



## Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

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# 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



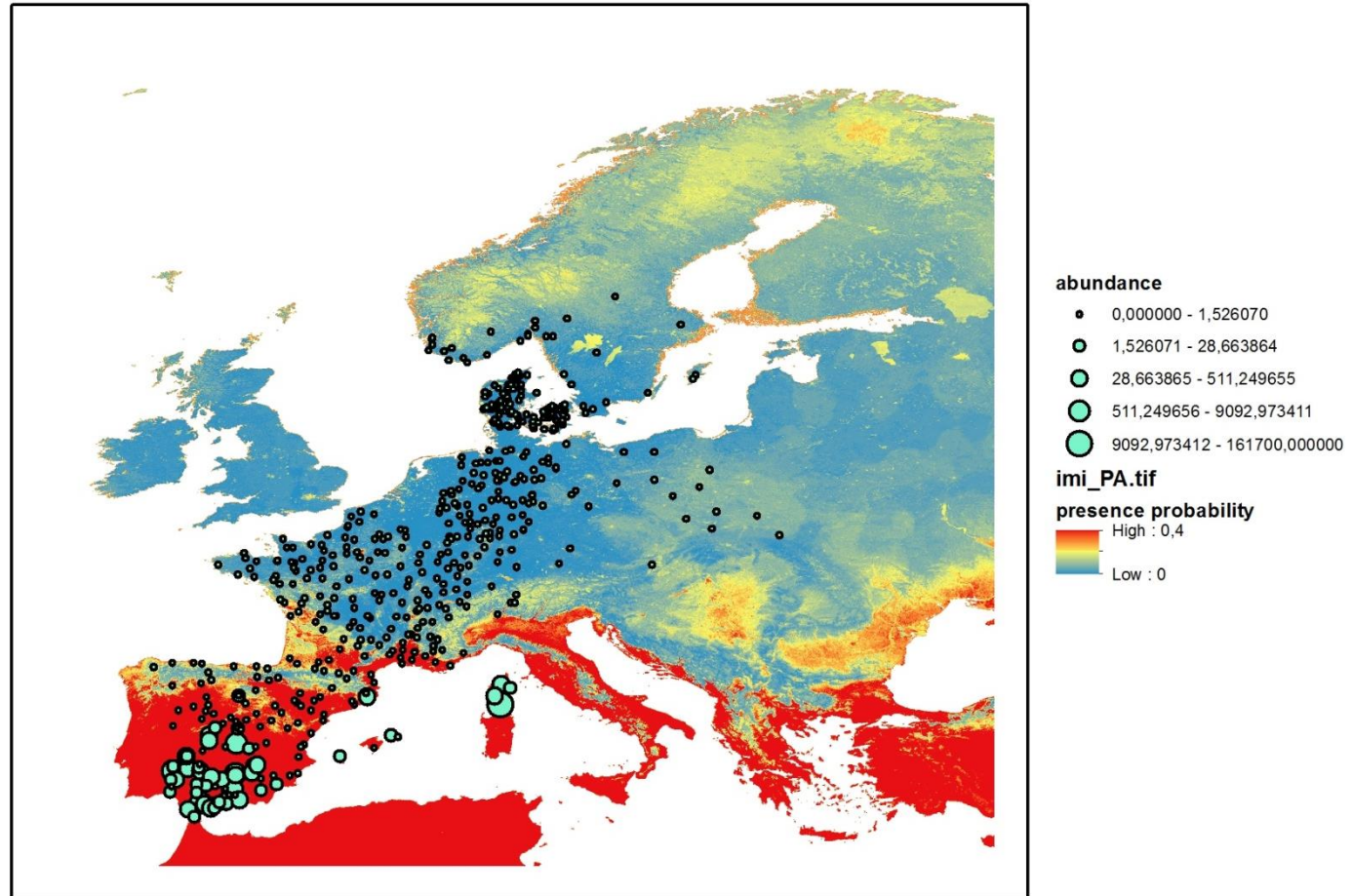
Founded by CoVetLab and InterReg

