Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

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Total number of authors:
14

Publication date:
2016

Document Version
Publisher's PDF, also known as Version of record

Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

Ana Carolina Cuellar, Kirstine Klitgaard Schou, Sara Moutailler, Patrick Fach, Sabine Delannoy, Fimme van der Wal, Aline de Koeier, Jan Chirico, Anna Aspán, Mikael Juremalm, Karen Mansfield, Paul Phipps, Tony Fooks and Rene Bødker

Founded by CoVetLab and InterReg

Introduction

Abstraktion of reality → **Modelling** → Predictions, planning

Spatial data → MAPS

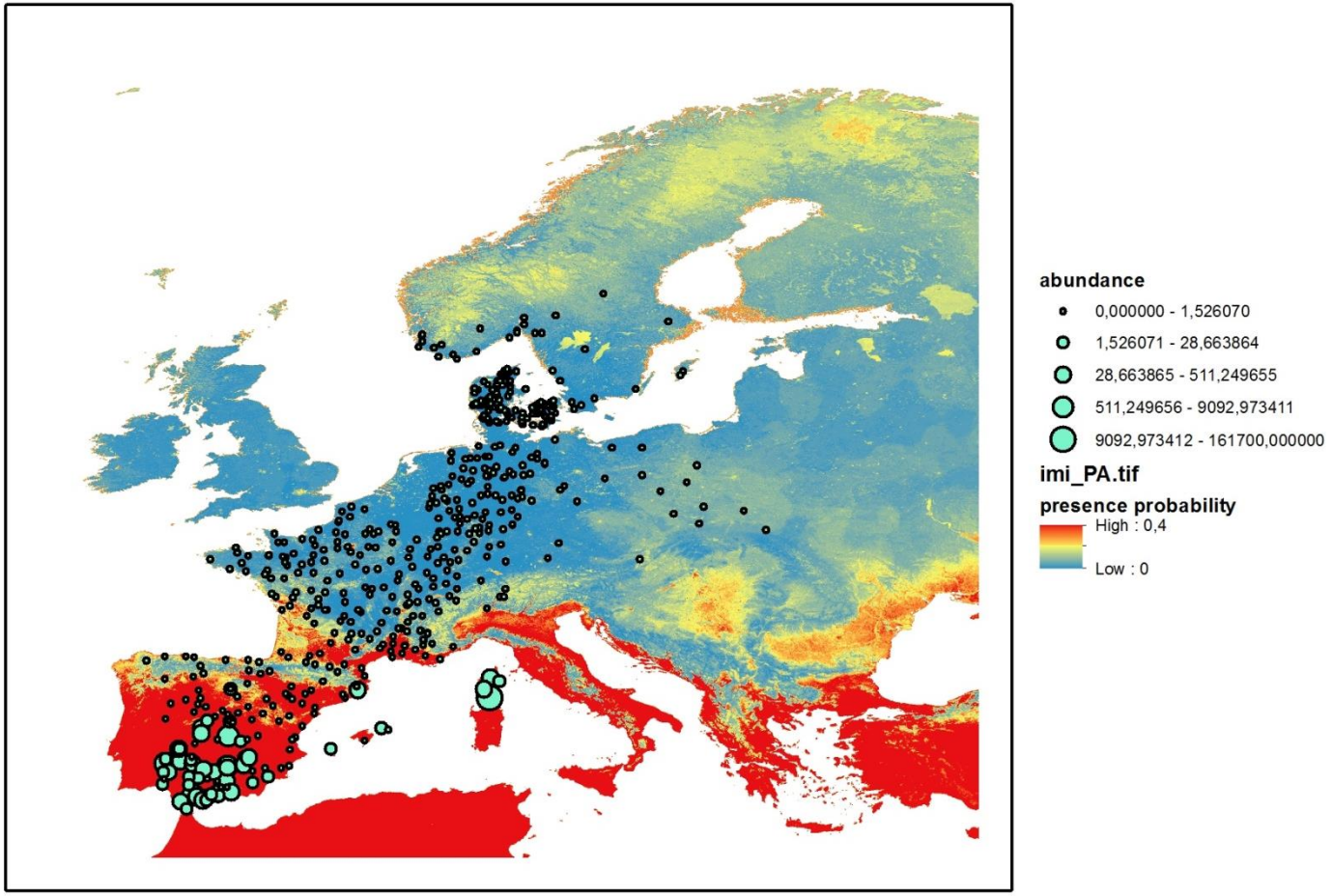
- Take samples at all sites
- Interpolation
- Predictive modelling

