WinBUGS 1.4.1

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The BUGS (Bayesian inference Using Gibbs Sampling) project is concerned with flexible software for the Bayesian analysis of complex statistical models using Markov chain Monte Carlo (MCMC) methods.

The project began in 1989 in the MRC Biostatistics Unit and led initially to the 'Classic' BUGS program, and then onto the WinBUGS software developed jointly with the Imperial College School of Medicine at St Mary's, London.

Development now also includes the OpenBUGS project in the University of Helsinki, Finland.

There are now many versions of BUGS, which can be confusing.

Example: Hierarchical model

- Data

School	y_i	σ_i
A	28.39	14.9
B	7.94	10.2
C	-2.75	16.3
D	6.82	11.0
E	-0.64	9.4
F	0.63	11.4
G	18.01	10.4
H	12.16	17.6

- Hierarchical model

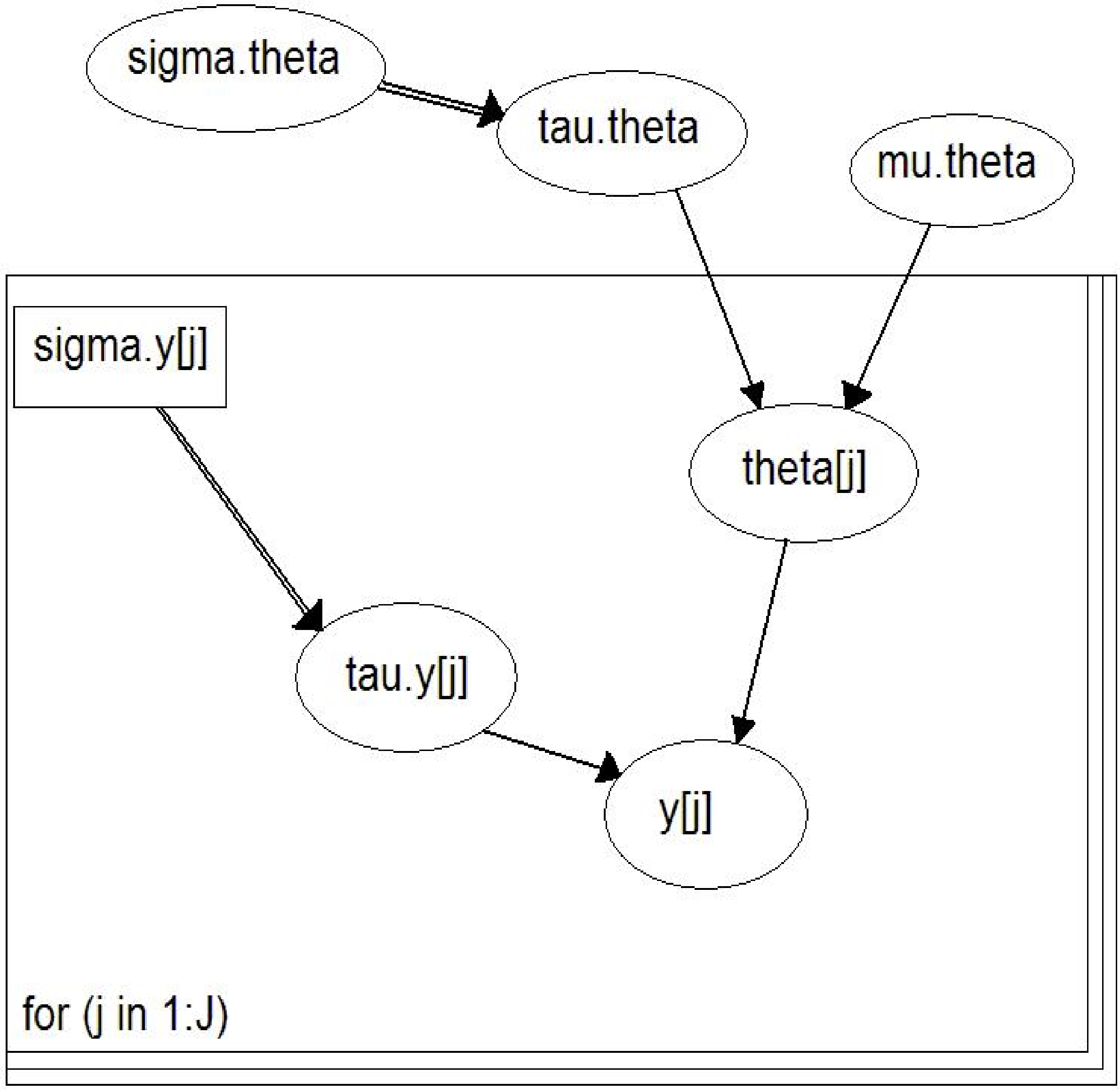
$$\begin{aligned} y_i &\sim N(\theta_i, \sigma_i^2) \\ \theta_i &\sim N(\mu_\theta, \sigma_\theta^2) \end{aligned}$$

for $i = 1, \ldots, I = 8$.