# Introduction

Abstraktion of reality  **Modelling**  Predictions, planning



# Culicioides imicola suitability map



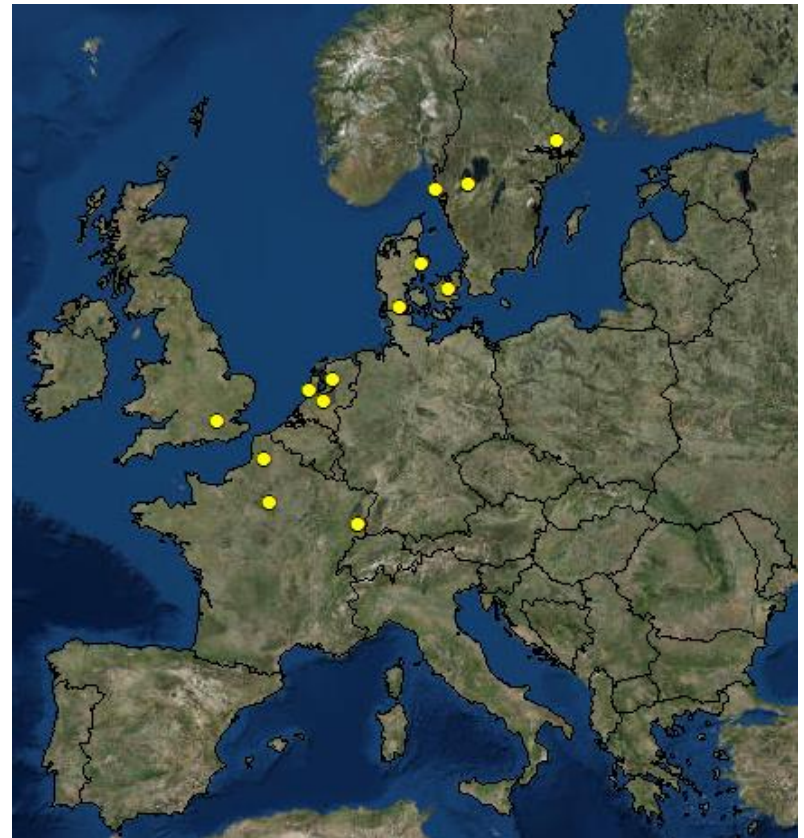
# Methods and materials

16000 ticks  
(*Ixodes ricinus*)