- Data
- Predictors

→ modelling → maps

(Presence-Absence (PA), Abundance)

Culicioides imicola suitability map

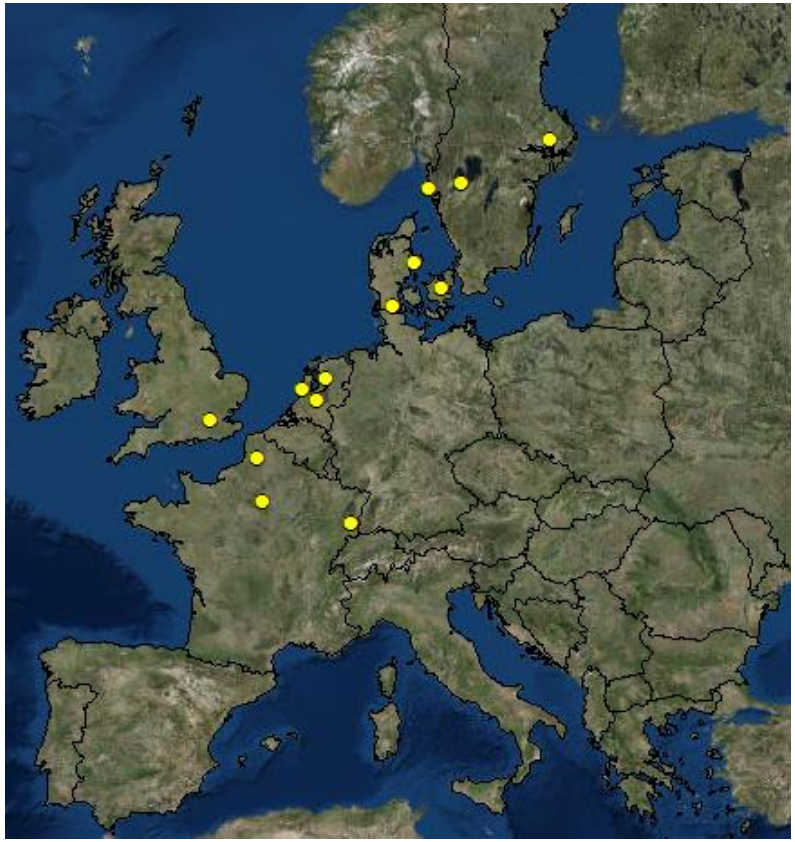


Methods and materials

16000 ticks
(*Ixodes ricinus*)

49 pools of 25 nymphs, per site

13 locations (England, Sweden, Denmark, Netherlands and France)



Pathogen detection (PCR techniques)

Pooled prevalence for fixed pool size and perfect tests

Pathogen prevalence

We use:
five species of Bacteria:

- *Borrelia Burgdorferi*
- *Borrelia Garinii*
- *Borrelia Miyamotoi*
- *Anaplasma phagocytophilum*
- Candidatus *N. mikurensis*

two species of parasites

- *Babesia divergens*
- *Babesia venatorum* (sp. EU1)

Data analysis

Machine learning techniques:

- Data drawn from unknown distribution, black box
- Predictive accuracy

Random Forest

Statistical analysis:

- Known data distribution
- P-value, confidence intervals

90 predictors: Remote sensing imagery (1km)

