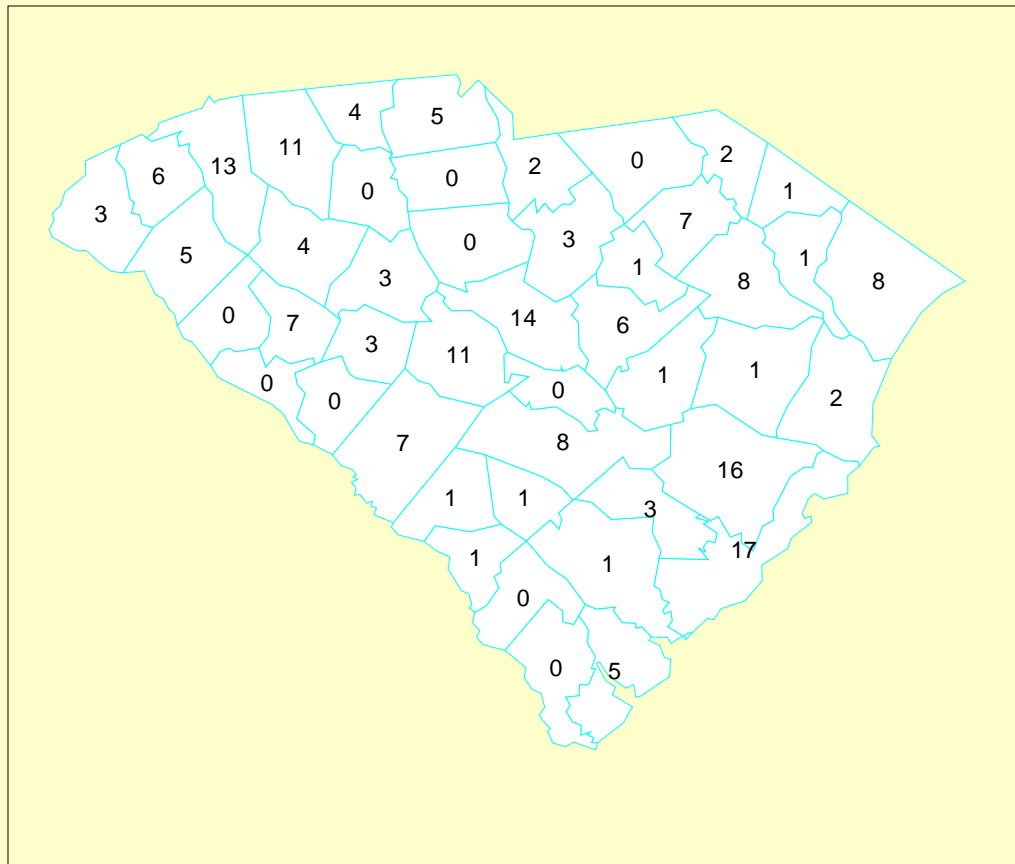# Introduction to Bayesian Mapping Methods

