

Nonparametric Bayesian Inference for Heterogeneously Mixing Epidemic Models

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Avian Influenza

Approach and Aims

From the outbreak of Avian Influenza, we observe the following data:

ID	Coordinates	Status	Culling Date
1	(5.32, 18.82)	Susceptible	NA
2	(2.90, 15.67)	Susceptible	NA
3	(2.86, 17.99)	Pre-Emptively Culled	3 rd May
4	(4.56, 18.01)	Culled	30 th April
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Using this data, we want to work out:

- If there is a spatial element to the spread of the disease?
- If so, how can we quantify this element?

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Homogeneous Mixing

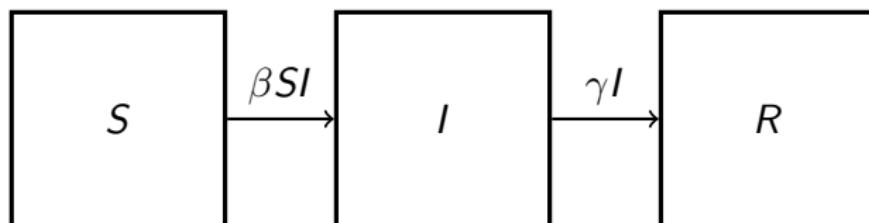


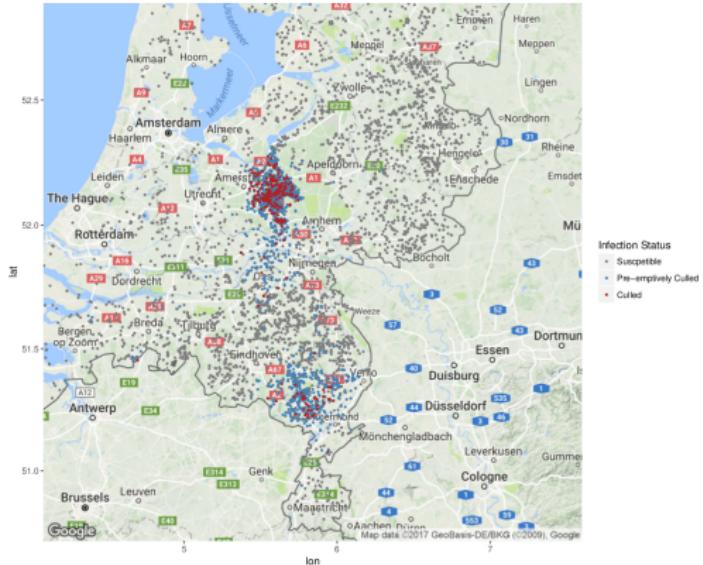
Figure: A homogeneously mixing SIR model.

Farms are either **Susceptible**, **Infected** or **Removed**.

- **Infections:** Infections occur according to a Poisson process with rate $\beta S_t I_t$.
- **Removals:** Individual j remains infectious for a time period drawn from an Exponential distribution, such that $r_j - i_j \sim \text{Exp}(\gamma)$.

Drawbacks of Homogeneous Mixing

- Suppose one farm is infected and m are susceptible.
- We generate the x , the number of infections, by sampling from a $\text{Poisson}(\beta m)$ distribution.
- We then choose x farms uniformly at random to be infected.



Heterogeneous Mixing

We need to include the distance between farms in the model. We compute the euclidean distance between each pair of farms farm i and j , $d_{i,j}$ and we make β a function of the distance.

$$\beta_{i,j} = f(d_{i,j})$$

Our heterogeneously mixing model builds on the homogeneously model, as we specify the infection and culling rates as follows:

- **Infections:** Infections occur according to an inhomogeneous Poisson process with a unique rate for each pair of farms, specified by $\beta_{i,j} = f(d_{i,j})$.
- **Removals:** Individual j remains infectious for a time period drawn from an Exponential distribution, such that $r_j - i_j \sim \text{Exp}(\gamma)$.

