BDA - Assignment 5

17/10/2021

Contents

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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)
```

We continue

```
density_ratio = function(alpha_propose, alpha_previous, beta_propose, beta_previous, x, y, n){
  likli_propose <- bioassaylp(alpha_propose, beta_propose, x, y, n)
  likli_previous <- bioassaylp(alpha_previous, beta_previous, x, y, n)

  prior_prop <- dmvnorm(c(alpha_propose,beta_propose),mu, sigma, log = TRUE)
  prior_prev <- dmvnorm(c(alpha_previous,beta_previous),mu, sigma, log = TRUE)

  prop = prior_prop + likli_propose
  prev = prior_prev + likli_previous

  res = exp(prop - prev)
  return(res)
}
```

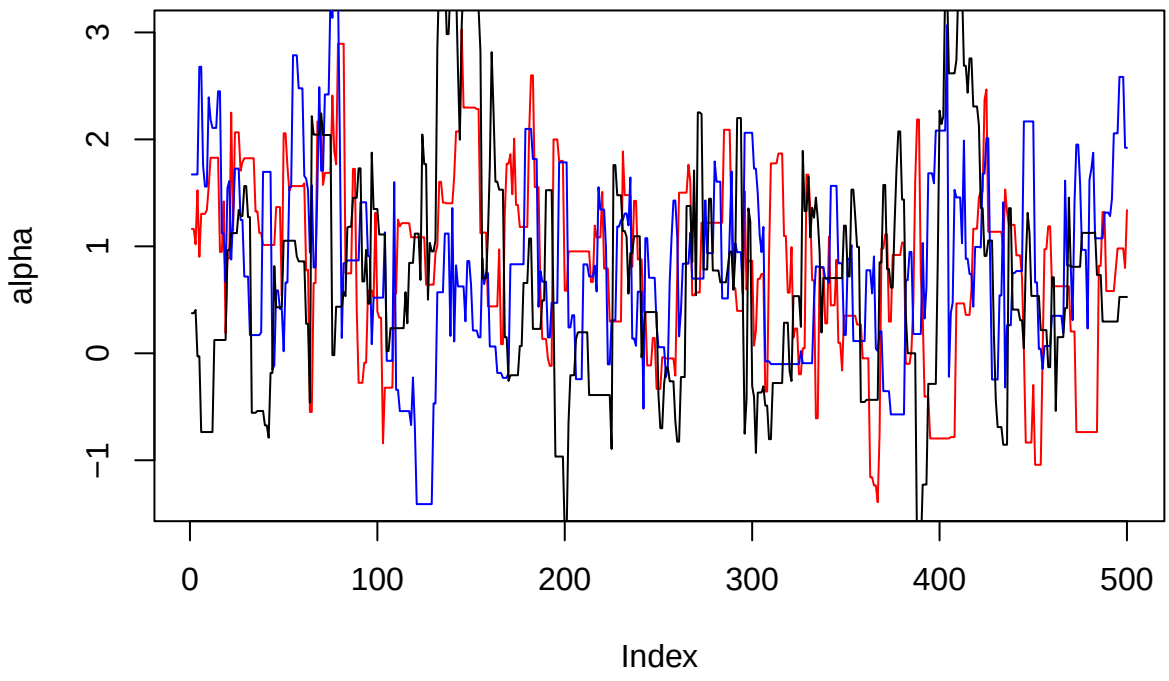
```
Metropolis_bioassay = function(n, alpha_previous, beta_previous, warmup_procent = 0.5){
  alphas = c()
  betas = c()
  for( i in 1:n){
    alpha_propose = rnorm(1, alpha_previous, 1)
    beta_propose = rnorm(1, beta_previous, 5)

     r = density_ratio(alpha_propose = alpha_propose, alpha_previous = alpha_previous, beta_propose = b
     r = min(1,r)
     if(r >= runif(1)){
       alpha_previous = alpha_propose
       beta_previous = beta_propose
     }
    alphas[i] = alpha_previous
    betas[i] = beta_previous
```