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- South Carolina congenital abnormality deaths 1990
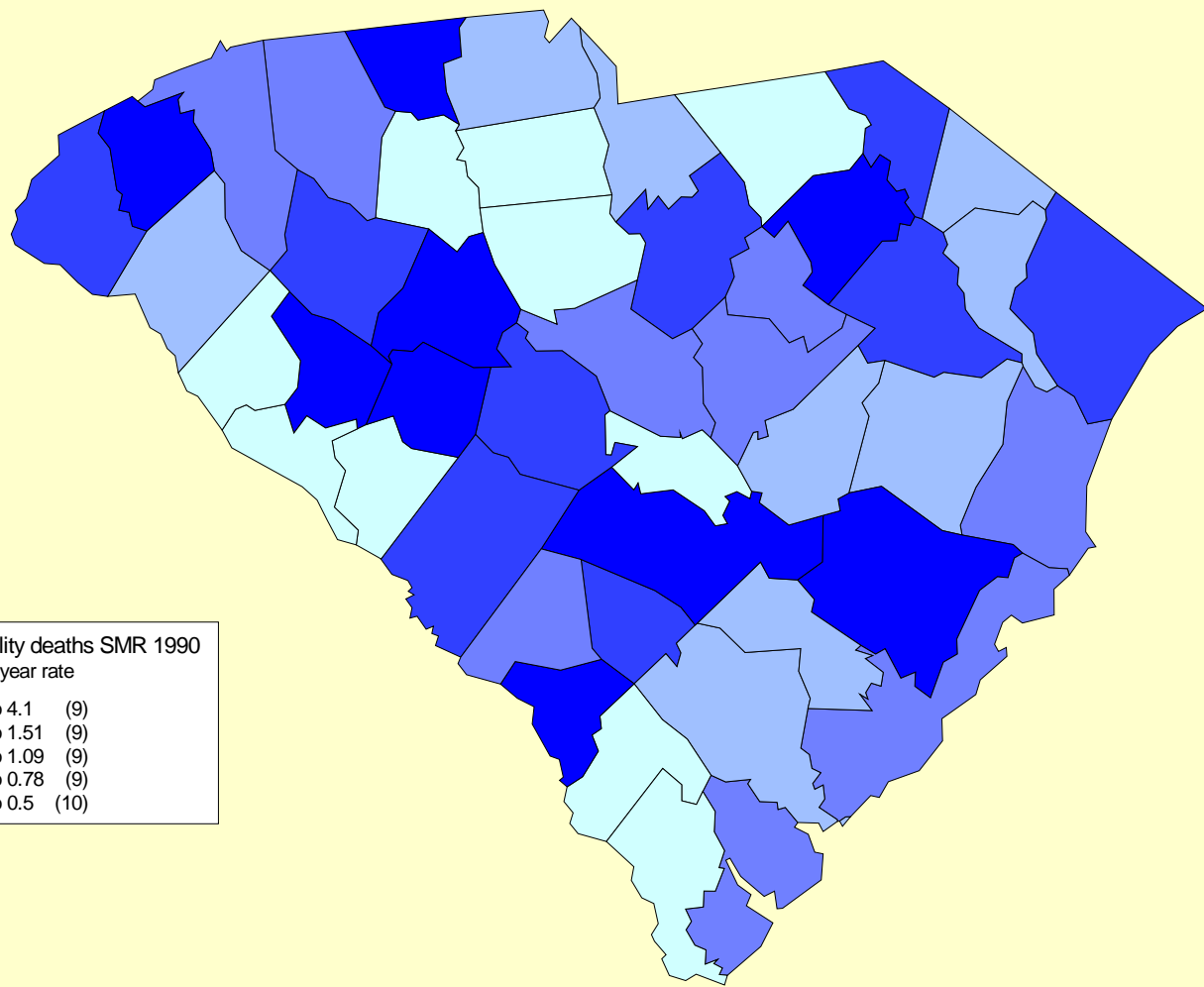
Mapping issues

- Relative risk estimation
- Disease Clustering
- Ecological analysis

Relative risk estimation

- SMRs (standardized mortality /morbidity ratios

Congenital abnormality deaths SMR 1990
using 8 year rate

■	1.51 to 4.1	(9)
■	1.09 to 1.51	(9)
■	0.78 to 1.09	(9)
■	0.5 to 0.78	(9)
■	0 to 0.5	(10)

CDC 2003 cancer
conference

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 $L(y, \theta)$:
- $L(y, \theta)$ 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