70 Fourier processed MODIS imagery:

- LST day
- LST night
- NDVI
- EVI

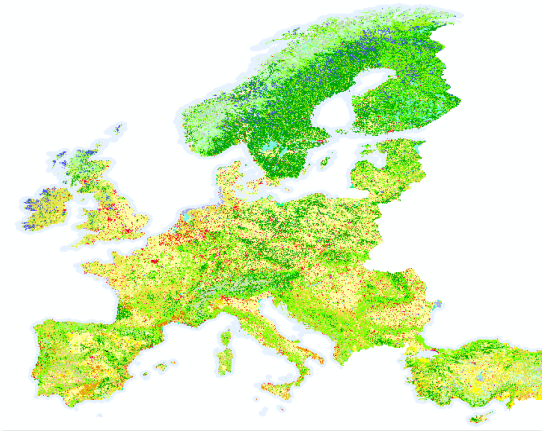
Modis: mean day temperture

-19 Worldclim imagery:

- Temperature and precipitation

Worldclim: mean precipation

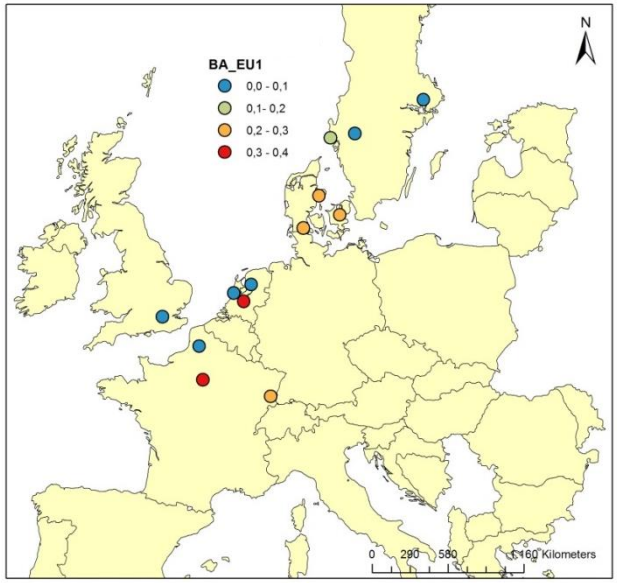
Corine Land Cover:



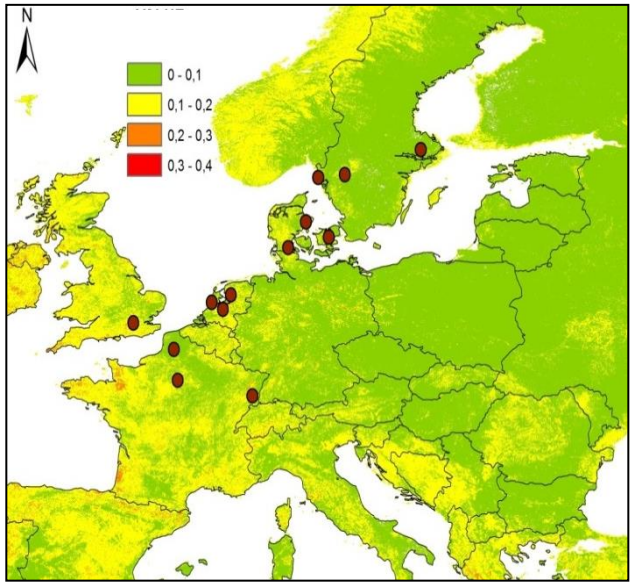
Results

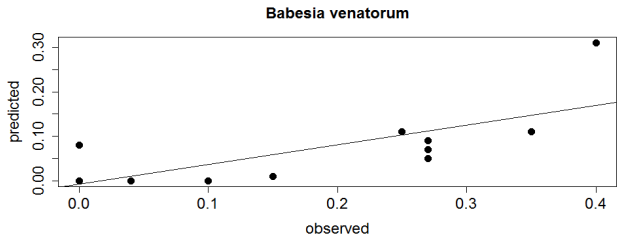
Babesia venatorum

%Prevalence



Probability of presence





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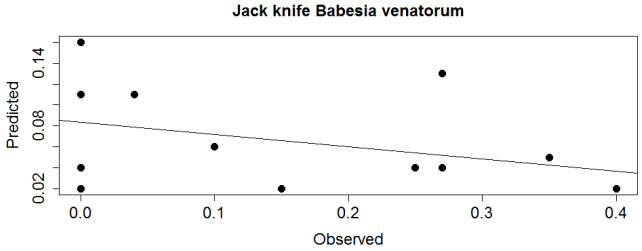

