

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

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

*Publication date:*  
2016

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

[Link back to DTU Orbit](#)

*Citation (APA):*  
Cuellar, A. C., Schou, K. K., Moutailler, S., Fach, P., Delannoy, S., van der Wal, F. J., ... Bødker, R. (2016). Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe Technical University of Denmark (DTU). [Sound/Visual production (digital)]., Örenäs, Sweden, 02/02/2016

## DTU Library

Technical Information Center of Denmark

---

### General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

# 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



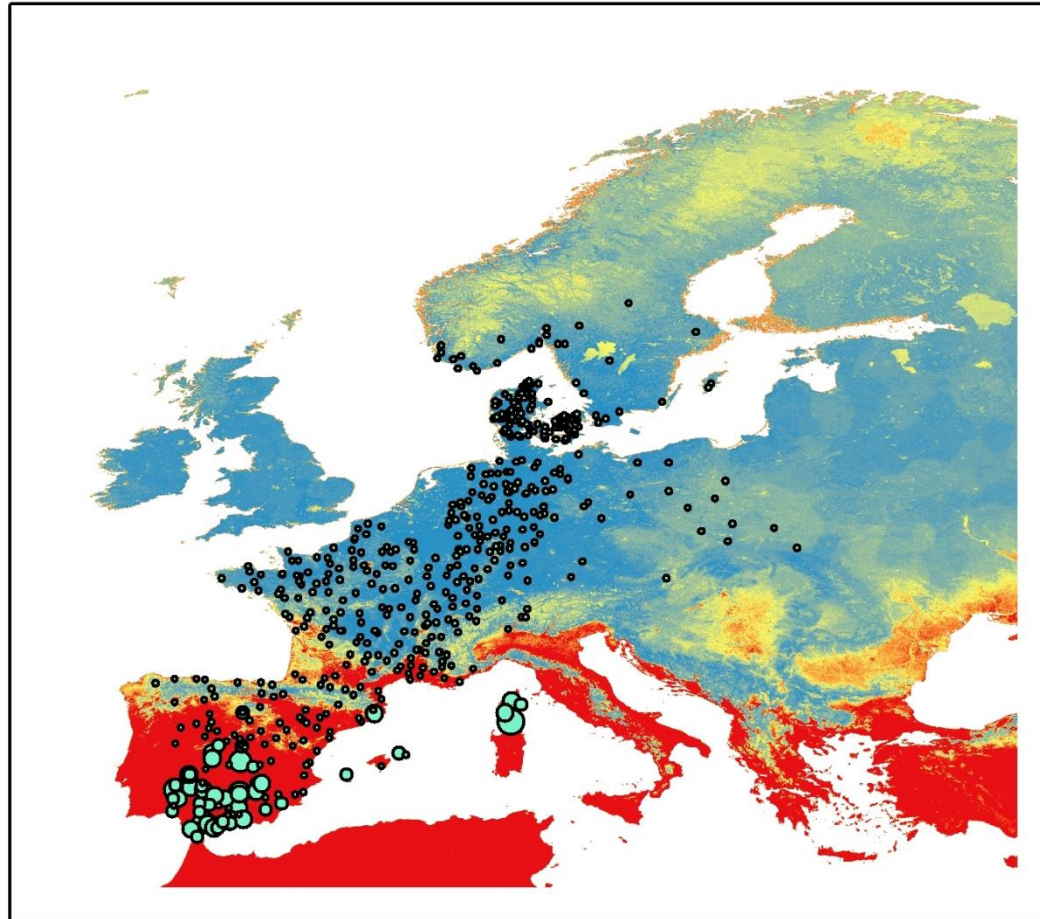
Founded by CoVetLab and InterReg

# Introduction

Abstraktion of reality  **Modelling**  Predictions, planning



# Culicioides imicola suitability map

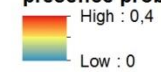


**abundance**

- 0,000000 - 1,526070
- 1,526071 - 28,663864
- 28,663865 - 511,249655
- 511,249656 - 9092,973411
- 9092,973412 - 161700,000000