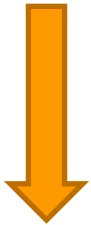


49 pools of 25 nymphs, per site

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 temperature

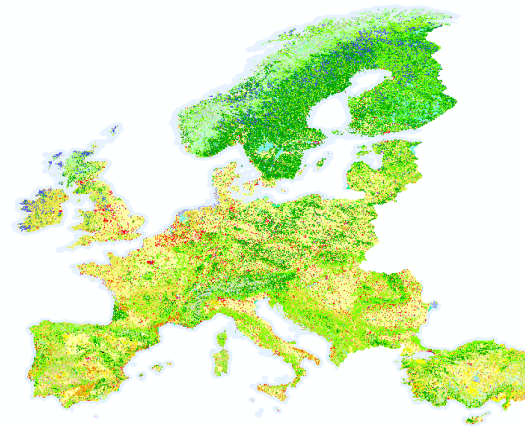
Worldclim: mean precipitation



## -19 Worldclim imagery:

- Temperature and precipitation

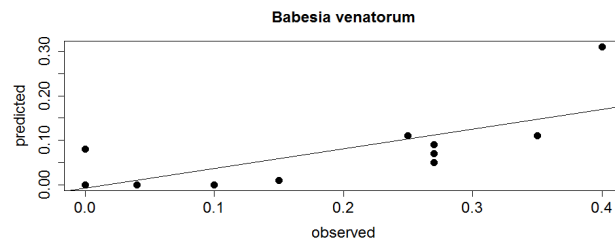
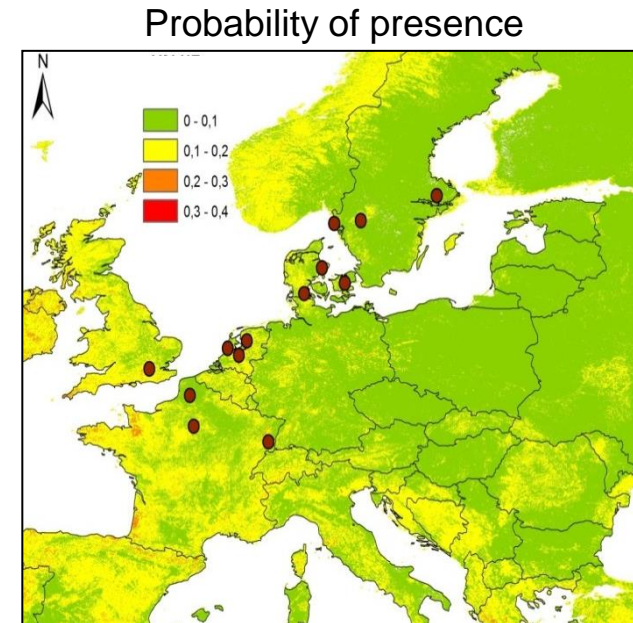
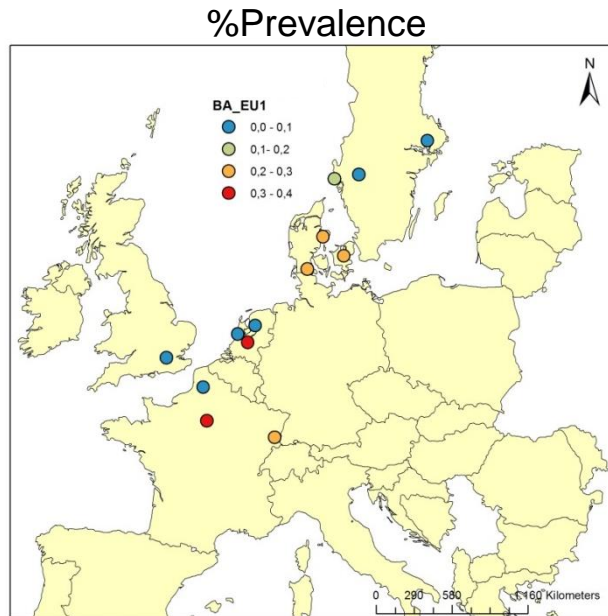
## Corine Land Cover:



