



# Hierarchical Bayesian modeling using SAS procedure MCMC: An Introduction

Ziv Shkedy

Interuniversity Institute for Biostatistics  
and statistical Bioinformatics  
CenStat, Hasselt University  
Agoralaan 1, B3590 Diepenbeek, Belgium

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# Overview

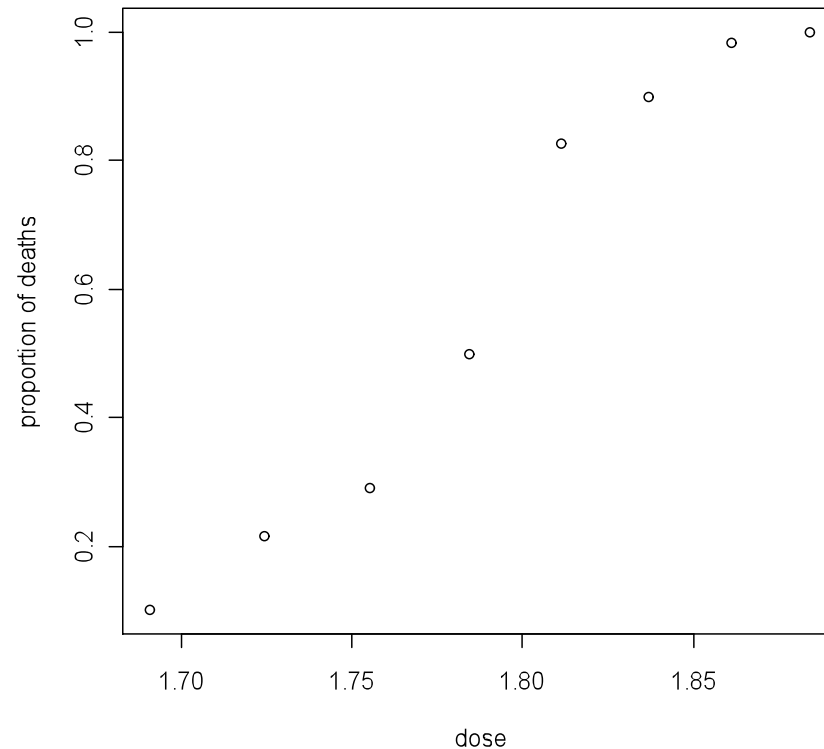
- Simple comparison between SAS procedure MCMC and Winbugs, 5 examples:
  1. Logistic regression model.
  2. Model selection using DIC.
  3. Diagnostic plot.
  4. Hierarchical Bayesian linear model.
  5. A change point model.

## Example 1:

Proc MCMC – syntax and comparison  
with Winbugs

# Dose-response modeling for binary data

- Analysis of binary dose response data.
- The numbers of beetles killed after 5 hour exposure to carbon Disulphide.
- N=8 different concentrations.



# Model formulation

$$r_i \sim B(n_i, \pi_i)$$

Likelihood and linear predictor

$$\text{logit}(\pi_i) = \alpha + \beta \times \text{dose}_i$$

$$\alpha \sim N(0, 1000)$$

Prior models for  $\alpha$  and  $\beta$

$$\beta \sim N(0, 1000)$$

# Syntax: Likelihood

## Winbugs

```
Model
{
for( i in 1 : N ) {
| r[i] ~ dbin(p[i],n[i])
logit(p[i]) <- alpha.star + beta * (x[i] - mean(x[]))
}
beta ~ dnorm(0.0,0.001)
alpha.star ~ dnorm(0.0,0.001)
}
```

## SAS

```
| proc mcmc data=beetles1 nbi=1000 nmc=10000 nthin=1      propcov=quanew monitor=
| (alpha beta) diag=(mcse ess) outpost=beetles1out seed=246810;
|
| parms (alpha beta) 0;
| prior alpha beta ~ normal(0, var = 10000);
| p = logistic(alpha + beta*(x-1.7934250));
| model r ~ binomial(n,p);
| run;
```

# Syntax: prior models for $\alpha$ and $\beta$

## Winbugs

```
Model
{
for( i in 1 : N ) {
r[i] ~ dbin(p[i],n[i])
logit(p[i]) <- alpha.star + beta * (x[i] - mean(x[]))
}
| beta ~ dnorm(0.0,0.001)
| alpha.star ~ dnorm(0.0,0.001)
}
```


## SAS

```
| proc mcmc data=beetles1 nbi=1000 nmc=10000 nthin=1      propcov=quanew monitor=
| (alpha beta) diag=(mcse ess) outpost=beetles1out seed=246810;
|
| parms (alpha beta) 0;
| prior alpha beta ~ normal(0, var = 10000);
| p = logistic(alpha + beta*(x-1.7934250));
| model r ~ binomial(n,p);
| run;
```

# Syntax: linear predictor

## Winbugs

```
Model
{
for( i in 1 : N ) {
r[i] ~ dbin(p[i],n[i])
logit(p[i]) <- alpha.star + beta * (x[i] - mean(x[]))
}
beta ~ dnorm(0.0,0.001)
alpha.star ~ dnorm(0.0,0.001)
}
```


$$\beta \times (x - \bar{x})$$

## SAS

```
proc mcmc data=beetles1 nbi=1000 nmc=10000 nthin=1      propcov=quanew monitor=
(alpha beta) diag=(mcse ess) outpost=beetles1out seed=246810;

parms (alpha beta) 0;
prior alpha beta ~ normal(0, var = 10000);
p = logistic(alpha + beta*(x-1.7934250));
model r ~ binomial(n,p);
run;
```



# Initial values

## Winbugs

```
list(alpha.star=0, beta=0)
```

## SAS

```
proc mcmc data=beetles1 nbi=1000 nmc=10000 nthin=1      propcov=quanew monitor=  
(alpha beta) diag=(mcse ess) outpost=beetles1out seed=246810;  
parms (alpha beta) 0;  
prior alpha beta ~ normal(0, var = 10000);  
p = logistic(alpha + beta*(x-1.7934250));  
model r ~ binomial(n,p);  
run;
```

# Output Winbugs and SAS

node	mean	sd	MC error	2.5%	median	97.5%	start	sample
alpha	<b>0.7438</b>	0.1372	0.001239	<b>0.4778</b>	0.7427	<b>1.018</b>	1000	10001
beta	<b>34.31</b>	2.892	0.03172	28.91	34.24	40.23	1000	10001

## The MCMC Procedure

### Posterior Summaries

Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
alpha	10000	<b>0.7543</b>	0.1381	0.6598	0.7580	0.8463
beta	10000	<b>34.5908</b>	2.8861	32.5108	34.4683	36.5581

### Posterior Intervals

Parameter	Alpha	Equal-Tail Interval		HPD Interval	
alpha	0.050	<b>0.4918</b>	<b>1.0381</b>	0.4857	1.0278
beta	0.050	29.3012	40.5697	29.0429	40.0955

# Options in the proc statement

## **proc mcmc**

data=beetles1

nbi=1000                      Burn in period (default=1000)

nmc=10000                    Number of iterations after the burn-in period

nthin=1                      Monitoring every iteration

propcov=quanew

monitor=(alpha beta)                      Parameter to monitor

diag=(mcse ess)

outpost=beetles1out

seed=246810;

In Winbugs: the update tool box and the sample monitor tool.

