Modelling the continental-scale spread of Schmallenberg virus in Europe

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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
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

(a) Cattle

(b) Sheep
Within-region force of infection

- Regional heterogeneity in transmission

(a) Cattle

(b) Sheep

NUTS2 region

force of infection ($\times 10^{-3}$)

force of infection ($\times 10^{-3}$)
Impact of underascertainment

- Using sero-survey data for Belgium and The Netherlands
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The Pirbright campus is being redeveloped.