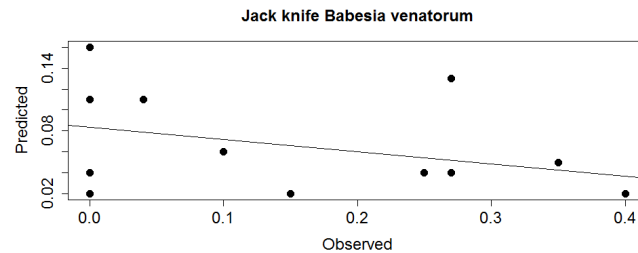


# Results

## *Babesia venatorum*



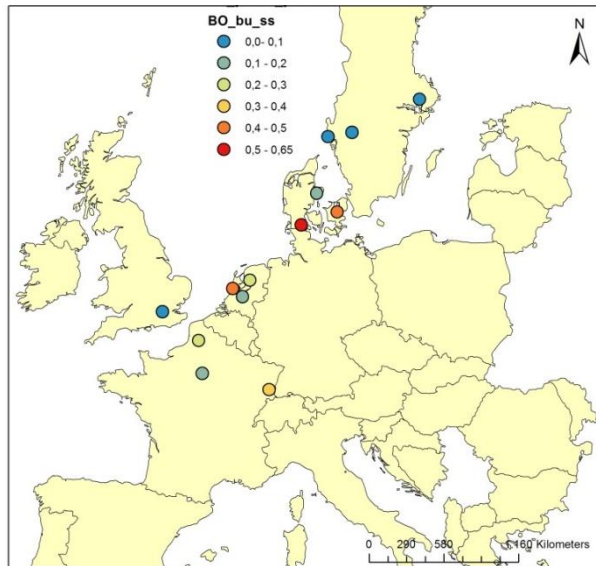
$P=0.003089$



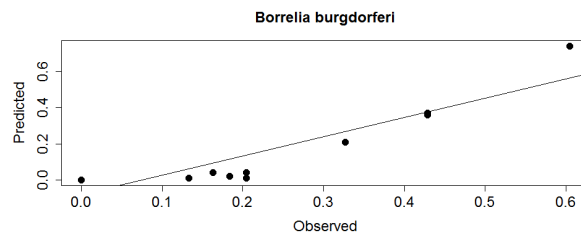
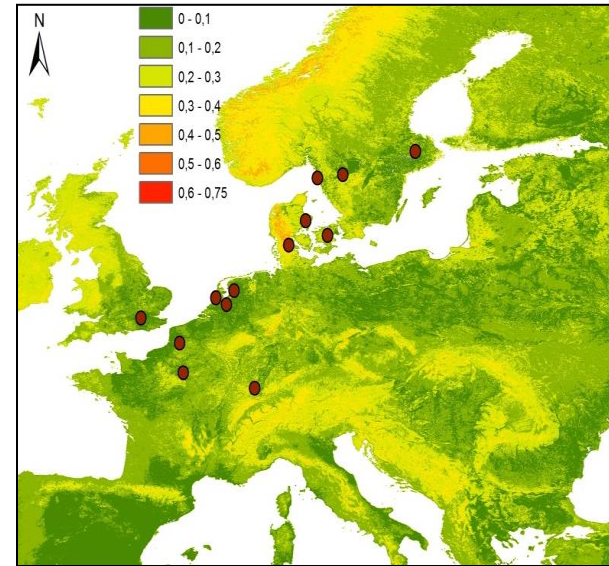
$P=0.2185$