- $y_i \sim \text{Poiss}(e_i \, \theta_i)$
- $\theta_i \sim \text{Gamma}(\alpha, \beta)$
- 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:
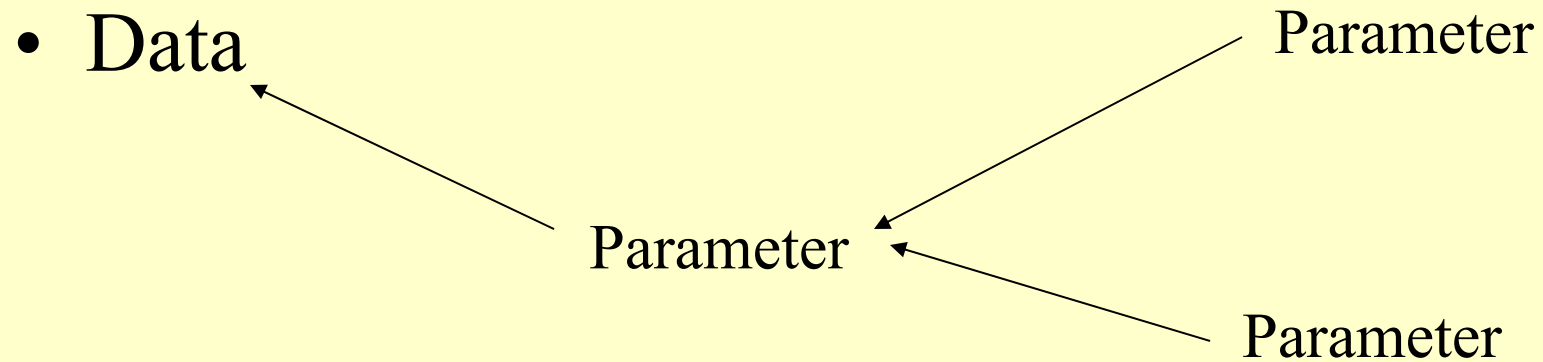- E.g. $\alpha \sim \exp(\upsilon), \beta \sim \exp(\rho)$

