Indian Buffet Epidemics

Ashley Ford, Gareth Roberts

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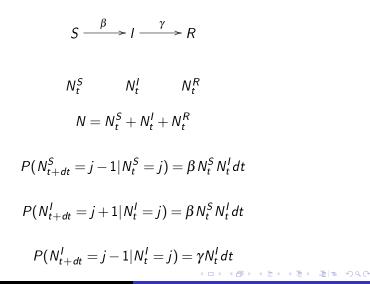
Outline





SIR Models

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SIR Models

- What data is available ?
 - Epidemic complete ?
 - Infection times ?
- MLE well known with full data
 - see Andersson and Britton (2000)
- Martingale estimator Becker and Hasofer (1997)
- MCMC estimates O'Neill and Roberts (1999)

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Indian Buffet Epidemics

- Need a model between homogeneous mixing and over complex models.
- Aim to fit the heterogeneity with two or three parameters that measure the departure from homogeneity.

Places and People

- Model heterogeneity in an epidemic amongst N people
- Each person belongs to 1 or more of many classes
 - e.g. households, schools, clubs, buses etcetera
- The classes are not specified
- A prior is put on class membership
 - represented as an $N \times K$ binary matrix Z
- An Indian Buffet Process

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Indian Buffet Process

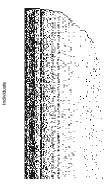
- Introduced by Griffiths and Ghahramani (2005)
- For each $k \; \psi_k$ is the probability that an individual is in class k
- $\psi_k \sim Beta(lpha/\kappa, 1)$ with lpha being the strength parameter of the IBP.
- The model for Z is: $z_{ik}|\psi_k \sim \textit{Bernoulli}(\psi_k)$ independently
- The process is obtained as $K \to \infty$

A culinary metaphor

- N customers enter a restaurant one after another.
- The *j*th customer selects each dish with probability m_k/j
 - where m_k is the number of previous customers who have chosen a dish.
- He then tries $Poisson(\alpha/j)$ new dishes.

MCMC Inference

Indian Buffet Process example



Classes

IBP Z generated with $N=260, K=260, \alpha=15$

315

Indian Buffet Epidemic

- The state of individual j is at time t is $x_{j,t} \in \{\mathsf{S},\mathsf{I},\mathsf{R}\}$.
- Given Z , infections are independent with transition rates given by
 - $P(x_{j,t+dt} = I | x_{j,t} = S, Z) = \sum z_{jk} \lambda_k N_{k,t}^I dt$
 - where $N'_{k,t}$ is the number that are in classs k and infective at time t and λ_k is the infection rate within group k.

•
$$N_{k,t}^{l} = \sum_{j} z_{jk} \mathbf{1}(x_{j,t} = l)$$

- A basic model has λ_k the same for all k.
- Intuitively it is reasonable to assume a greater per person infection rate in a small group such as a household

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$$\lambda_k = \lambda N_k^{-v}$$

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MCMC Inference

MCMC Inference

- Augmented data
- Parameterisation
- Proposal

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Summary

- A new model for epidemics incorporating heterogenity has been introduced.
- Initial steps towards inference taken.
- Planned developments
 - Develop MCMC algorithms
 - Apply to real data
- Questions

MCMC Inference

The parameters $\theta = (\lambda, \alpha, \gamma, \nu, K)$. The log liklihood when the epidemic is observed on $[0, T_{max}]$

$$\log f(T', T^{R}|z, \theta) = \sum \log \eta_{j}(T_{j}^{I}) - \int_{0}^{T_{\max}} \sum \eta_{j}(t) dt + \sum \log g(T_{j}^{R} - T_{j}^{I}) + \sum \log 1 - G(T_{\max} - T_{j}^{I})$$
(1)

where η_j is the instantaneous rate of infections on individual j g and G are the pdf and cdf of time to recovery

$$\eta_j(t) = \sum_k z_{jk} \lambda_k N_{k,t-}^J$$
⁽²⁾

$$\eta_j(t) = \lambda \sum_k z_{jk} N_{k,t-}^l / N_k^v$$
(3)

Random Walk Metropilis MCMC

Given complete data, i.e. observed infection and recovery times, the likelihood factorises so γ can be independently estimated. The steps in the algorithm are:

- ${\small \textcircled{0}} \hspace{0.1in} \lambda \sim \!\! \mathsf{MH} \hspace{0.1in} \mathsf{using} \hspace{0.1in} \mathsf{a} \hspace{0.1in} \mathsf{random} \hspace{0.1in} \mathsf{walk} \hspace{0.1in} \mathsf{with} \hspace{0.1in} \mathsf{Gaussian} \hspace{0.1in} \mathsf{steps}, \hspace{0.1in} \mathsf{folding} \hspace{0.1in} \mathsf{at} \hspace{0.1in} 0$
- 2 $lpha \sim$ MH using a random walk with Gaussian steps, folding at 0
- **3** $Z \sim MH$ on Z, proposal .
 - At each step K i.i.d. column flip probabilities ψ_k are sampled from a beta distribution with parameters K and 0.8/K.

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2 Within each column, each bit is flipped independently with probability ψ_k .

These parameters where chosen so that the expected number of flips is close to 1 but there is a small chance of a large number of flips. Appendix

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Diffusion Models

Defining
$$x_t = N_t^S / N$$
 and $y_t = N_t^I / N$ we can approximate the process
as an SDE
 $dx = -\beta xy dt + \sqrt{\beta xy / N} dB_1(t)$
 $dy = (\beta xy - \gamma y) dt - \sqrt{\beta xy / N} dB_1(t) + \sqrt{\gamma y / N} dB_2(t)$
where dB_{1} and dB_{2} are independent Brownian motions.

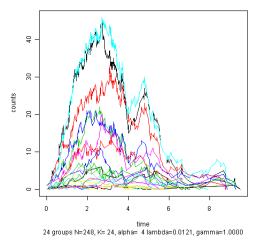
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Infectives in each group

Indian Buffet Epidemic Groups IBp75eg2



Martingale estimation

A significant result is that of Becker and Hasofer (1997) An epidemic process has two obvious martingales

$$dM_1(t) = dN_t^S + \beta N_t^S N_t^I$$
(4)

$$dM_2(t) = dN_t^R - \gamma N_t^I \tag{5}$$

setting $\theta = \beta / \gamma$ two less obvious martingales

$$dM_3(t) = dM_1(t) + \theta N_t^S dM_2(t)$$
(6)

$$M_4(t) = \delta M_2(t) + \int_0^t H(\theta, \tau) dM_3 \tag{7}$$

For Further Reading I

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Stochastic Epidemic Models and Their Statistical Analysis. Springer, 2000.

T.L. Griffiths and Z. Ghahramani. Infinite latent feature models and the Indian buffet process (tech. rep. no. 2005-001). Gatsby Computational Neuroscience Unit, 2005.

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Estimation in epidemics with incomplete observations. Journal of the Royal Statistical Society. Series B (Methodological), 59(2):415–429, 1997.