



# Modelling the continental-scale spread of Schmallenberg virus in Europe

Simon Gubbins  
Head of Transmission Biology



# Part I

## Introduction

# Schmallenberg virus (SBV)

- First detected in Germany and The Netherlands in summer 2011
- Affects cattle and sheep:
  - mild or no clinical signs in adults
  - malformation in calves/lambs (referred to as AHS cases)
- Transmitted by *Culicoides* biting midges



from Garigliany et al. (2012) Antiviral Research, 95, 82-87

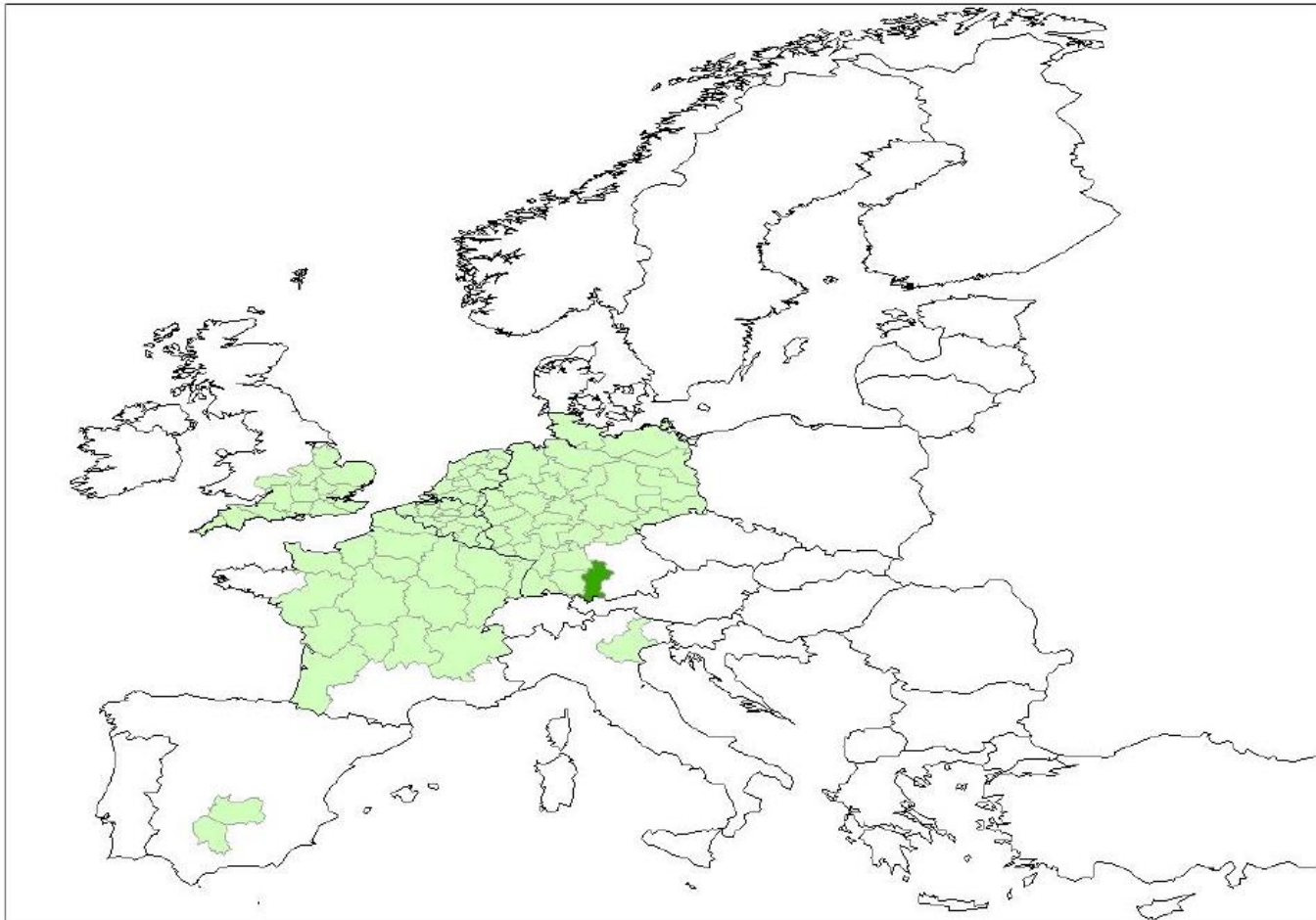
# What epidemic data?

- Member states reported cases to EFSA
- For each NUTS2 region, date and number of cattle and sheep farms reporting AHS cases:
  - not all cases confirmed as SBV
  - possibility of under-ascertainment
- Demographic data available from Eurostat at same scale