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Parametric Infection Rates

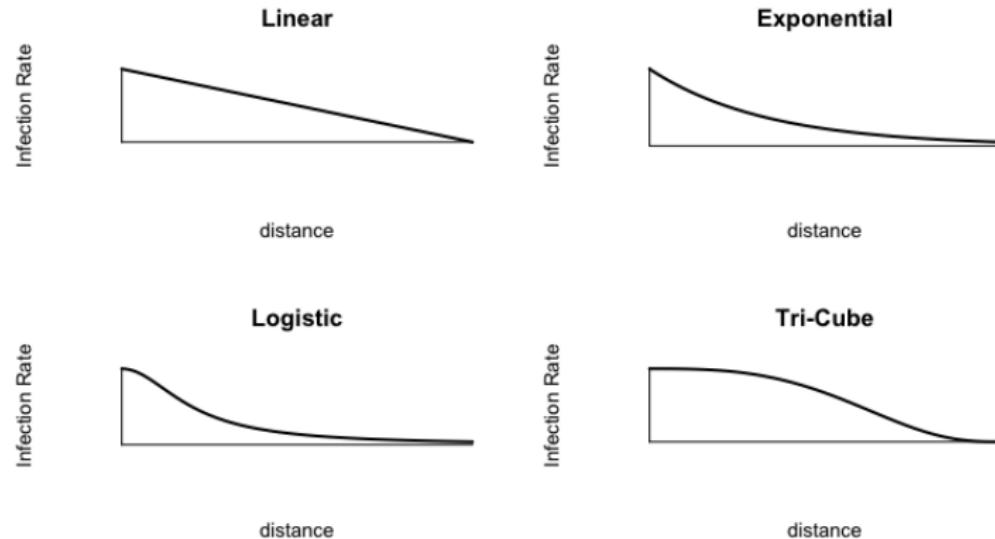


Figure: Four Possible Infection Rates.

Parametric Models for Avian Influenza

Parametric inference for this data set has already been carried out by Boender *et al.* (2007). They proposed five models and used AIC to choose the best of the proposed models.

Model	Infection Rate
1	$\beta_{i,j} = \beta_0$
2	$\beta_{i,j} = \frac{\beta_0}{1+d_{i,j}}$
3	$\beta_{i,j} = \frac{\beta_0}{1+d_{i,j}^2}$
4	$\beta_{i,j} = \frac{\beta_0}{1+d_{i,j}^\alpha}$
5	$\beta_{i,j} = \frac{\beta_0}{1+(d_{i,j}/\beta_1)^\alpha}$

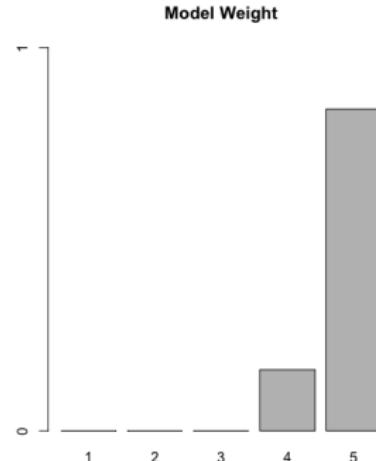


Figure: Model Weights for the different Infection Rates.

