BDA - Assignment 6

24/10/2021

1

We start by pre-calculating the mean μ and covariance metrics Σ

```
corr = 0.6
a_std = 2
b_std = 10

mu = c(0,10)
sigma = matrix( c(a_std^2, a_std*b_std*corr, a_std*b_std*corr, b_std^2),nrow = 2)
```

Here is the stan model used for the assignment

```
data {
  int<lower=0> N;
  vector[N] x;
  int<lower=0> n[N];
  int<lower=0> y[N];
  vector[2] mu;
  matrix[2,2] sigma;
}
parameters {
  vector[2] theta;
}
model {
  theta ~ multi_normal(mu, sigma);
  for (k in 1:N) {
    y[k] ~ binomial_logit(n[k],theta[1] + theta[2]*x[k]);
  }

}
```

Let us create the data used by stan

```
data <- list(
  N = length(bioassay$x), #Number of data points
  x = bioassay$x,         #Outcome
  n = bioassay$n,         #Total draws
  y = bioassay$y,         #Successes
  mu = mu,                #Mean vector
  sigma = sigma           #Covariance matrix
)
```

```
fit1 = sampling(stanmodel,
  data = data,            # named list of data
  chains = 4,             # number of Markov chains
  warmup = 1000,          # number of warmup iterations per chain
  iter = 2000,              # total number of iterations per chain
  cores = 1,                # number of cores (could use one per chain)
  refresh = 0               # no progress shown
  )
```

We have chosen to use a chain length of 2000 with a warmup of 1000. We are simulating 4 chains.

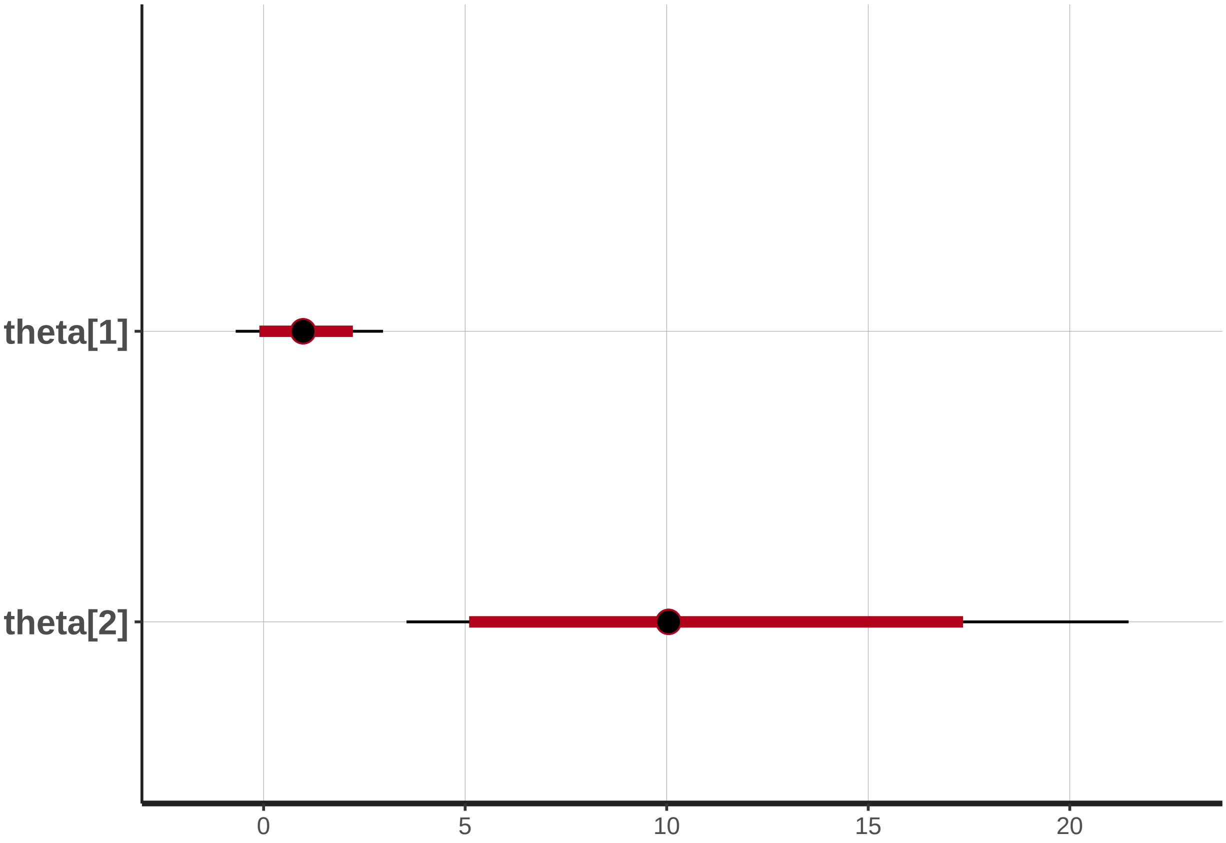
Let us print the model

```
print(fit1)
```

```
## Inference for Stan model: 2dc9fd89244b41be37b26fa255d63416.
## 4 chains, each with iter=2000; warmup=1000; thin=1;
## post-warmup draws per chain=1000, total post-warmup draws=4000.
##
##           mean se_mean   sd  2.5%   25%   50%   75% 97.5% n_eff Rhat
## theta[1]  1.03    0.02 0.92 -0.69  0.41  0.98  1.61  2.96  1371    1
## theta[2] 10.73    0.13 4.76  3.55  7.11 10.05 13.69 21.46  1322    1
## lp__     -7.17    0.03 1.04 -9.97 -7.60 -6.85 -6.42 -6.15  1248    1
##
## Samples were drawn using NUTS(diag_e) at Fri Oct 22 12:32:37 2021.
## For each parameter, n_eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor on split chains (at
## convergence, Rhat=1).
```

