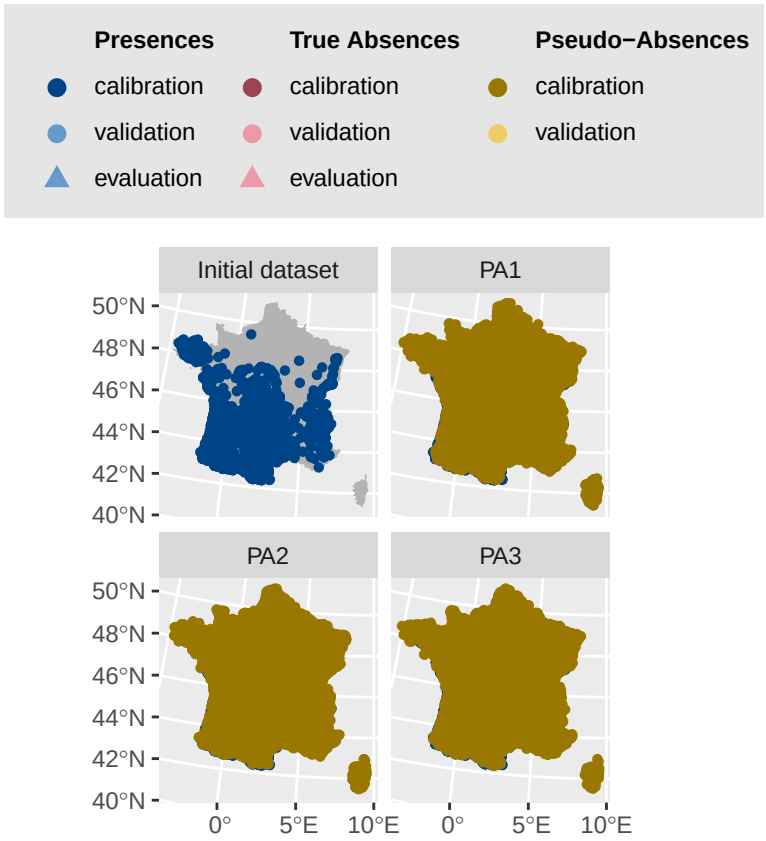
The final habitat suitability maps were generated using 3 families of machine learning algorithms (SDM models):

- neural network: artificial neural network (ANN)
- bagging model: random forest (RF)
- boosting model: Extreme gradient boosting (XGBOOST)

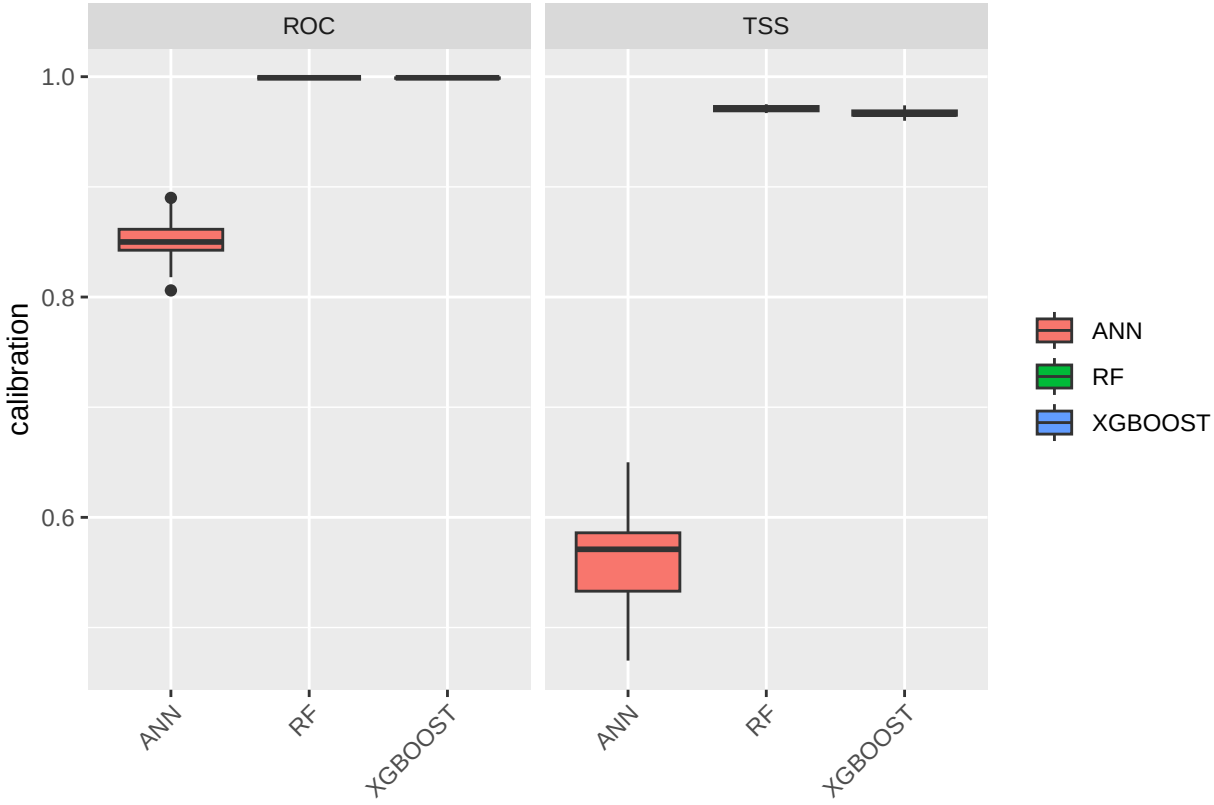
For each family, 15 models were generated using different presence/pseudo-absence composition within the calibration/validation dataset. Each model was calibrated using 80% of the initial dataset and the remaining 20% was used to produce validation indicators (ROC and TSS). All models that passed the validation threshold (i.e., TSS $>$ 0.6) were combined to produce ensemble models (either using probability mean, probability weighted mean or committee averaging). Finally, we produced a map of presence probability for the group from each ensemble model.