**imi\_PA.tif**

**presence probability**



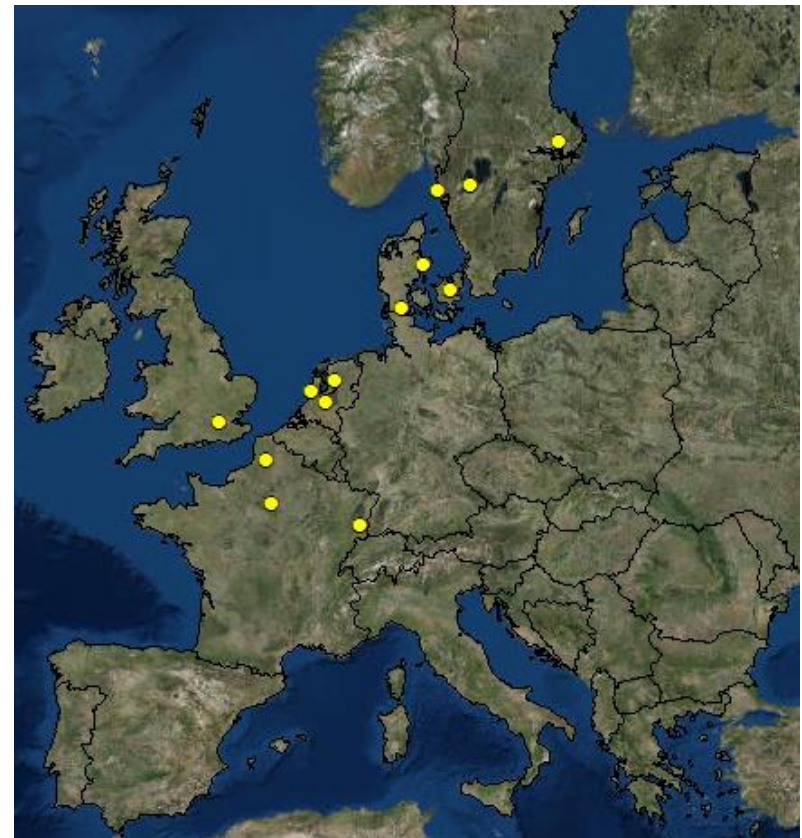
# Methods and materials

16000 ticks  
(*Ixodes ricinus*)