## Example 2:

Model Selection using the deviance information criterion

## Three alternative models for the data

$$\pi_i = \frac{e^{\alpha + \beta \times d_i}}{1 + e^{\alpha + \beta \times d_i}}$$

$$\pi_i = 1 - \exp(-e^{\alpha + \beta \times d_i})$$

$$\pi_i = \phi(\alpha + \beta \times d_i)$$

Link function:

Logit

C-log-log

probit

# Specification of the link functions in Winbugs and SAS

logit

```
logit(p[i])<-alpha.star+beta*(x[i]-mean(x[]))
```

```
p = logistic(alpha + beta*(x-1.7934250));
```

cloglog

```
cloglog(p[i])<-alpha.star + beta * (x[i]-mean(x[]))
```

```
p = 1-exp(-exp(alpha + beta*(x-1.7934250)));
```

probit

```
probit(p[i]) <- alpha.star + beta * (x[i]-mean(x[]))
```

```
w=alpha+beta*(x-1.7934250);
```

```
p = cdf('normal', w, 0, 1);
```

# Model Selection using DIC

```
proc mcmc data=beetles1 nbi=1000 nmc=10000 nthin=1 propcov=quanew  
monitor=(alpha beta) diag=(mcse ess) outpost=beetles1out seed=246810 DIC;
```

```
parms (alpha beta) 0;  
prior alpha beta ~ normal(0, var = 10000);  
p = logistic(alpha + beta*(x-1.7934250));  
model r ~ binomial(n,p);  
run;
```

In Winbugs: the DIC tool box.

# SAS and Winbugs output

DIC values for the logit model

Winbugs

Dbar = post.mean of -2logL; Dhat = -2LogL at post.mean of stochastic nodes

	Dbar	Dhat	pD	DIC
r	39.402	37.431	1.972	41.374
total	<b>39.402</b>	37.431	<b>1.972</b>	<b>41.374</b>

SAS

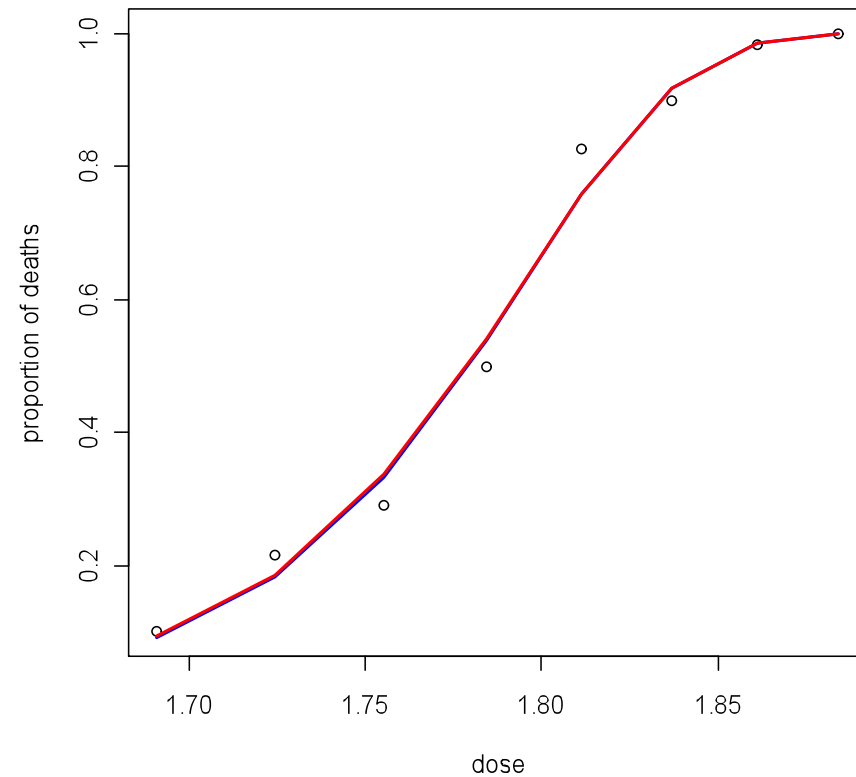
Deviance Information Criterion

Dbar (posterior mean of deviance)	<b>39.466</b>
Dmean (deviance evaluated at posterior mean)	37.447
pD (effective number of parameters)	<b>2.019</b>
DIC (smaller is better)	<b>41.485</b>



# DIC, data and posterior means

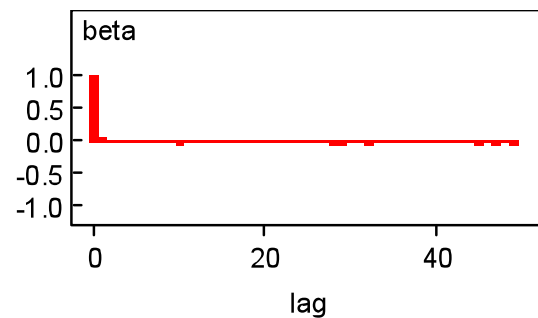
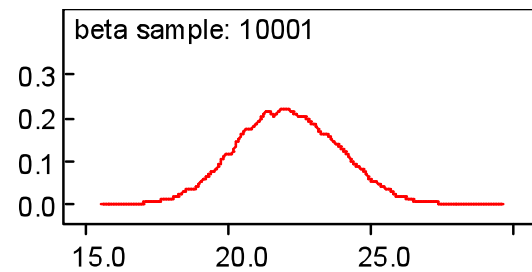
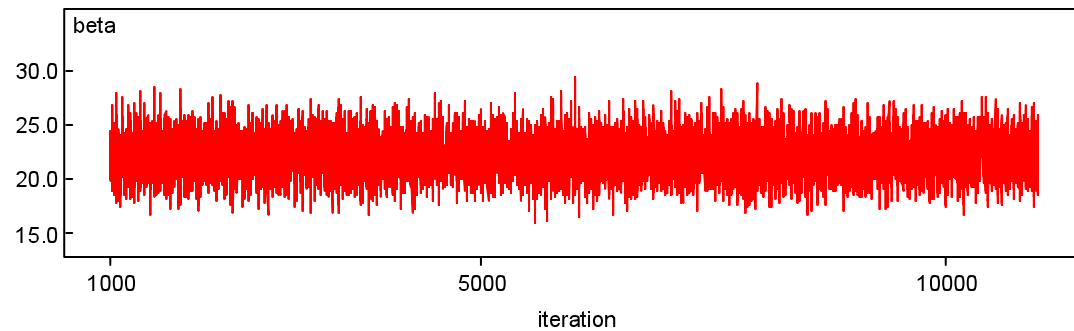
model	DIC SAS	DIC WinBUGs
logit	41.485	41.374
c-log-log	<b>33.801</b>	<b>33.715</b>
probit	40.284	40.347



# Example 3:

## Diagnostic plots

# Diagnostic plot in Winbugs



Winbugs: Inference tool

# The ods statement for the diagnostic plot

**ods graphics on;**

```
proc mcmc data=beetles1 nbi=5000 ntu=1000 nmc=20000 nthin=2 propcov=quanew diag=(mcse ess) outpost=beetles1out seed=246810 DIC;
```

```
parms (alpha beta) 0;
```

