

# BDA - Assignment 6

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## Exercise 1

```
library(rstan)
rstan_options(auto_write = TRUE)
options(mc.cores = parallel::detectCores())
library(aaltobda)
data('bioassay')

rho = 0.5
mu1 = 0; sd1 = 2
mu2 = 10; sd2 = 10
mu = c(mu1, mu2)
cov = matrix(c(sd1^2, sd1*sd2*rho, sd1*sd2*rho, sd2^2), 2)
```

```
bioassay <- "
data {
  int J;
  int y[J];
  int n[J];
  vector[J] x;
  matrix[2, 2] cov;
  vector[2] mu;
}

parameters {
  vector[2] theta;
}

model {
  theta ~ multi_normal(mu, cov);
  y ~ binomial_logit(n, theta[1] + theta[2] * x);
}
"
bioassay_data = list(J = 4,
                     y = c(0, 1, 3, 5),
                     n = c(5, 5, 5, 5),
```

```

x = c(-0.86, -0.30, -0.05, 0.73),
mu = mu,
cov = cov)

fit = stan(model_code=bioassay, data=bioassay_data)
monitor(fit)

## Inference for the input samples (4 chains: each with iter = 2000; warmup = 0):
##
##           Q5  Q50  Q95 Mean  SD  Rhat Bulk_ESS Tail_ESS
## theta[1] -0.4  0.9  2.7  1.0 0.9    1    1206    1514
## theta[2]  4.0 10.0 19.1 10.5 4.6    1    1269    1713
## lp__      -9.2 -6.8 -6.1 -7.1 1.1    1    1498    1752
##
## For each parameter, Bulk_ESS and Tail_ESS are crude measures of
## effective sample size for bulk and tail quantities respectively (an ESS > 100
## per chain is considered good), and Rhat is the potential scale reduction
## factor on rank normalized split chains (at convergence, Rhat <= 1.05).

```

## Exercise 2

For convergence analysis, I use Rhat from package rstan. This package uses Rhat which is a potential scale reduction factor on split chains. The split chains method allows us to address the non-stationarity of chains.

From the above results we see that Rhat for parameters alpha and beta are both 1, which is the desired value at convergence. This means that as the number of draws increases the Rhat statistic approaches 1:

$$\lim_{n \rightarrow \infty} R = 1$$

## Exercise 3

```

draws = as.data.frame(fit)[,1:2]
plot(draws, type = 'p', xlim=c(-4,8), ylim=c(-10,40), pch = 19, lwd=0.1, cex=0.4,
     col='midnightblue', main='Scatterplot of the draws', xlab='Alpha', ylab='Beta')

```

**Scatterplot of the draws**