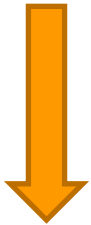


49 pools of 25 nymphs, per site

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

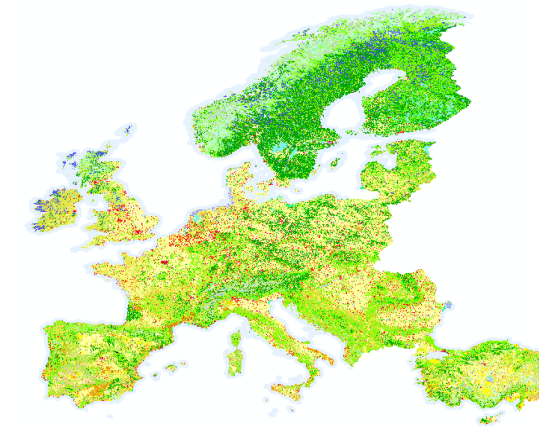
Worldclim: mean precipitation



## -19 Worldclim imagery:

- Temperature and precipitation

## Corine Land Cover:

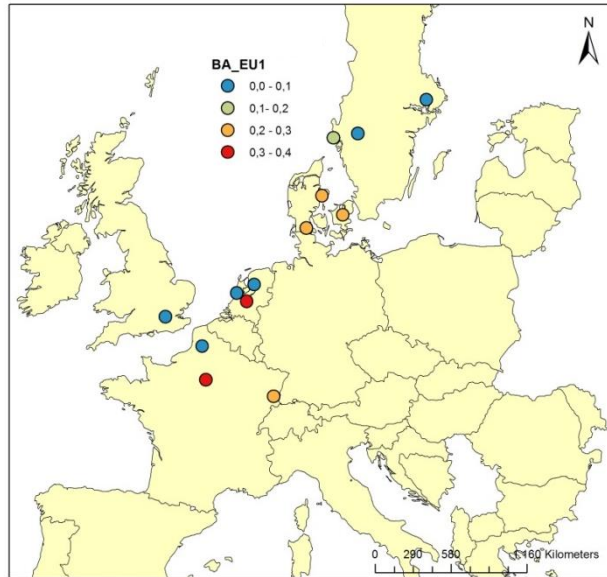




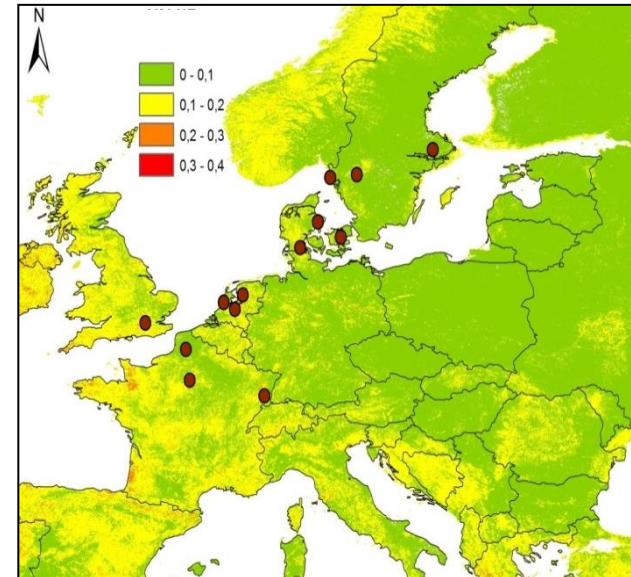
# Results

## *Babesia venatorum*

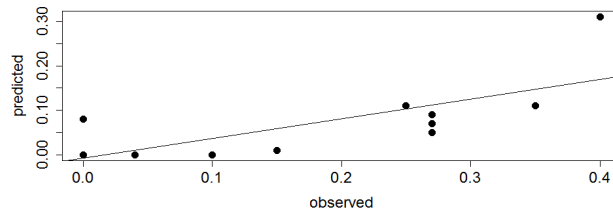
%Prevalence



Probability of presence

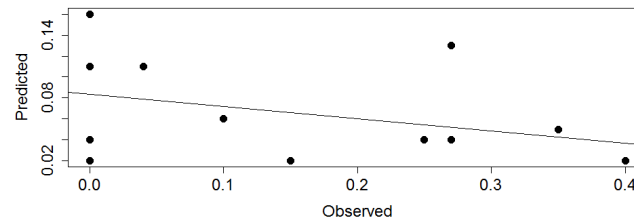


*Babesia venatorum*



$P=0.003089$

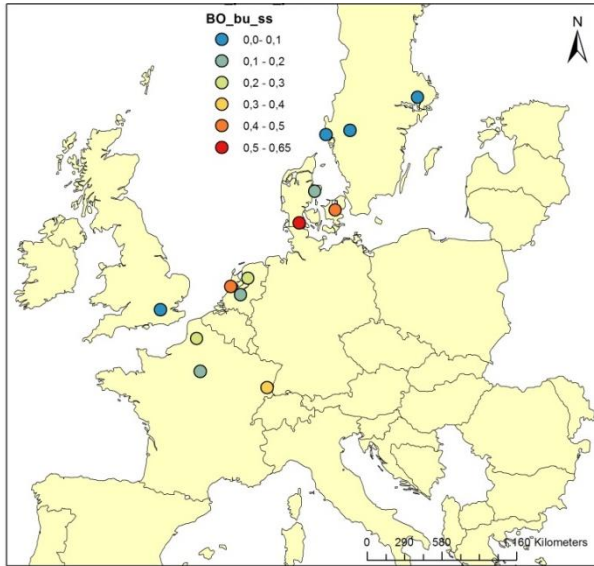
Jack knife *Babesia venatorum*



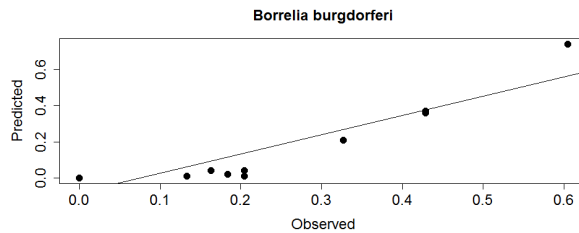
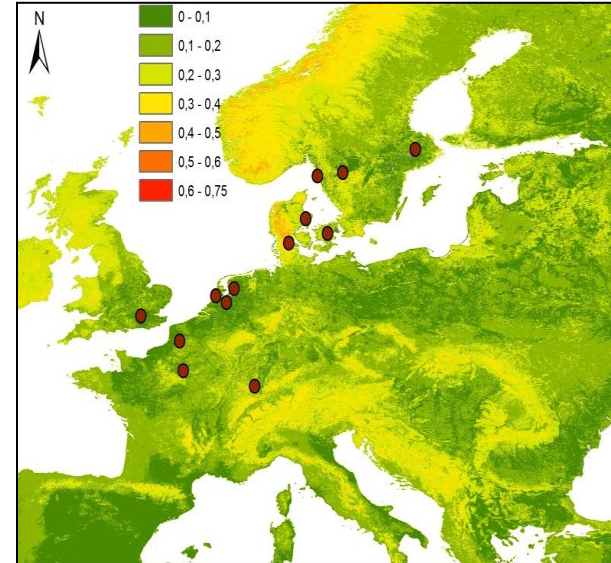
$P=0.2185$