- Hyperprior

$$\begin{aligned} \mu_\theta &\sim N(0, 10^6) \\ \sigma_\theta &\sim U(0, 100) \end{aligned}$$

Graphical model



Bugs code

```
model;
{
   for( j in 1 : J ) {
      theta[j] ~ dnorm(mu.theta,tau.theta)
   }
   for( j in 1 : J ) {
      y[j] ~ dnorm(theta[j],tau.y[j])
   }
   mu.theta ~ dnorm( 0.0,1.0E-6)
   tau.theta <- pow(sigma.theta, -2)
   for( j in 1 : J ) {
      tau.y[j] <- pow(sigma.y[j], -2)
   }
   sigma.theta ~ dunif(0,100)
}
```

Bugs from R - R2WinBUGS

```
install.packages("R2WinBUGS")
library("R2WinBUGS")
data(schools)
J       <- nrow(schools)
y       <- schools$estimate
sigma.y <- schools$sd
data    <- list("J","y","sigma.y")
inits   <- function(){
  list(theta=rnorm(J,0,100),mu.theta=rnorm(1,0,100),
       sigma.theta=runif(1,0,100))
}
schools.sim = bugs(data,inits,
  model.file="hierarchicalmodel.bug",
  parameters=c("theta","mu.theta","sigma.theta"),
  n.chains=3,n.iter=2000,n.burnin=1000,n.thin=1,
  bugs.directory="c:/Program Files/WinBUGS14/",
  codaPkg=FALSE)
print(schools.sim)
plot(schools.sim)
```

Nonlinear growth curve

Extracted from WinBugs

Carlin and Gelfand (1991) present a nonconjugate Bayesian analysis of the following data set from Ratkowsky (1983):

Dugong (sea cows)	1	2	3	...	26	27
Age (X)	1.00	1.50	1.50	...	29.0	31.50
Length (Y)	1.80	1.85	1.87	...	2.27	2.57

Carlin and Gelfand (1991) model this data using a nonlinear growth curve with no inflection point and an asymptote as x_i tends to infinity:

$$\begin{aligned} y_i &\sim N(\mu_i, \tau^{-1}) \\ \mu_i &= \alpha + \beta\gamma^{x_i} \end{aligned}$$

for $i = 1, \ldots, 27$, $\alpha, \beta > 1$ and $0 < \gamma < 1$.

Standard noninformative priors are adopted for α, β and τ, and a uniform prior on (0,1) is assumed for γ.

- WinBugs code

```
model{
  for( i in 1 : N ) {
    y[i] ~ dnorm(mu[i], tau)
    mu[i] <- alpha - beta * pow(gamma,x[i])
  }
  alpha ~ dnorm(0.0, 1.0E-6)
  beta ~ dnorm(0.0, 1.0E-6)
  gamma ~ dunif(0.0, 1.0)
  tau ~ dgamma(0.001, 0.001)
}
```

- R code

```
x = c(1.0,1.5,1.5,1.5,2.5,4.0,5.0,5.0,7.0,8.0,8.5,
      9.0,9.5,9.5,10.0,12.0,12.0,13.0,13.0,14.5,
      15.5,15.5,16.5,17.0,22.5,29.0,31.5)
y = c(1.80,1.85,1.87,1.77,2.02,2.27,2.15,2.26,2.47,
      2.19,2.26,2.40,2.39,2.41,2.50,2.32,2.32,2.43,
      2.47,2.56,2.65,2.47,2.64,2.56,2.70,2.72,2.57)
N     <- length(x)
data  <- list("x","y","N")
inits <- function(){
  list(alpha=1,beta=1,tau=1,gamma=0.9)
}
nonlinear.sim = bugs(data,inits,
     model.file="nonlinearmodel.bug",
     parameters=c("alpha","beta","tau","gamma"),
     n.chains=1,n.iter=10000,n.burnin=5000,n.thin=1,
     bugs.directory="c:/Program Files/WinBUGS14/",
     codaPkg=FALSE)
```

