1. Analyze the following data with one-way anova model in BUGS. The data are in tabular format, 4 measurements per group, 5 groups. Compare the group means and draw a box-plot of their posterior distributions. Can we conclude difference between (any or some) groups? Compute $P(\mu_i > \mu_i' \mid \text{data})$ and $\min(P(\beta_i > 0 \mid \text{data}), P(\beta_i < 0 \mid \text{data}))$ for $i, i' \in \{1,2,3,4,5\}$. Check also the posterior of σ. (The data were generated from N([1,2,3,4,5],2^2)). Implement the model with CR constraints and then with STZ constraints, and finally the simple model without intercept (no constraints then). Check the 2D-posterior distributions of the pairs (β_i, β_i') in each case (Correlation Tool in BUGS).

$$y_{i,j} \sim \mathrm{N}(\mu_i, \sigma^2) \quad \tau \sim \Gamma(0.001, 0.001)$$
$$\mu_i = \beta_0 + \beta_i \quad i = 1,2,3,4,5, \text{and } j = 1,2,3,4.$$

```
  list(y=structure(.Data=c(
  -0.34,  1.34, 3.25, 0.22,
   0.89, -0.07, 1.08, 4.56,
   4.12,  1.90, 2.45, 0.27,
   4.95,  2.44, 2.34, 4.62,
   3.62,  9.84, 6.14, 4.63),.Dim=c(5,4)))

 model{
for(i in 1:5){ # groups
  m[i] <- inprod(beta[],X[i,1:6]) # mean of group i
for(j in 1:4){ # measurements
y[i,j] ~ dnorm(mu[i,j],tau)
mu[i,j] <- inprod(beta[1:6],X[i,1:6])
             # X=dummies given in data list
}}
tau ~ dgamma(0.001,0.001); s <- pow(tau,-0.5)
for(i in 1:6){beta[i] ~ dnorm(0,0.001)}
 # beta[1] is intercept
}
  list(tau=1,beta=c(0,0,0,0,0,0))
  list(y=structure(.Data=c(
  -0.34,  1.34, 3.25, 0.22,
   0.89, -0.07, 1.08, 4.56,
   4.12,  1.90, 2.45, 0.27,
   4.95,  2.44, 2.34, 4.62,
   3.62,  9.84, 6.14, 4.63),.Dim=c(5,4)),
  # simple model without intercept,
  # so beta[1] is redundant (no constraints):
 X=structure(.Data=c(0,1,0,0,0,0,
                     0,0,1,0,0,0,
                     0,0,0,1,0,0,
                     0,0,0,0,1,0,
                     0,0,0,0,0,1),.Dim=c(5,6)))
 # STZ dummies:
  X=structure(.Data=c(1,-1,-1,-1,-1,-1,
                      1,0,1,0,0,0,
```

```
                        1,0,0,1,0,0,
                        1,0,0,0,1,0,
                        1,0,0,0,0,1),.Dim=c(5,6)))
 # CR dummies:
  X=structure(.Data=c(1,0,0,0,0,0,
                        1,0,1,0,0,0,
                        1,0,0,1,0,0,
                        1,0,0,0,1,0,
                        1,0,0,0,0,1),.Dim=c(5,6)))
# the data were generated from N(c(1,2,3,4,5),2^2)
```

2. Analyze the following data with two-way anova model with interactions in BUGS. The data are in tabular format, 8 measurements per group, 5×5 groups defined by two 5-level factors. Can we conclude any of the interactions to be relevant? (The data were generated using CR constraints with $\alpha_2, \ldots, \alpha_5 = 1, 2, 3, 4$, $\beta_2, \ldots, \beta_5 = 2, 4, 6, 8$, $\gamma_{i,j} = 0$ except $\gamma_{5,5} = 3$, and $\sigma = 2$). Compute DIC. Draw box-plots of all parameters α, β, γ. If you collect them in a single vector, you could plot them all against true values using 'Model Fit' in 'Comparison Tool'. Then compute a model with only main effects and $\gamma_{5,5}$ while setting $\gamma_{i,j} = 0$ for other interactions. Compute DIC and compare with previous model. Finally, try with the second data set, which was generated from the same 'true model' but with $\sigma = 0.5$. The estimates should now be better because of reduced 'noise' in the data.

$y_{i,j,k} \sim \mathrm{N}(\mu_{i,j}, \sigma^2) \quad \tau \sim \Gamma(0.001, 0.001)$
$\mu_{i,j} = \beta_0 + \alpha_i + \beta_j + \gamma_{i,j} \quad i = 1, \ldots, 5, \text{and } j = 1, \ldots, 5, \text{and } k = 1, \ldots, 8.$
CR constraints can be imposed