# *Borrelia burgdorferi*

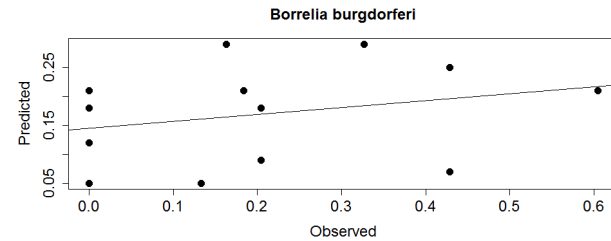
### %Prevalence



### Probability of presence



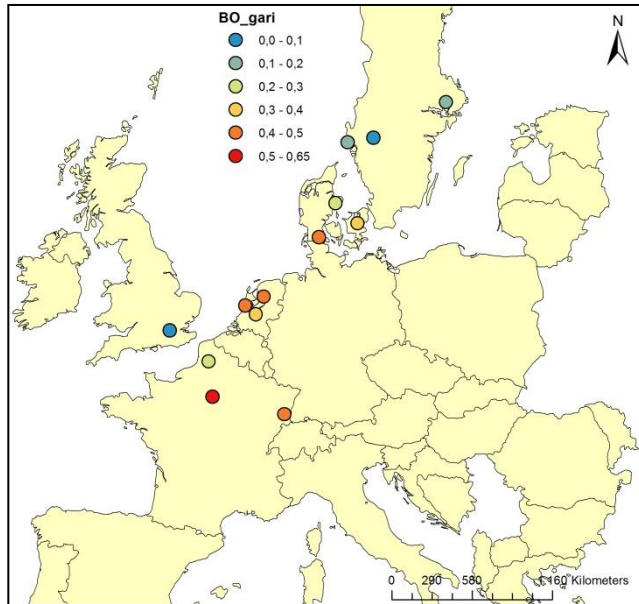
$P < 0,001$



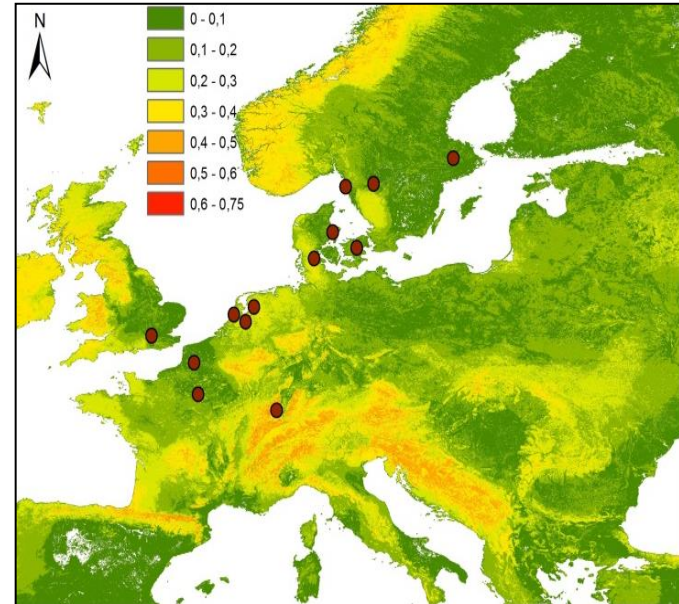
$P = 0.3739$

# Borrelia garinii

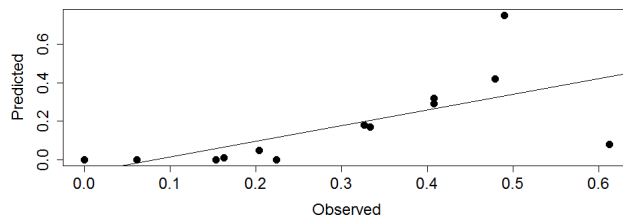
### %Prevalence



### Probability of presence

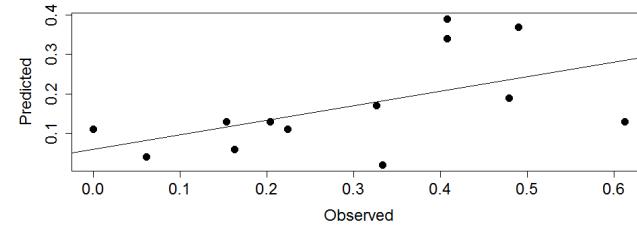


### Borrelia garinii



P=0,01456