# *Borrelia burgdorferi*

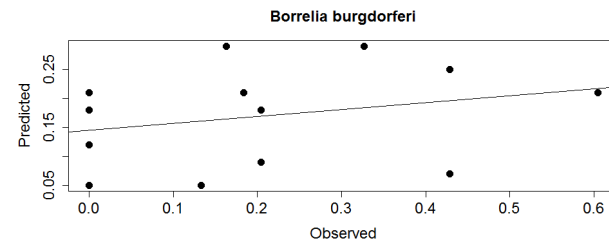
%Prevalence



Probability of presence



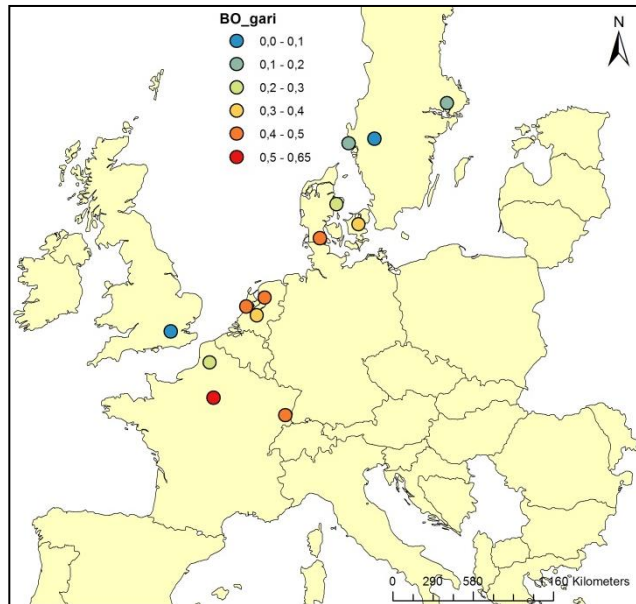
$P < 0,001$



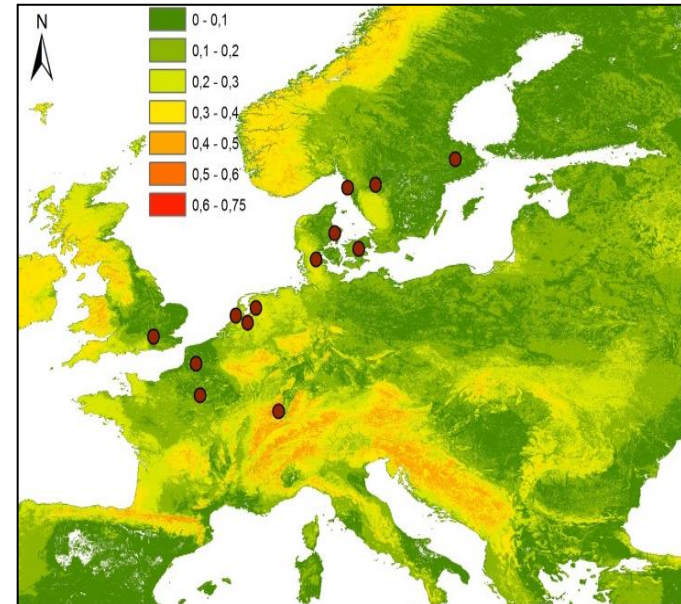
$P = 0.3739$

# *Borrelia garinii*

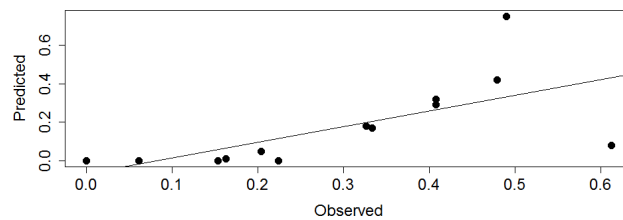
