Predicting spatial prevalence of tick pathogens in Northern Europe using satellite imagery

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Predicting spatial prevalence of tick pathogens in Northern Europe using satellite imagery

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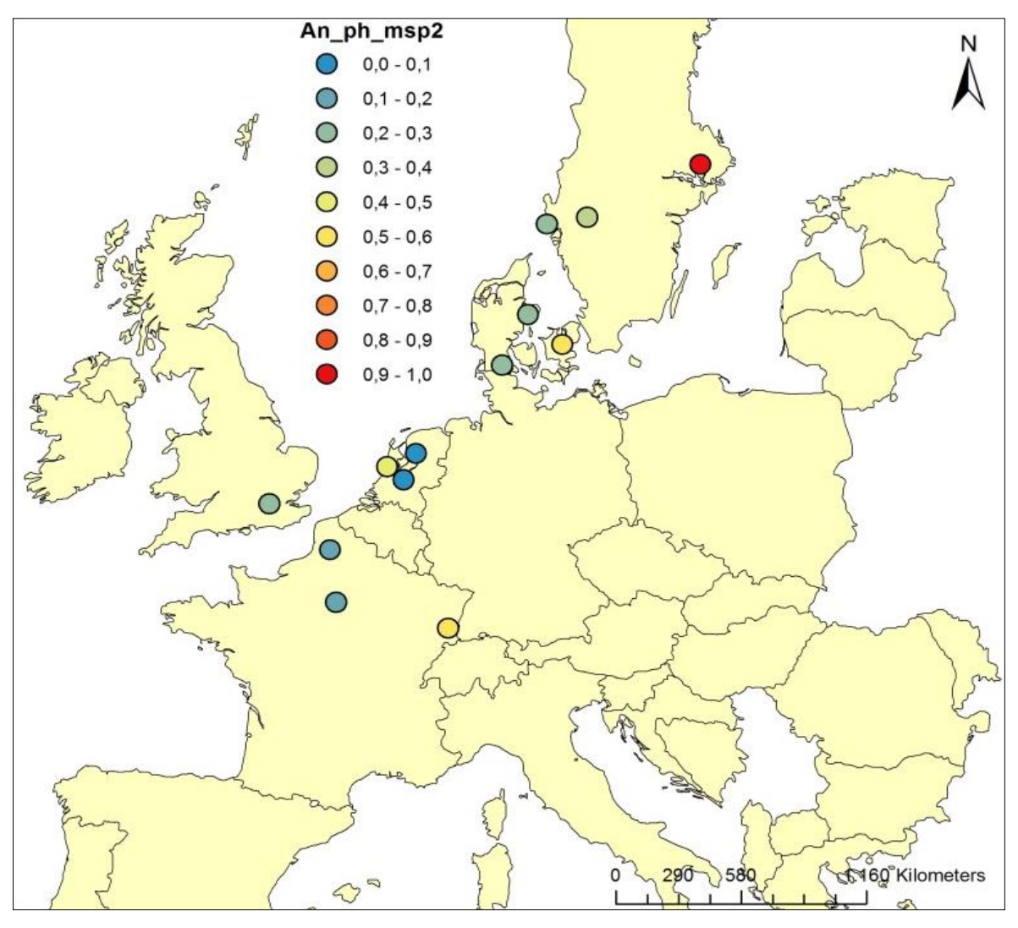
Background

- Spatial distribution of ticks and the pathogens they transmit is a key tool to assess human risk for tick borne diseases
- Tick pathogens are related to the presence of suitable hosts which depend on environmental factors
- We hypothesis therefore that the spatial prevalence can be modelled using predictors variables obtained from Earth Observation satellites (Big Data).

