A dynamic spatio-temporal model to investigate the effect of movements of animals on the spreading of Bluetongue BTV-8 in Belgium

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Abstract: When Bluetongue Virus Serotype 8 (BTV-8) was first detected in Northern Europe in 2006, several guidelines were immediately put into place with the goal to protect farms and stop the spreading of the disease. This however did not prevent further rapid spread of BTV-8 across Northern Europe, which has resulted to substantial economic losses, particularly in the sheep and cattle industry (Wilson and Mellor, 2009).

A better understanding of the BTV-8 transmission is needed to be able to define appropriate control guidelines. Using information on the 2006 Bluetongue outbreak in cattle farms in Belgium, a spatio-temporal transmission model was formulated, similar to the model proposed by Hooten et al (2010) for Influenza in North America. The model quantifies the local transmission of the disease between farms within a municipality, the short-distance transmission between farms across neighboring municipalities and the long-distance transmission as a result of the movement of animals. Different municipal-level covariates (i.e. farm density, land composition variables, temperature and precipitation) were assessed as possibly influencing each component of the transmission process.

The model allows to predict the dynamic spreading of the disease for different scenarios. This is especially useful in investigating the impact of movement (or lack of movement) of animals between farms in the transmission of bluetongue.

Keywords: Bluetongue, Movement, Spatio-temporal model, Dynamic model

1 Introduction

The livestock and poultry industry have been battling for decades the emergence and recurrence of various infectious animal diseases. Bluetongue (BT), which is a non-contagious, insect-borne infectious disease of ruminants, has become one of the most important diseases of livestock especially in Europe where a series of incursions took place, largely under the influence of climate change (Szmaragd et al, 2009).

When BTV-8 was first detected in the Netherlands and subsequently in Belgium, Luxemburg, Germany and France in 2006, several guidelines were immediately put into place: a 150 km surveillance zone was established around the first reported cases and a 20 km standstill zone was set up around the infected farms, within which, all ruminants must be kept inside at night, all movement of live animals on or off farms is prohibited, and the use of insecticide is compulsory in an effort to eradicate the *Culicoides* mites that carry the disease. In the protection and surveillance zones, strict controls must be carried out on all live animals and movement of live ruminants in or out of the zones is banned. This however did not prevent further rapid spread of BTV-8 across Northern Europe, which has resulted to substantial economic losses, particularly in the sheep and cattle industry (Wilson and Mellor, 2009).

To better understand the BTV-8 transmission, information on the 2006 Bluetongue outbreak in Belgium was used. A spatio-temporal transmission model was proposed to quantify the local transmission of the disease between farms within a municipality, the transmission between farms across neighbouring municipalities and transmission as a result of the movement/transport of animals. The model then allows to predict the dynamic spreading of the disease for different scenarios.

2 Materials and Methods

2.1 Data

The 2006 Bluetongue outbreak information for Belgium used in this study was extracted from the data collected by BT-DYNVECT for the bluetongue occurences in the Northern Europe region. Figure 1 details the observed spatial and temporal trend of the BT outbreak in Belgium where the number of infected farms (farms with at least 1 reported case of infected animal) per municipality were counted. Out of the 40,141 farms in Belgium (spread across 576 municipalities), a total of 582 cases of infected farms were observed coming from 205 different municipalities.

Different covariates deemed as influential for the spread of BT were also investigated, namely:

- Farm Density per municipality (number of farms/sq.km.) and land area
- Land Usage Variables: *Compostional proportion of Pasture, Forest, and Urban areas relative to the Crop area*
- Average Weekly Temperature and Precipitation
- Animal transportation information