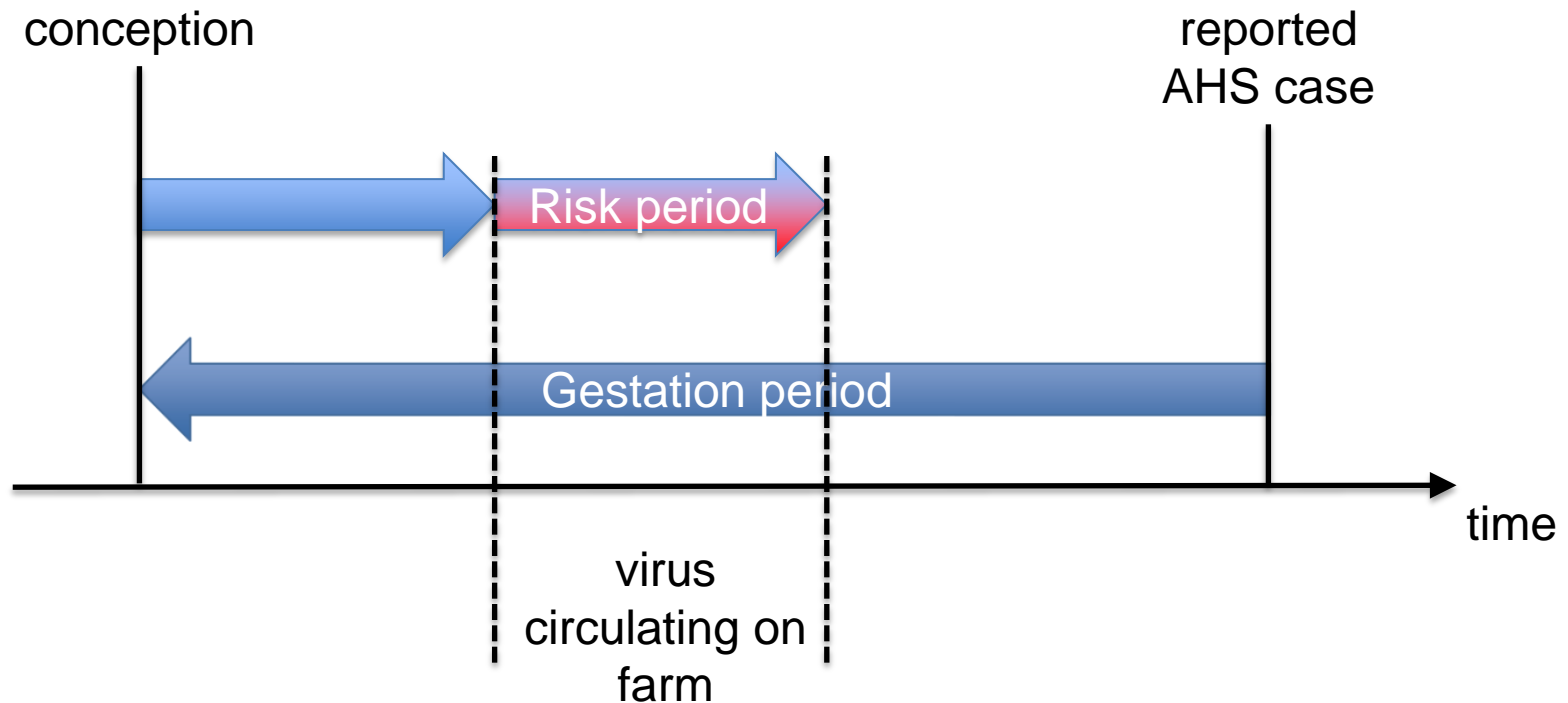
# Regions reporting AHS cases

Up to end April 2012



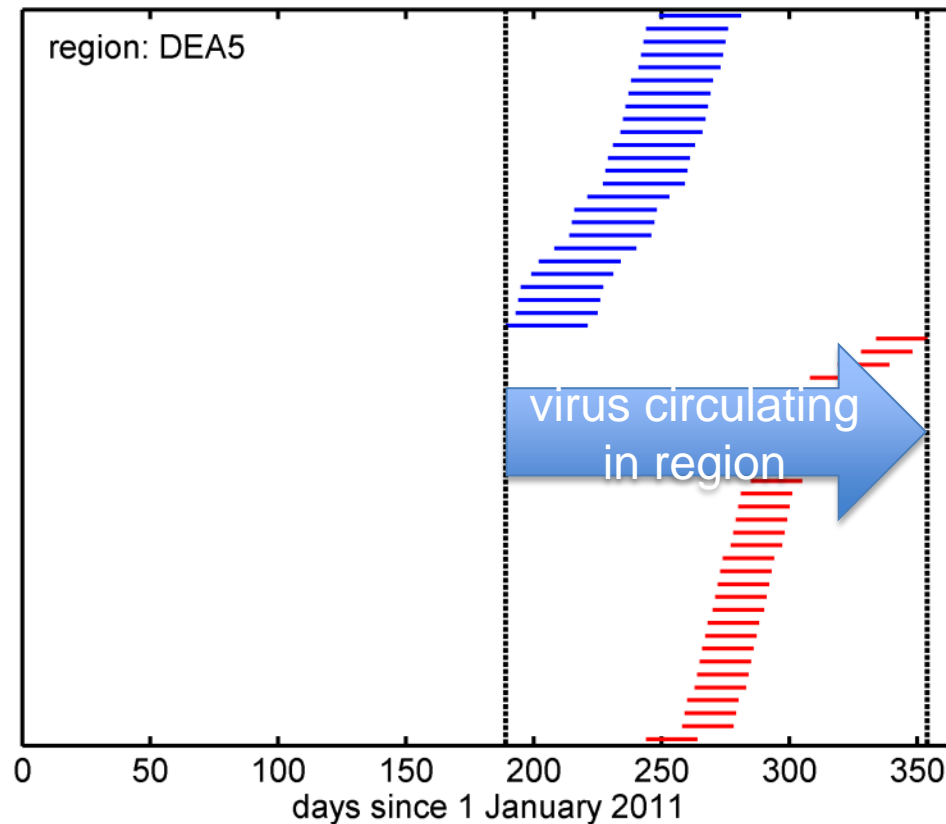
# Reconstructing the epidemic (1)

- How can we infer when SBV was circulating from reported AHS cases?
  - based on Akababe virus, there is a risk period during gestation for AHS cases



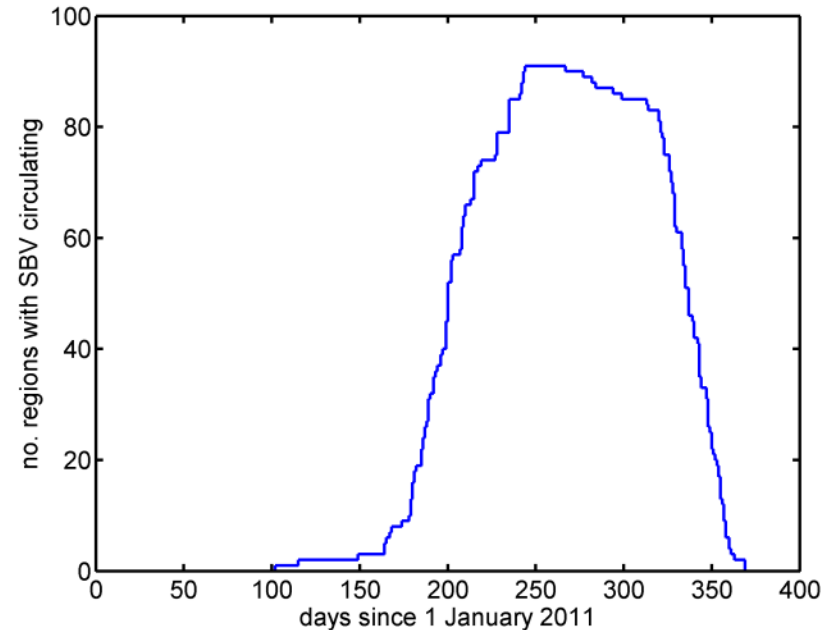
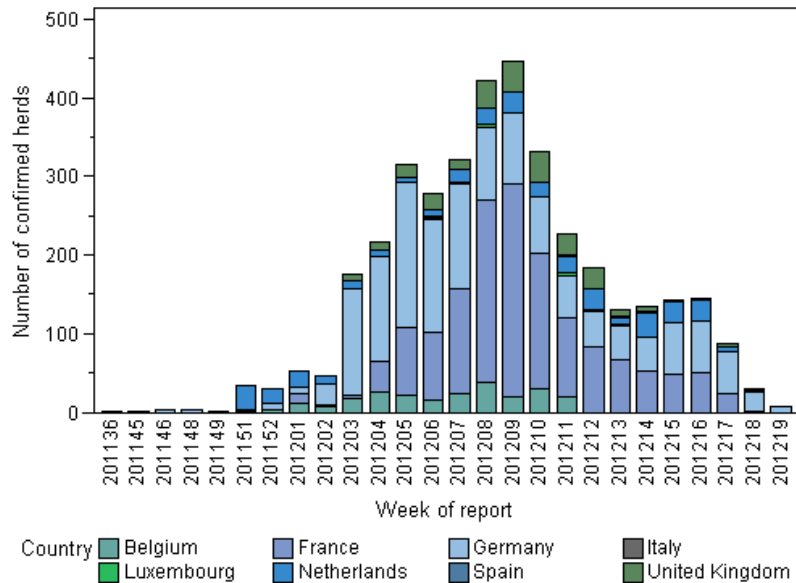
# Reconstructing the epidemic (2)