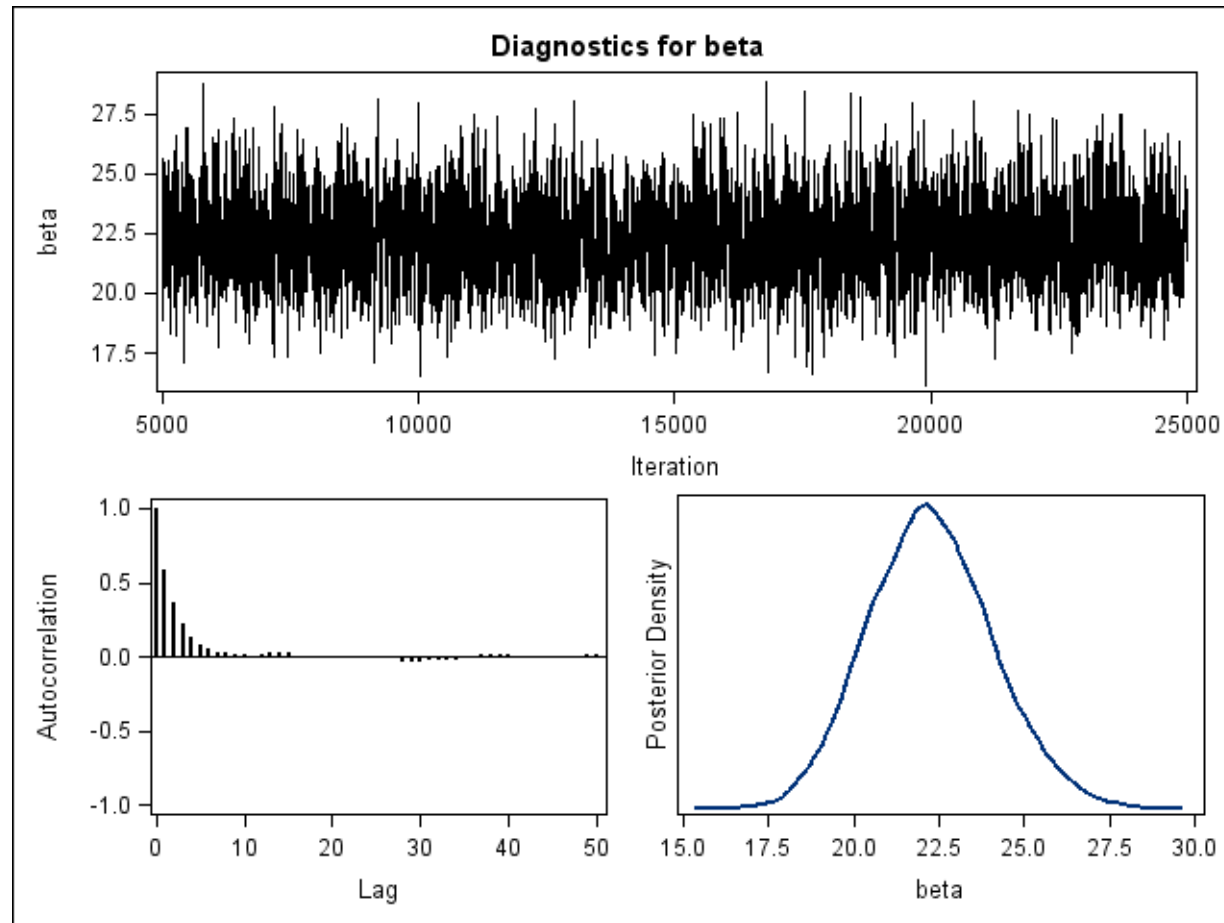
```
prior alpha beta ~ normal(0, var = 10000);
```

```
p = 1-exp(-exp(alpha + beta*(x-1.7934250)));
```

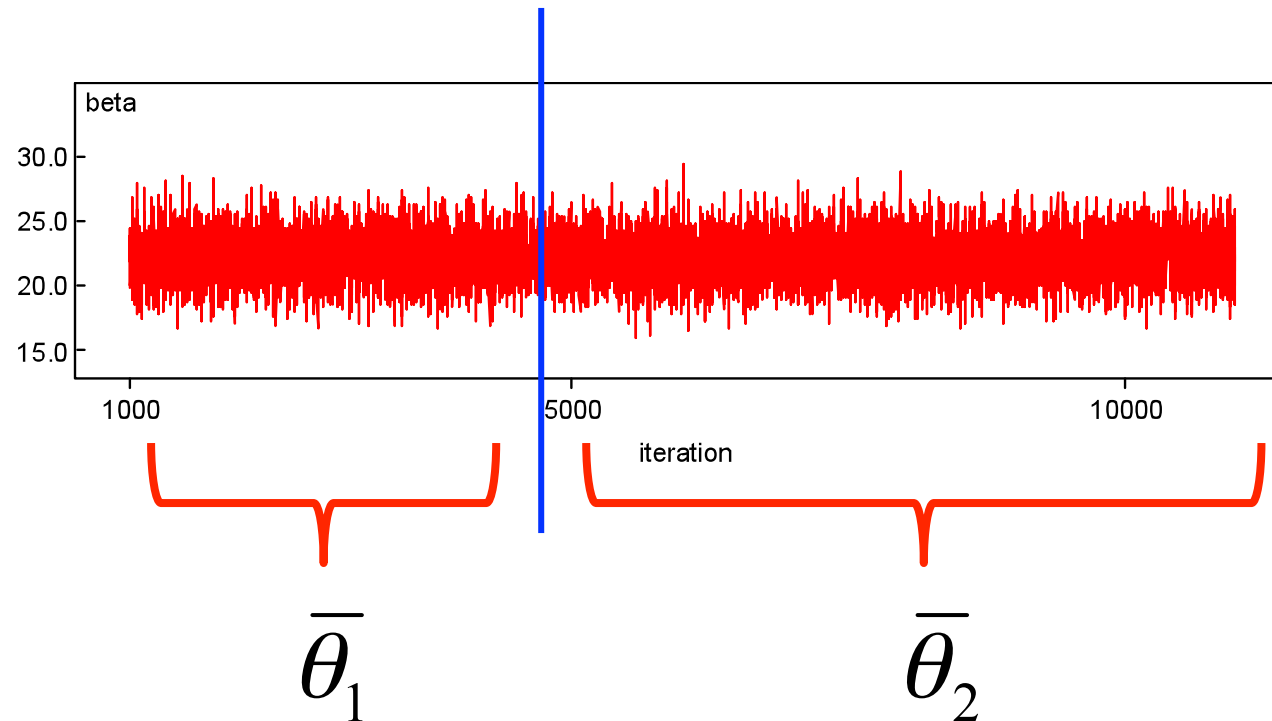
```
model r ~ binomial(n,p);
```

```
run;
```

# Diagnostic plot in SAS

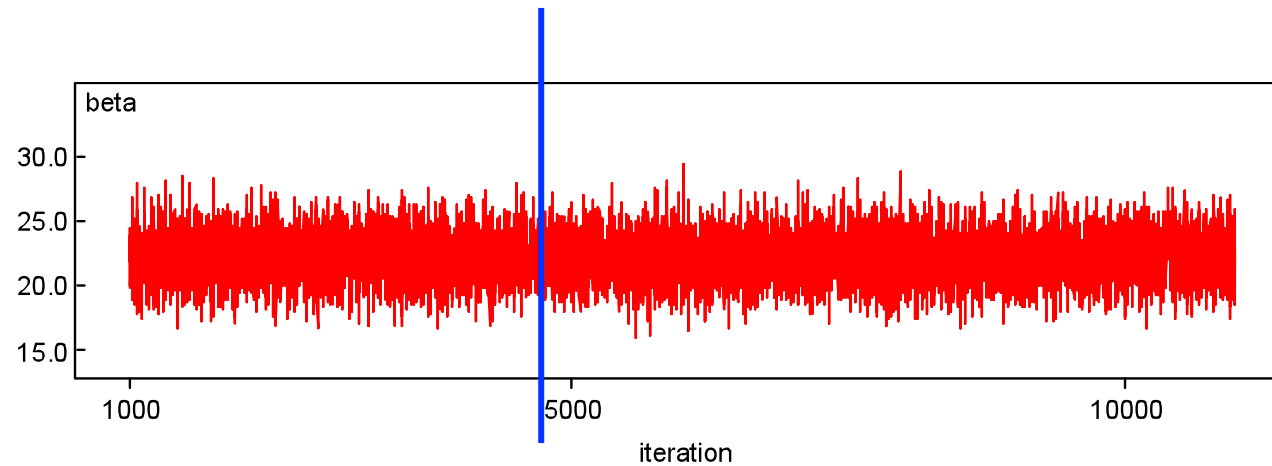


# Geweke diagnostic in SAS



We want to compare between the posterior means of two different parts of the chain.