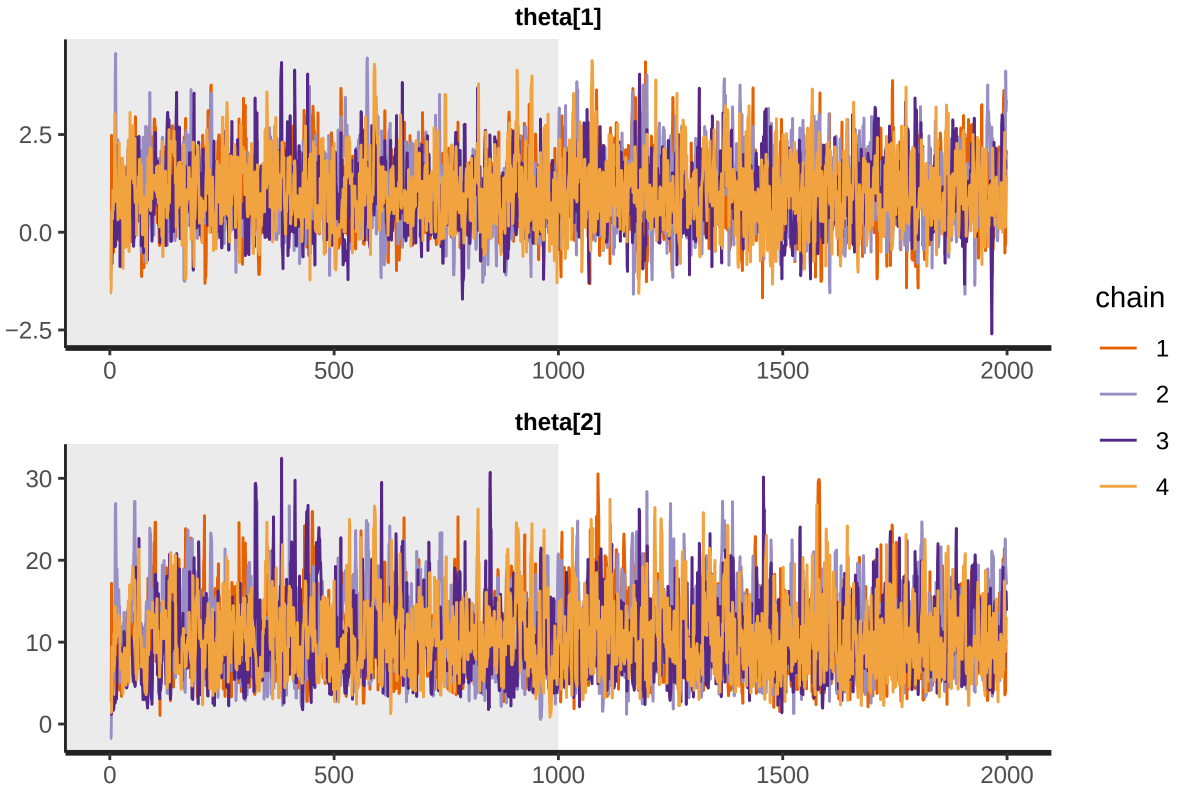
and here we can see how the parameters alpha and beta are distributed

```
plot(fit1, probs=c(.05,.5,.95))
```