- Apply this to each farm reporting AHS cases in a region



# The reconstructed epidemic

- Assuming same risk period as for Akabane virus
  - cattle: days 64-96; sheep: days 30-50







# Part II

## Modelling approach

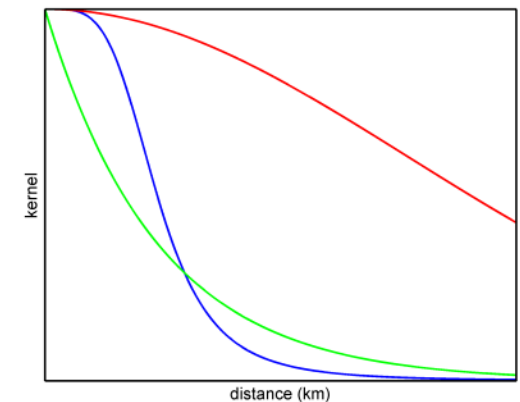
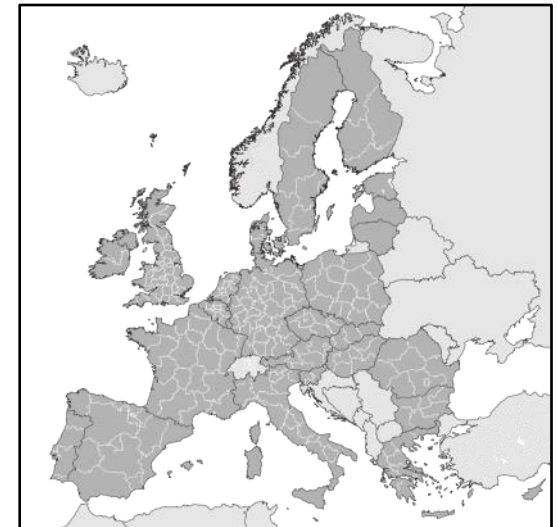
# Modelling the spread of SBV

- Simple model for the transmission of SBV in Europe
  - scenarios for 2012
- Model applied at level of NUTS2 regions
  - i.e. same as the data
  - includes EU28, Norway, Switzerland
- The model has three components:
  - transmission between regions
  - duration of transmission period
  - within-region transmission (but no dynamics)



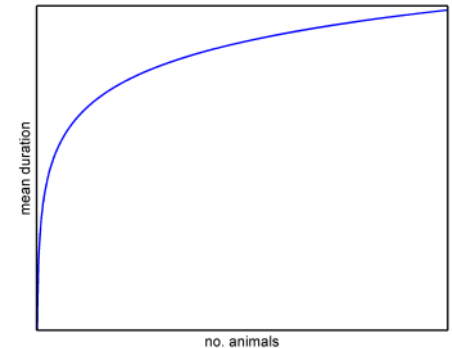
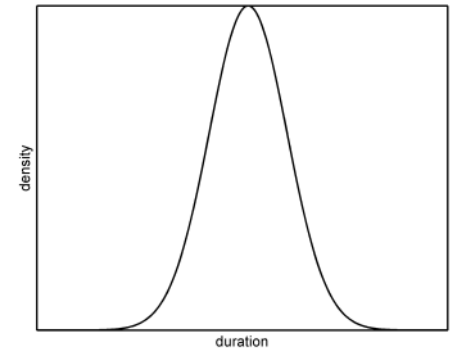
# Transmission between regions

- Force of infection depends on:
  - distance between region centroids
  - number of cattle and sheep farms
  - seasonal vector activity
- Cattle and sheep holdings assumed to be equally infectious/susceptible
- Different kernels considered:
  - fat-tailed, Gaussian, exponential
  - density-dependent vs -independent



# Duration of transmission period

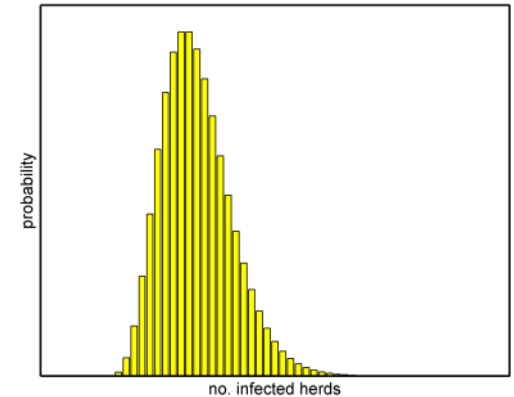
- This is the period during which SBV circulates within a region
- It was assumed to follow a (truncated) Normal distribution
- Mean depends on region demography:
  - no dependency (i.e. constant)
  - log no. animals
  - log no. farms
  - log mean farm size



# Within-region transmission

- Number of infected cattle and sheep farms assumed to follow a Poisson distribution
- Expected number of infected farms (e.g. cattle):

$$\mu_C = \text{force of infection} \times \\ \text{no. cattle farms} \times \\ \text{seasonal vector activity}$$



# Parameter estimation

- Bayesian methods used to estimate parameters for each component of the model:
  - facilitates incorporating uncertainty in model predictions
  - adaptive Metropolis algorithm with non-informative priors
- Compare different models
  - only present results for best-fit model
- Assess impact of underascertainment
  - requires additional data (e.g. serological surveys)