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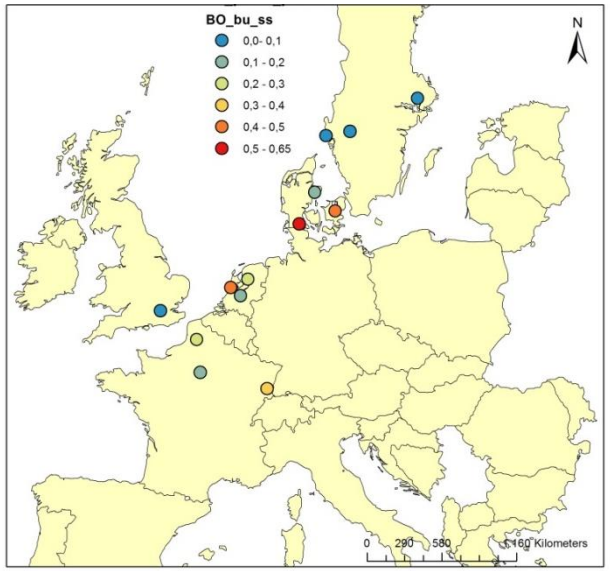
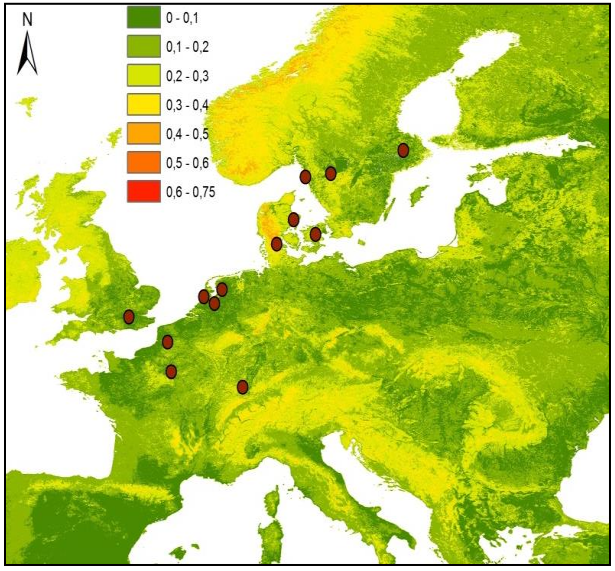
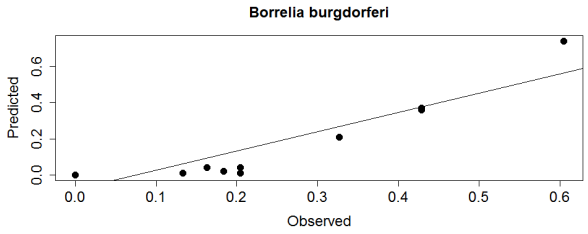
Borrelia burgdorferi

%Prevalence



Probability of presence





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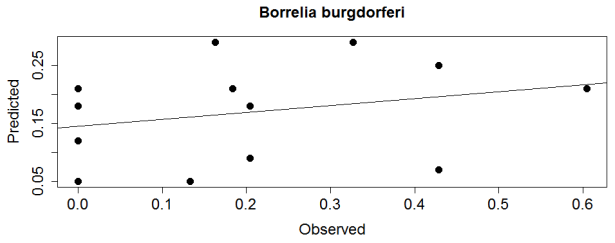

