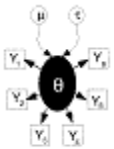


Salm: extra - Poisson variation in dose - response study

Breslow (1984) analyses some mutagenicity assay data (shown below) on salmonella in which three plates have been processed at each dose *i* of quinoline and the number of revertant colonies of TA98 Salmonella measured. A certain dose-response curve is suggested by theory.

dose of quinoline (μg per plate)

0	10	33	100	333	1000
15	16	16	27	33	20
21	18	26	41	38	27
29	21	33	69	41	42

This is assumed to be a random effects Poisson model allowing for over-dispersion. Let x_i be the dose on the plates *i*1, *i*2 and *i*3. Then we assume

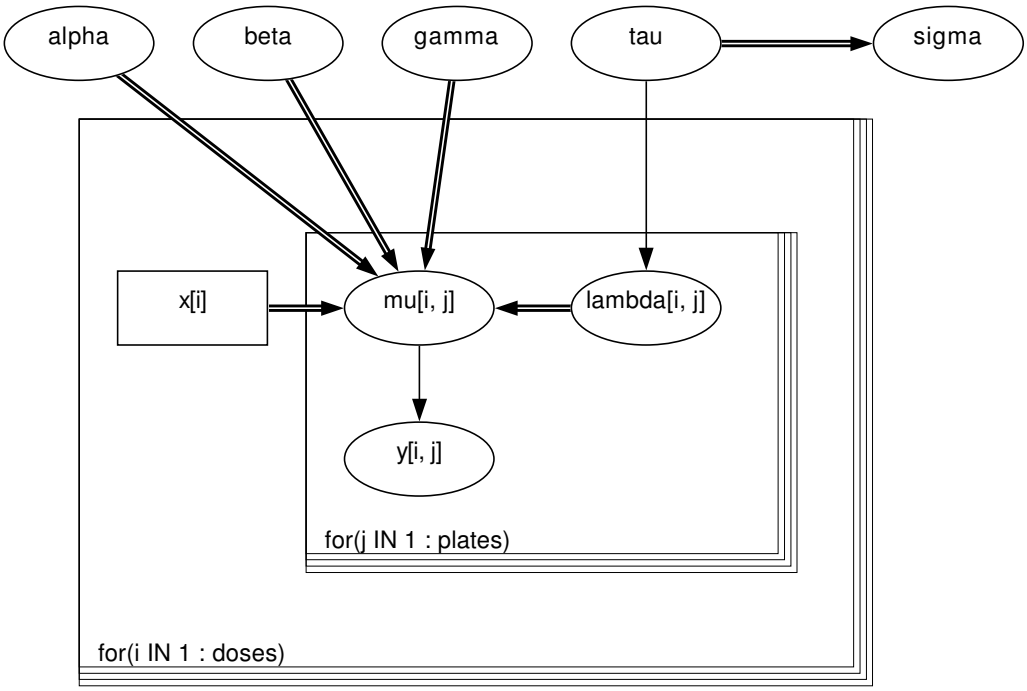
$$y_{ij} \sim \text{Poisson}(\mu_{ij})$$

$$\log(\mu_{ij}) = \alpha + \beta \log(x_i + 10) + \gamma x_i + \lambda_{ij}$$

$$\lambda_{ij} \sim \text{Normal}(0, \tau)$$

α , β , γ , τ are given independent ``noninformative" priors. The appropriate graph is shown

Graphical model for salm example



BUGS *language for salm example*

```
model
{
   for( i in 1 : doses ) {
      for( j in 1 : plates ) {
         y[i , j] ~ dpois(mu[i , j])
         log(mu[i , j]) <- alpha + beta * log(x[i] + 10) +
            gamma * x[i] + lambda[i , j]
         lambda[i , j] ~ dnorm(0.0, tau)
      }
   }
   alpha ~ dnorm(0.0,1.0E-6)
   beta ~ dnorm(0.0,1.0E-6)
   gamma ~ dnorm(0.0,1.0E-6)
   tau ~ dgamma(0.001, 0.001)
   sigma <- 1 / sqrt(tau)
}
```

Data (click to open)

Inits (click to open)

Results

A 1000 update burn in followed by a further 10000 updates gave the parameter estimates

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
alpha	2.193	0.3874	0.01118	1.438	2.194	2.959	1001	10000
beta	0.3059	0.1054	0.003266	0.09692	0.3065	0.5131	1001	10000
gamma	-9.577E-4	4.525E-4	1.48E-5	-0.001837	-9.622E-4	-3.196E-5	1001	10000
sigma	0.2608	0.08077	0.002114	0.1305	0.2512	0.4472	1001	10000

These estimates can be compared with the quasi-likelihood estimates of Breslow (1984) who reported α = 2.203 +/- 0.363, β = 0.311 +/- 0.099, γ = -9.74E-4 +/- 4.37E-4, σ = 0.268