

1 EXAMPLE 1: BIRTHWEIGHT & ESTRIOL LEVEL

1.1 Model (Bug file)

```

model example1;
const n=31; # n=sample size
var  estriol[n], # estriol level of pregnant woman
     birth[n],  # birthweight
     mu[n],     # regression expected value
     a.star,a,b,tau,s2; # model parameters,
                        # tau = precision, s2=1/tau error variance
data estriol,birth in 'estriol.dat';
inits in 'estriol2.ini';
{
#     definition of likelihood function
#
#     for (i in 1:n) {
#         birth[i]~dnorm( mu[i], tau ); # random component
#         systematic component & link function
#         mu[i]<-a.star+b*(estriol[i]-mean(estriol[]));
#     }
#     prior distributions
#
#     a.star~dnorm( 0, 1.0E-04 ); # normal prior for a
#     b~dnorm( 0, 1.0E-04 ); # normal prior for b
#     tau~dgamma( 1.0E-04 , 1.0E-04 ); # gamma prior for precision
#     s2<-1/tau;
#     a<-a.star-b*mean(estriol[]);
#
}

```

1.2 Initial Values (estriol2.ini)

```
list(a.star=0.0, b=0.0, tau=1.0)
```

1.3 Data (estriol.dat)

```

7      25
9      25
9      25
12     27
14     27
16     27
16     24
14     30
16     30
16     31
17     30
19     31
21     30
24     28
15     32
16     32
17     32
25     32
27     34
15     34
15     34
15     35
16     35
19     34
18     35
17     36
18     37
20     38
22     40
25     39
24     43

```

2 EXAMPLE 2: BEETLES DATASET

2.1 Model (Bug file)

```

model beetles;
const
  N = 8;      # number of doses
var
  r[N],p[N],x[N],n[N],alpha,alpha.star,beta,r.hat[N], odds.ratio;
data x, n, r in "beetles.dat";
inits in "beetles.in";
{
  for (i in 1:N) {
    r[i] ~ dbin(p[i], n[i]);
    logit(p[i]) <- alpha.star + beta*(x[i]-mean(x[]));
    r.hat[i] <- p[i]*n[i]; # fitted values
  }
  alpha.star ~ dnorm(0.0, 1.0E-3);
  beta ~ dnorm(0.0, 1.0E-3);
  alpha <- alpha.star - beta*mean(x[]);
  odds.ratio <- exp( beta )
}

```

2.2 Initial Values (beetles.ini)

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

2.3 Data (beetles.dat)

```

1.6907  59   6
1.7242  60  13
1.7552  62  18
1.7842  56  28
1.8113  63  52
1.8369  59  53
1.8610  62  61
1.8839  60  60

```

3 EXAMPLE 3: WAIS & SENILITY SYMPTOMS

3.1 Model (Bug file)

```

model example3;
const n=54;          # number of observations
var   wais[n],      # wais measurement
      symptom[n],  # symptom binary indicator
      p[n],        # probability of symptom appearance
      alpha,       # alpha parameter
      beta,        # beta parameter
      odds.ratio,  # odds ratio
      x.fifty,    # value of x for p=1/2
      p.meanx;    # fitted probability for x=mean(x)
data wais, symptom in 'wais.dat';
inits in 'wais.ini';
{
#       Likelihood Definition
  for (i in 1:n) {
#           random component
            symptom[i]~dbern( p[i] );
#           systematic component & link function
            logit( p[i] ) <- alpha + beta * wais[i];
  }
#       calculation of odds ratio
  odds.ratio<-exp(beta);
#       priors for alpha and beta
  alpha~dnorm(0.0, 0.00001);
  beta~dnorm(0.0, 0.00001);
#       x.fifty
  x.fifty<- -alpha/beta
#       symptom probability for mean of observed wais
  p.meanx<-exp( alpha+beta*mean(wais[]) )/
  (1+exp(alpha+beta*mean(wais[]) ) )
}

```

3.2 Initial Values (wais.ini)

```
list( alpha=0.0, beta=0.0 )
```

3.3 Data (wais.dat)

```

9      1
13     1
6      1
8      1
10     1
4      1
14     1
8      1
11     1
7      1
9      1
7      1
5      1
14     1
13     0
16     0
10     0
12     0
11     0
14     0
15     0
18     0
7      0
16     0

```

9	0
9	0
11	0
13	0
15	0
13	0
10	0
11	0
6	0
17	0
14	0
19	0
9	0
11	0
14	0
10	0
16	0
10	0
16	0
14	0
13	0
13	0
9	0
15	0
10	0
11	0
12	0
4	0
14	0
20	0