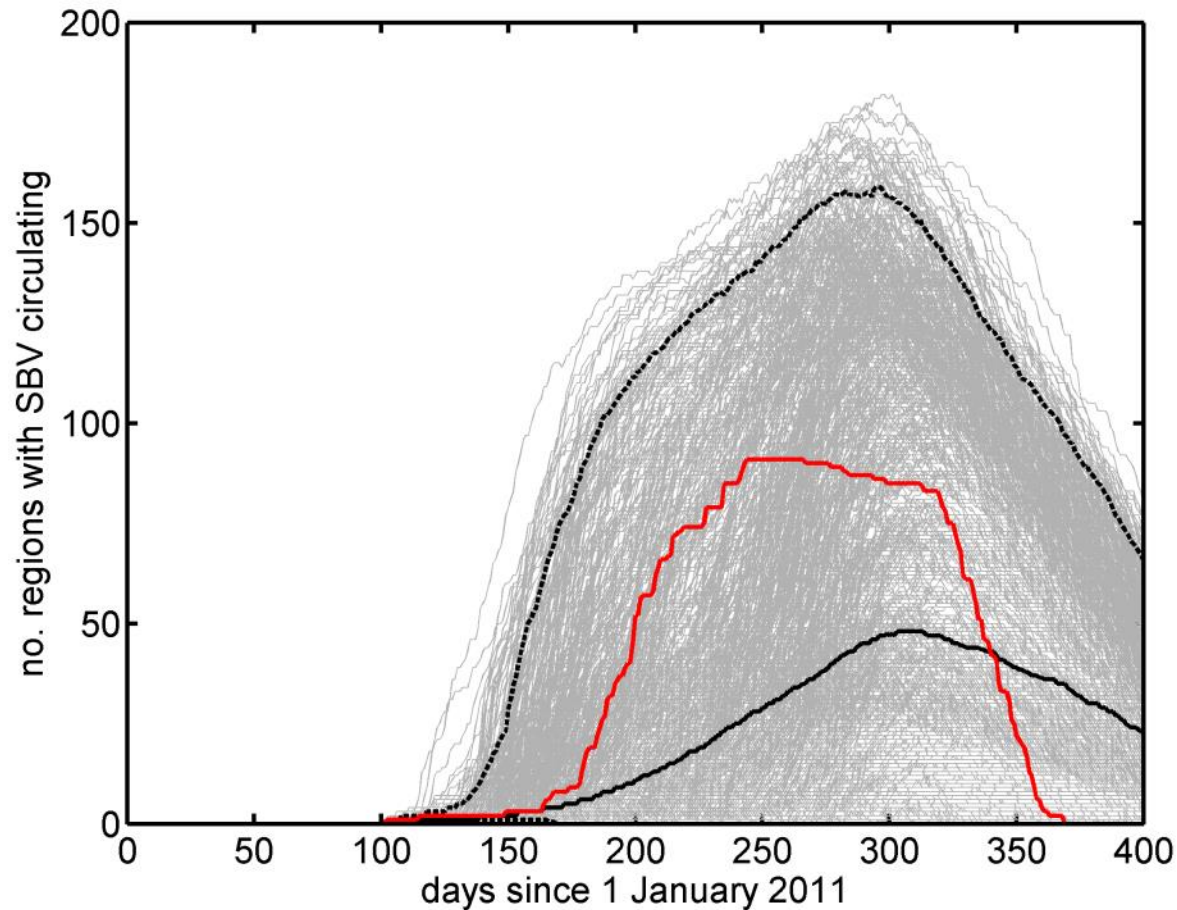


## **Part III**

Geographical spread in 2011 and scenarios for 2012

# Time-course for 2011

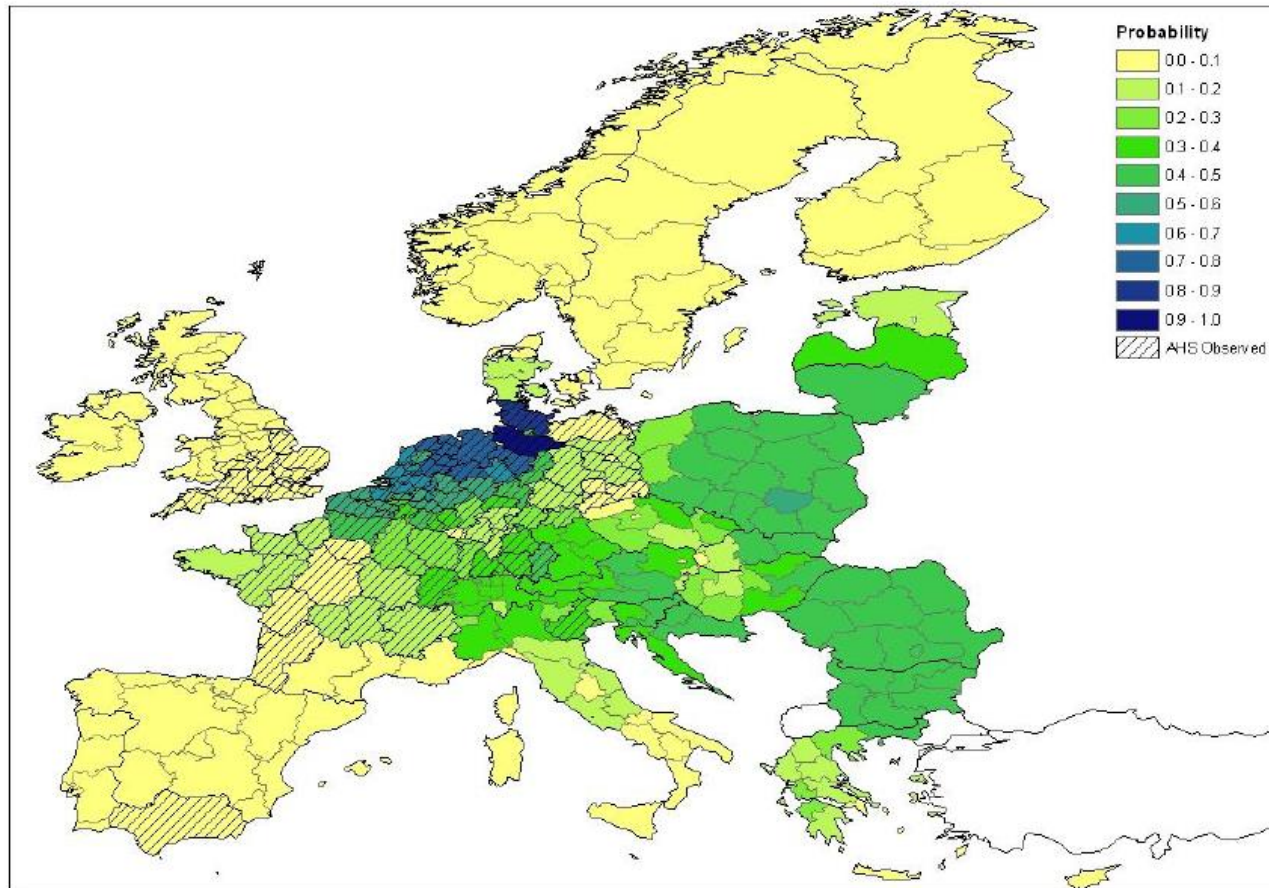
- Fat-tailed density-dependent kernel





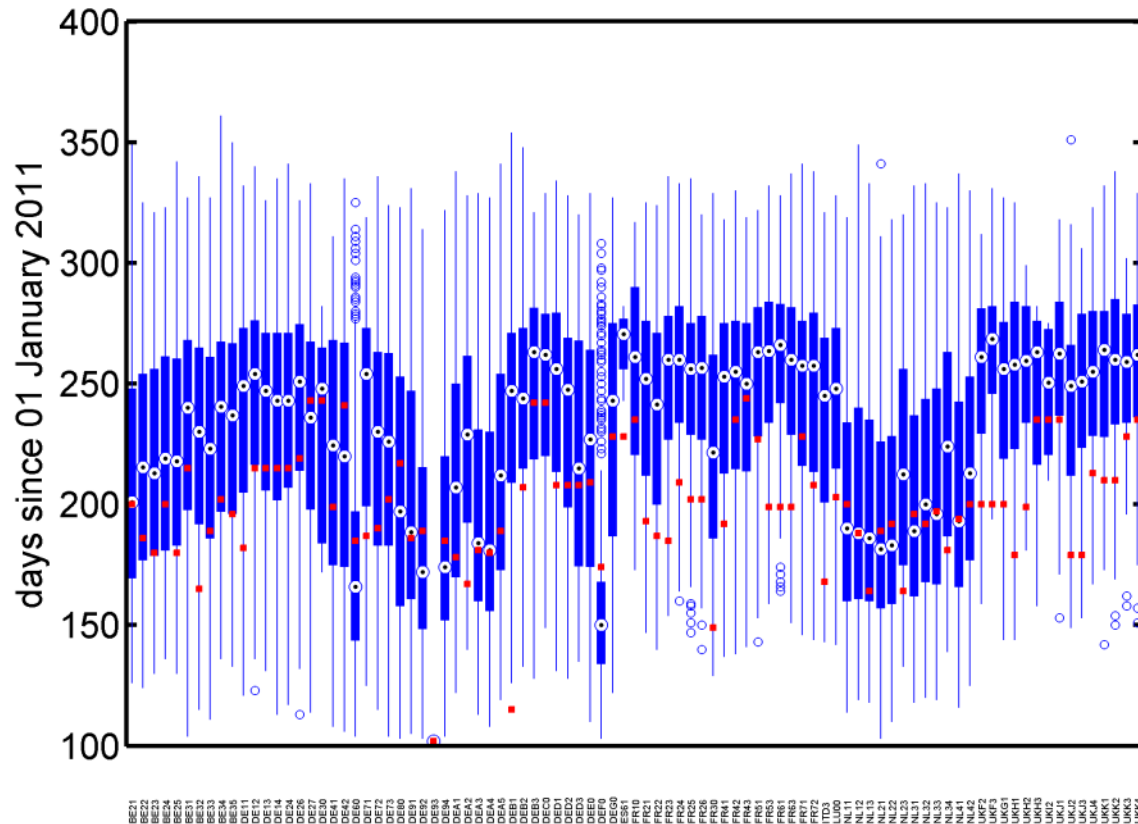
# Geographical spread in 2011

- Fat-tailed density-dependent kernel