Objectives

- To model the probability of presence of different ticks pathogens in five European countries using environmental variables extracted from satellite imagery
- To map the probability of presence of ticks pathogens
- To analyze if the probability of presence its correlated to the ticks pathogen prevalence

Methods



Observed prevalence of tick pathogens

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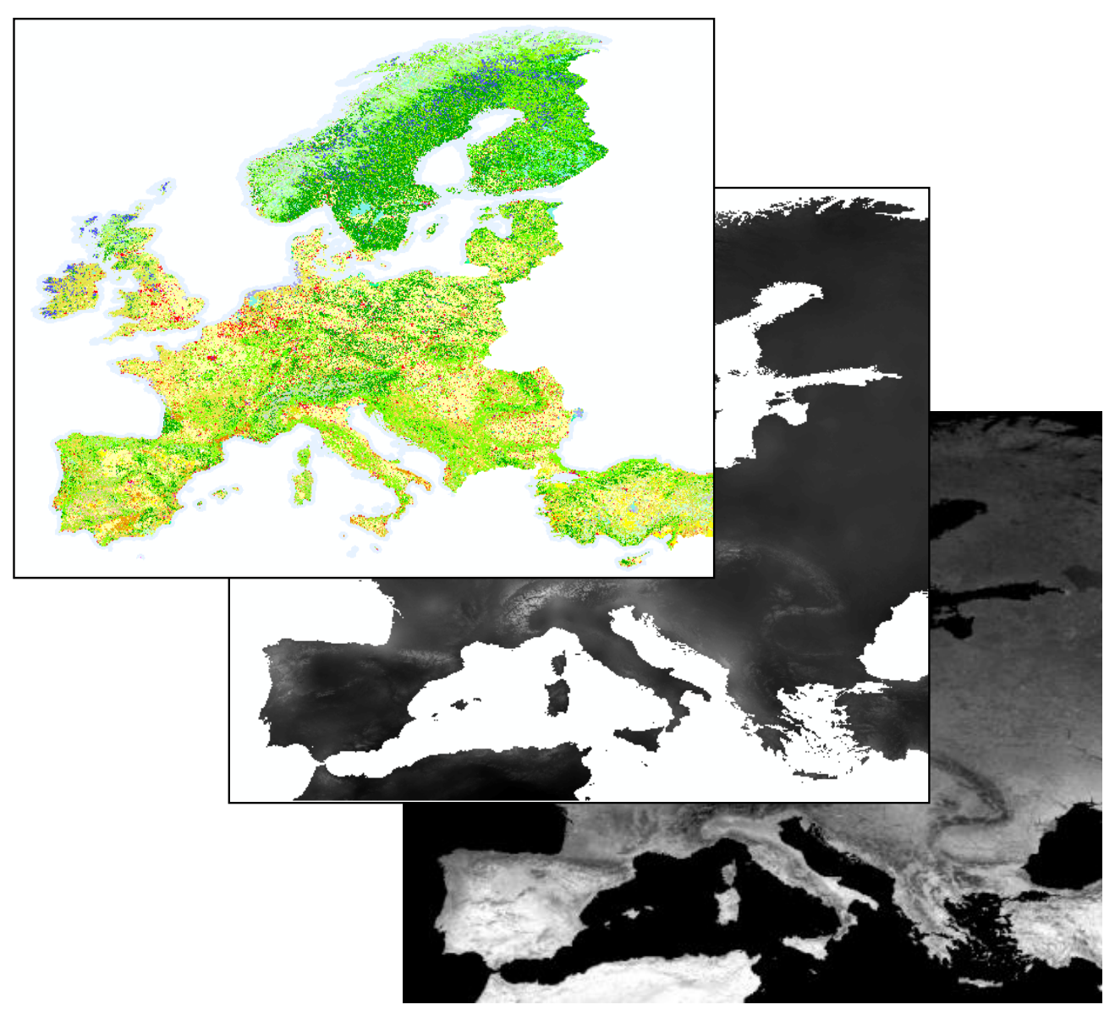
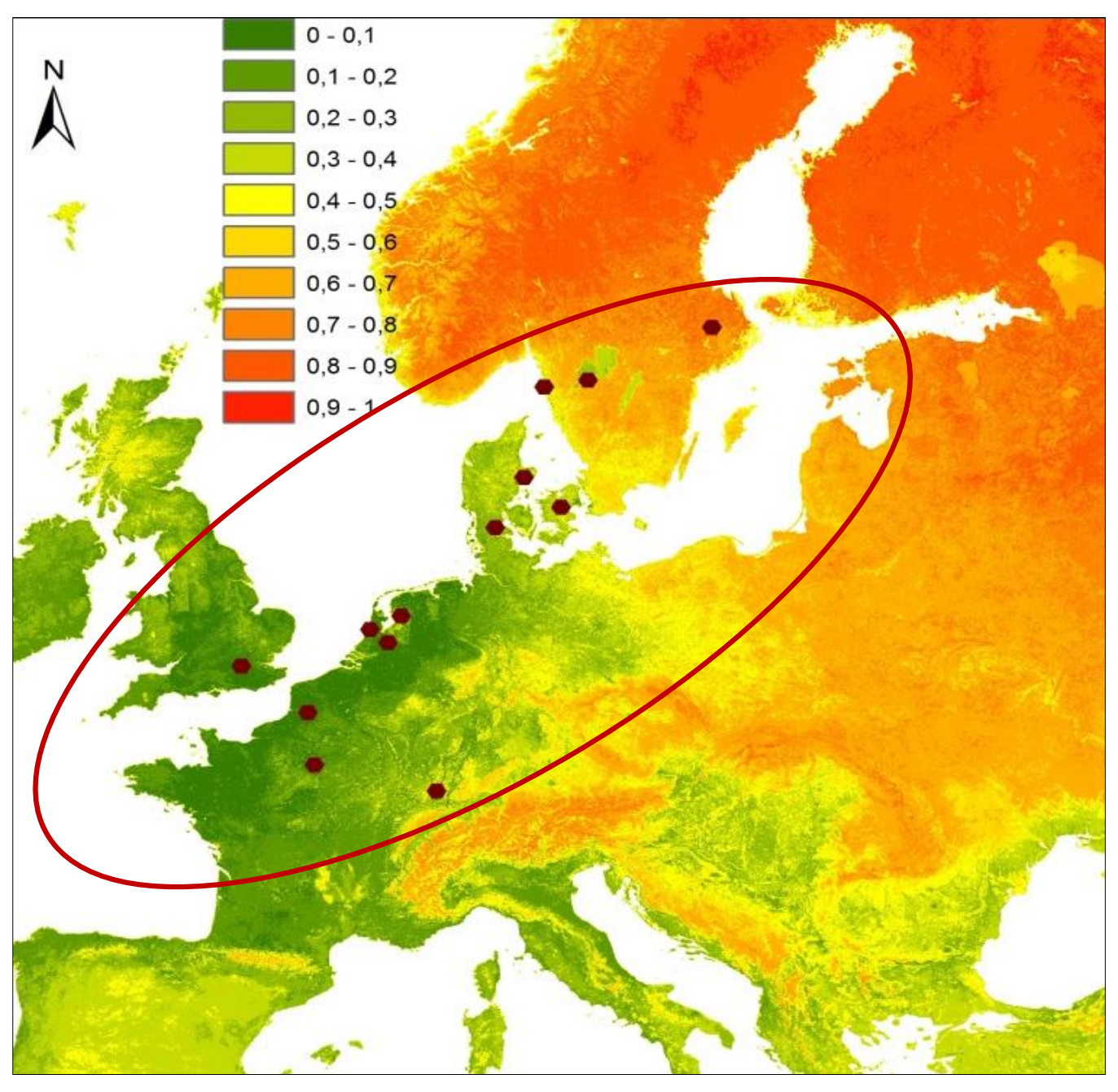