First data set:

```
 # data generated with sigma=2:
list(N=8,z=structure(.Data=c( -3.11, -2.97, -0.99, 1.59, -0.39,
-5.39, -2.97, 1.17, -1.54, 2.51, 1.03, 1.18, 4.06, 3.46, 4.27, 4.01,
7.2, 2.77, 5.19, 3.53, 4.66, 3.56, 5.91, 1.3, 5.85, 5.61, 5.03,
5.39, 4.78, 4.72, 5.9, 4.19, 8.82, 5.76, 5.22, 6.25, 8.59, 8.15,
8.59, 9.52, 2.02, 0.56, 1.14, 3.27, 3.78, 0.6, 0.04, 0.38, 2.85,
4.37, 5.67, 3.64, 2.78, -0.38, 3.44, 3.54, 6.18, 4.36, 3.12, 0.03,
6.81, 3.27, 7.19, 0.95, 7.09, 7.57, 8.4, 7.71, 7.53, 10.16, 5.97,
6.6, 11.36, 8.99, 8.66, 8.67, 11, 8.42, 9.2, 7.34, 1.6, 3.78, 4.91,
2.87, 1.99, 5.21, 1.16, -1.75, 6.26, 4.58, 3.8, 5.84, 3.84, 6.02,
1.83, 5, 5.46, 4.47, 10.14, 6.38, 3.56, 7.21, 4.47, 8.39, 7.42,
8.33, 9.41, 6.89, 7.72, 3.29, 9.27, 7.78, 9.06, 8.29, 11.85, 10.32,
12.25, 6.71, 9.67, 8.06, 3.73, 3.76, 4.64, 2.56, 1.19, 3.08, 5.19,
3.94, 4.46, 7.94, 2.64, 4.03, 6.72, 6.83, 5.17, 5.97, 8.21, 4.73,
7.85, 5.05, 8.53, 8.83, 3.24, 8.93, 9.68, 9, 3.89, 9.83, 10.71, 11,
4.08, 11.17, 9.3, 13.48, 8.29, 10.05, 7.79, 10.46, 9.33, 9.5, 7.86,
-0.93, 2.15, 2.61, 6.74, 4.29, 5.78, 6.85, 4.1, 4.85, 7.48, 7.77,
5.61, 9.09, 1.52, 6.44, 5.55, 7.9, 10.3, 8.58, 9.35, 6.52, 7.55,
5.04, 10.2, 8.8, 8.16, 9.79, 10.6, 9.83, 5.39, 8.05, 16.32, 13.86,
```

```
16.69, 15.68, 18.09, 15.86, 15.26, 14.29), .Dim = c(5, 5,
8)),betatrue=c(0,1,2,3,4,2,4,6,8,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3))
```

Second data set:

```
 # data generated with sigma=0.5:
list(N=8,z=structure(.Data=c(0.17, -0.23, 0.73, -0.27, 0.19, 0.09,
-0.28, -0.94, 1.95, 1.92, 1.88, 2.48, 2.07, 2.44, 2.41, 2.26, 4.47,
3.86, 4.45, 3.67, 5.32, 4.42, 3.8, 3.32, 5.73, 5.57, 5.95, 6.14,
5.59, 5.32, 5.9, 6.04, 7.86, 8.69, 7.89, 7.15, 8.56, 7.86, 7.16,
8.13, 0.75, 1.03, 1.35, 0.64, 0.45, 0.89, 1.32, 1.36, 2.76, 2.42,
2.84, 2.64, 3.53, 3.07, 1.93, 2.27, 5.21, 4.99, 5.29, 5.07, 4.84,
5.79, 5.51, 5.02, 6.95, 6.55, 8.17, 7.14, 7.45, 6.43, 7.4, 7.81,
8.82, 9.35, 8.12, 8.48, 9.29, 9.15, 9.21, 8.71, 1.12, 3.26, 2.17,
2.63, 1.77, 0.89, 2.91, 1.51, 4.15, 4.07, 4.22, 3.96, 3.35, 4.88,
4.32, 3.47, 5.38, 5.67, 6.74, 7.23, 5.19, 6.3, 6.22, 6.88, 8.3,
7.73, 8.08, 7.91, 7.83, 8.17, 8.24, 7.61, 10.56, 10.77, 10.85,
10.12, 10.75, 9.62, 9.95, 10.18, 3.87, 3.02, 2.28, 1.89, 3.5, 3.32,
2.34, 2.85, 5.23, 4.88, 4.7, 4.93, 4.18, 5.46, 4.42, 5.14, 6.61,
6.68, 6.19, 7.25, 7.68, 6.76, 7.88, 6.23, 8.95, 9.13, 8.92, 8.86,
8.95, 8.99, 9.44, 8.8, 10.45, 11.74, 11.59, 11.39, 11.23, 11.2,
12.08, 10.1, 3.71, 4.54, 3.22, 4.02, 3.8, 4.57, 4.3, 3.48, 5.6,
5.58, 6.12, 6.82, 6.83, 5.51, 6.78, 5.35, 8.2, 7.74, 8.11, 7.8,
7.93, 8.47, 8.47, 7.65, 10.32, 9.8, 9.56, 10.13, 10.5, 10.51, 10.07,
9.55, 15.31, 15, 15.58, 15.06, 14.5, 15.16, 15.66, 15.28), .Dim =
c(5, 5,
8)),betatrue=c(0,1,2,3,4,2,4,6,8,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,3))

model{
# CR dummies
for(i in 1:5){
for(j in 1:5){
X[i,j,1] <- 1 # constant term
for(u in 2:5){X[i,j,u] <- equals(i,u)  }   # groups 2:5 of variable A
for(v in 2:5){X[i,j,4+v] <- equals(j,v) }  # groups 2:5 of variable B
for(k in 1:4){X[i,j,9+k] <- X[i,j,2]*X[i,j,5+k] }  # interactions A2 B(k+1)
for(k in 1:4){X[i,j,13+k] <- X[i,j,3]*X[i,j,5+k] }  # interactions A3 B(k+1)
for(k in 1:4){X[i,j,17+k] <- X[i,j,4]*X[i,j,5+k] }  # interactions A4 B(k+1)
for(k in 1:4){X[i,j,21+k] <- X[i,j,5]*X[i,j,5+k] }  # interactions A5 B(k+1)
m[i,j] <-  inprod(beta[1:25],X[i,j,1:25]) # group means as parameters
mobs[i,j] <- mean(z[i,j,1:N]) # observed group means
for(r in 1:N){
z[i,j,r] ~ dnorm(mu[i,j,r],tau)
mu[i,j,r] <- inprod(beta[1:25],X[i,j,1:25])
}}}
tau ~ dgamma(0.001,0.001); s <- pow(tau,-0.5)
```

```
for(k in 1:25){beta[k] ~ dnorm(0,0.001);axis[k]<-k;bt[k]<-betatrue[k]}
#for(k in 10:24){beta[k]<-0} # for setting all except the last interactions zeros
# beta[1] = intercept
# beta[2:5] = main effects A2...A5
# beta[6:9] = main effects B2...B5
# beta[10:25] = interactions (A2...A5)x(B2...B5)
}
# initials:
list(beta=c(0,0,0,0,0,0,0,0,0,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,NA,0),tau=1)
list(beta=c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),tau=1)
```