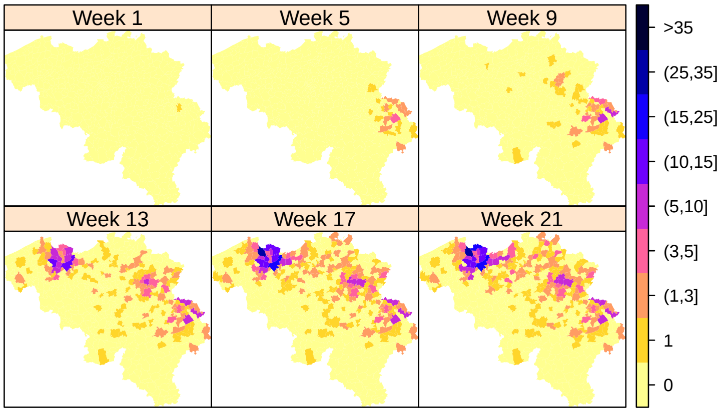

FIGURE 1. *Spatial trend of number of newly infected farms in Belgium for 2006. Week 1 refers to July 16-22, 2006.*

2.2 Infection Model

We model the infectious status of the farm and assumed that once a farm become infected, it is infectious until the winter period. Each farm was classified into either susceptible (no animals infected with BTV-8), infected or infectious class (at least one reported case of infected animal). The SI model for BT is a closed population model, where for a given time t at municipality i, the number of susceptible farms $S_{i,t}$ plus the number of infectious/infected farms $I_{i,t}$ sums up to the total number of farms for each municipality i, N_i. Thus, $S_{i,t} + I_{i,t} = N_i$. The susceptible component could then be rewritten as the difference of the total number of farms and the number of infectious cases, while the number of infectious farms at time point t, is just the sum of the total number of newly infected farms (Y) until time point t and is given by:

$$S_{i,t} = N_i - I_{i,t} \tag{1}$$

$$I_{i,t} = \sum_{k=1}^{t} Y_{i,k} \tag{2}$$

This number of newly infected farms can then be modeled as a binomial random variable which depends on the number of susceptible farms at the previous time point $(S_{i,t-1})$ and a parameter $\theta_{i,t}$. Thus, $Y_{i,t} \sim bin(\theta_{i,t}, S_{i,t-1})$

and

$$logit(\theta_{i,t}) = \begin{cases} (\beta_1 + \mathbf{X}\boldsymbol{\beta}_{int}) + between + move & \text{if } I_{i,t-1} = 0 \\ & \\ (\beta_2 + \mathbf{X}\boldsymbol{\beta}_{int}) + within + between + move & \text{if } I_{i,t-1} > 0 \end{cases} \tag{3}$$

The parameter $\theta_{i,t}$ was formulated as a function of the previous infectious population and is composed of at most four additive terms representing the different transmission scenarios, similar to the method by Hooten et al (2010):

1. The first component of the model ($(\beta_1 + \mathbf{X}\boldsymbol{\beta}_{int})$ and $(\beta_2 + \mathbf{X}\boldsymbol{\beta}_{int})$) gives the background transmission which represents the general risk of infection per municipality. The risk changes depending on whether or not the municipality had an infection at the previous time point.

2. The local or within municipality transmission of BT is given by:

$$within = (\mathbf{X}_W \boldsymbol{\beta}_W)\, I_{i,t-1} \tag{4}$$

3. Between municipality transmission represents the effect of the infectious state of neighbouring municipalities at previous time point ($I_{j,t-1}$), together with some municipal-level covariates. The binary weight $b_{i,j}$, represents the contiguity of municipalities i and j.

$$between = \mathbf{X}_B \boldsymbol{\beta}_B \sum_{j=1}^{N} b_{i,j} \mathbf{I}\left(I_{j,t-1} > 0\right) \tag{5}$$

   where $\mathbf{I}(\cdot)$ is the indicator function.

4. Transmission through animal transport, where the movement of animals from municipality j to municipality i is quantified through $a_{i,j}$, along with the infection status of municipality j where the movement originated ($I_{j,t-1}$) is given by:

$$move = \mathbf{X}_A \boldsymbol{\beta}_A \sum_{j=1}^{N} a_{i,j} \mathbf{I}\left(I_{j,t-1} > 0\right) \tag{6}$$

When $I_{j,t-1} > 0$, random effects can be included in each of the terms to account for extra heterogeneity in the data.