Model hierarchy
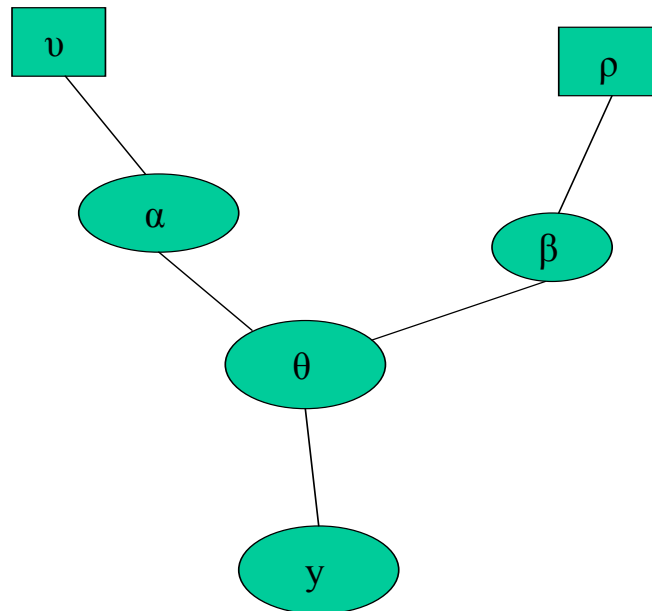
Summary

- 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

A basic Hierarchy

- Data

Parameter

Parameter

Parameter

- Data   1st level   2nd level
-     distribution   distribution

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)
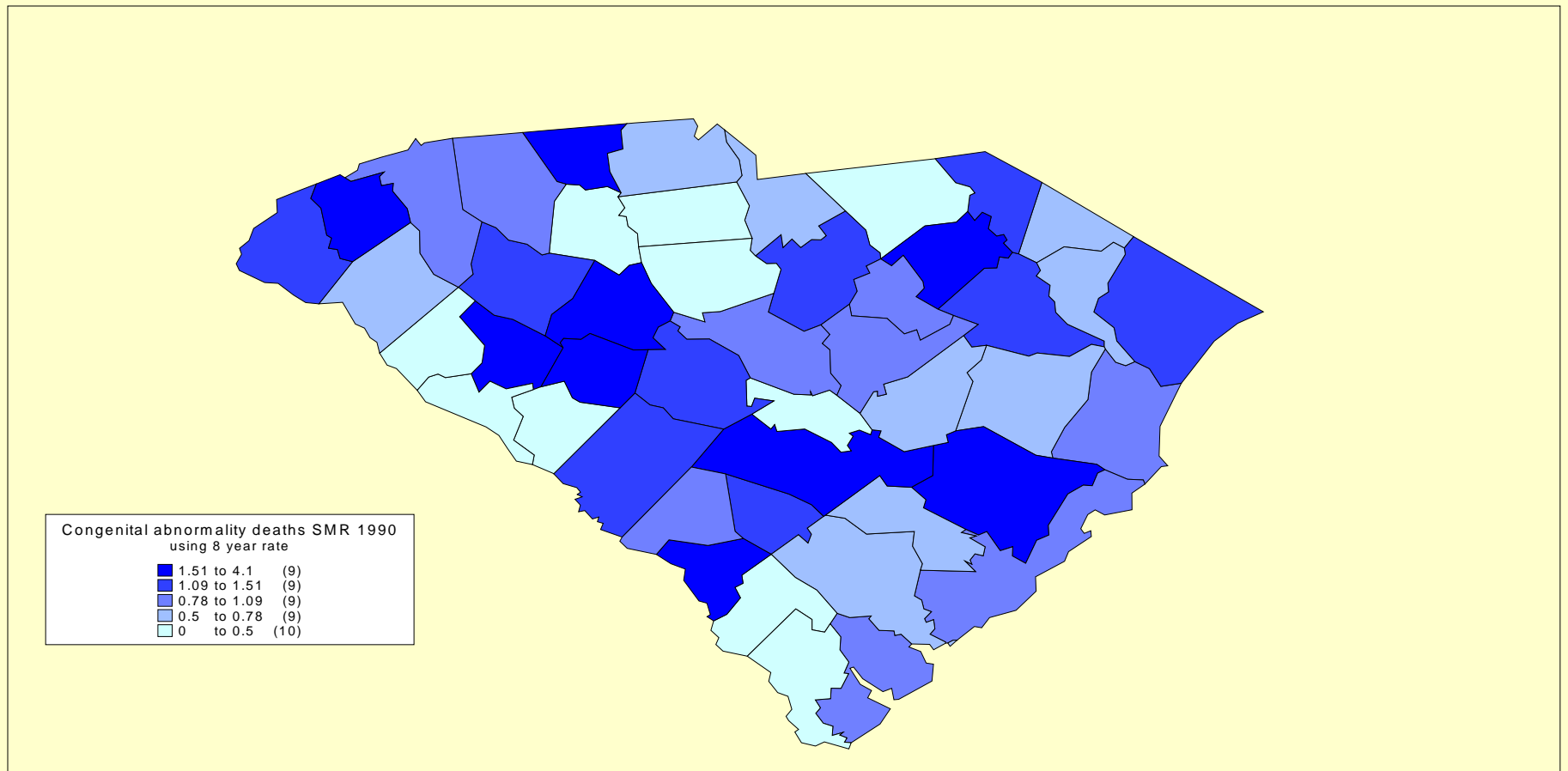
Disease Mapping on WinBUGS