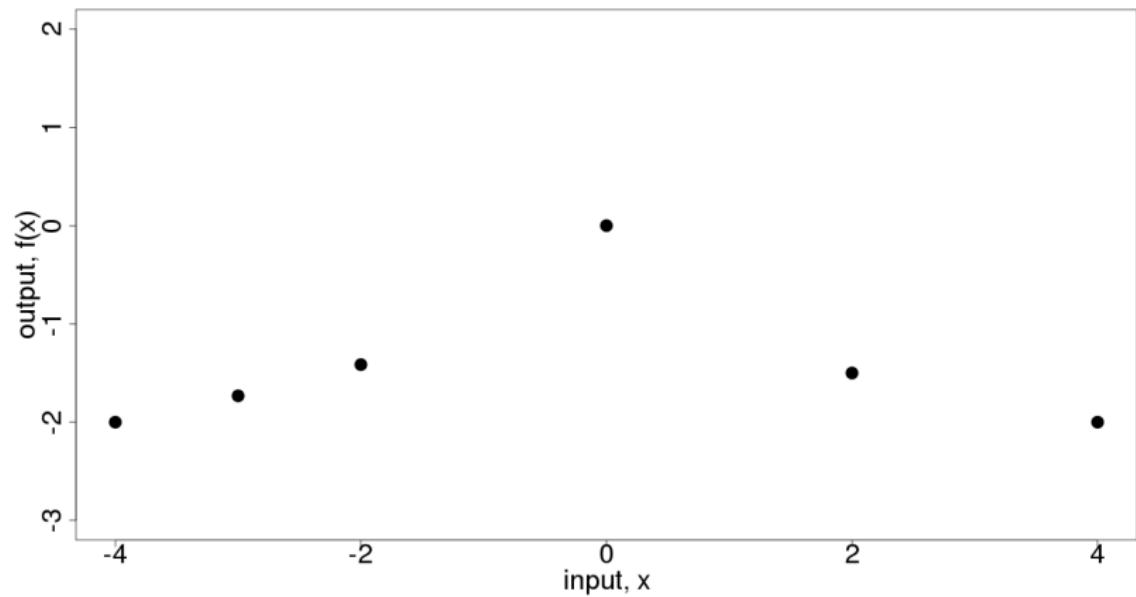
Inference for Nonparametric Models

Our nonparametric methodology use Gaussian Processes (GPs) to estimate $\beta_{i,j}$.

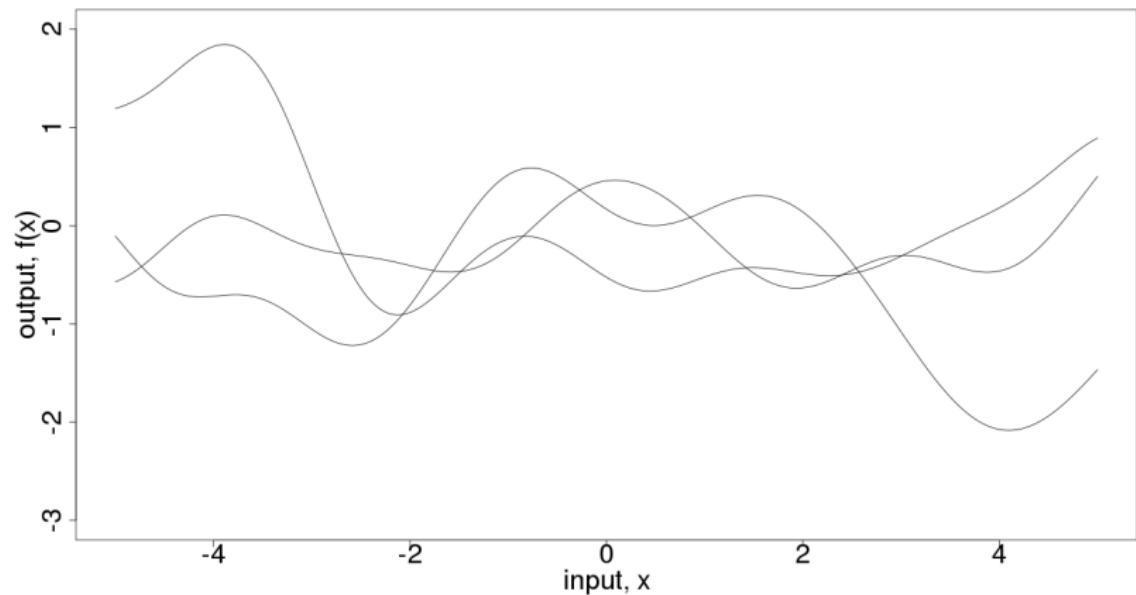
- GPs are a generalisation of the multivariate Gaussian distribution to a function space.
- We use GPs to assign a prior distribution over a function space.
- We need to control the signal variance and volatility.

$$f(\mathbf{x}) \sim \mathcal{GP}(\mathbf{0}, \Sigma)$$

Data



GP Prior Distribution



Posterior Distribution

Avian Influenza Likelihood

The augmented likelihood function for this model is given by

$$\pi(\mathbf{i}, \mathbf{r} | \boldsymbol{\beta}, \gamma) \propto \underbrace{\exp \left(- \sum_{j=1}^n \sum_{k=1}^N \beta_{j,k} ((r_j \wedge i_k) - (i_j \wedge i_k)) \right)}_{\text{Total Infectious Pressure}} \\ \times \underbrace{\prod_{\substack{j=1 \\ j \neq \kappa}}^n \left(\sum_{k \in \mathcal{Y}_j} \beta_{k,j} \right)}_{\text{Pressure infectives put on each susceptible}} \\ \times \underbrace{\prod_{j=1}^n f(r_j - i_j | \gamma)}_{\text{Infectious period distribution}} .$$

Avian Influenza Priors

We put a GP prior on the infection rate β , where the covariance matrix is based on the distances between the farms.

$$\log \beta \sim \mathcal{GP}(\mathbf{0}, \Sigma).$$

We put a vague Exponential prior on the infectious period distribution parameter.

$$\gamma \sim \text{Exp}(0.01).$$

We use MCMC to estimate β and γ , as well as estimating the day each farm was infected.