# Geweke diagnostic in SAS



```
proc mcmc ..... DIAGNOSTICS=GEWEKE;
```

output

## Geweke Diagnostics

Parameter	z	Pr >  z
alpha	1.2652	0.2058
beta	0.4371	0.6620

# Example 4:

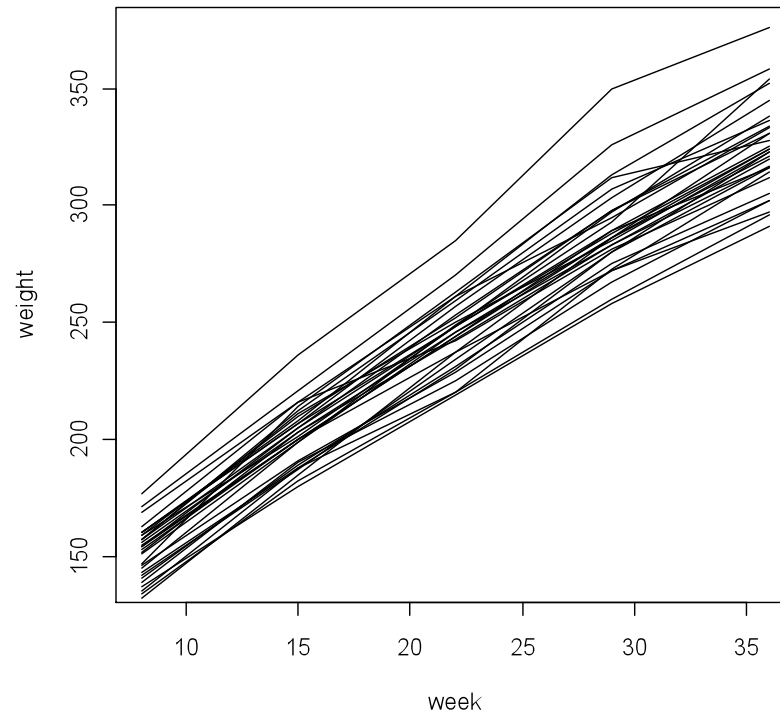
## hierarchical linear mixed model

Rats: a normal hierarchical model (Example volume I in winbugs)



# The rat data

- 30 young rats whose weights were measured weekly for five weeks.
- Variability among subjects.
- Increasing variability over time.



**Rats: a normal hierarchical model (Example volume I in winbugs)**

# Model formulation

**Linear mixed model** with random intercept and random slope:

$$y_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i}) \times t_{ij} + \varepsilon_{ij}$$

The parameters  $\beta_0$  and  $\beta_1$  are the fixed effects,  $b_{0i}$  and  $b_{1i}$  are random intercept and slope.

$$\varepsilon_{ij} \sim N(0, \sigma_\varepsilon^2)$$

$$b_{0i} \sim N(0, \sigma_{b_0}^2)$$

$$b_{1i} \sim N(0, \sigma_{b_1}^2)$$

**Rats: a normal hierarchical model (Example volume I in winbugs)**

# Procedure Mixed: random intercept and random slope

```
proc mixed data=rat;  
class id;  
model y=time/s;  
repeated id/type=simple;  
random intercept time/subject=id type=simple;  
run;
```



$$\begin{bmatrix} b_{0i} \\ b_{1i} \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_{b_0}^2 & 0 \\ 0 & \sigma_{b_1}^2 \end{bmatrix} \right)$$

# Hierarchical Bayesian model: model formulation

A random intercept and random slope model:

$$y_{ij} \sim N\left((\beta_0 + b_{0i}) + (\beta_1 + b_{1i}) \times t_{ij}, \sigma_\varepsilon^2\right)$$

Prior models for  $\beta$ s

$$\beta_0 \sim N(0, \sigma_{\beta_0}^2)$$

$$\beta_1 \sim N(0, \sigma_{\beta_1}^2)$$

Prior models for  $b_{0i}$   
and  $b_{1i}$

$$b_{0i} \sim N(0, \sigma_{b_0}^2)$$

$$b_{1i} \sim N(0, \sigma_{b_1}^2)$$

Hyperprior for the  
variance components

$$\sigma_\varepsilon^{-2} \sim \text{gamma}(\delta_0, \delta_1)$$

# Procedure MCMC: “random intercept and random slope”

```
proc mcmc data=rat ntu=1000 thin=1 nmc=10000 seed=7893  
  propcov=quanew diag=(mcse ess) outpost=ratout  
  monitor=(beta0 beta1 s2 s30 s31) DIC;
```

```
array b0[30];  
array b1[30];
```

Specification of the subject specific parameters

```
parms beta0 0 beta1 0;  
parms b0: 0;           Initial  
parms b1: 0;           values  
parms s2 1 ;  
parms s30 1 s31 1;
```


```
prior beta0: ~ normal(0, var = 10000);  
prior beta1: ~ normal(0, var = 10000);  
prior b0  : ~ normal(0, var = s30);  
prior b1  : ~ normal(0, var = s31);
```

priors

```
prior s2: ~ igamma(0.001, scale = 1000);  
hyperprior s30 ~ igamma(0.001, scale = 1000);  
hyperprior s31 ~ igamma(0.001, scale = 1000);
```

priors

```
mu = (beta0+b0[id])+(beta1+b1[id])*time;  
model y ~ normal(mu, var = s2);  
run;
```


$$\mu_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i}) \times t_{ij}$$

# Specification of the mean

Data for the first two subjects

Obs	time	y	id	ti
1	8	151	1	-14
2	15	199	1	-7
3	22	246	1	0
4	29	283	1	7
5	36	320	1	14
6	8	145	2	-14
7	15	199	2	-7
8	22	249	2	0
9	29	293	2	7
10	36	354	2	14

```
array b0[30];  
array b1[30];
```

$$b_{0,1}, b_{0,2}, \dots, b_{0,30}$$
$$b_{1,1}, b_{1,2}, \dots, b_{1,30}$$

```
mu = (beta0+b0[id])+(beta1+b1[id])*time;
```

$$\mu_{ij} = (\beta_0 + b_{0i}) + (\beta_1 + b_{1i}) \times t_{ij}$$

# Proc MIXED and proc MCMC

## PROC MIXED

Cov Parm Subject Estimate

Intercept id 106.31  
time id 0.2417  
id 36.8340

Solution for Fixed Effects  
Standard

Effect	Estimate	Error	DF	t Value	Pr >  t
Intercept	106.57	2.2365	29	47.65	<.0001
time	6.1857	0.1028	29	60.18	<.0001