We can now plot all chains to examine graphically if they converge.

```
traceplot(fit1, inc_warmup = TRUE, nrow = 2)
```



2

We use the built in function for Rhat from Rstan

```
diagnostics = monitor(fit1)
```

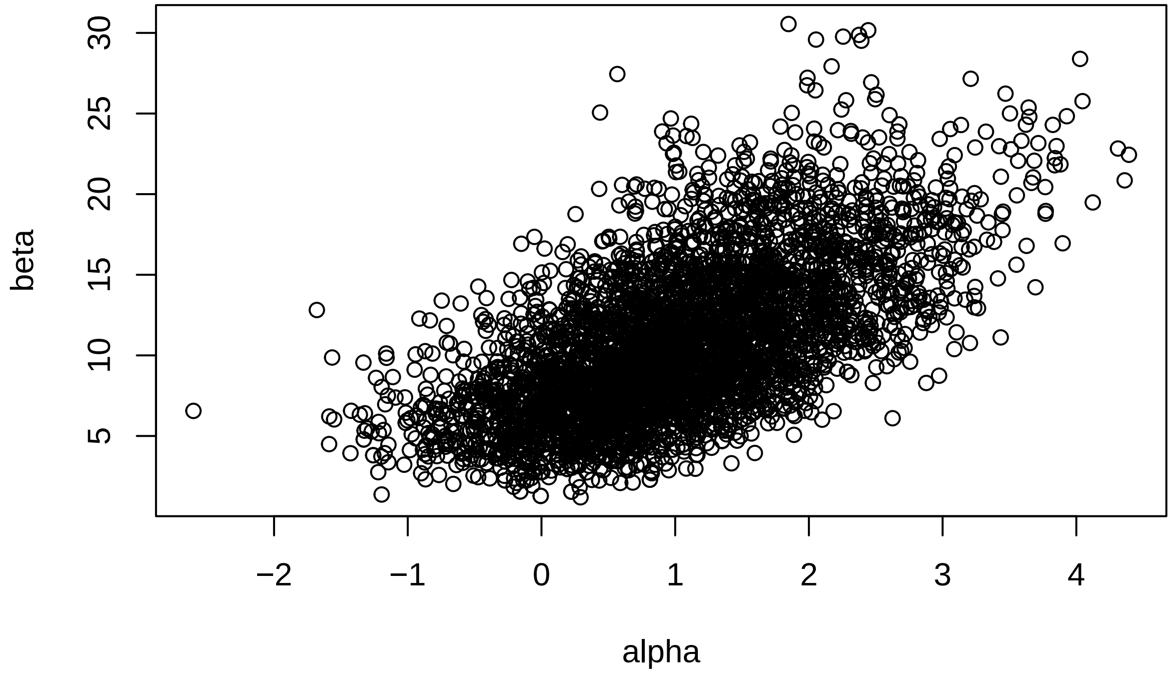
```
## Inference for the input samples (4 chains: each with iter = 2000; warmup = 0):
##
##             Q5  Q50  Q95 Mean  SD  Rhat Bulk_ESS Tail_ESS
## theta[1] -0.4  1.0  2.6  1.0 0.9     1     1393     1697
## theta[2]  4.2 10.0 19.7 10.7 4.8     1     1405     1583
## lp__     -9.3 -6.8 -6.2 -7.2 1.0     1     1406     1846
##
## 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).
```

The $\widehat{R}_\alpha$ is 1.00 and $\widehat{R}_\beta$ is 1.00.

3

Let us scatter plot the parameters

```
theta = extract(fit1)$theta
alpha = theta[,1]
beta = theta[,2]
plot(alpha,beta)
```



We can conclude that the plot is very similar to last weeks plot and the plot from the course book.

4.

The following tech was used for the assignment:

1. OS: Windows 10
2. Language: R
3. Interface used: Rstan

I had no installation or compilation error. I ran everything locally. I found the documentation quite lacking, I found no explanation for the `y ~ dist(para1,para2)` kind of syntax and when to use it and when to use normal `y = dist(y,para1,para2)` syntax.