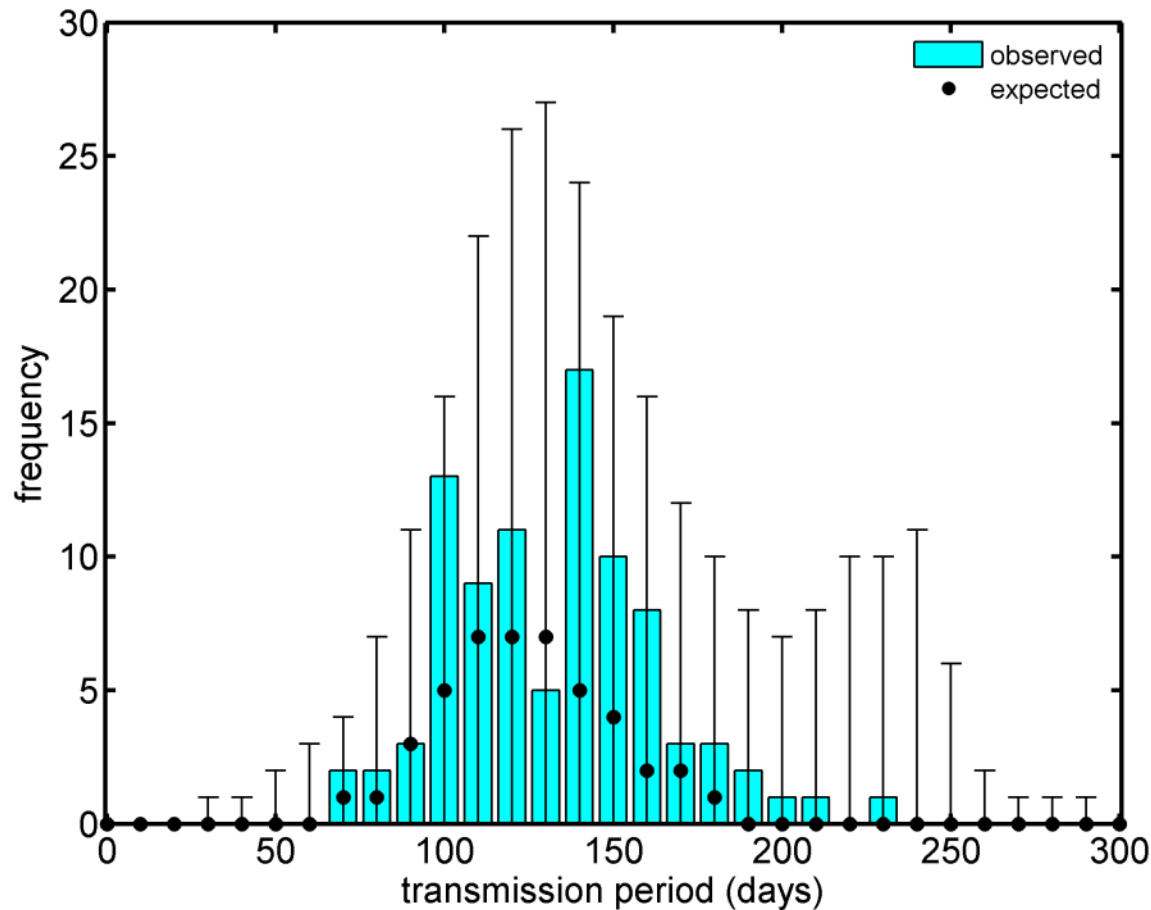
# Timing of infection in 2011

- Fat-tailed density-dependent kernel



# Duration of transmission period

- Mean depends on log no. animals



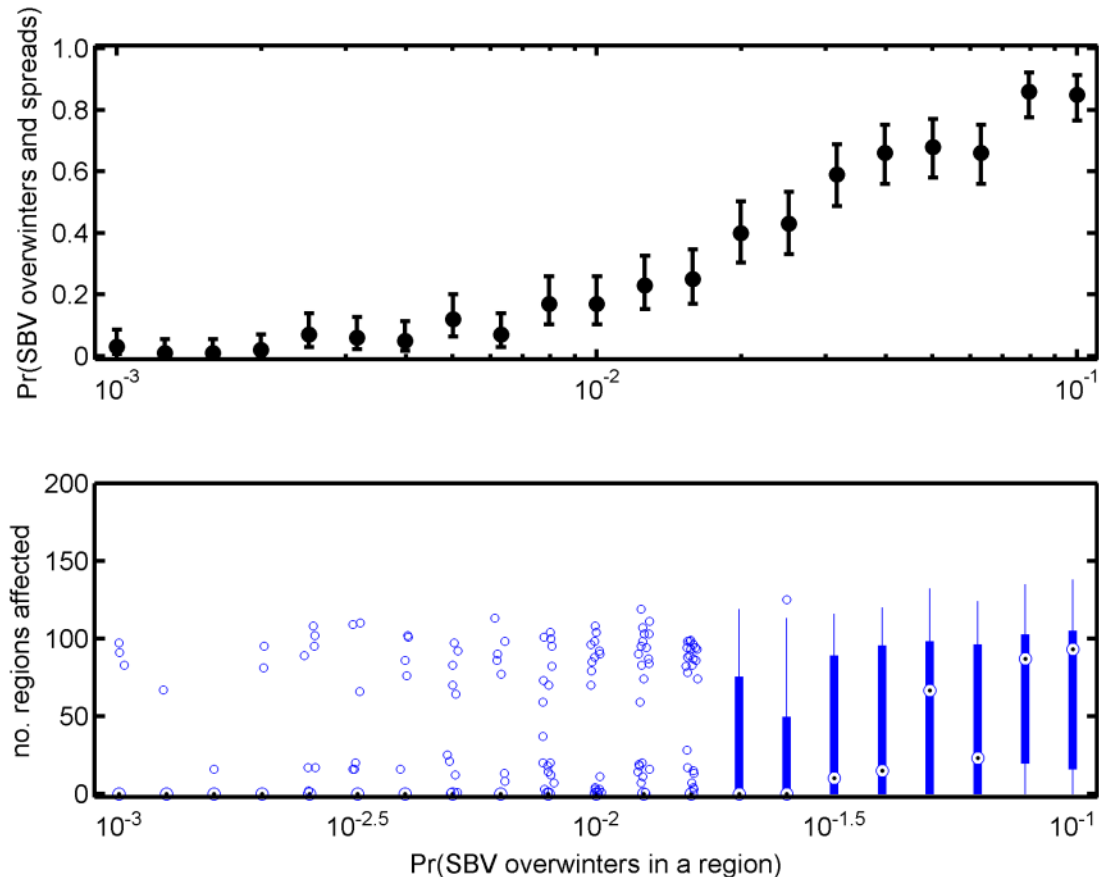
# Scenarios for SBV in 2012

## Model assumptions

1. Regions infected during 2011 have experienced a complete outbreak (i.e. no additional spread)