%Prevalence



Probability of presence

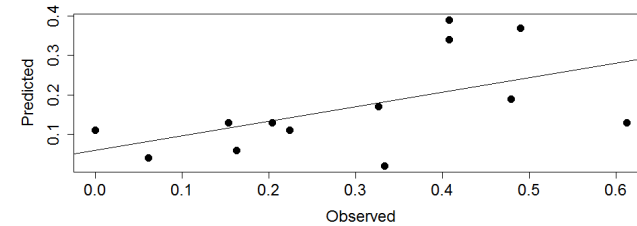


*Borrelia garinii*



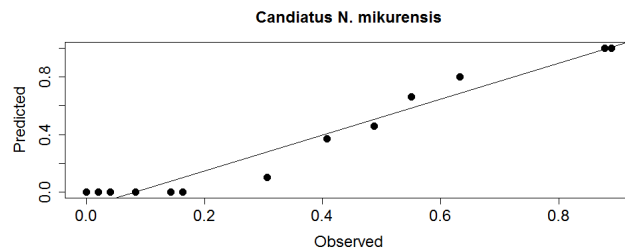
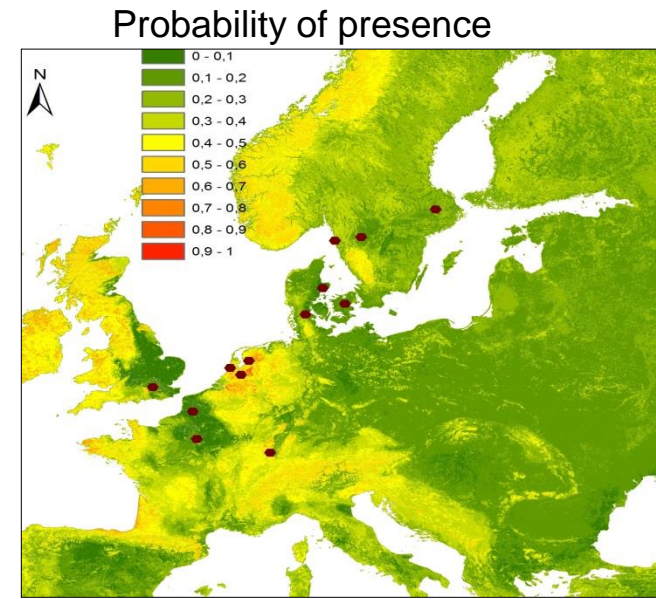
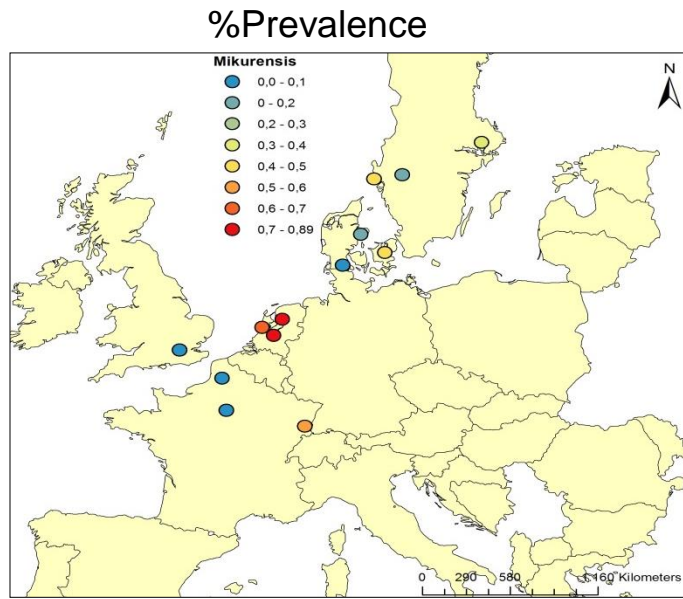
$P=0,01456$

