Risk assessment from small scale and early phase epidemics

Kokouvi M. Gamado1, Glenn Marion1 and Thibaud Porphyre2

Biomathematics and Statistics Scotland, Edinburgh, UK 1
The Roslin Institute, University of Edinburgh, Edinburgh, UK2

Background

- Emerging and re-emerging pathogens usually lead to small scale epidemics
- Analysis of historical outbreaks informs control of future outbreaks
- Risk assessment is crucial to inform policy on potential new incursions

Aim

- Infer historic outbreak characteristics from just observed cases (and small)
- Predict future evolution of ongoing outbreaks from its early phase
- Use data from small historic and ongoing outbreaks to select between models

Modelling framework

- An individual location, eg a farm, makes an infectious contact with a susceptible individual at rate \( \beta_j \) assumed to be

\[ \beta_j = \beta_0 h_j, \]

\( \beta_0 \) being the contact rate. \( \beta_j \) is known as a spatial kernel transmission function and 4 forms widely used in the disease modelling literature are considered:

- \( K_1: h_j = \exp\left(-\tau d_j \right) \)
- \( K_2: h_j = \left(1 + \left( \frac{d_j}{\alpha} \right)^\gamma \right)^{-1} \)
- \( K_3: h_j = 1 - \exp\left(- \frac{d_j}{\alpha} \right)^{-1} \)

- Once infected the time to detection is assumed to follow a left-truncated gamma distribution:

\[ R_i - I_i \sim T(\alpha, \gamma, c), \]

- The likelihood of observing the detections \( R_i, I_i \) is

\[ L = \prod_{i=1}^{n} \sum_{j=1}^{K} \beta_j \exp\left( -S \right) \gamma^{\alpha_i} \exp\left( -\gamma \sum_{i=1}^{n} (R_i - I_i)^{-1} \right) \]

where \( S = \sum_{i=1}^{n} \sum_{j=1}^{K} \beta_j (R_i, I_i - I_i) \)

Inference

Bayesian inference

- The distribution of the model parameters and latent variables given the data is

\[ \pi(\theta, l|R) \propto L(R, l|\theta)\pi(\theta), \]

- Metropolis-Hastings within Gibbs algorithm
- Non-centered parameterisation for computational efficiency

Parameters and latent variables updated simultaneously and helps reduce autocorrelation

Model assessment and selection

- DIC = “goodness of fit” + “complexity”
- Problems: non invariance to reparameterisation, lack of consistency, weak theoretical justification with multiple definitions in the case of latent variables – 2 used
- Bayesian Latent residuals (LR): inferred from data, iid uniform r.v. if fitted model consistent with data generation process
- LR constructed to test different components of model

Assess performance for historic outbreaks: simulated data

- Coverage properties: true parameters are contained 95% in the CI
- Uncertainty of the estimates reduces as the epidemic size increases
- Evaluate the amount of data size needed for model selection
- Increasing epidemic size increases the accuracy of identifying the correct model with the LR

Classical Swine Fever in East Anglia Norfolk in 2000

- Data

\( N = 1703 \) farms with exact location or coordinates
- Times and location of 16 detected cases

- Inference and predictions

Kw with 95% CI

\[ K_1 = 429.301 156.682 27.78 \]
\[ K_2 = 517.229 157.021 10.672 \]
\[ K_3 = 352.761 156.055 32.832 \]
\[ K_4 = 411.096 157.703 19.477 \]

LR assessment correlates better with predicted risk

Inference during early phase of outbreak

- Predict future evolution of outbreak under various kernels
- Assess using ROC curve
- More observations imply better prediction

Summary

- Infer outbreak characteristics from small and ongoing outbreaks e.g. 16 CSF cases
- Novel model selection tools based on LR allow selection of models e.g. kernels
- LR approach leads to more reliable risk assessment

Reference


Acknowledgment

K.M.Gamado(kokouvi@bioss.ac.uk), G.Marion(glenn@bioss.ac.uk), T.Porphyre(T.Porphyre@ed.ac.uk)