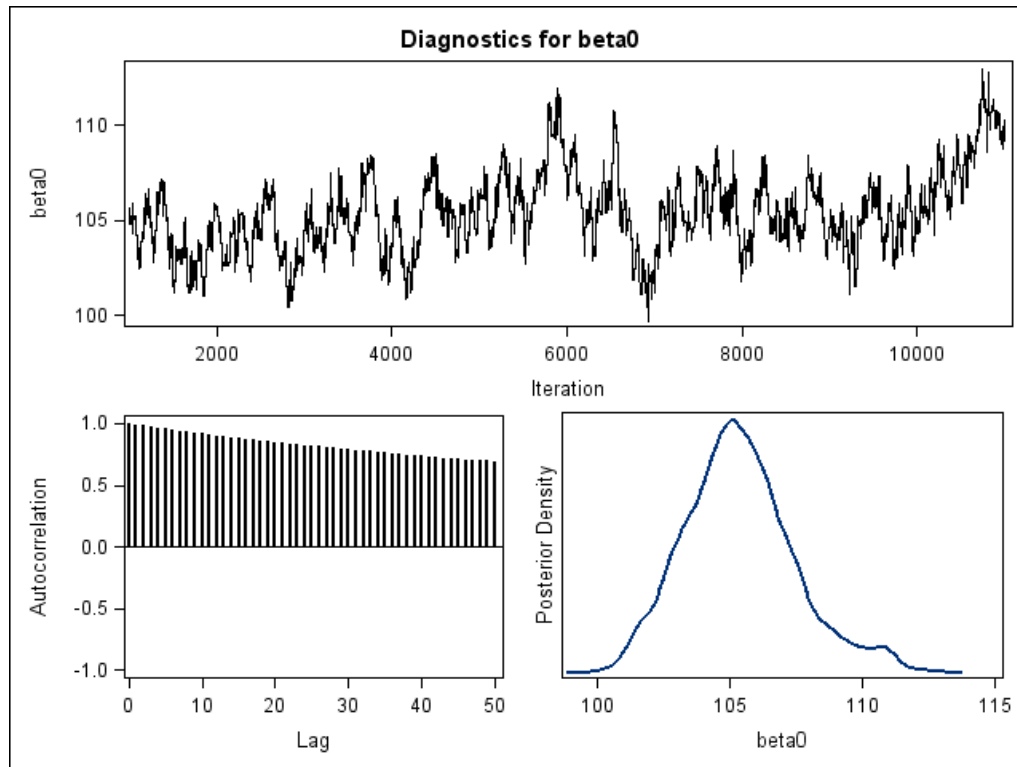
## PROC MCMC

The MCMC Procedure

Posterior Summaries

Parameter	N	Standard		Percentiles		
		Mean	Deviation	25%	50%	75%
beta0	10000	105.4	2.1007	104.0	105.2	106.6
beta1	10000	5.7521	0.4385	5.4631	5.7193	6.0234
s2	10000	78.1745	10.5917	70.4747	77.2854	84.4435
s30	10000	114.9	39.0045	89.1155	108.6	132.5
s31	10000	71.5748	19.6891	57.5063	68.1735	82.5253

# Diagnostic plot for the intercept



Convergence problems:  
slow mixing and high  
correlation.

Hierarchical centering.



# Hierarchical centering: model formulation

A random intercept and random slope model:

$$y_{ij} \sim N(b_{0i} + b_{1i} \times t_{ij}, \sigma_{\varepsilon}^2)$$

Prior models for  $b_{0i}$   
and  $b_{1i}$

$$b_{0i} \sim N(\beta_0, \sigma_{b_0}^2)$$

$$b_{1i} \sim N(\beta_1, \sigma_{b_1}^2)$$

Hyperprior models  
for  $\beta$ s

$$\beta_0 \sim N(0, \sigma_{\beta_0}^2)$$

$$\beta_1 \sim N(0, \sigma_{\beta_1}^2)$$

Hyperprior for the  
variance components

$$\sigma_{\varepsilon}^{-2} \sim \text{gamma}(\delta_0, \delta_1)$$



The mean of the “random” effects is not zero but the “fixed” effects.

# Winbugs program for the rat data

```
Model
{
for( i in 1 : N ) {
  for( j in 1 : T ) {
    Y[i , j] ~ dnorm(mu[i , j],tau.c)
    mu[i , j] <- (alpha[i] + beta[i] * (x[j] - xbar))
  }
alpha[i] ~ dnorm(alpha.c,alpha.tau)
beta[i] ~ dnorm(beta.c,beta.tau)
}
tau.c ~ dgamma(0.001,0.001)
sigma.y <- 1/tau.c
sigma.alpha <- 1/alpha.tau
sigma.beta <- 1/beta.tau
alpha.c ~ dnorm(0.0,1.0E-6)
alpha.tau ~ dgamma(0.001,0.001)
beta.c ~ dnorm(0.0,1.0E-6)
beta.tau ~ dgamma(0.001,0.001)
alpha0 <- alpha.c - xbar * beta.c
}
```



Prior models for  $b_{0i}$  and  $b_{1i}$

$$b_{0i} \sim N(\beta_0, \sigma_{b_0}^2)$$

$$b_{1i} \sim N(\beta_1, \sigma_{b_1}^2)$$

# SAS program for the rat data

```
proc mcmc data=rat ntu=1000 thin=1 nmc=10000 seed=7893
    propcov=quanew diag=(mcse ess) outpost=ratout
    monitor=(beta0 beta1 s2 s30 s31) DIC;
array b0[30];
array b1[30];

parms beta0 0 beta1 0;
parms b0: 0;
parms b1: 0;
parms s2 1 ;
parms s30 1 s31 1;

prior beta0: ~ normal(0, var = 10000);
prior beta1: ~ normal(0, var = 10000);
prior b0 : ~ normal(beta0, var = s30);
prior b1 : ~ normal(beta1, var = s31);
prior s2: ~ igamma(0.001, scale = 1000);
hyperprior s30 ~ igamma(0.001, scale = 1000);
hyperprior s31 ~ igamma(0.001, scale = 1000);

mu = b0[id]+b1[id]*time;
model y ~ normal(mu, var = s2);
run;
```



$$b_{0i} \sim N(\beta_0, \sigma_{b_0}^2)$$
$$b_{1i} \sim N(\beta_1, \sigma_{b_1}^2)$$

# Winbugs and SAS output

## Winbugs

node	mean	sd	MC error	2.5%	median	97.5%	start	sample
alpha0	106.5	3.656	0.04112	99.44	106.5	113.8	1000	10001
beta.c	6.185	0.1062	0.0013	5.975	6.185	6.395	1000	10001
Sigma.alpha	219.3	64.82	0.6982	125.0	208.3	372.1	1000	10001
sigma.beta	0.2728	0.09908	0.001621	0.1266	0.2572	0.5129	1000	10001
sigma.y	37.25	5.687	0.09148	27.61	36.73	49.69	1000	10001