2. However, they act as a source of infection for seeding outbreaks in 2012, with a given probability of overwintering
3. If SBV overwinters in a region, it remains a risk until the end of June

# Scenarios: overwintering

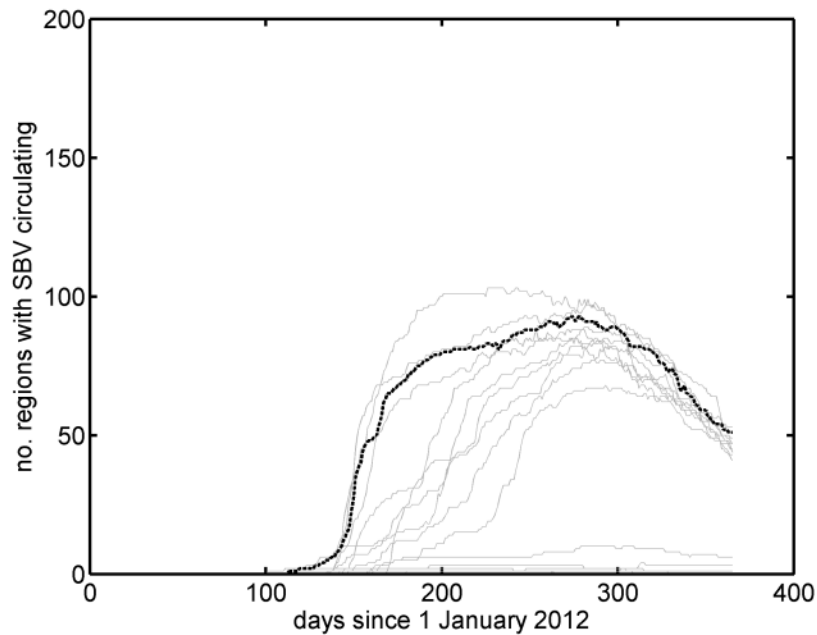
- Outcome in 2012 depends critically on probability of overwintering