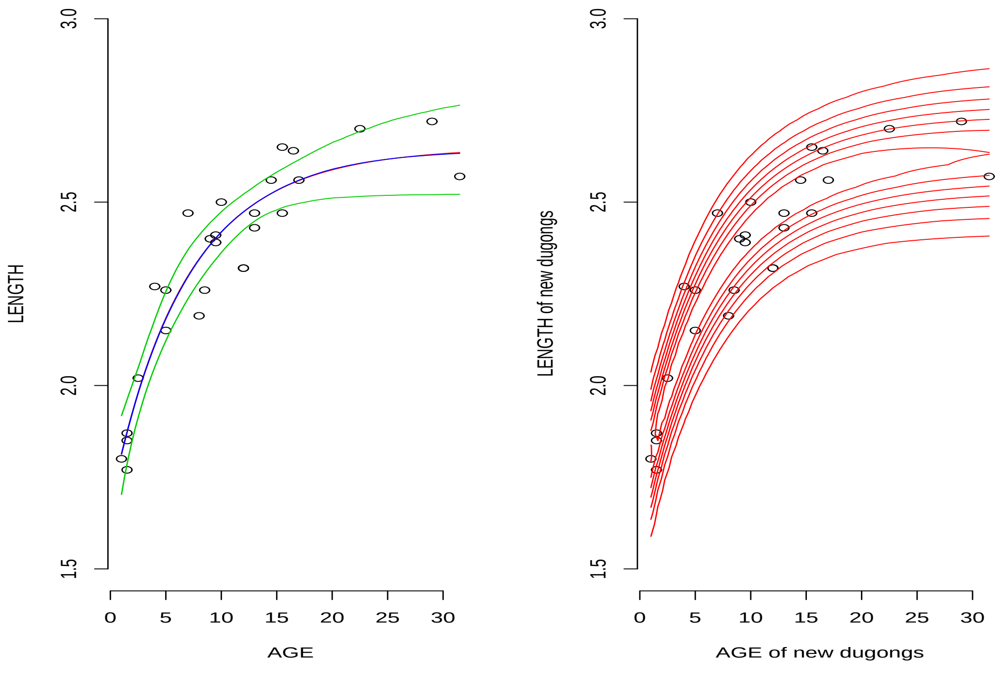
- Posterior summary

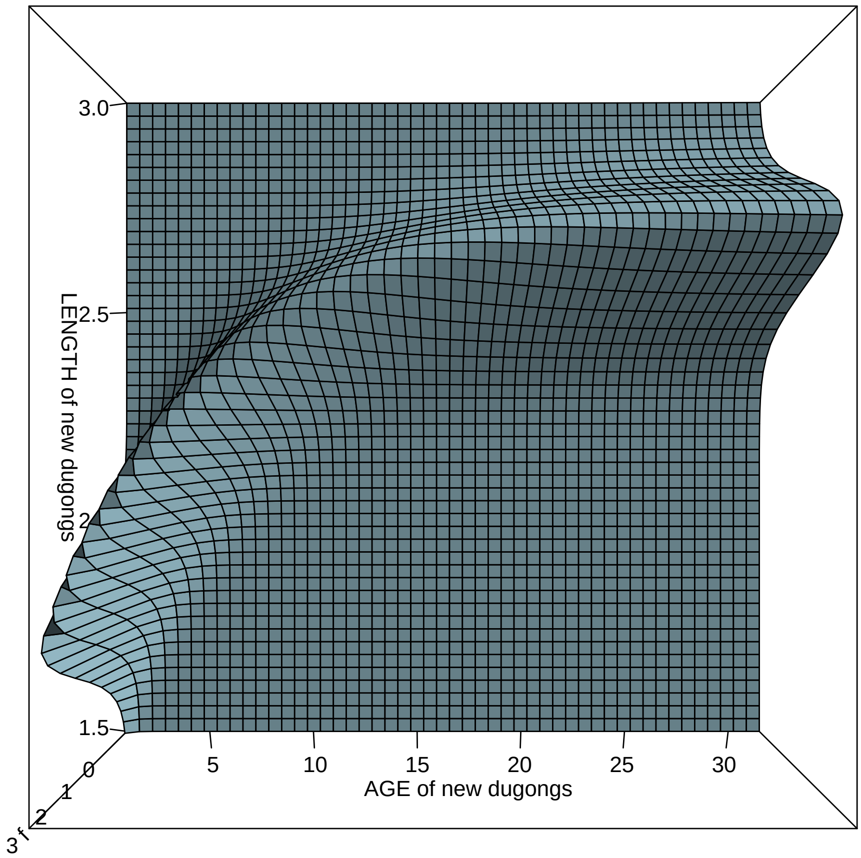
	α	β	τ	γ
1st Qu.	2.600	0.9244	85.06	0.8418
Median	2.643	0.9739	104.70	0.8646
Mean	2.652	0.9755	107.80	0.8607
3rd Qu.	2.694	1.0240	127.20	0.8845

- Posterior inference for

mean function : $E(y|x) = \alpha + \beta\gamma^x$

predictive : $p(y_{new}|x_{new}, \mathbf{x}, \mathbf{y})$




3.0
2.5
2
1.5
LENGTH of new dugongs
0
1
2
3
f
5
10
15
20
25
30
AGE of new dugongs

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