Environmental predictors from satellite imagery

Data collection: pools of 25 *Ixodes ricinus* nymphs from 13 sites (England, France, Netherlands, Denmark, Sweden)

Machine Learning modelling
Random Forest



Probability of presence map

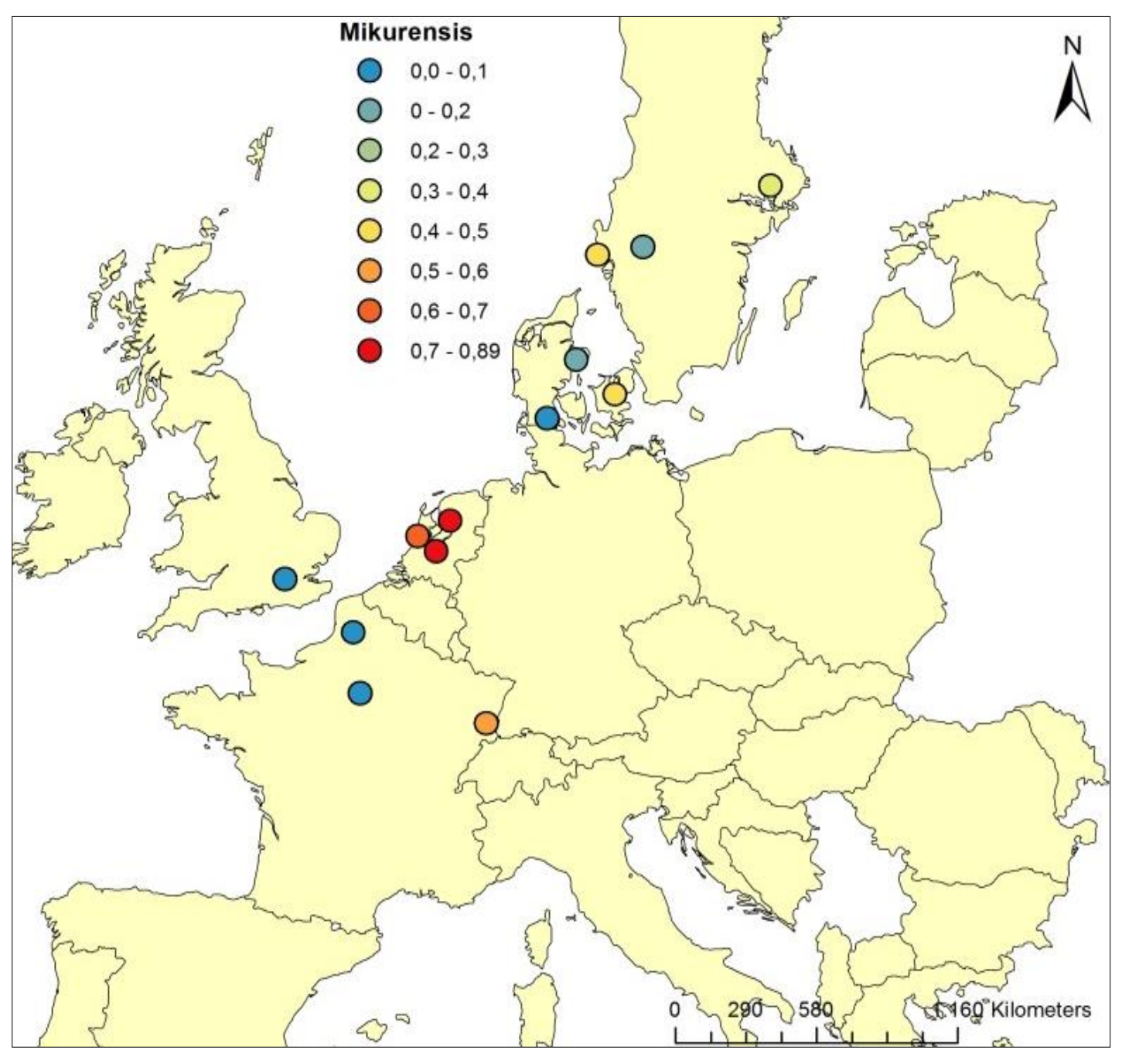
Model validation: Jackknife

Results

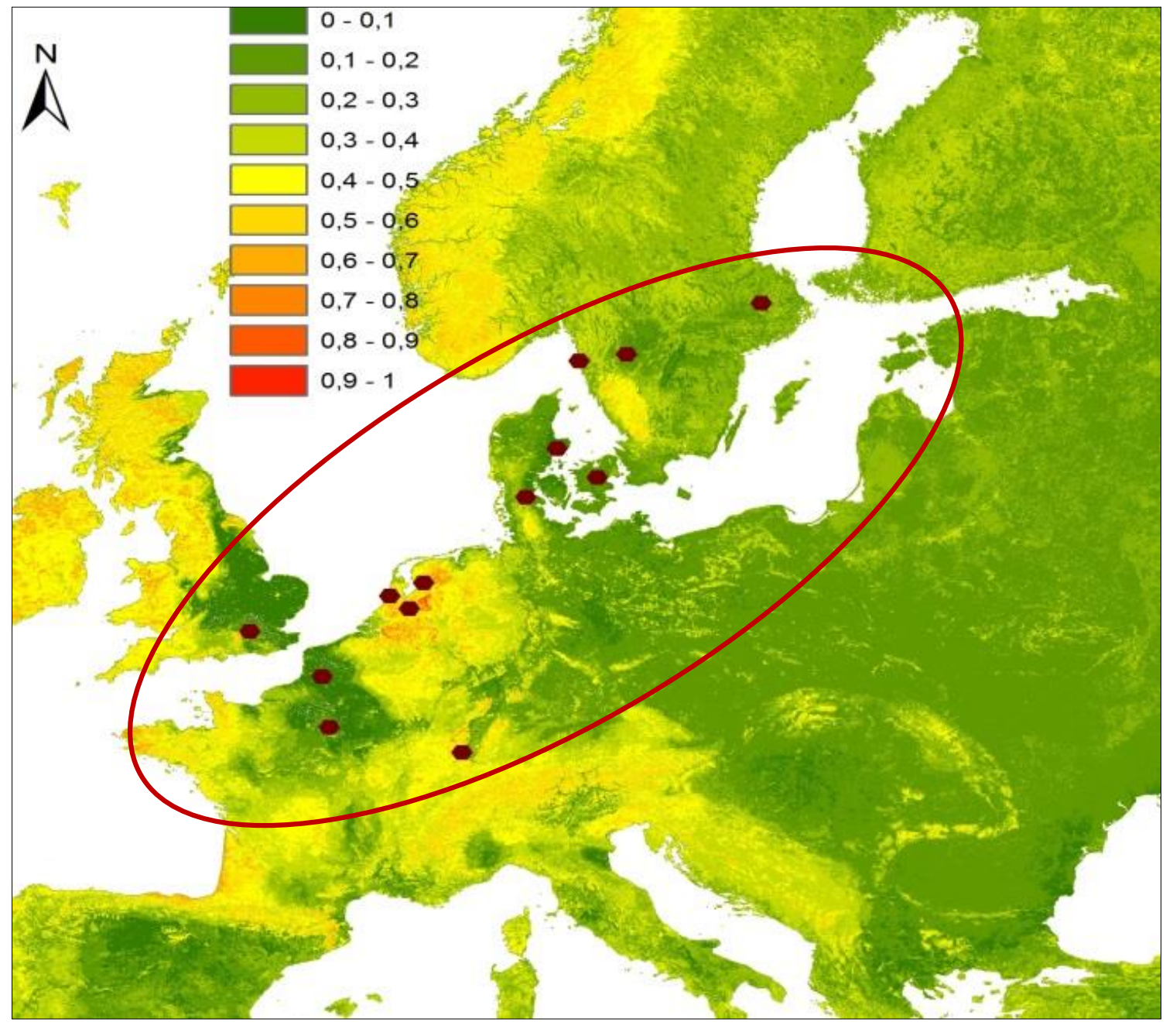
The model was significant for 2/7 of the species.