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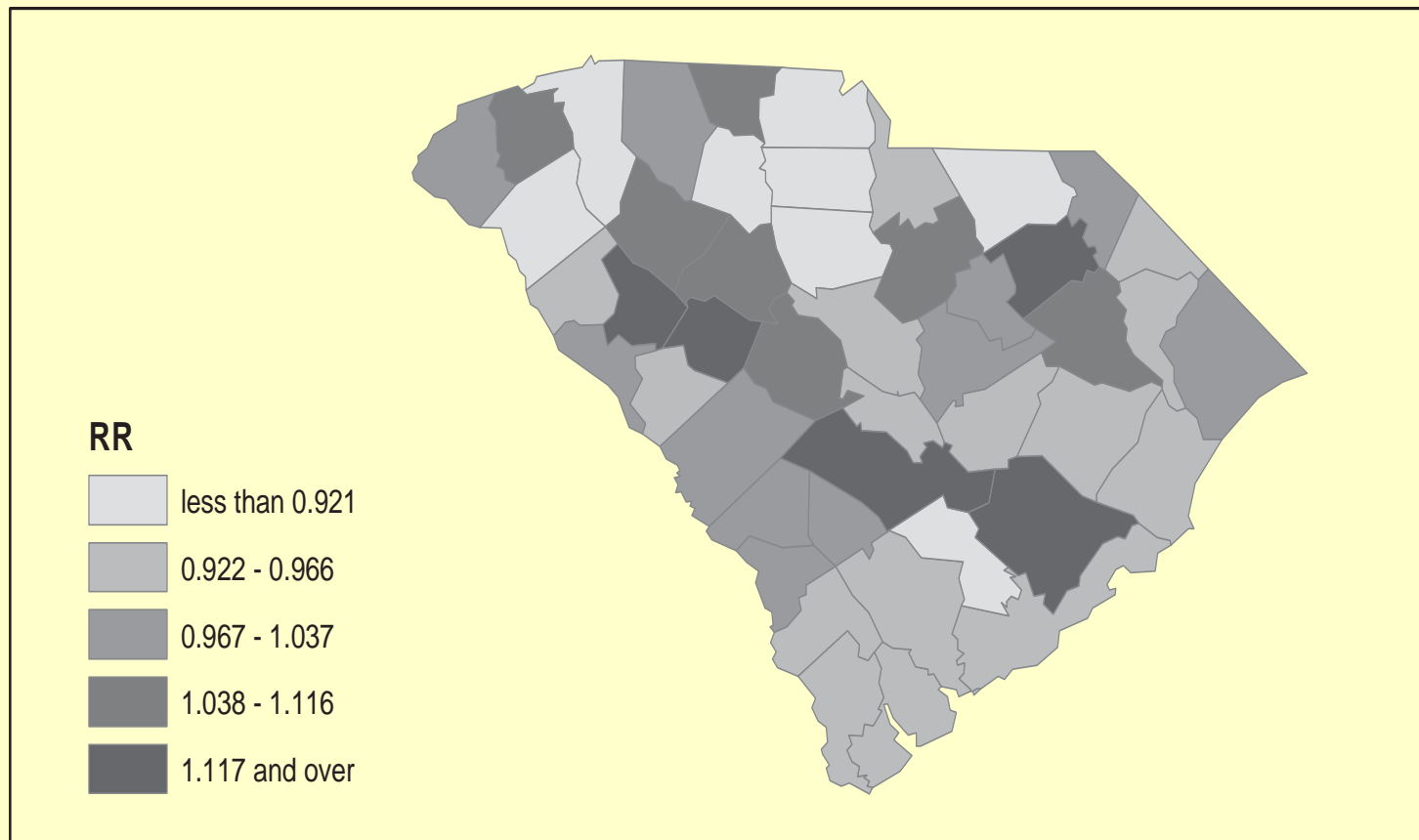 - Putative health hazards (focused clustering)
  - Ecological analysis

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

Congenital abnormality deaths SMR 1990
using 8 year rate

■ 1.51 to 4.1 (9)
■ 1.09 to 1.51 (9)
■ 0.78 to 1.09 (9)
■ 0.5 to 0.78 (9)
□ 0 to 0.5 (10)

