Modelling density wild boar populations in Europe for wildlife disease control

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Context and objectives

Wild boar populations have had a sharp growth and are a huge concern, due to a high risk of transmission diseases. Recent outbreaks of African swine fever in Europe have caused sanitary controls to reduce the risk of disease transmission.

European countries are making a big effort to determine numbers and where are they distributed. However, abundance failed in quantifying species abundance at high spatial resolution predictions.

Our **aim** was to assess different modelling approaches to produce predictions of species abundance at high spatial resolution predictions.

Materials and methods

3 modeling approaches to predict wild boar

A) RAW model	*B) Density model*	*C) iCAR model*
1) GLM (RV_1 ~ AREA * NUT) 2) GLM(Residuals ~EV)	GLM (RV_2~ EV)	INLA(RV_2~ EV)

Data used for modeling Europe

55844 hunting yield (HY) collected data for 31 countries with different resolution scale

Response variable

- RV_1: Maximum HY
- RV_2: Densities (HY divided by area)
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Explanatory Variables (EV)

- Climatic,
- Land cover,
- 4 Bioclimatic zones

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- Area
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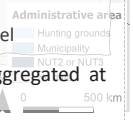
- NUTS level

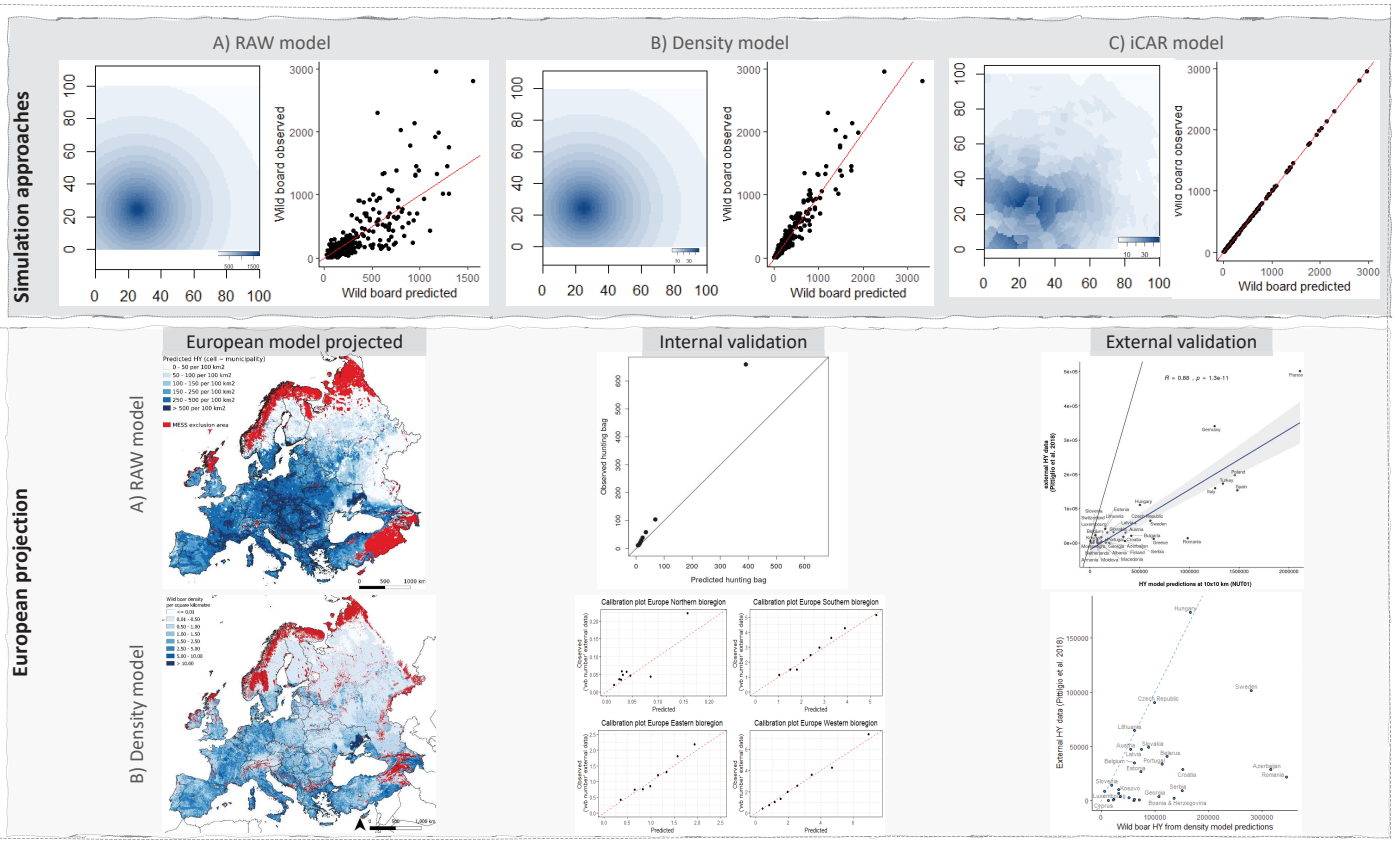
Variables with VIF<2 were selected for constructing the model



Model predictions were downscaled to a 2x2km grid and aggregated at country to compare predictions with an external dataset.

Tidyverse, sf, MASS, usdm, Hmisc, modEvA, spdep, INLA were the R packages used for managing data, modelling and predict.

Results



Conclusions

- European models showed similar results as simulation models in terms of internal validation adjustment.
- iCAR model tested improved both approaches and it is expected that this approach reduces more the overprediction shown at European scale, what could not be yet tested and is a challenge.
- Different approaches showed similar geographical pattern at European scale, although density model predictions reduced the overprediction of RAW model predictions (external validation).
- There is a trade-off between having close-fitting predictions which could help to focus the effort in controlling wildlife populations to decrease the risk of disease transmission and applying spatial autocorrelation models for all Europe.

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