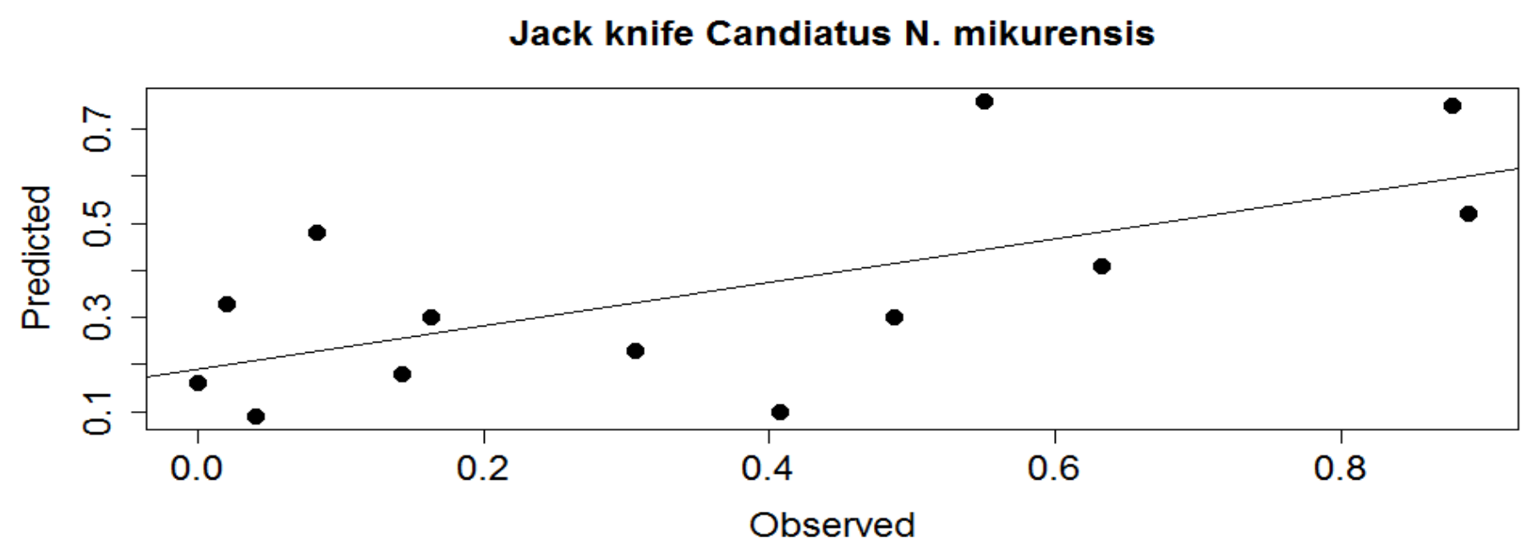
Candidatus *Neoehrlichia mikerensis*

Observed Prevalence



Probability of presence





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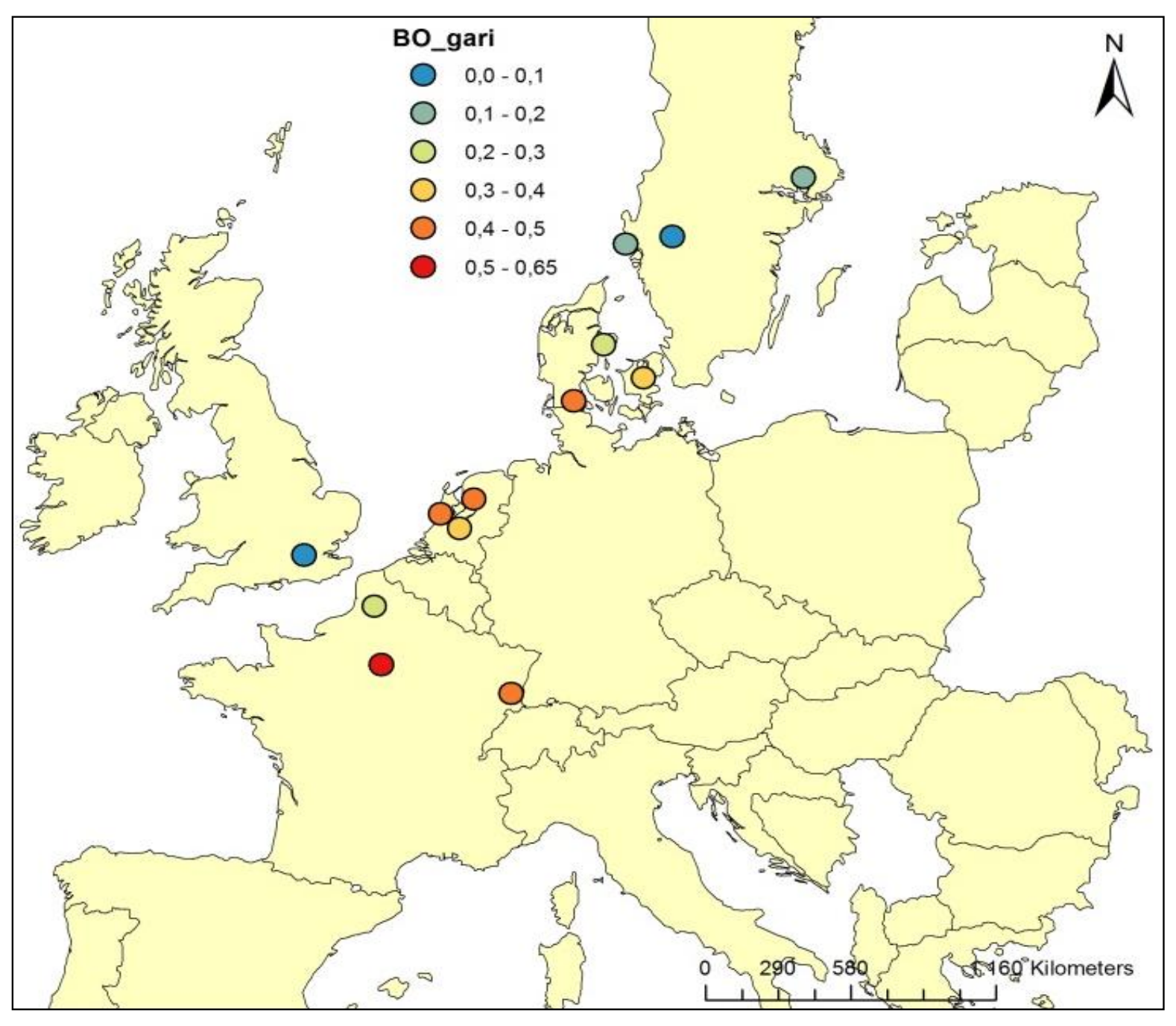
