

Introduction to Bayesian Mapping Methods

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 South Carolina congenital abnormality deaths 1990



Mapping issues

- Relative risk estimation
- Disease Clustering
- Ecological analysis

Relative risk estimation

• SMRs (standardized mortality /morbidity ratios



Some notation

- For each region on the map:
- y_i is the count of disease in the ith region
- e_i is the expected count in the ith region
- θ_i is the relative risk in the ith region
- The SMR is just $smr_i = y_i / e_i$
- This is just an estimate of θ_i

SMR problems

- Notoriously unstable
- Small expected count can lead to large SMRs
- Zero counts aren't differentiated
- The SMR is *just the data!*

Smoothing for risk estimation

- Modern approaches to relative risk estimation rely on smoothing methods
- These methods often involve additonal assumptions or model components
- Here we will examine only one approach:
 Bayesian modeling

Bayesian Modeling

Some statistical ideas:

- Likelihood.....we usually assume that counts of disease have a Poisson distribution so that y_i has a Poisson distribution with expected value $e_i \theta_i$
- We usually write this as $y_i \sim Pois(e_i \theta_i)$ for short
- The counts have a Poisson likelihood

Likelihood

- The counts have a joint probability of arising based on the likelihood $L(y, \theta)$:
- L(y, θ) is the product of Poisson probabilities for each of the regions
- This tells us how *likely the data are given* the expected rates $(e_i \theta_i)$
- It also tells us what the most likely values of θ are given the data observed.

Maximum Likelihood

- The SMR is the value of θ which gives the highest likelihood for the data (under a simple Poisson model)....this is called *maximum likelihood (ML)*
- This approach is often used in statistics to get good estimates of parameters
- Here we go beyond ML

Smoothing using Bayesian methods

- One way to produce smoother relative risk estimators is to assume that the risk has a distribution
- In Bayesian terms this is called a *prior distribution*
- In the Poisson count example the commonest prior distribution is to assume that θ_i has a Gamma distribution

A simple Hierarchy

- $y_i \sim Poiss(e_i \theta_i)$
- $\theta_i \sim \text{Gamma}(\alpha, \beta)$
- This a very simple example which allows the risk to vary according to a distribution
- α and β are unknown herea nd we can either try to estimate them from the data OR give then a distribution also:
- E.g. $\alpha \sim \exp(\upsilon), \beta \sim \exp(\rho)$

Model hierarchy



Summary

- Bayesian models are useful for smoothing disease relative risk estimates
- They use prior distributions for parameters
- The priors can be multi-level
- The prior distributions can control the model results
- Sensitivity to prior distributions is important



Modern Posterior inference

- Unlike the usual ML estimates of risk, a Bayesian model is described by a distribution and so a range of values of risk will arise (some more likely than others)
- Posterior distributions are sampled to give a range of these values (*posterior sample*)
- This contains a large amount of information about the parameter of interest

A Bayesian Model

- A Bayesian model consists of a likelihood and prior distributions
- The product of the likelihood and the prior distributions gives the most important distribution: *the posterior distribution*
- In Bayesian modeling all the inference about parameters is made from the posterior distribution.

Posterior Sampling

- The posterior distribution gives information about the *distribution* of parameters: not just about the most likely value
- It is now relatively simple to obtain samples of parameters from posterior distributions
- The commonest method for this is *Gibbs Sampling*

WinBUGS

- This package has been set up to provide relatively easy access to Gibbs Sampling for a range of hierarchical models
- The package is very flexible and implements Gibbs Sampling (and other Markov Chain Monte Carlo (MCMC) methods)
- It also includes a GIS module called GeoBUGS which allows the mapping of the resulting fitted parameters (e.g. relative risks)

Disease Mapping on WinBUGS

- WinBUGS is a very powerful tool which can be applied to:
 - Relative risk estimation
 - Putative health hazards (focused clustering)
 - Ecological analysis

A Simple Example

- South Carolina congenital abnormality deaths 1990
- Data: counts of deaths in counties of South Carolina
- Expected rates available as age x sex adjusted rates
- The SMR map is next:

SMR for congenital anomalies



Gamma Poisson model: WinBUGS



Using WinBUGS

- WinBUGS is a windowed version of the BUGS package. BUGS stands for Bayesian inference using Gibbs Sampling
- The package must be programmed to sample form Bayesian models
- For simple models there is an interactive Doodle editor; more complex models must be written out fully.

WinBUGS Introduction

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Doodle Editor

- The doodle editor allows you to visually set up the ingredients of a model
- It then automatically writes the BUGS code for the model

BUGS code and Doodle stages

```
model
                                                                         stochastic
                                                                                  density:
                                                                                          dnorm
                                                        ٧[i]
                                                                 type:
                                                name:
                                                        0.0
                                                                 precision
                                                                         tau
                                                                                  lower bound
                                                                                                   upper bound
                                                mean
ł
for (i in 1:m)
{
    y[i]~dpois(mu[i])
    log(mu[i])<-log(e[i])+v[i]
    theta[i]<-exp(v[i])
    v[i]~dnorm(0,tau)
}
                                                                          ¥[i]
}
```



Final doodle



Demonstration

Demonstration

- Doodle example with simple nodes
- SC congenital anomalies 1990
- Example 6.1.2 (burn-in 2000, final 6000 iterations)
- Example 6.1.3 Log-normal model (6000 iterations)
- Example 6.1.5 CAR –normal model (15000 iterations)

Extensions

- Space-time modeling (Section 6.1 6)
- Mixture modeling (section 6.1.7)
- Focused clustering (analysis of putative health hazards) (Chapter 7)
- Binomial models (Section 8.3.2)
- Ecological regression (chapter 8)
- Spatial survival analysis (Chapter 9)

Conclusions

- WinBUGS provides a *free* and relatively easy-to-use tool for disease mapping with small area count data
- Allows state-of-the-art approach to relative risk and ecological regression
- Available from:

www.mrc-bsu.cam.ac.uk/bugs