

Bayesian modelling with applications to sheep pox epidemic data

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Features of epidemic data

- Spatio-temporal nature.
- Environmental noise.
- Multicollinearity issues.
- Presence of excess zeros.

Motivating example

- Sheep pox is a highly contagious viral infection of sheep that can have devastating consequences.
- Major sheep pox epidemic in Evros Prefecture, northeastern Greece during 1994-98.
- Included 35,440 dead animals and 250 infected farms.

Bayesian regression modelling

- We adopt the Bayesian paradigm for modelling the weekly frequencies of disease occurrence incorporating various factors such as spatial information, environmental covariates and autoregressive (O-U type) processes.
- We ameliorate the existing methodologies by improving accuracy of predictions through the incorporation of spatial information, implementing suitable zero-inflated distributions, dealing with correlated data and introducing an epidemic interpretation via a branching process approximation.

Let Y_{ij} be the number of occurrences for the i th year and the j th week ($i=0,1,2,3,4$; $j=0,1,\dots,52$). Poisson and ZIP models are special cases of:

$$Y_{ij} \sim g(y_{ij} | \theta_{ij}; p_{ij})$$

$$g(y_{ij} | \theta_{ij}; p_{ij}) = p_{ij} I_{\{y_{ij}=0\}} + (1 - p_{ij}) f(y_{ij} | \theta_{ij})$$

$$\theta_{ij} = h(\mu_{ij}) = \log(\mu_{ij})$$

$$\log(\mu_{ij}) = \mathbf{X}_{ij} \Theta^* + \beta + b_i + U_{ij} + \theta_\tau * y_{i(j-1)} + K(\Theta, \kappa)$$

where $\Theta = (\Theta_\beta, \Theta_\tau, \Theta_\kappa)^T$ comprises of fixed-effects parameters β , AR(1) parameter associated with number of cases in previous week (θ_τ) and parameters of transmission kernel functions, b_i yearly random effects and U_{ij} an O-U process adjusting for serial correlation.

Epidemic control

- We connect the Poisson component of our model to a suitable branching process.
- Using this representation we obtain the probability of epidemic extinction by solving $\exp(q\lambda) = q \exp(\lambda)$
- For ZIP model: $prob(\text{extinction}) = 1 \wedge (q(\lambda_{ij}) + p_{ij})$
- We decompose the average rate of infection to its endemic and epidemic components:

$$\lambda = \lambda_{endemic} \cdot \lambda_{epidemic} = \exp(\Theta_{endemic} + \Theta_{epidemic})$$

Results

Major findings:

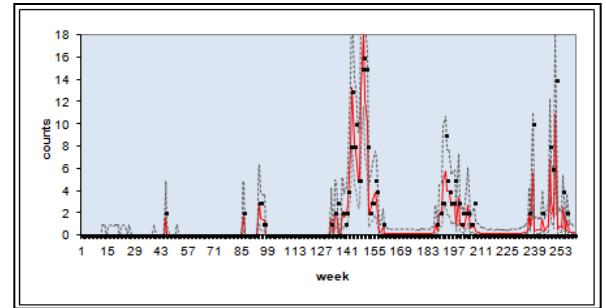
- Temperature levels had the strongest influence on disease spread
- Epidemic spread is also sensitive to distance between infected herds.

	temperature			distance
	min	average	max	
min	q=0.78	q=0	q=1	q=0.61
median	q=0.66	q=0.66	q=0.66	q=0.66
max	q=0.41	q=1	q=0	q=0.66

Table 1: Estimated average extinction probabilities (q) for different covariate combinations

	min	median	max
$\lambda_{endemic}$	0.17	2.84	121.6
$\lambda_{epidemic}$	1.27	1.005	3.19

Table 2: Endemic/epidemic decomposition of λ



Predicted vs observed counts based on the fit of the best (ZIP-type) model

Discussion

We have proposed a unified approach for effectively dealing with frequent problems of epidemic data. Our modelling framework extends similar approaches (Choi *et al.*, 2012; Branscum *et al.*, 2008) in various ways:

- Incorporation of spatial information.
- Adopt g-prior-based approaches for coping with multicollinearity problems between covariates, especially those of environmental and/or meteorological data nature.
- Use of suitable distributions for modelling excess zeros datasets, particularly the zero-inflated Poisson (ZIP) distribution.
- Combine branching process theory with Bayesian regression models to identify epidemic potential.

Future directions

- Model selection has been solely based on standard (deviance-based) predictive approaches. The temporal nature of this type of data suggests a sequential approach.
- Explore continuous (DeWijts type) spatio-temporal models