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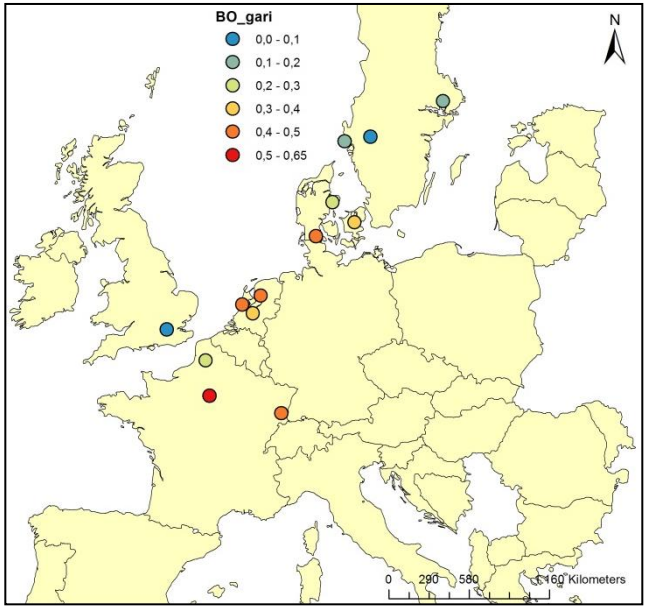
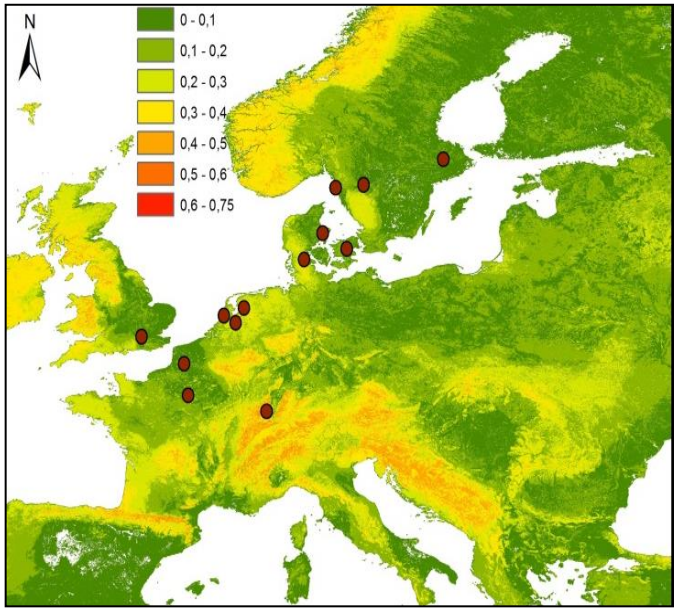
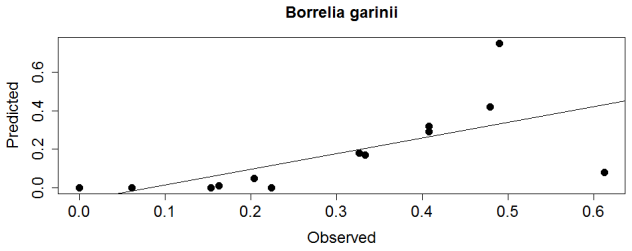
Borrelia garinii

%Prevalence



Probability of presence





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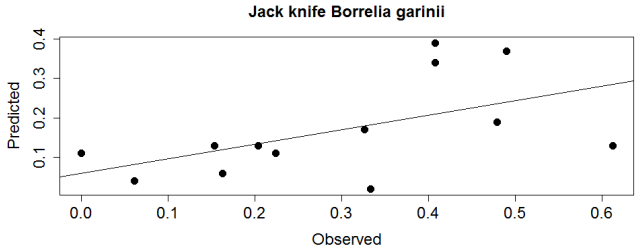