```
  }
  alpha_final = na.omit(alphas[n*warmup_procent+1:n])
  beta_final = na.omit(betas[n*warmup_procent+1:n])
  return(cbind(alpha_final,beta_final))
}
```

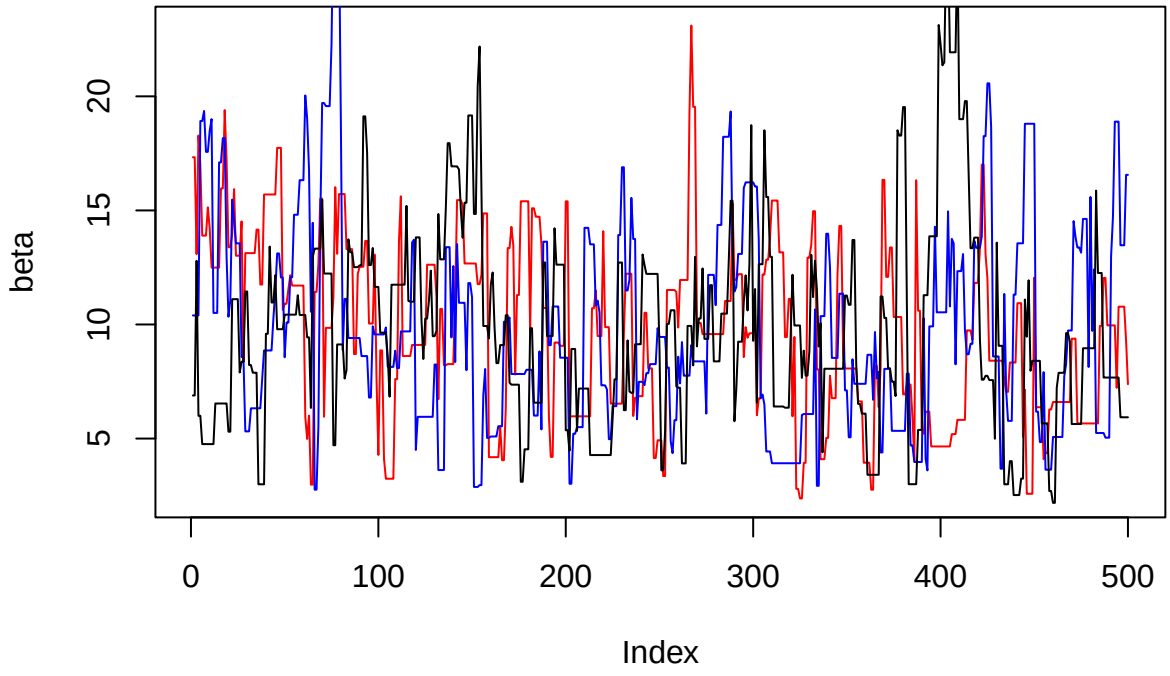
```
n=1000
warmup_procent = 0.5
thetas1 = Metropolis_bioassay(n, 0, 10, warmup_procent)
thetas2 = Metropolis_bioassay(n, 2, 15, warmup_procent)
thetas3 = Metropolis_bioassay(n, -2, 5, warmup_procent)
```

```
plot(thetas1[,1],
     type='l',
     col='red',
     ylab='alpha')
lines(thetas2[,1],
     type='l',
     col='blue')
lines(thetas3[,1],
     type='l',
     col='black')
```




```
plot(thetas1[,2],
     type='l',
     col='red',
     ylab='beta')
```

```
lines(thetas2[,2],
     type='l',
     col='blue')
lines(thetas3[,2],
     type='l',
     col='black')
```




```
alphas = cbind(thetas1[,1],thetas2[,1],thetas3[,1])
alpha_Rhat = Rhat(alphas)
betas = cbind(thetas1[,2],thetas2[,2],thetas3[,2])
betas_Rhat = Rhat(betas)
```

The values are $\widehat{R}_\alpha = 1.03$ and $\widehat{R}_\beta = 1.03$.