Jack knife *Borrelia garinii*

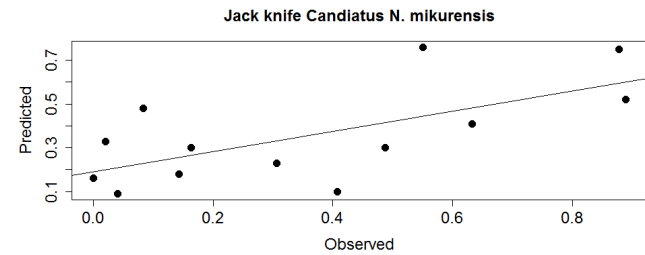


$P=0,05589$

# Candidatus *Neoehrlichia mikereensis*



$P < 0,001$

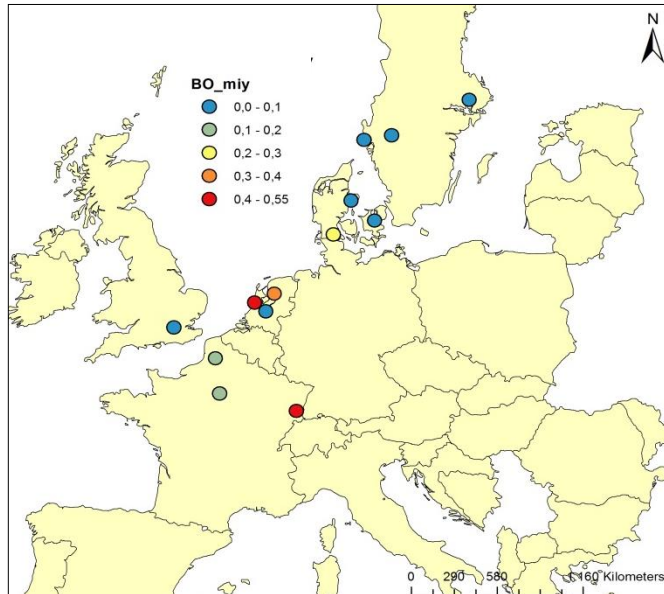


$P = 0,01523$

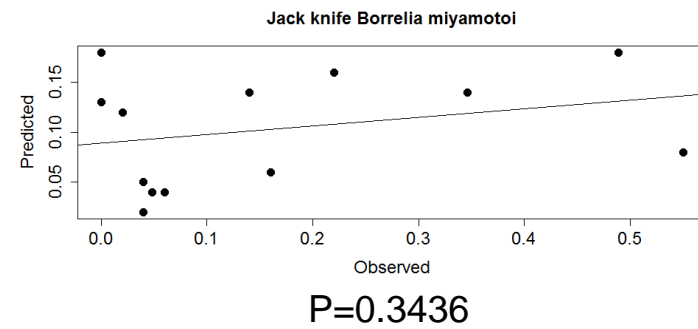
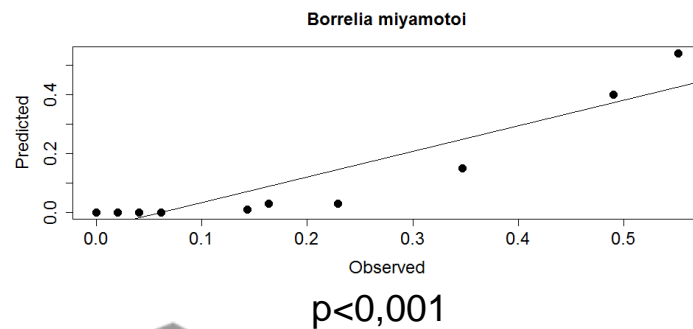
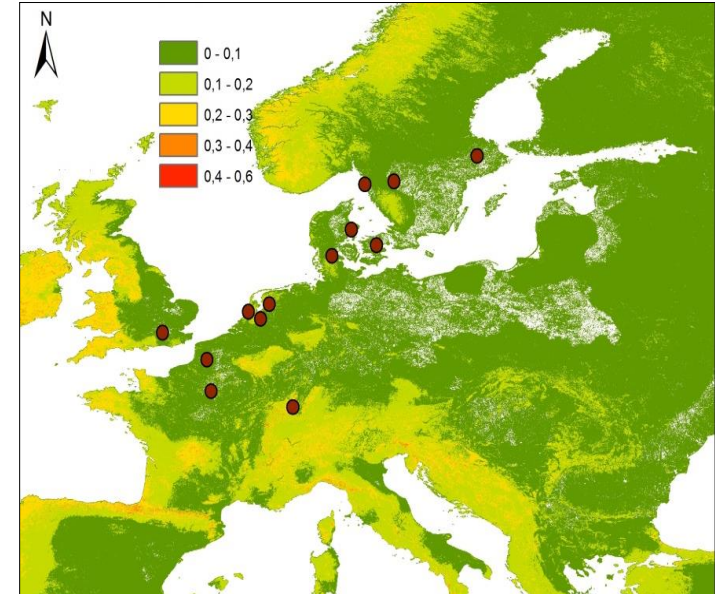