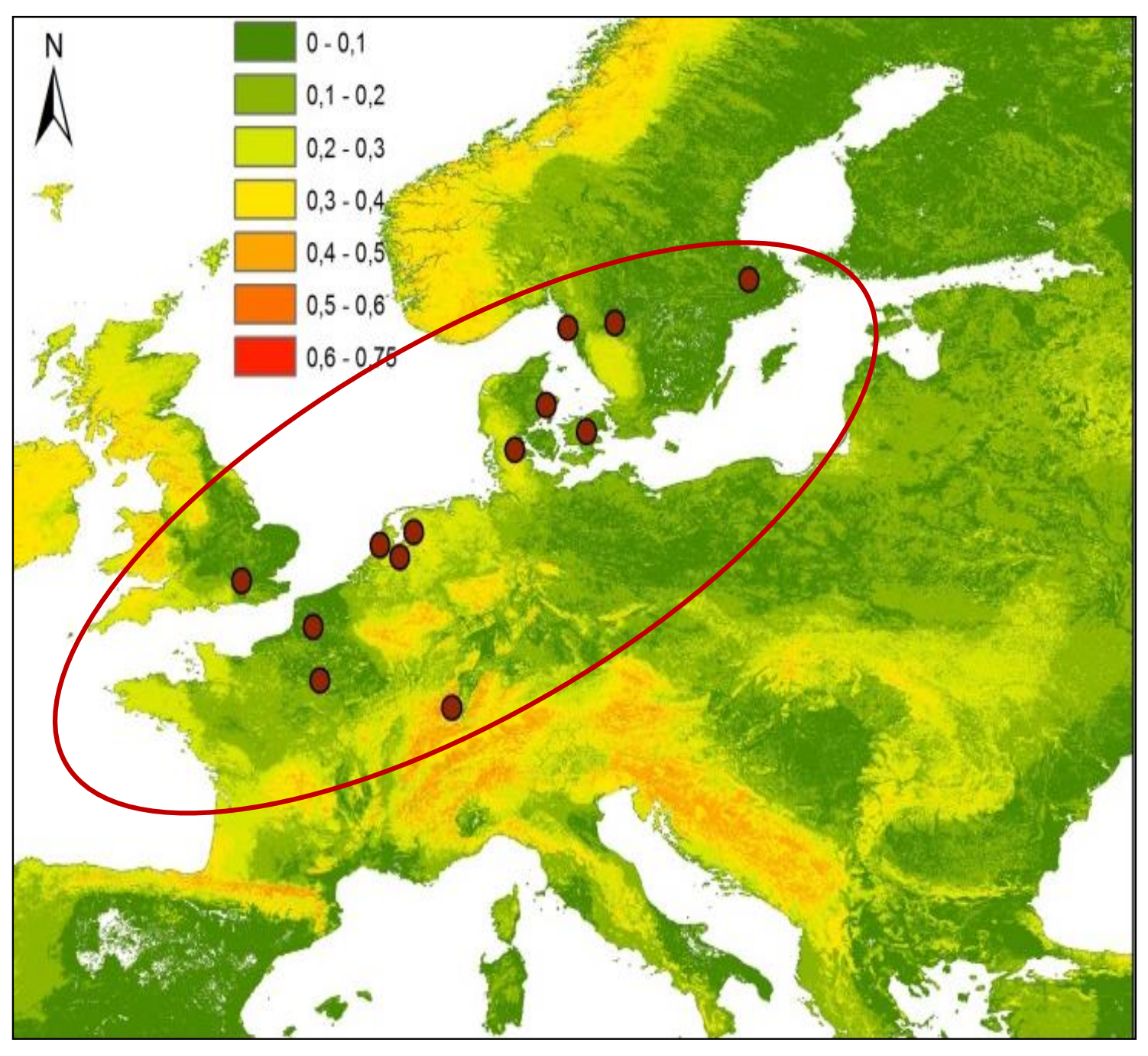
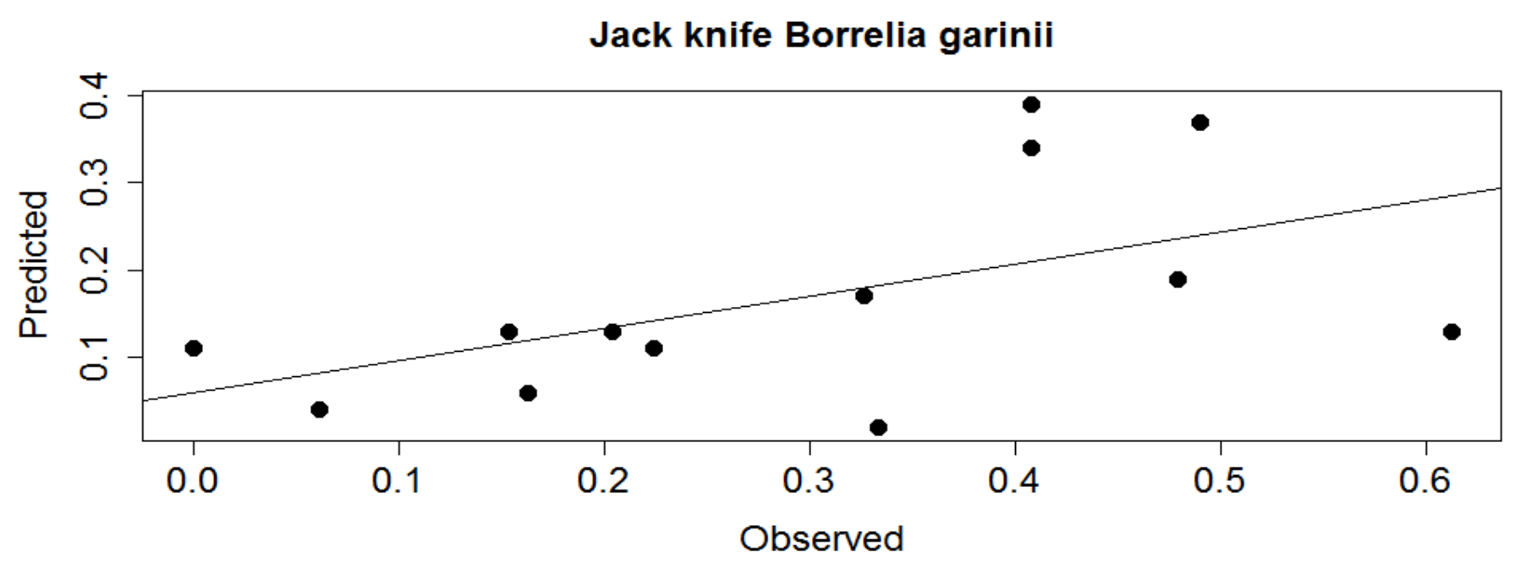
Borrelia garinii

Observed Prevalence



Probability of presence





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Conclusion

- Pathogen prevalence differed between sites
- Observed prevalences fit the environmental data
- It is possible to predict and model spatial variation in prevalence of some tick-borne pathogens

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