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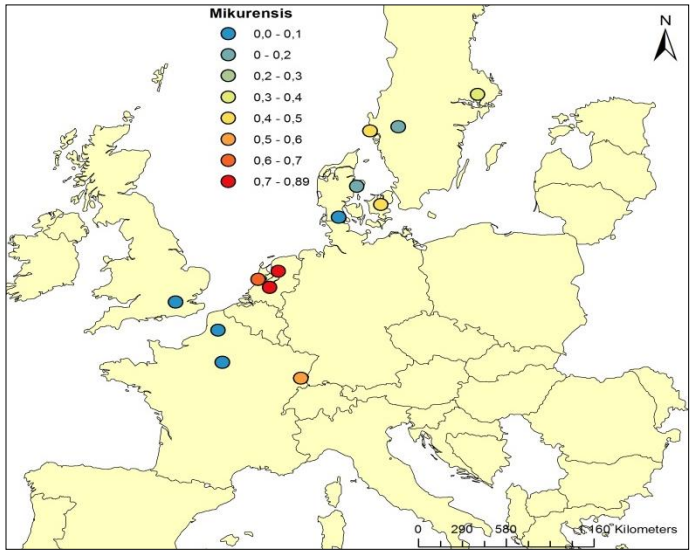
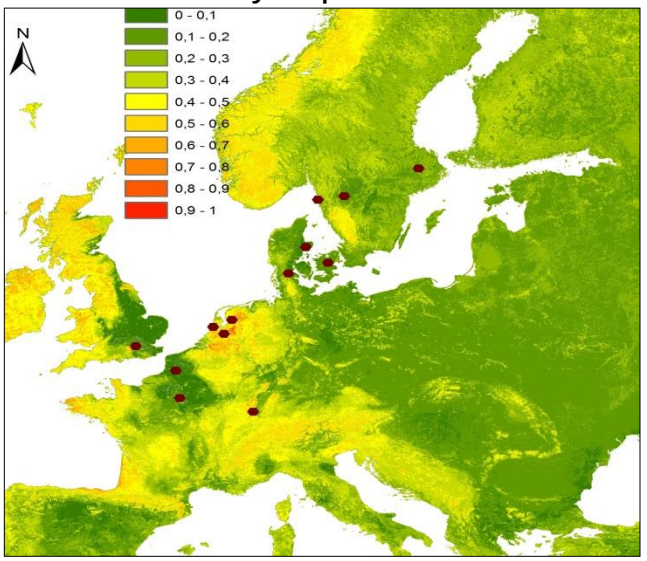
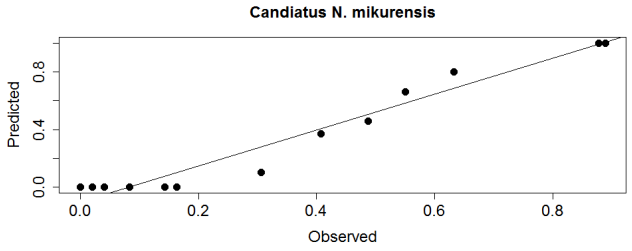
Candidatus *Neoehrlichia mikerensis*

%Prevalence



Probability of presence





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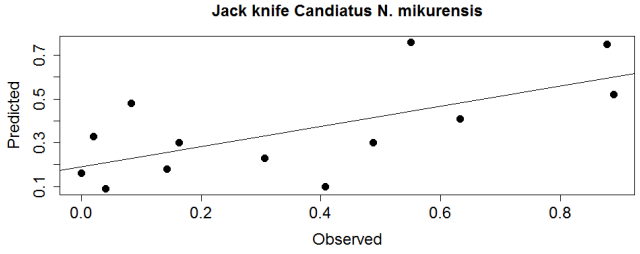