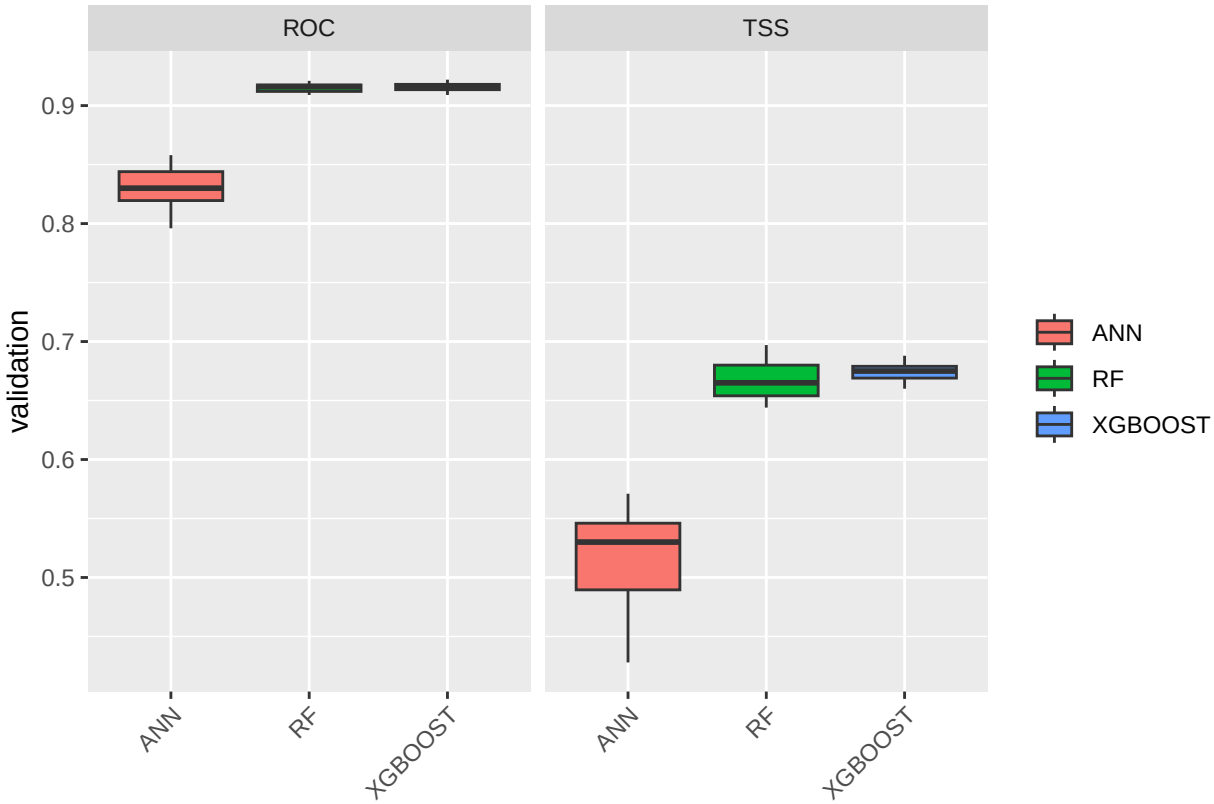
Explanatory variables that were used in these models included the same variables as the one used for environmental PCA (work task 1 for functional group definition).