# *Borrelia miyamotoi*

%Prevalence

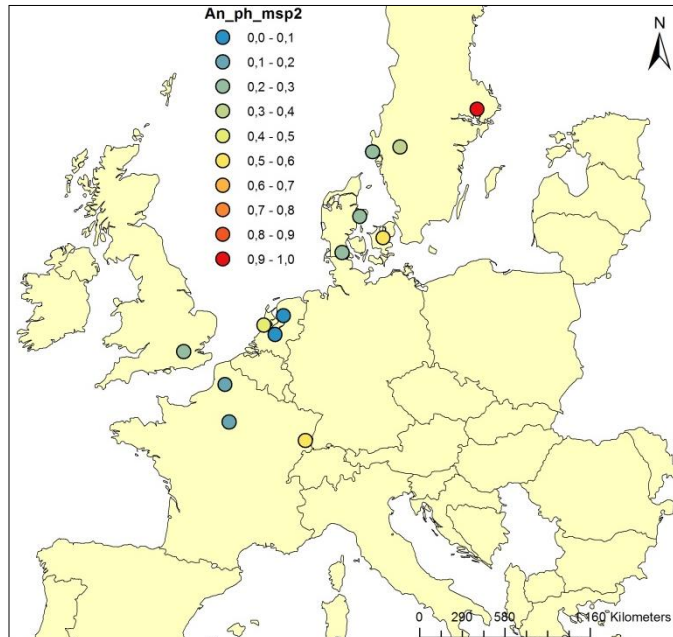


Probability of presence

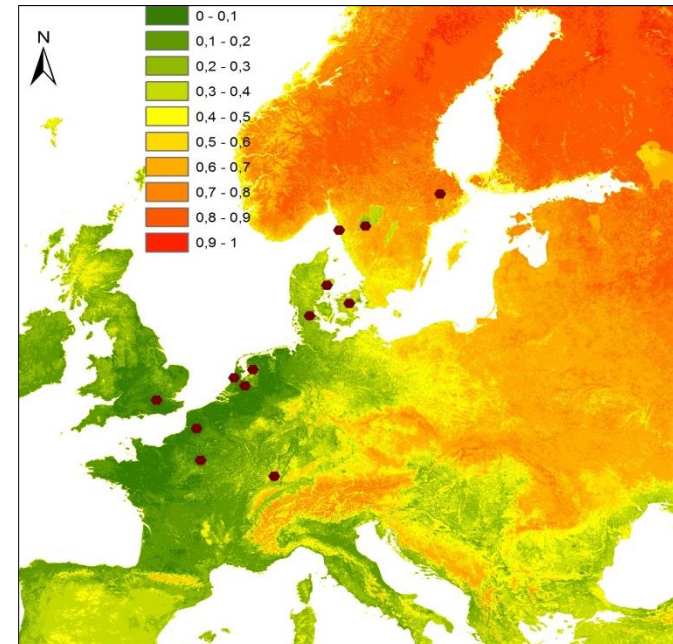


# *Anaplasma phagocytophilum*

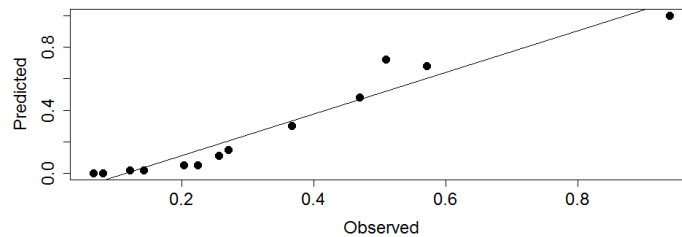
%Prevalence



Probability of presence

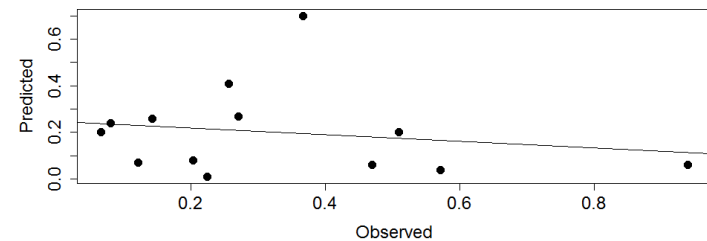


*Anaplasma phagocytophilum*



$P < 0,001$

*Anaplasma phagocytophilum*



$P = 0.5486$

# Discussion/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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