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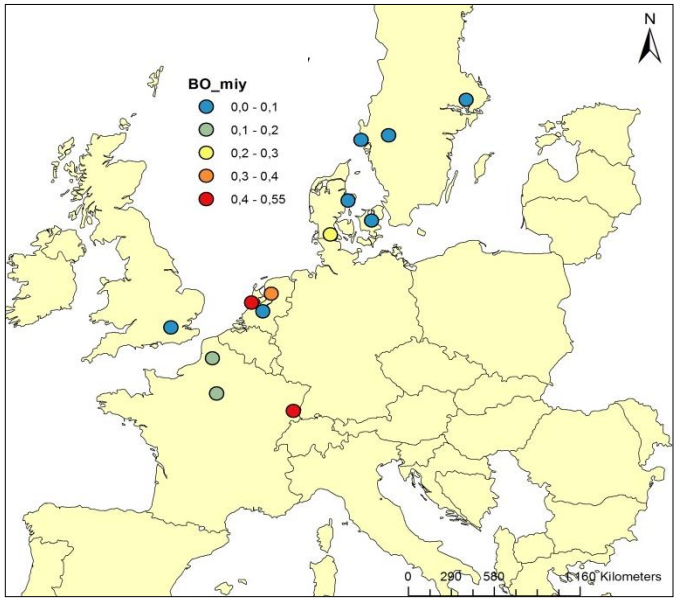
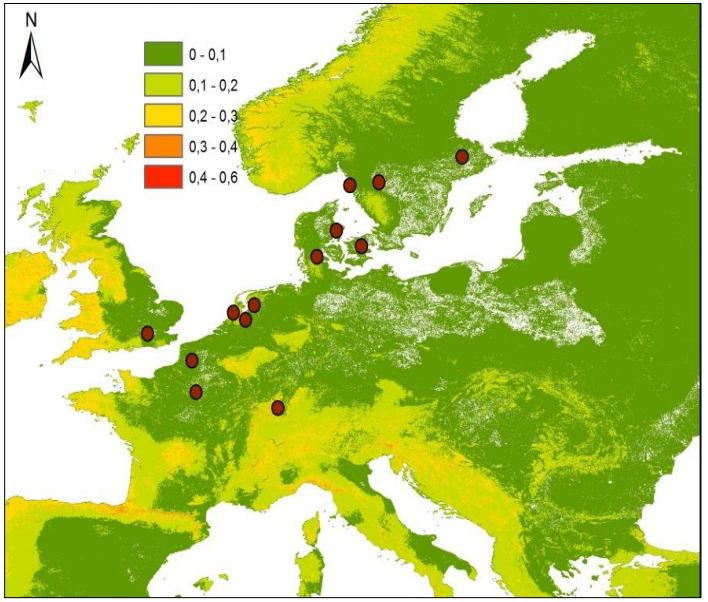
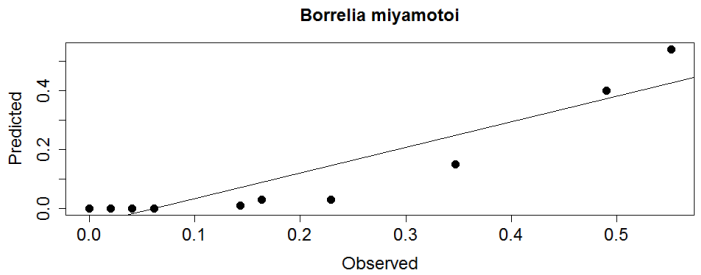
Borrelia miyamotoi

%Prevalence



Probability of presence





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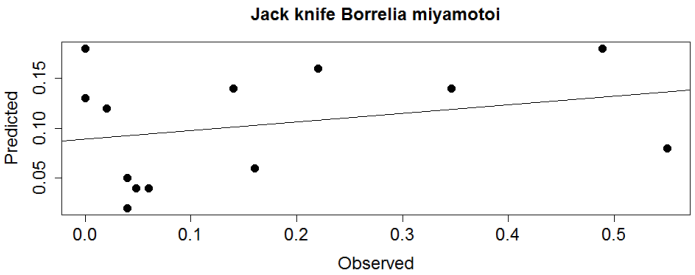
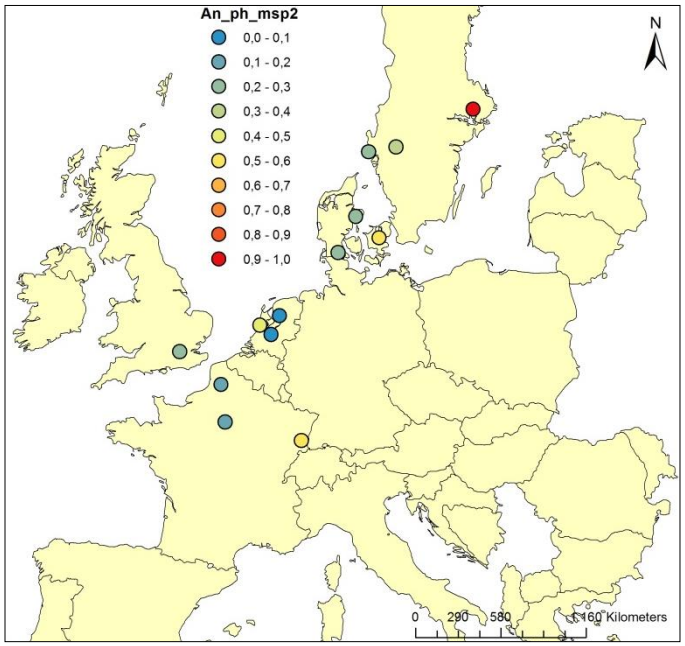