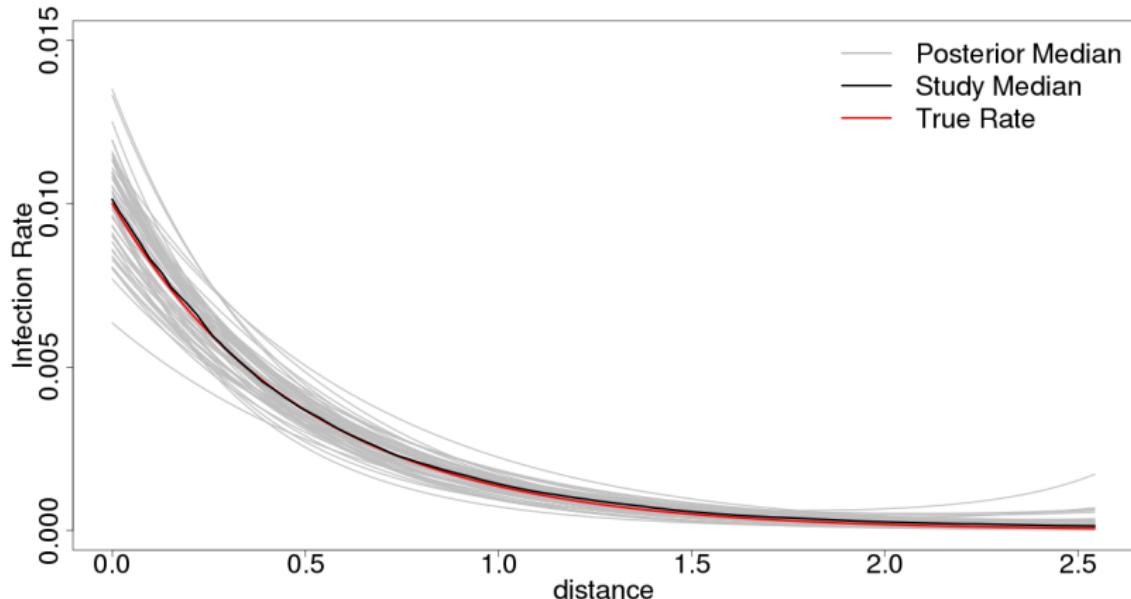
MCMC Algorithm

Algorithm 1 Structure of the MCMC algorithm

- 1: Initialise the chain with estimates $\gamma^{(0)}$, $\mathbf{f}^{(0)}$, $I^{(0)}$, and $\mathbf{i}^{(0)}$
Repeat the following steps
 - 2: Sample γ from the conditional distribution $\pi(\gamma|\lambda, \mathbf{i}, \mathbf{r}, \chi_\gamma)$ using a Gibbs sampler
 - 3: Sample \mathbf{f} using an underrelaxed proposal method for a Metropolis Hastings algorithm
 - 4: Sample I using a Metropolis Hastings algorithm
 - 5: Update \mathbf{i} , the vector of infection times
-

Simulation Study

We generated the positions of 1000 farms, and simulated 250 outbreaks with the same infection rate. Only using the positions and removal times, we estimated the infection rate.



Avian Influenza Results

We then applied the GP inference method to the Avian Influenza data set and compared our model to the parametric model.