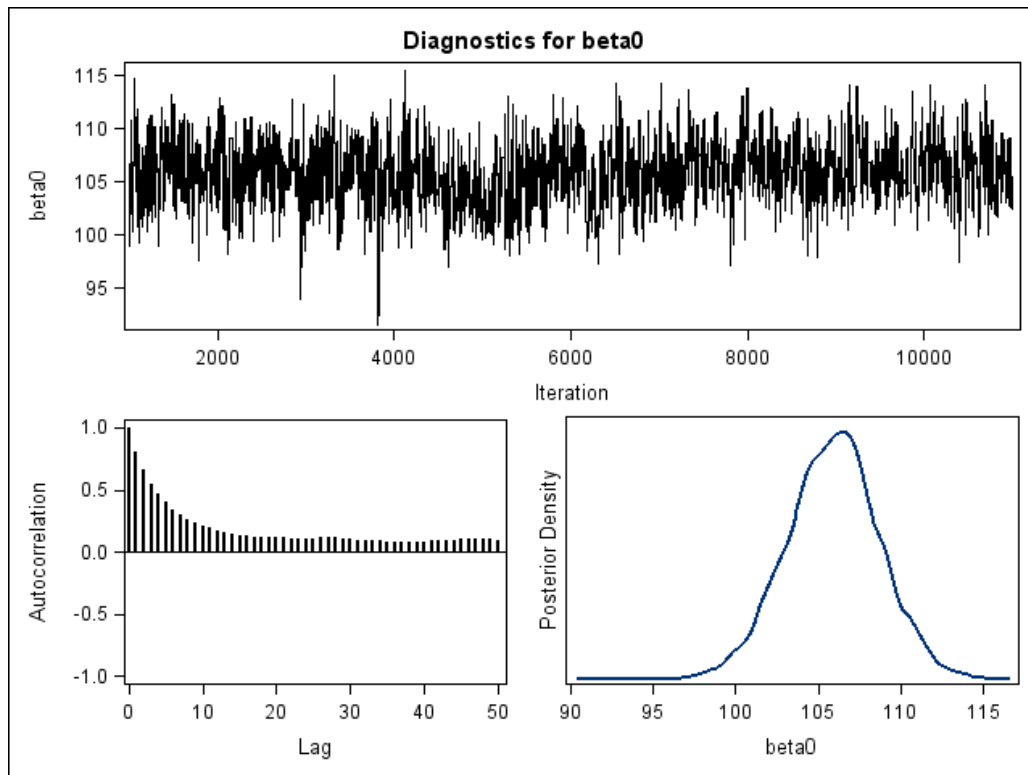
## SAS

The MCMC Procedure

Posterior Summaries

Parameter	N	Standard		Percentiles		
		Mean	Deviation	25%	50%	75%
beta0	10000	105.9	2.8147	104.1	106.0	107.7
beta1	10000	6.2014	1.5549	5.1696	6.1859	7.2083
s2	10000	58.1899	7.9568	52.7546	57.3587	63.0212
s30	10000	191.4	64.1846	146.4	179.2	222.6
s31	10000	73.4174	19.7368	59.6083	70.6727	84.4961

# Diagnostic plot for the intercept

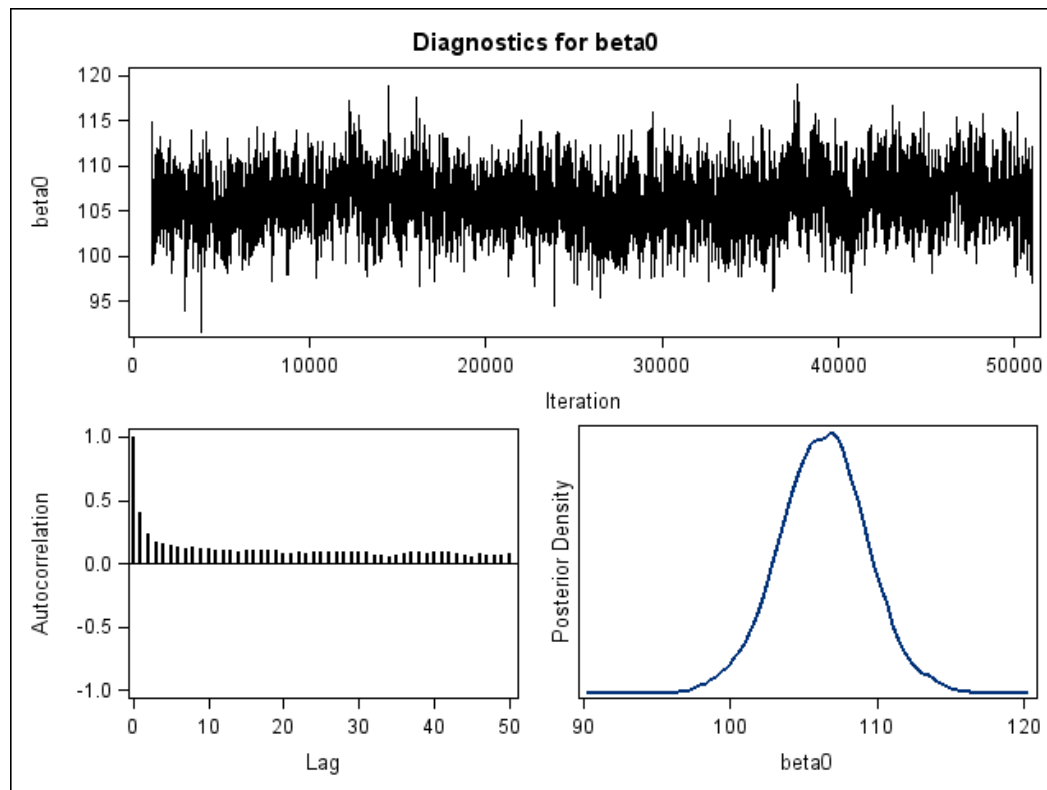


Convergence problems:  
slow mixing and high  
correlation.

Hierarchical centering

# Improving convergence

```
proc mcmc data=rat nbi=1000 thin=5 nmc=50000 seed=7893.....
```



We can run the model for higher number of iteration and monitor every  $k$  ( $k=5$  in our example) iterations.

# Winbugs and SAS output

## Winbugs

node	mean	sd	MC error	2.5%	median	97.5%	start	sample
alpha0	106.5	3.656	0.04112	99.44	106.5	113.8	1000	10001
beta.c	6.185	0.1062	0.0013	5.975	6.185	6.395	1000	10001
Sigma.alpha	219.3	64.82	0.6982	125.0	208.3	372.1	1000	10001
sigma.beta	0.2728	0.09908	0.001621	0.1266	0.2572	0.5129	1000	10001
sigma.y	37.25	5.687	0.09148	27.61	36.73	49.69	1000	10001

## SAS

Parameter	N	Standard		Percentiles		
		Mean	Deviation	25%	50%	75%
beta0	10000	106.3	2.9998	104.3	106.3	108.3
beta1	10000	6.1629	1.5786	5.1264	6.1772	7.1907
s2	10000	55.3038	8.3116	49.4731	54.4440	60.1196
s30	10000	223.2	72.8559	172.2	210.8	261.9
s31	10000	73.9487	20.4162	59.2302	70.3625	85.2244

# Example 5:

## A changepoint model



# Changepoint models

- The simplest changepoint model assumes that  $y_i \sim P_1(y|\theta_1)$ ,  $i = 1, 2, 3, \dots, k$  and  $y_i \sim P_2(y|\theta_2)$   
 $i = k + 1, k + 2, \dots, n$ .
- Note that  $P_1$  and  $P_2$  are assumed to be known, in our example  $P_1$  and  $P_2$  are both Poisson.

# Changepoint model

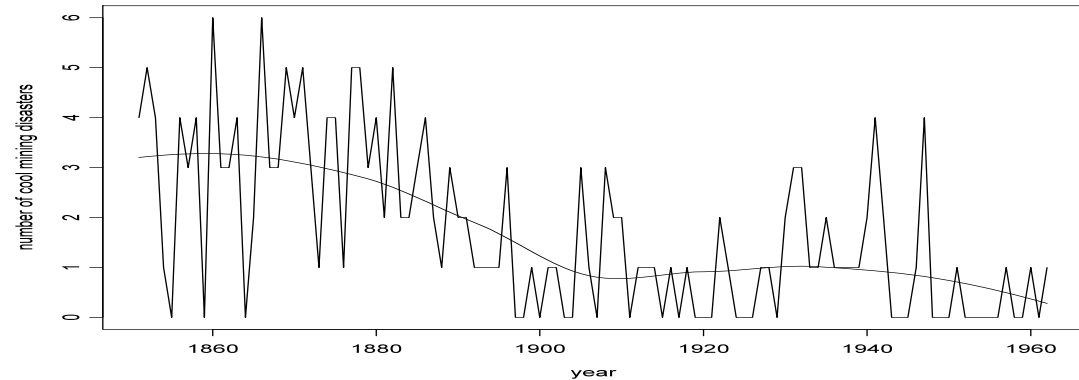
- The likelihood for this model is given by

$$P(y | \theta) = \prod_{i=1}^k P_1(y | \theta_1) \prod_{i=k+1}^n P_1(y | \theta_2)$$

- The model assumes that there is a change in the location (and scale) of  $y$  and that the change occurred at  $k$ .