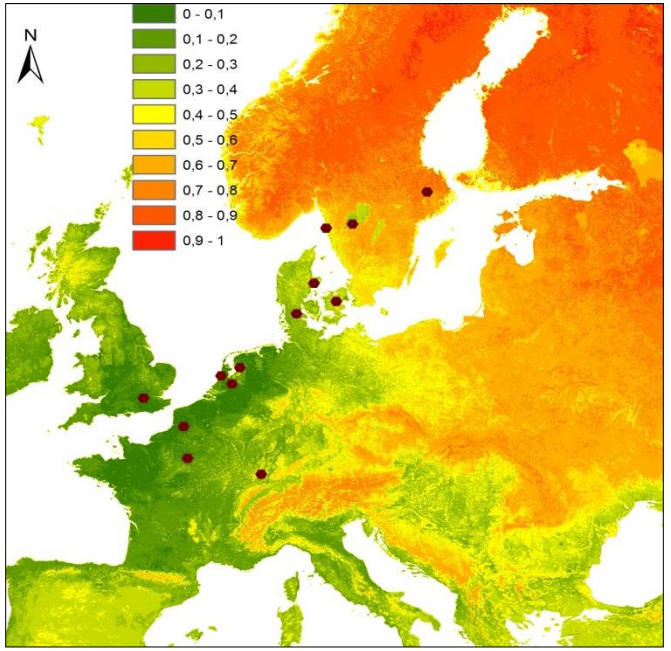
P=0.3436

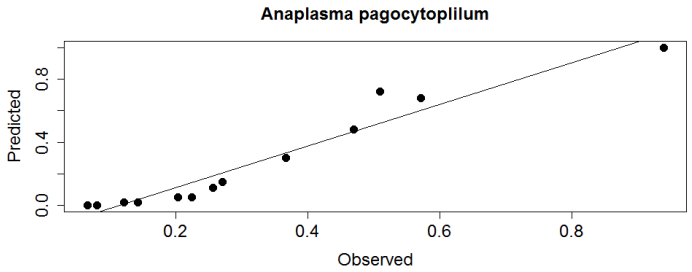
Anaplasma phagocytophilum

%Prevalence



Probability of presence





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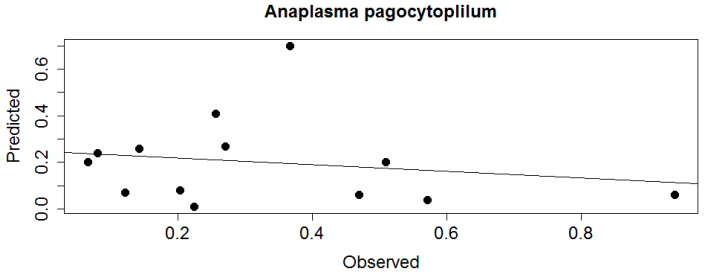

P=0.5486

Discusion/conclusion

- Pathogens prevalence differ between sites
- First attempt to model tick pathogens using environmental variables from remote sensing data
- Observed prevalences fit the environmental data ☺
- Overfitting: few observations
- Other algorithms like Boosted Regression Trees

Thank you
for your attention

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