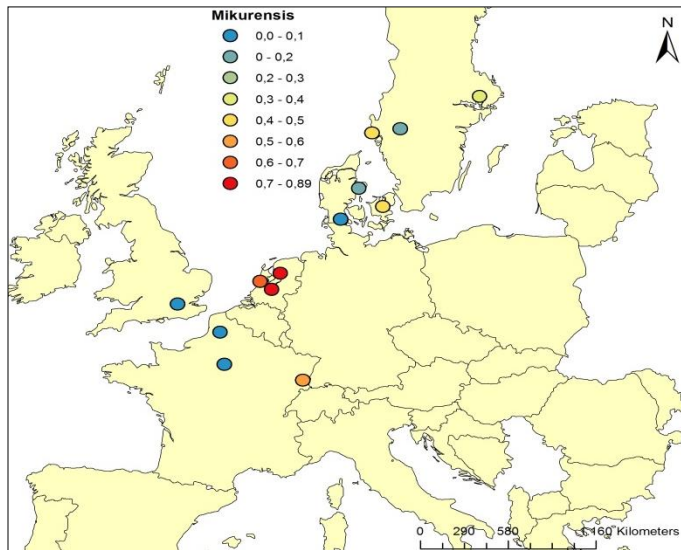
### Jack knife Borrelia garinii



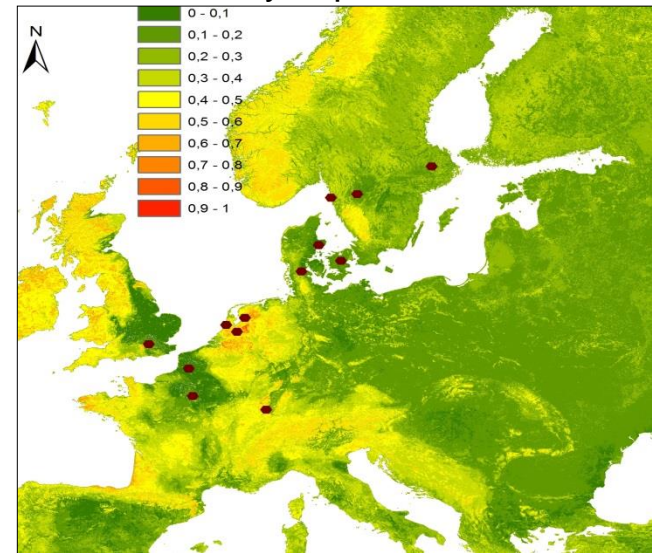
P=0,05589

# Candidatus *Neoehrlichia mikerensis*

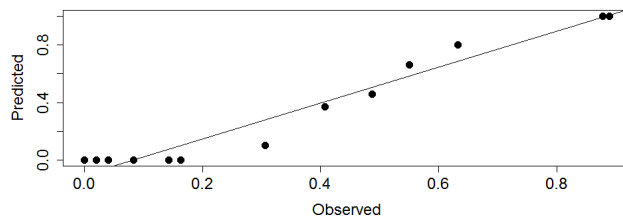
### %Prevalence



### Probability of presence

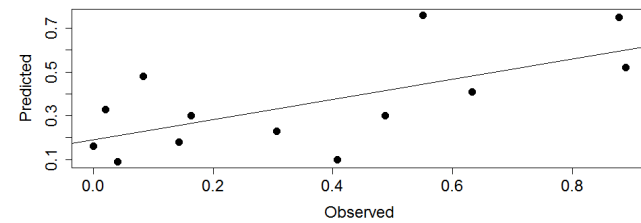


### Candiatus *N. mikerensis*



$P < 0,001$