4 EXAMPLE 4: BREAST CANCER & AGE AT 1st BIRTH

4.1 Model (Bug file)

```

model example4;
const n=4;      # number of cells
var  status[n], # study group (1=case, 0=control)
     age[n],    # age at 1st birth (0=age<30, 1=age>29)
     counts[n], # cell counts
     lambda[n], # expected number of cells
     mu,        # constant parameter
     a,         # status effect
     b,         # age effect
     ab,        # interactio between status and age
     odds.ratio; # odds ratio
data status, age, counts in 'breast.dat';
inits in 'breast.ini';
{
#      Likelihood Definition
  for (i in 1:n) {
#          random component
    counts[i]~dpois( lambda[i] );
#      systematic component & link function
    log( lambda[i] ) <- mu + a*status[i] +b*age[i]+
ab*status[i]*age[i];
  }
#      calculation of odds ratio
  odds.ratio<-exp(ab);
#      priors for model parameters
  mu~dnorm(0.0, 0.00001);
  a~dnorm(0.0, 0.00001);
  b~dnorm(0.0, 0.00001);
  ab~dnorm(0.0, 0.00001);
}

```

4.2 Initial Values (breast.ini)

```
list(mu=0, a=0, b=0, ab=0)
```

4.3 Data (breast.dat)

```

1 1 683
1 0 2537
0 1 1498
0 0 8747

```

5 EXAMPLE 5: 2x2x2 COMMON ODDS RATIO ESTIMATION: PASSIVE SMOKING & CANCER ADJUSTING FOR SMOKING STATUS

5.1 ANALYSIS 1: DIFFERENT RISK PER SMOKING STATUS

5.1.1 Model (Bug File)

```

model ex5notcommonOR;
const n=8,
      p=4;
var
  smoking[n],
  status[n],
  passive[n],
  counts[n],
  b[2,p],
  lambda[n],
  or[2];
data smoking, status, passive, counts in 'smoke.dat';
inits in 'smoke.ini';
{
#
#      model for 1st table (nonsmokers)
#      for (i in 1:4) {
#          counts[i]~dpois( lambda[i] );
#          log(lambda[i])<- b[1,1] + b[1,2]*status[i] +
b[1,3]*passive[i] + b[1,4]*status[i]*passive[i];
#      }
#
#      model for 2nd table (smokers)
#      for (i in 5:8) {
#          counts[i]~dpois( lambda[i] );
#          log(lambda[i])<- b[2,1] + b[2,2]*status[i] +
b[2,3]*passive[i] + b[2,4]*status[i]*passive[i];
#      }
#      priors
#      for (i in 1:2){
#          for (j in 1:p){
#              b[i,j]~dnorm(0.0, 1.0E-04)
#          }
#      }
#      odds ratios
#      or[1]<-exp(b[1,4])
#      or[2]<-exp(b[2,4])
}

```

5.1.2 Initial Values (smoke.ini)

```
list(b=c(0,0,0,0,0,0,0,0))
```

5.1.3 Data (smoke.dat)

```

0 1 1 120
0 1 0 111
0 0 1 80
0 0 0 155
1 1 1 161
1 1 0 117
1 0 1 130
1 0 0 124

```

5.2 ANALYSIS 2: COMMON RISK PER SMOKING STATUS

5.2.1 Model (Bug File)

```

model ex5commonOR;
const n=8,
      p=4;
var
  smoking[n],
  status[n],
  passive[n],
  counts[n],
  b[2,p-1],
  ab,
  lambda[n],
  or;
data smoking, status, passive, counts in 'smoke.dat';
inits in 'smoke2.ini';
{
#
#      model for 1st table (nonsmokers)
#      for (i in 1:4) {
#          counts[i]~dpois( lambda[i] );
#          log(lambda[i])<- b[1,1] + b[1,2]*status[i] +
b[1,3]*passive[i] + ab*status[i]*passive[i];
#      }
#
#      model for 2nd table (smokers)
#      for (i in 5:8) {
#          counts[i]~dpois( lambda[i] );
#          log(lambda[i])<- b[2,1] + b[2,2]*status[i] +
b[2,3]*passive[i] + ab*status[i]*passive[i];
#      }
#      priors
#      for (i in 1:2){
#          for (j in 1:p-1){
#              b[i,j]~dnorm(0.0, 1.0E-04);
#          }
#      }
#      ab~dnorm(0.0, 1.0E-04);
#      odds ratios
#      or<-exp(ab)
}