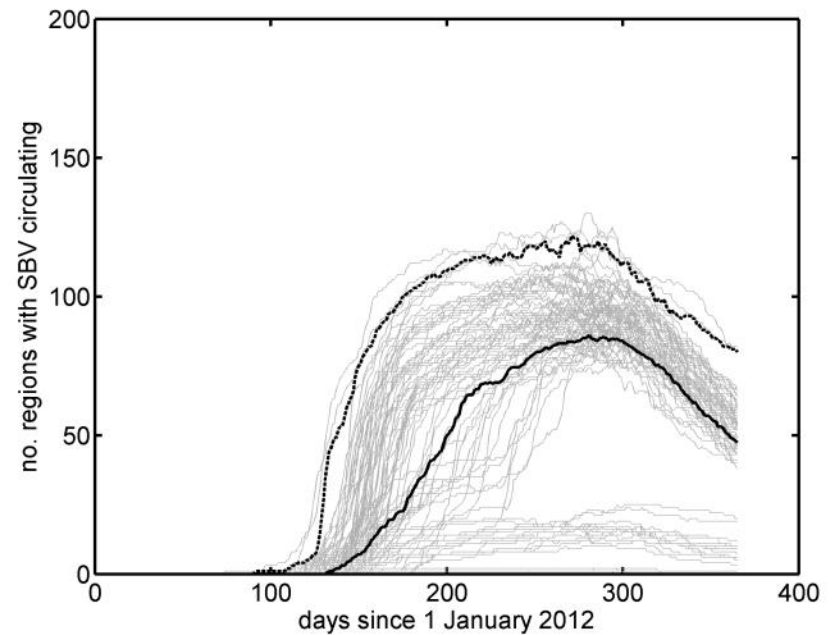
# Scenarios: time-course

- Predicted time-course in 2012

Pr(overwintering in region)=0.01



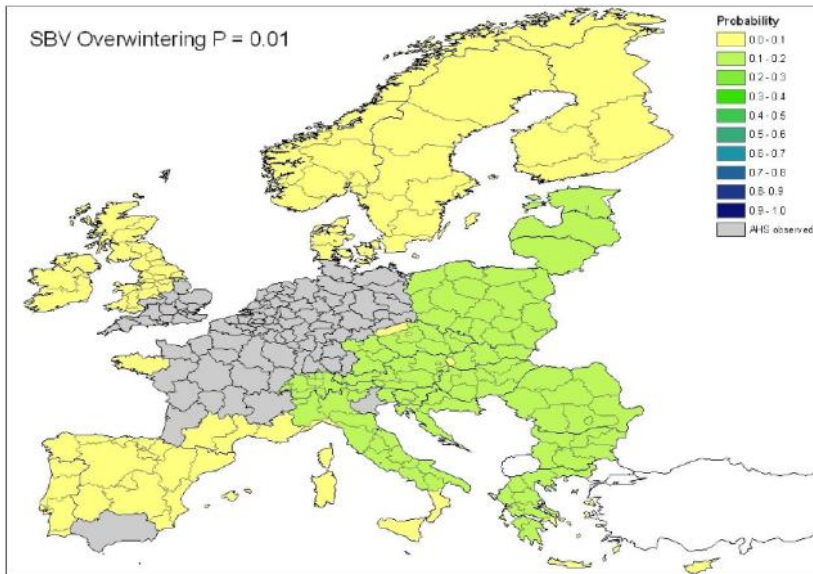
Pr(overwintering in region)=0.1



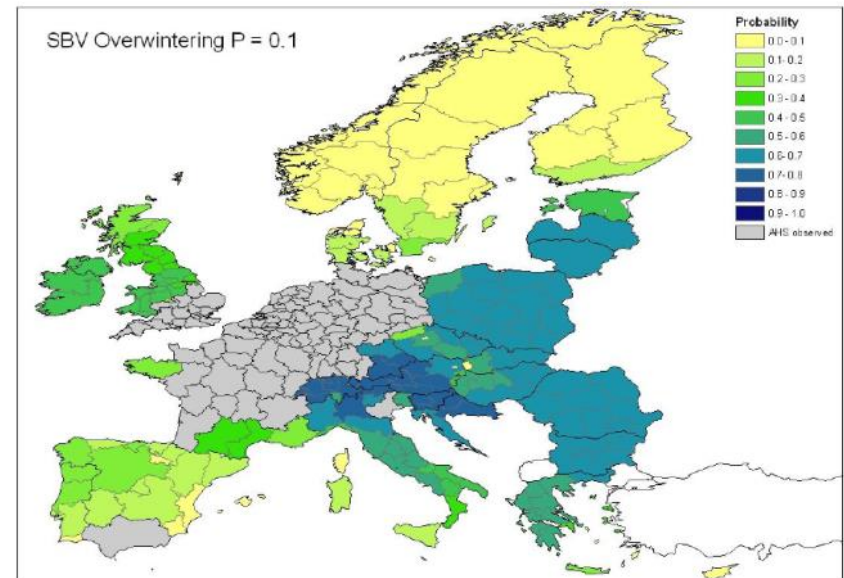
# Scenarios: geographic spread

- Predicted geographic spread in 2012

Pr(overwintering in region)=0.01



Pr(overwintering in region)=0.1



# Scenarios: conclusions

If SBV overwinters, the model predicts:

- it is likely to re-emerge between mid-April and the end of May in 2012
- the outbreak is likely to be of a similar size to the one occurred in 2011, though in regions previously unaffected