### Jack knife Candiatus *N. mikerensis*

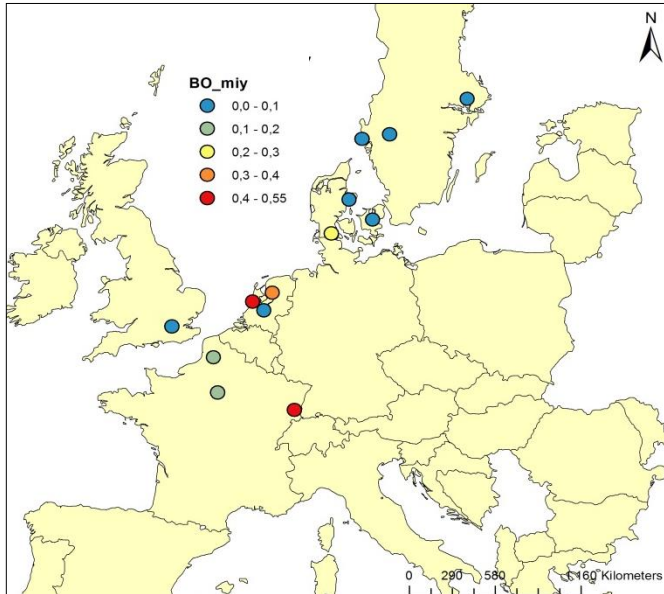


$P = 0,01523$

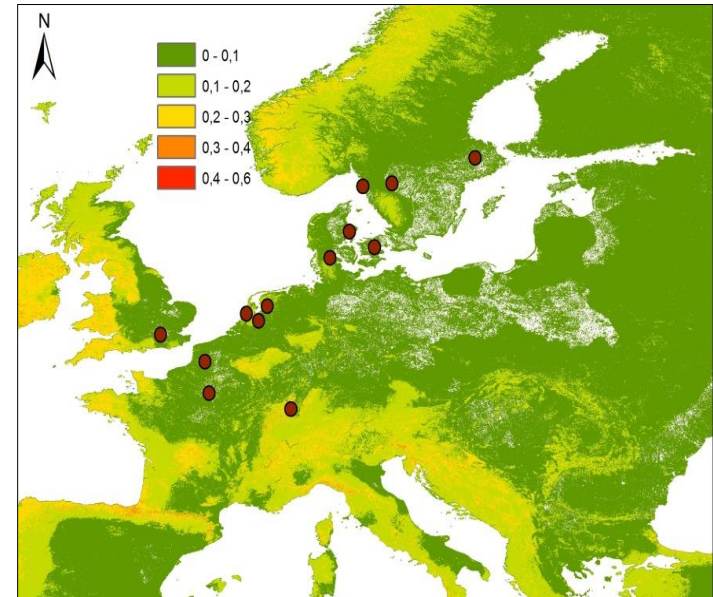


# Borrelia miyamotoi

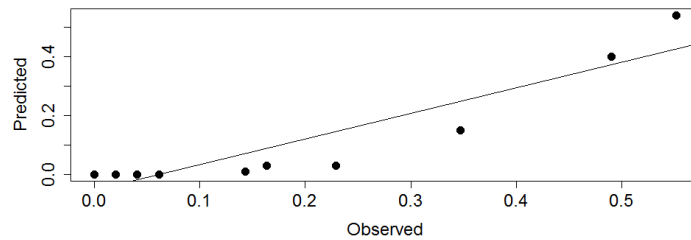
### %Prevalence



### Probability of presence

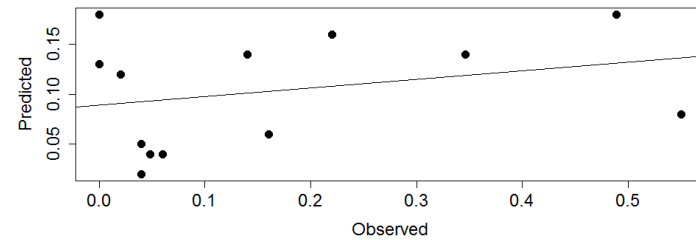


### Borrelia miyamotoi



$p < 0,001$

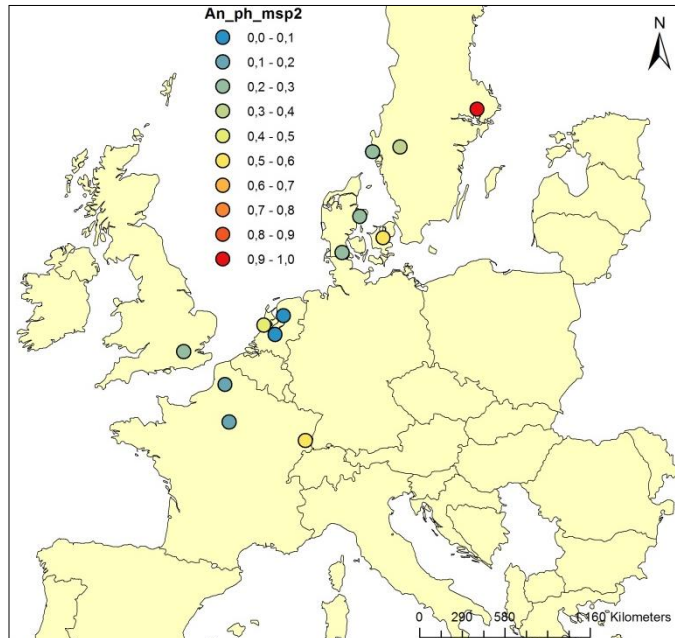
### Jack knife Borrelia miyamotoi



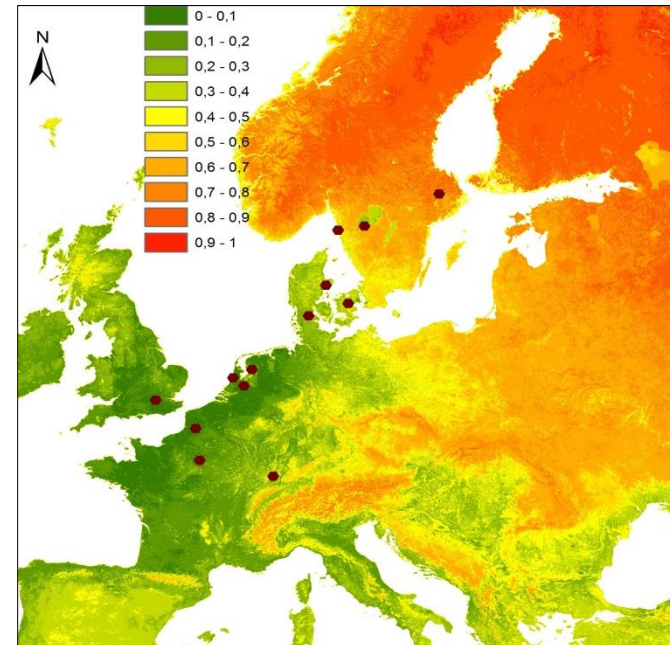