# The British coal mining disasters data

The British coal mining disasters data by year (1=1851, 112=1962).



Number of events by year, over a period of 112 years.

# Model formulation

- We assume that the number of events  $y_i$  is a Poisson random variable.

$$y_i \sim \begin{cases} \text{Poisson}(\lambda_1) & \text{time} \leq \tau \\ \text{Poisson}(\lambda_2) & \text{time} > \tau \end{cases}$$

- In this model, the mean is change from  $\lambda_1$  to  $\lambda_2$  at year  $k + 1$ .
- $k$ , the year of the change is unknown but we know that  $1 < k < 112$ .

# Model formulation

We formulate the following hierarchical model:

$$y_i \sim \text{Poisson}(\mu_i) \quad \text{likelihood}$$

$$\mu_i = I_i \times \lambda_1 + (1 - I_i) \times \lambda_2$$

$$\lambda_i \sim N(0, 10000) \quad \text{Prior (for the mean)}$$

$$k \sim U(1, 112) \quad \text{Prior for the changepoint}$$

- Note that  $k$  is assumed to be a random variable which follows a uniform distribution.
- This means that we assume that the changepoint can occur at each year between the first and the last year.

# Winbugs program

```
model
```

```
{
```

```
  for( i in 1 : N ) {
```


```
    y[i] ~ dpois(mu[i])
```

```
    log(mu[i]) <- lambda[J[i]]
```

```
    J[i] <- 1 + step(year[i] - x.change - 0.5)   $J_i = \begin{cases} 1 & t_i \geq \tau \\ 2 & t_i < 0 \end{cases}$ 
```

```
  }
```

```
  for( j in 1 : 2 ) {
```

```
    lambda[j] ~ dnorm(0.0,1.0E-6)  Prior for the mean
```

```
  }
```

```
  x.change ~ dunif(1,112)  Prior for the changepoint
```

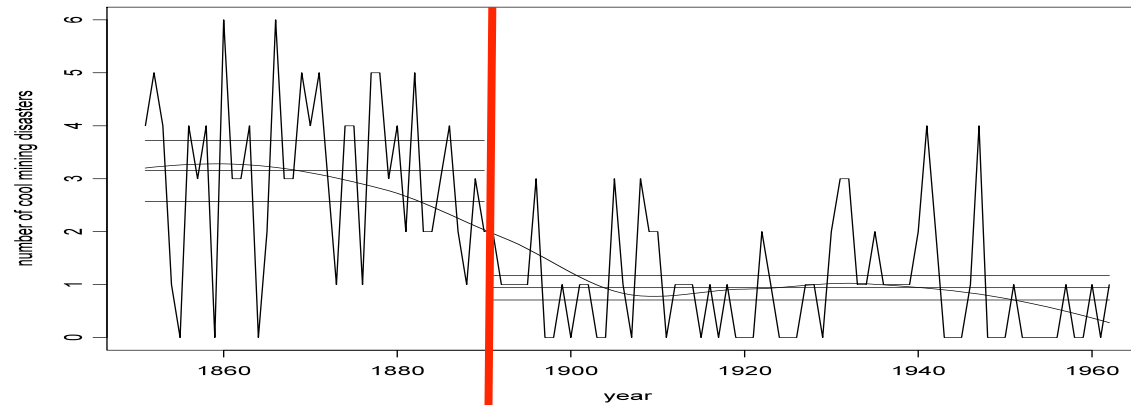
```
}
```

# Posterior means

The changepoint in the means occurred at year 40.  
Posterior means: 3.14 for the first period and 1.07 for the second period.

<b>node</b>	<b>mean</b>	<b>sd</b>	<b>MC error</b>	<b>2.5%</b>	<b>median</b>	<b>97.5%</b>	<b>start</b>	<b>sample</b>
x.change	39.22	2.476	0.0212	35.1	39.44	44.48	1000	20000
mu[1]	3.141	0.2965	0.002096	2.597	3.128	3.753	1000	20000
mu[112]	1.076	0.06495	4.924E-4	1.002	1.059	1.242	1000	20000

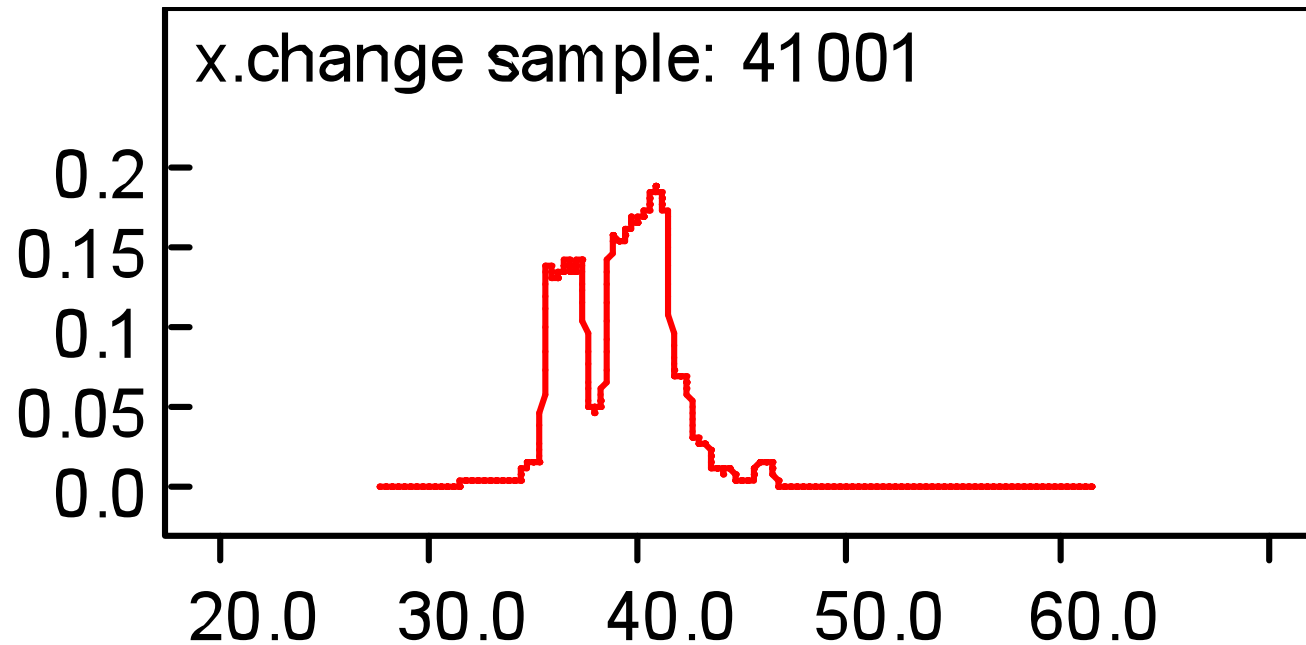
# Data, posterior means (for the means) and 95% credible intervals



The change point at month 40



# Density estimate for the posterior distribution of the changepoint



The density estimate for the posterior distribution of the changepoint suggests that a more complicated model is needed with possibly two changepoints.