3 Results

Results from model fitting revealed that all investigated covariates where found to influence (on varying degree) the transmission risk. Temperature and precipitation, most especially affected significantly the risk of BT transmission within and between muncipalities. This result was not surprising since other authors (i.e. Purse et al, 2004 and Szmaragd et al, 2009) have already reported these findings. Proportion of pasture, forest, and urban areas relative to the crop are was also found to significantly affect the transmission risk, although not so in the within transmission, but more in the between transmission.

Figures 2 and 3 give the deterministic and stochastic prediction results from the fitted model. To compute for the predicted weekly values, observed data from the previous week was used in the deterministic prediction model. In the case of the stochastic prediction, only data until the 7th week of outbreak was used (79 observed cases) and the model was then allowed to predict the rest of the outbreak period. A total of 1000 simulations was done (depicted in gray lines in plots b and c in Figure 2), with the median stochastic prediction given by the black line. The model managed to capture farely well both the temporal and spatial trend of the infection, with most observed points falling within the 90% bootstrap interval as given in Figure 2.

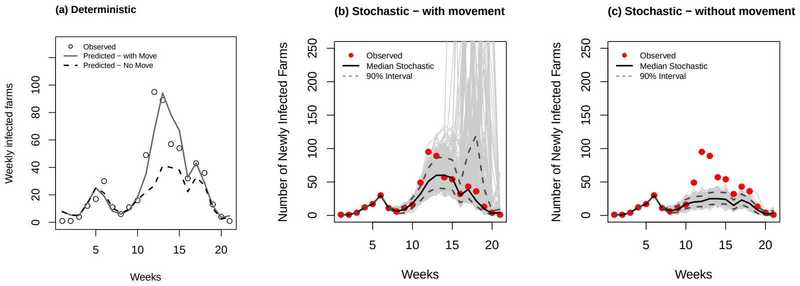

FIGURE 2. *Deterministic and Stochastic weekly number of infected farms with and without animal movements (gray lines are the predictions from 1000 stochastic simulations).*

To investigate the impact of movement of animals in the transmission of bluetongue, Figures 2 and 3 also shows the deterministic and stochastic prediction from the model with movement set to 0. For the stochastic prediction, only data until 7 weeks of the outbreak was used and thus, movement restriction was assumed to start from week 8. We can see in the temporal plots the reduction of the number of newly infected cases, and hence reduction in the number of cumulative infections per municipality when there is movement restriction. Maps of the spread of BT with and without animal movements from week 8 shows fewer cases of predicted BT infection especially in the East and West Flanders region where a high number of

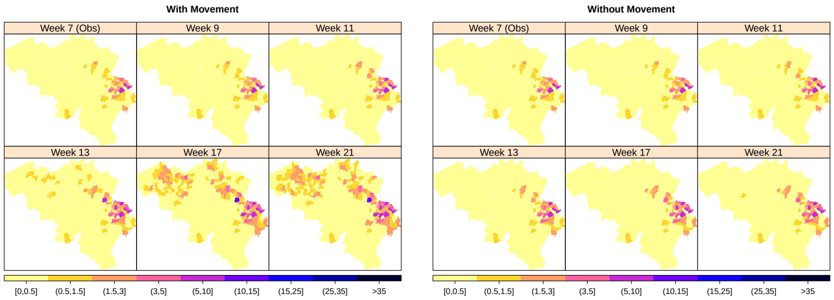

FIGURE 3. *Median stochastic prediction of the spatial trend of the cumulative number of infected farms with and without animal movements.*

incoming movements took place. This reduction in the predicted number of cases then suggests that animal movements had a significant impact in the spread of BT.

4 Conclusion

The dynamic model developed for the 2006 BT outbreak in Belgium managed to capture the spatial and temporal trend of the infection. By subdividing the model into the different transmission sources, it was shown that the transport of animals played a significant role in the spreading of the disease.

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