$P = 0.3436$

# *Anaplasma phagocytophilum*

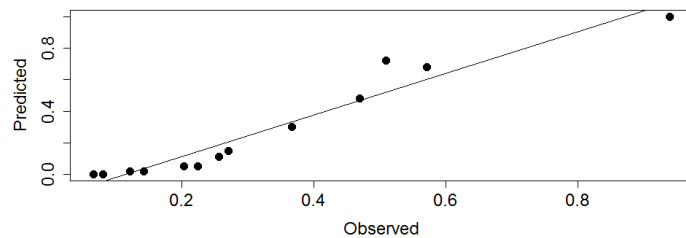
%Prevalence



Probability of presence

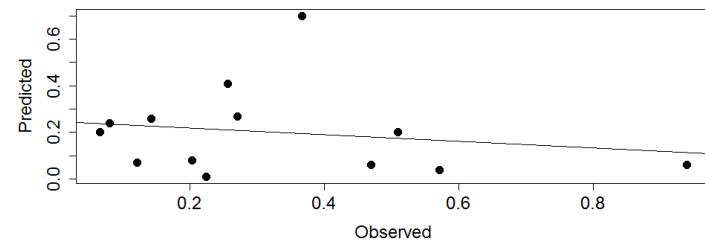


*Anaplasma pagocytoplilum*



$P < 0,001$

*Anaplasma pagocytoplilum*



$P = 0.5486$

# 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**

***Ana Carolina Cuellar***  
[anacu@vet.dtu.dk](mailto:anacu@vet.dtu.dk)