# Proc MCMC

## Winbugs

```
model
{
  for( i in 1 : N ) {
    y[i] ~ dpois(mu[i])
    log(mu[i]) <- lambda[J[i]]
    J[i] <- 1 + step(year[i] - x.change- 0.5)
  }
  for( j in 1 : 2 ) {
    lambda[j] ~ dnorm(0.0,1.0E-6)
  }
  x.change ~ dunif(1,112)
}
```

## SAS

```
ods graphics on;
proc mcmc data=change
  outpost=changeout seed=24860
  ntu=1000 nmc=20000
  propcov=quanew diag=(mcse ess)
  monitor=(cp lambda);
```

**array lambda[2];**

parms cp 10;

parms lambda1 4 lambda2 4;

**prior lambda: ~ normal(0, v = 1e6);**

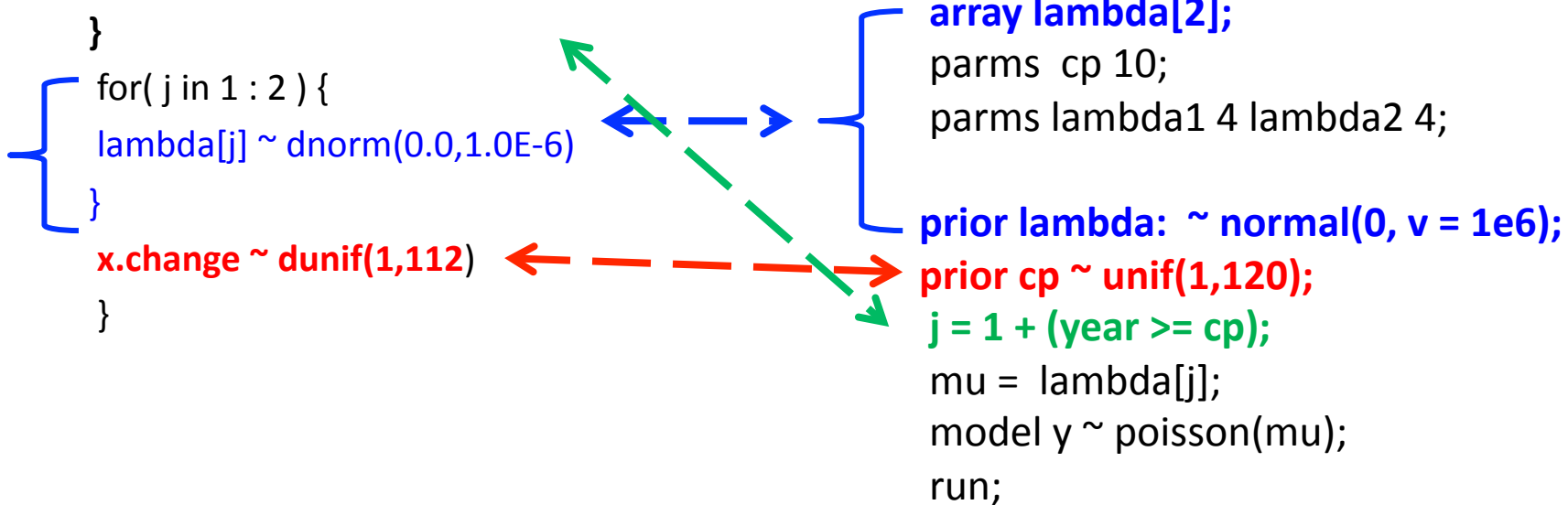
**prior cp ~ unif(1,120);**

**j = 1 + (year >= cp);**

mu = lambda[j];

model y ~ poisson(mu);

run;



# Winbugs and SAS output

## Winbugs

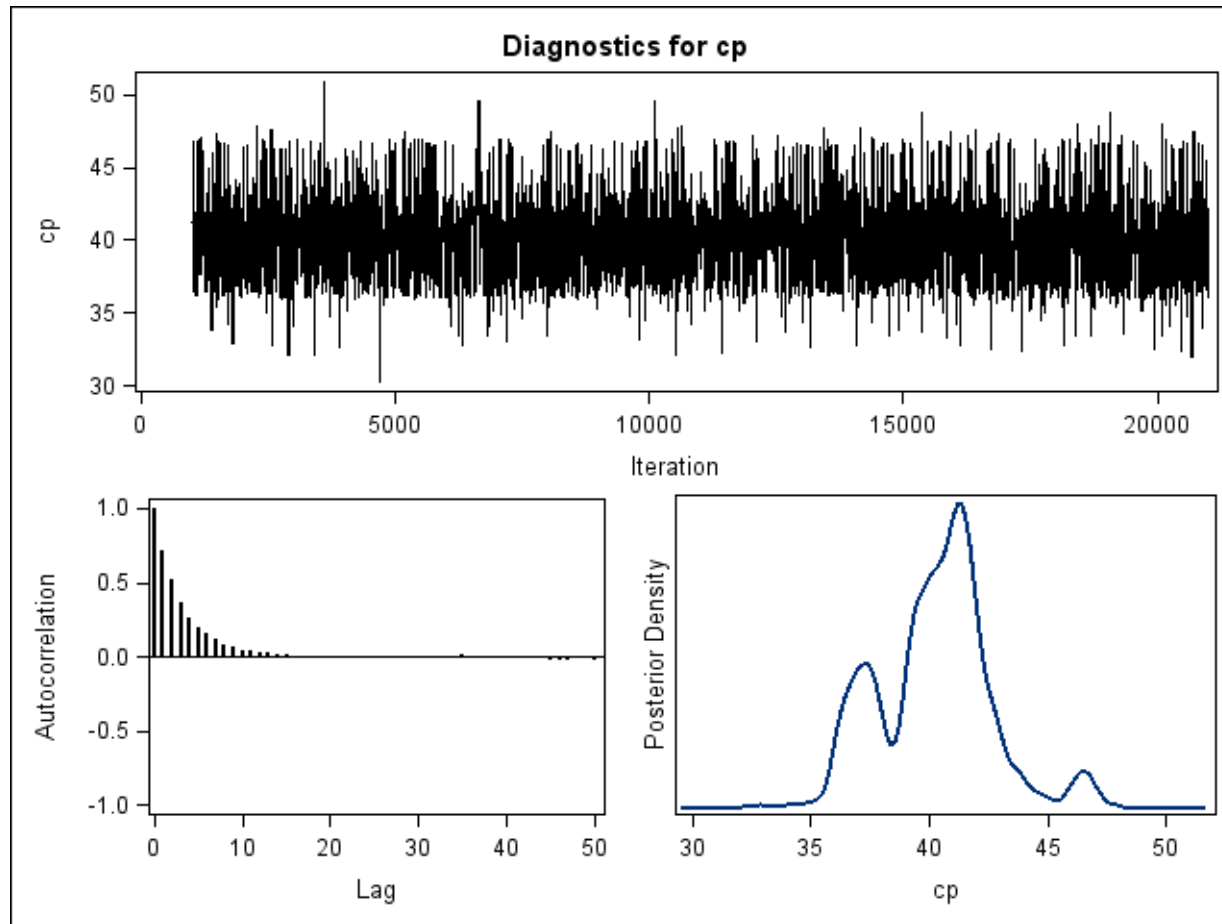
node	mean	sd	MC error	2.5%	median	97.5%	start	sample
x.change	<b>39.22</b>	2.476	0.0212	35.1	39.44	44.48	1000	20000
mu[1]	3.141	0.2965	0.002096	2.597	3.128	3.753	1000	20000
mu[112]	1.076	0.06495	4.924E-4	1.002	1.059	1.242	1000	20000

## SAS

The MCMC Procedure  
Posterior Summaries

Parameter	N	Mean	Standard Deviation	Percentiles		
				25%	50%	75%
cp	20000	<b>40.2860</b>	2.4217	38.9566	40.4605	41.6282
lambda1	20000	3.1500	0.2952	2.9455	3.1390	3.3407
lambda2	20000	0.9377	0.1205	0.8538	0.9312	1.0173

# Density estimate for the posterior distribution of the changepoint



Thank you !!!