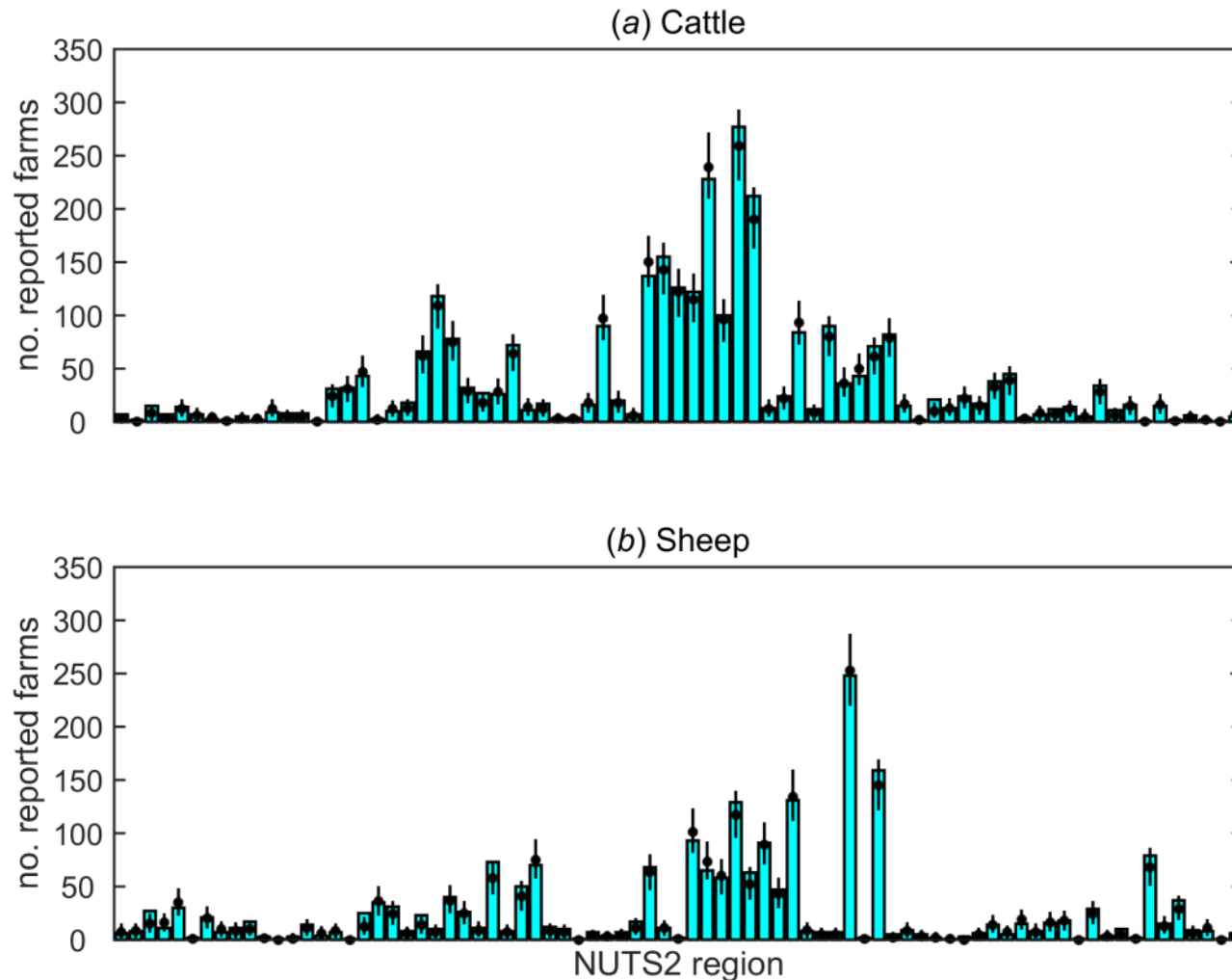




# Part IV

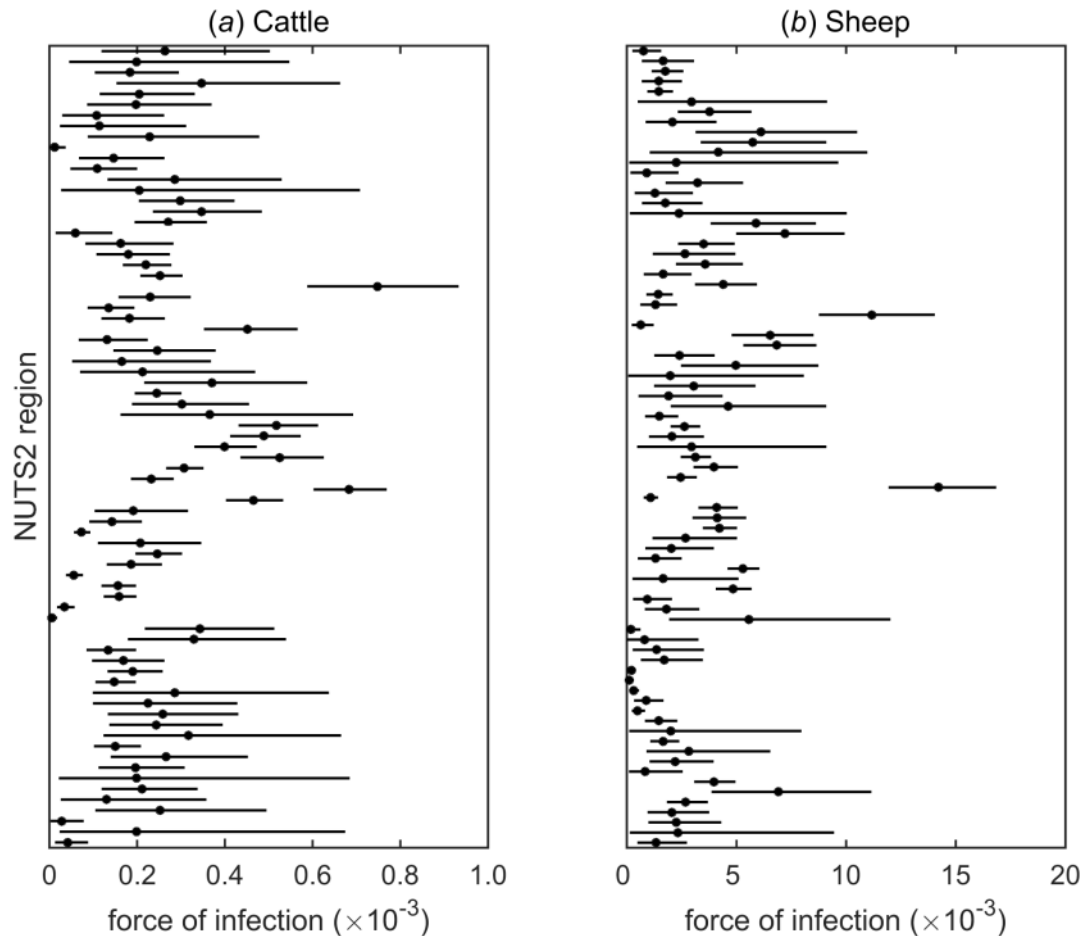
## Within-region transmission

# Affected farms in a region



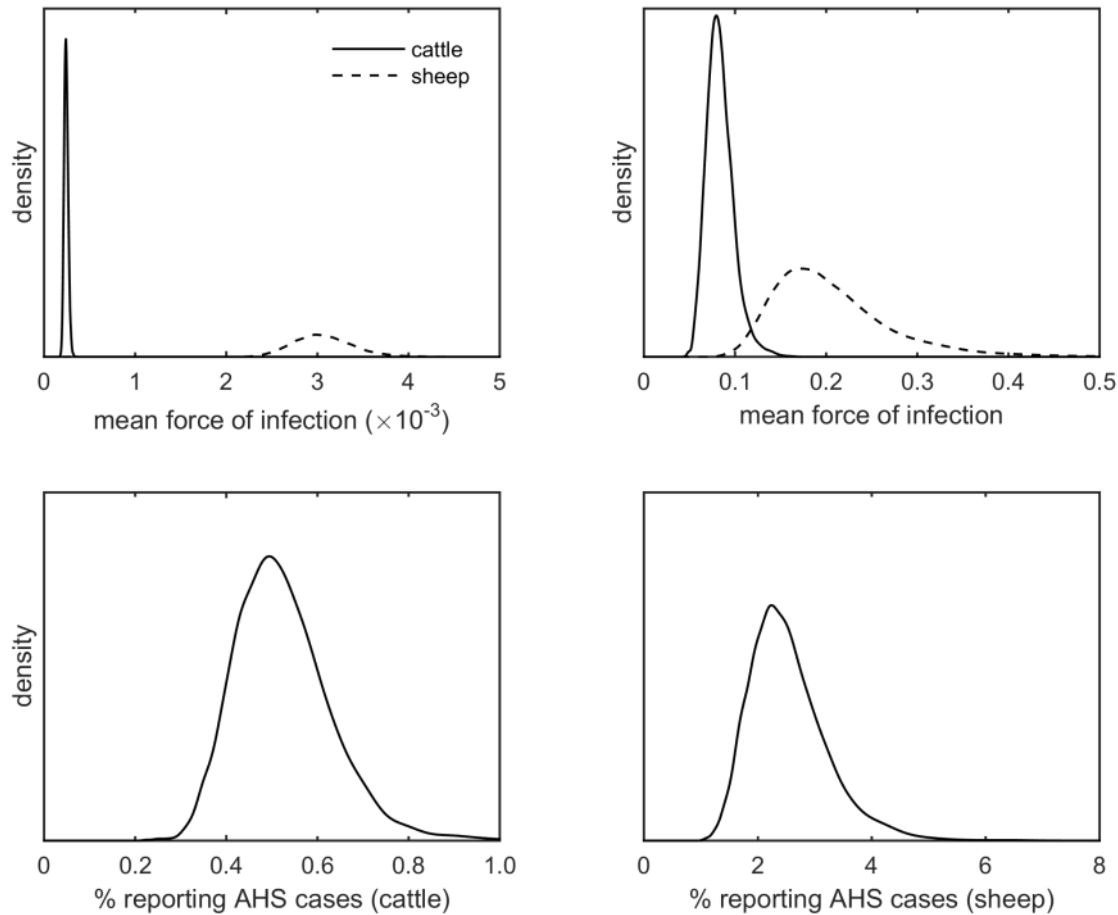
# Within-region force of infection

- Regional heterogeneity in transmission



# Impact of underascertainment

- Using sero-survey data for Belgium and The Netherlands



# Acknowledgements

## EFSA SBV working groups

Thomas Balenghien

Rene Bødker

Anette Bøtner

Aline de Koeijer

Anthony Wilson

Matthew Baylis

Brigitte Cay

Richard Elliot

Antoine Poskin

Claire Ponsart

Stefan Zientara

## EFSA

José Cortinas Abrahantes

Ana Afonso

Angeliki Vlachou

Frank Berthe

Anna Zuliani

Katriina Willgert

Jane Richardson

Eugen Christoph

Didier Verloo

Andrea Bau



The Pirbright campus is being redeveloped