Gamma Poisson model: WinBUGS

RR

	less than 0.921
	0.922 - 0.966
	0.967 - 1.037
	1.038 - 1.116
	1.117 and over

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.
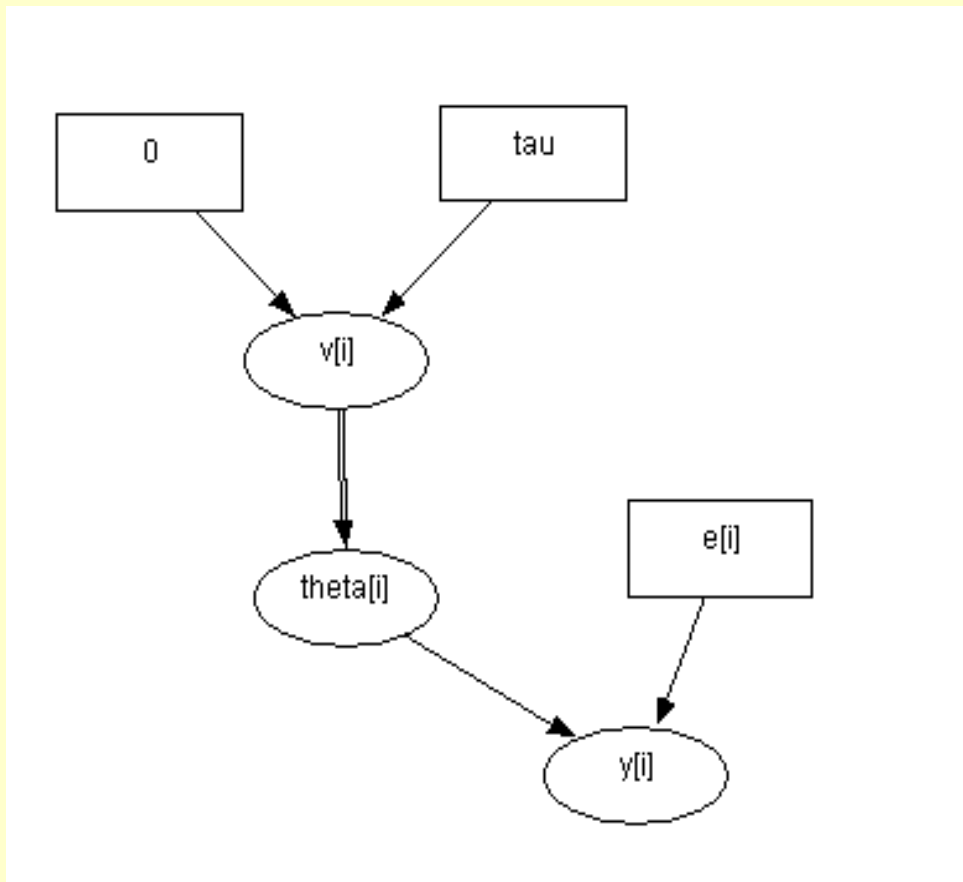
WinBUGS Introduction
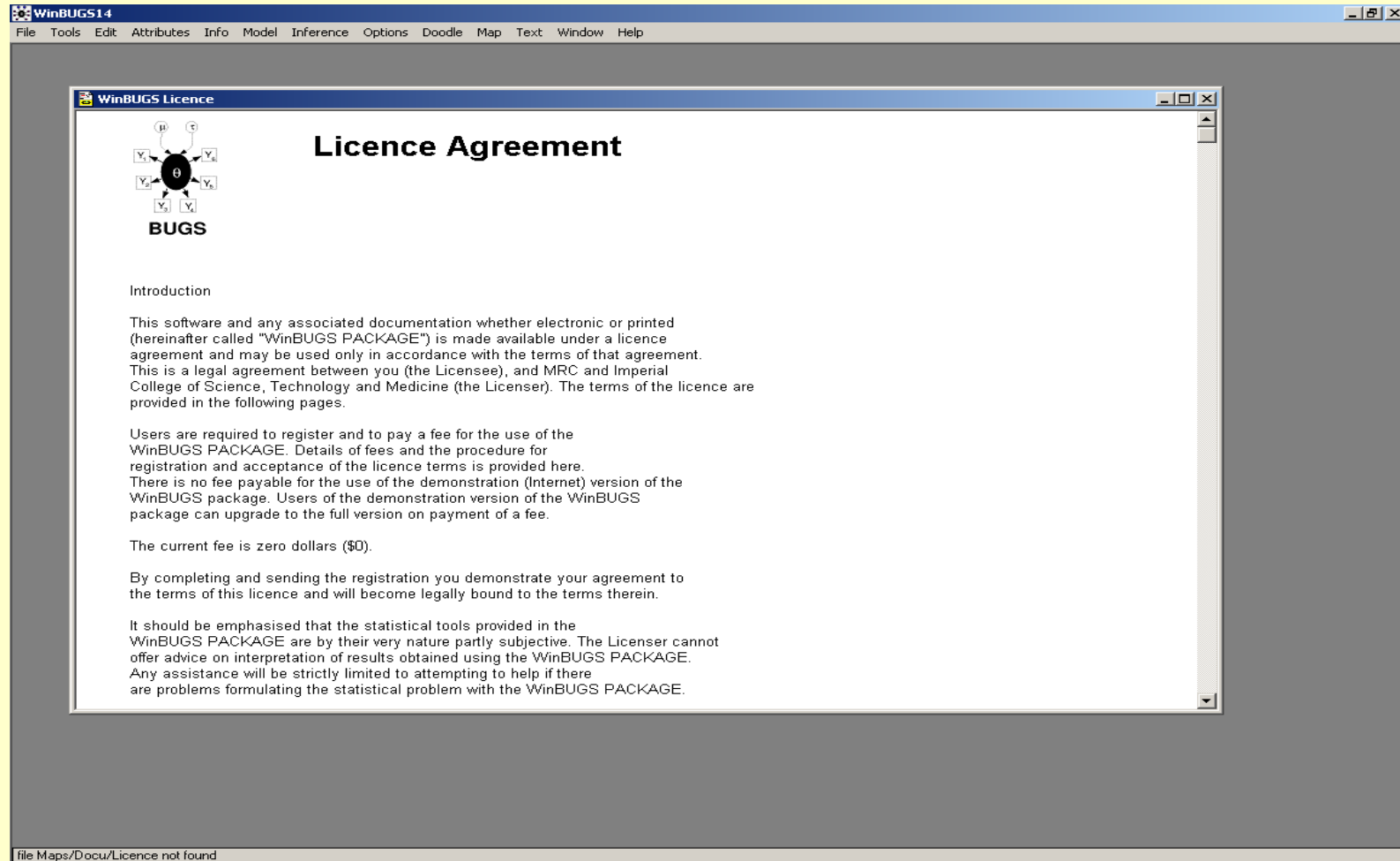
Doodle Editor