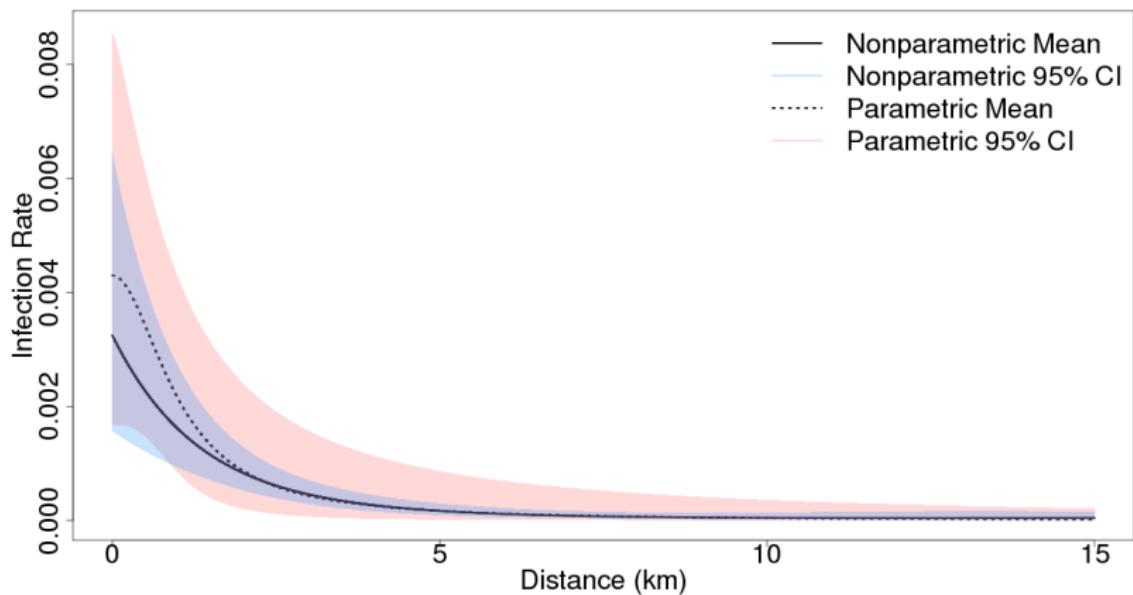


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Conclusion

Throughout this talk, we have shown that:

- We can model infection rates non-parametrically with GPs,
- We do not need to make restrictive assumptions about the parametric form of the infection rate,
- We can do this for large data sets without having to deal with large covariance matrices.

We can improve and build on this method by:

- Including more covariates, such as the number of animals on each farm,
- Extend this to include information about the type of animals on each farm.

References

- Boender, G. J., Hagenaars, T. J., Bouma, A., Nodelijk, G., Elbers, A. R. W., de Jong, M. C. C. and van Boven, M. (2007). Risk Maps for the Spread of Highly Pathogenic Avian Influenza in Poultry. *PLoS Computational Biology*, 3(4), pp. 704-712.
- Rasmussen, C. E. and Williams, C. K. I. (2006). *Gaussian Processes for Machine Learning*. USA: MIT Press.
- Xu, X., Kypraios, T. and O'Neill, P. D. (2016). Bayesian non-parametric inference for stochastic epidemic models using Gaussian Processes. *Biostatistics*, 17(4), pp. 619-633.
- Jewell, C. P., Kypraios, T., Christley, R. M. and Roberts, G. O. (2009). A novel approach to real-time risk prediction for emerging infectious diseases: A case study in Avian Influenza H5N1. *Preventive Veterinary Medicine*, 91(1), pp. 19-28.

Gaussian Processes Overview

- A Gaussian Process is a collection of random variables, any finite number of which have a joint Gaussian Distribution. (Rasmussen and Williams, 2007).
- We describe the log of the infection rate fully through the GP, this ensure the infection rate is always positive.

$$\log \beta_{i,j} \sim \mathcal{GP}(\mathbf{0}, \Sigma).$$

- We use the squared exponential covariance function to define the covariance matrix.

$$\Sigma = k(\mathbf{d}, \mathbf{d}'; \alpha, l) = \alpha^2 \exp \left(-\frac{(\mathbf{d} - \mathbf{d}')^2}{l^2} \right).$$

GPs and Epidemic Models

We put a GP prior on $\beta_{i,j}$ and use under-relaxed MCMC to give estimate this rate.

- 1 Propose new infection rate based on current one.

$$\log \beta'_{i,j} = \sqrt{1 + \delta^2} \log \beta_{i,j} + \delta \nu,$$

$$\nu \sim \mathcal{GP}(\mathbf{0}, \Sigma).$$

- 2 Evaluate likelihood of proposed infection rate.
- 3 Accept new rate based on probability of proposed against current rate being the true rate.

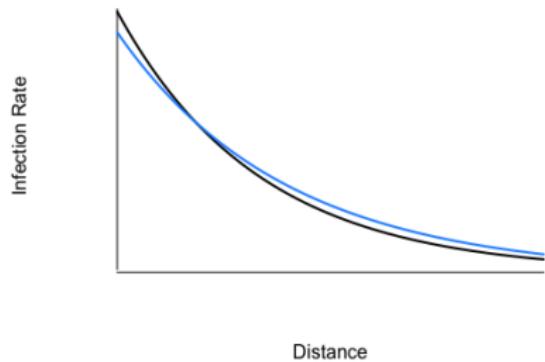


Figure: Current infection rate (black) and proposed rate (blue).