3. In the bioassay example, fit the separate lines model where

$$\mu_i = \beta_{0,\text{drug}_i} + \beta_{1,\text{drug}_i} \log(\text{dose}_i)$$

Check the plausibility of parallel lines assumption (corresponds to slope difference $\beta_{1,2} - \beta_{1,1}$).

```
 list( n=24,
 y=c(68.8, 67.6, 68.1, 67.6,  69.0, 67.9, 68.6, 68.3,
     61.4, 59.8, 62.3, 60.6,  60.9, 60.3, 61.6, 61.8,
     53.5, 51.9, 53.6, 52.2,  53.8, 54.9, 54.1, 54.2),
 dose=c(0.025, 0.025, 0.025, 0.025, 0.025, 0.025, 0.025, 0.025,
        0.050, 0.050, 0.050, 0.050, 0.050, 0.050, 0.050, 0.050,
        0.100, 0.100, 0.100, 0.100, 0.100, 0.100, 0.100, 0.100),
 drug=c(1,1,1,1,2,2,2,2, 1,1,1,1,2,2,2,2, 1,1,1,1,2,2,2,2) )
```

Simple parametrization with no need for constraints:

```
 model{
    # model's likelihood
    for (i in 1:n){
        y[i] ~ dnorm( mu[i], tau )
        mu[i] <- beta0[drug[i]] + beta1[drug[i]]*log(dose[i])
    }
    # prior distributions
    beta0[1] ~ dnorm( 0.0, 0.001)  # constant for standard treatment
    beta0[2] ~ dnorm( 0.0, 0.001)  # constant for test treatment
    beta1[1]  ~ dnorm( 0.0, 0.001) # slope for standard treatment
    beta1[2]  ~ dnorm( 0.0, 0.001) # slope for test treatment
   tau ~ dgamma( 0.001, 0.001) # precision of regression model
s <- 1/sqrt(tau) # standard error of regression
#
slope.difference<-beta1[2]-beta1[1]
# test for slope difference>0
p2 <- 1-step(slope.difference)
 }
```

Parametrization with CR or STZ constraints, using design matrix:

```
 model{
    for (i in 1:n){
        # creating the design matrix
        X[i,1]<-1.0          # beta1=constant term
        X[i,2]<- log(dose[i]) # beta2=log dose
        X[i,3]<- equals( drug[i], 2 ) # beta3=CR dummy for test treatment
        #X[i,3]<- equals( drug[i], 2 )-equals( drug[i], 1 )# beta3=STZ dummy
        X[i,4]<-X[i,2]*X[i,3]#beta4=interaction between dose and drug (slope difference)
        # model likelihood
        y[i] ~ dnorm( mu[i], tau )
        mu[i] <- inprod( beta[], X[i,])
    }
    # prior distributions
    for (j in 1:4){ beta[j]~dnorm( 0.0, 0.001) }
    tau ~ dgamma( 0.001, 0.001) # precision of regression model
    s <- 1/sqrt(tau) # standard error of regression
slope.difference<-beta[4] # CR
# slope.difference<-beta[4] # STZ
# test for slope difference>0
p2 <- step(slope.difference)
}
```