- The doodle editor allows you to visually set up the ingredients of a model

- It then automatically writes the BUGS code for the model
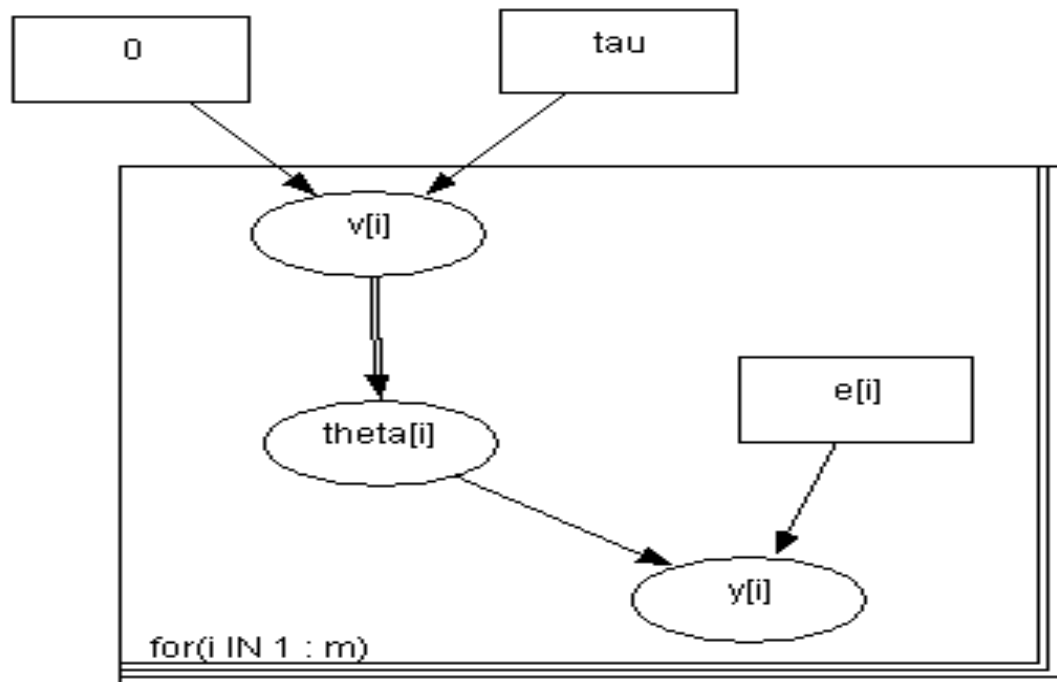
BUGS code and Doodle stages

```
model
{
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)
}
}
```

name:	v[i]	type:	stochastic	density:	dnorm	
mean	0.0	precision	tau	lower bound		upper bound

v[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