Distribution of presences and generated pseudo-absences:

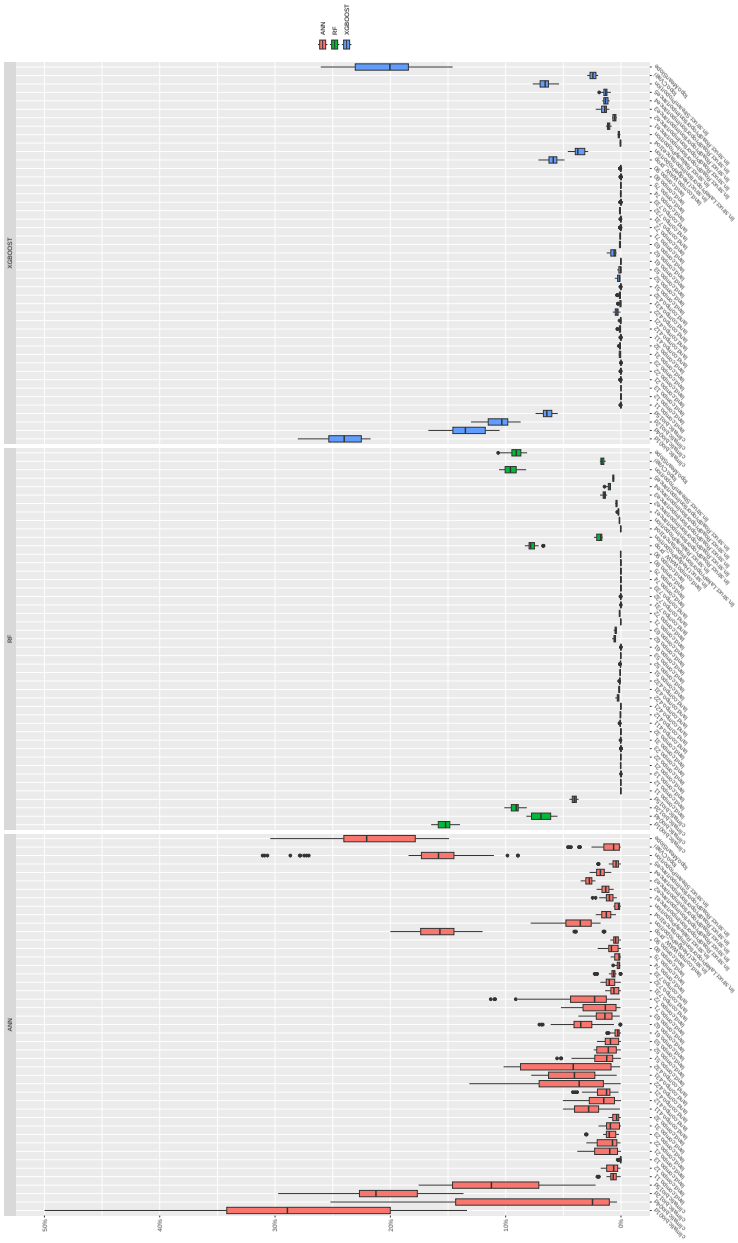
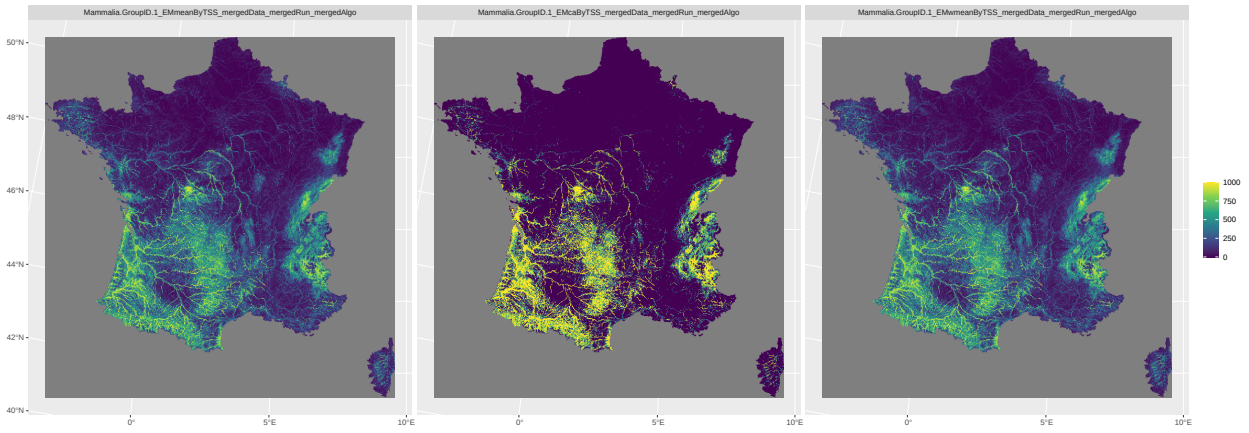


Distribution of evaluation metrics for the calibration and validation datasets:




ROC
TSS
validation
0.9
0.8
0.7
0.6
0.5
ANN
RF
XGBOOST
ANN
RF
XGBOOST
ANN
RF
XGBOOST

Importance of the environmental variables for the calculation of presence probabilities:



Projection of the ensemble models over the whole territory to predict group presence probabilities (multiplied by 1000 here):