```

5.2.2 Initial Values (smoke2.ini)

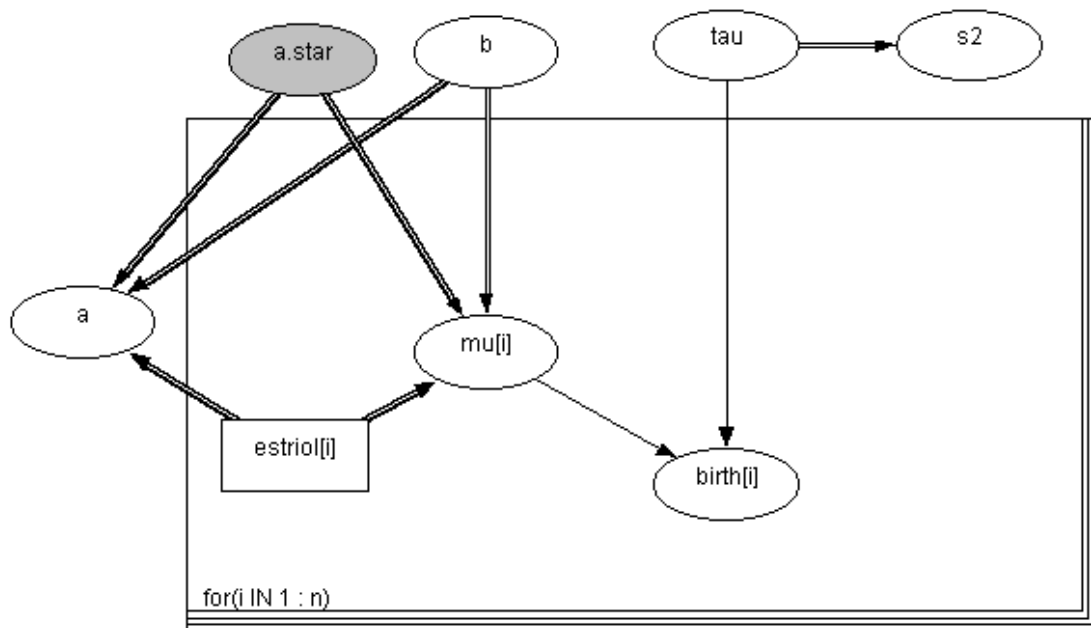
```
list(b=c(0,0,0,0,0,0),ab=0)
```

6 WINBUGS EXAMPLE: BIRTHWEIGHT & ESTRIOL LEVEL

```

{
#      definition of likelihood function
#
#      for (i in 1:n) {
#          birth[i]~dnorm( mu[i], tau ); # random component
#          mu[i]<-a.star+b*(estriol[i]-mean(estriol[])); # systematic
component
#          & link function
#      }
#      prior distributions
#
#      a.star~dnorm( 0, 1.0E-04 ); # normal prior for a
#      b~dnorm( 0, 1.0E-04 ); # normal prior for b
#      tau~dgamma( 1.0E-04 , 1.0E-04 ); # gamma prior for precision
#      s2<-1/tau;
#      a<-a.star-b*mean(estriol[]);
#
#      list(a.star=0.0, b=0.0, tau=1.0) # initial values
#
# data
list(n=31)
estriol[] birth[]
7      25
9      25
9      25
12     27
14     27
16     27
16     24
14     30
16     30
16     31
17     30
19     31
21     30
24     28
15     32
16     32
17     32
25     32
27     34
15     34
15     34
15     35
16     35
19     34
18     35
17     36
18     37
20     38
22     40
25     39
24     43

```



7 A SIMPLE HYPOTHESIS TEST: WINBUGS EXAMPLE

```

model estriol;
{
#   definition of likelihood function
#
  for (i in 1:n) {
    birth[i]~dnorm( mu[i], tau ); # random component
    mu[i]<-a.star+gamma*b*(estriol[i]-mean(estriol[])); # systematic component
    #   & link function
  }
#   prior distributions
#
  a.star~dnorm( 0, 1.0E-04 ); # normal prior for a
  b~dnorm( 0, 1.575); # normal prior for b
  gamma~dbern(0.5);
  tau~dgamma( 1.0E-04 , 1.0E-04 ); # gamma prior for precision
  s2<-1/tau;
  a<-a.star-b*mean(estriol[]);
}
list(a.star=0.0, b=0.0, tau=1.0,gamma=1)
  
```