

# Metropolis-Hastings

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## Metropolis-Hastings

Our target distribution is  $\text{Beta}(6,4)$  and our proposal distribution is  $\phi_{prop}|\phi_{old} \sim \text{Beta}(c\phi_{old}, c(1-\phi_{old}))$ , for some constant  $c$ . First, we implement several functions which will be used in calculating posterior distribution. Here, we define likelihood function which gives the log-likelihood value of the parameter, and also prior function that gives the log density value of the parameter. The density used in the likelihood function is  $\text{Beta}(6,4)$  since it is our target distribution, and the density used in the prior function is  $\text{Uniform}[0,1]$  since our start value is from  $\text{Uniform}[0,1]$ . In addition, since the parameters in Beta distribution have to be larger than 0, for  $c > 0$ ,  $\phi < 1$ .

```
a <- 6
b <- 4

likelihood <- function(param){
  singlelikelihoods = dbeta(param, a, b, log = T)
  return(singlelikelihoods)
}

prior <- function(param){
  pr = dunif(param, min=0, max=1, log = T)
  return(pr)
}

posterior <- function(param){
  return (exp(likelihood(param) + prior(param)))
}
```

Posterior function can be calculated by multiplying likelihood function and prior function. However, we used log in the likelihood function and the prior function, so we need to convert them into  $\exp(\text{likelihood} + \text{prior})$  in the posterior function.

```
metropolis_MCMC <- function(startvalue, iterations, c){
  chain = array(dim = c(iterations+1,1))
  chain[1,] = startvalue
  for (i in 1:iterations){
    proposal = rbeta(1, c*chain[i,], c*(1-chain[i,]))
    probab = (posterior(proposal)*dbeta(chain[i,],c*proposal,c*(1-proposal)))/
      (posterior(chain[i,])*dbeta(proposal, c*chain[i,], c*(1-chain[i,])))
    if (runif(1) < probab){
      chain[i+1,] = proposal
    }else{
      chain[i+1,] = chain[i,]
    }
  }
  return(chain)
}
```

After implementing all the functions that are required to obtain a chain, then we can finally define metropolis\_MCMC function that can yield a chain. Note that

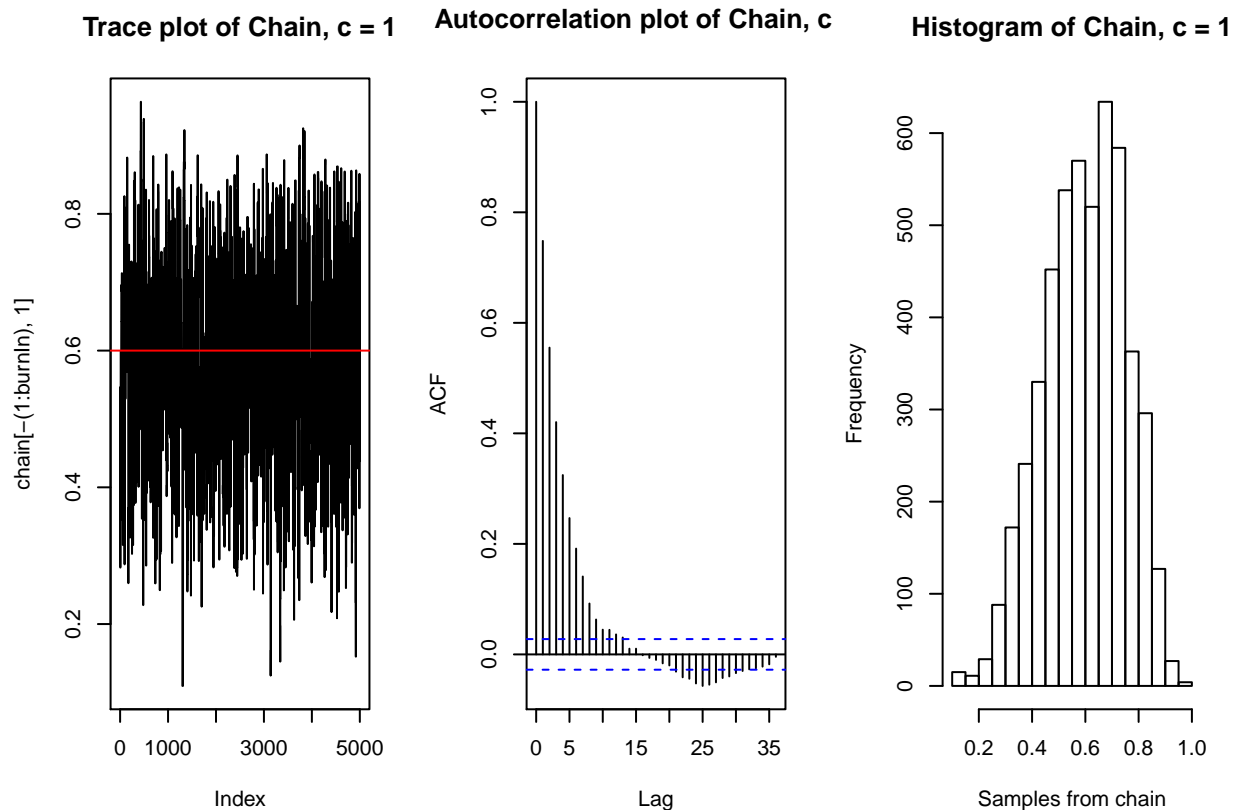
$$\begin{aligned}\phi_{new} &= \phi_{proposal} \text{ with probability } \alpha(\phi_{old}, \phi_{new}) \\ &= \phi_{old} \text{ with probability } 1 - \alpha(\phi_{old}, \phi_{new})\end{aligned}$$

where  $\alpha(\phi_{old}, \phi_{new}) = \min(1, \frac{p(\phi_{new})q(\phi_{old}|\phi_{new})}{p(\phi_{old})q(\phi_{new}|\phi_{old})})$ . Here,  $p(\phi)$  is the posterior function, and  $q(\phi_{new}|\phi_{old})$  is our proposal functions that follows  $Beta(c\phi_{old}, c(1 - \phi_{old}))$ . Since Beta distribution is asymmetric, the probability form cannot be simplified to the ratio of posterior functions. Hence, we need to calculate the probability by using posterior functions and proposal functions.

Next, we can finally get the chain using `metropolis_MCMC` function with the startvalue generated from `Uniform(0,1)`. We also generate random values from `Beta(6,4)` for the comparison.

```
startvalue <- runif(1, 0, 1)
chain=metropolis_MCMC(startvalue, 10000, c=1)
test <- rbeta(10000, 6, 4)

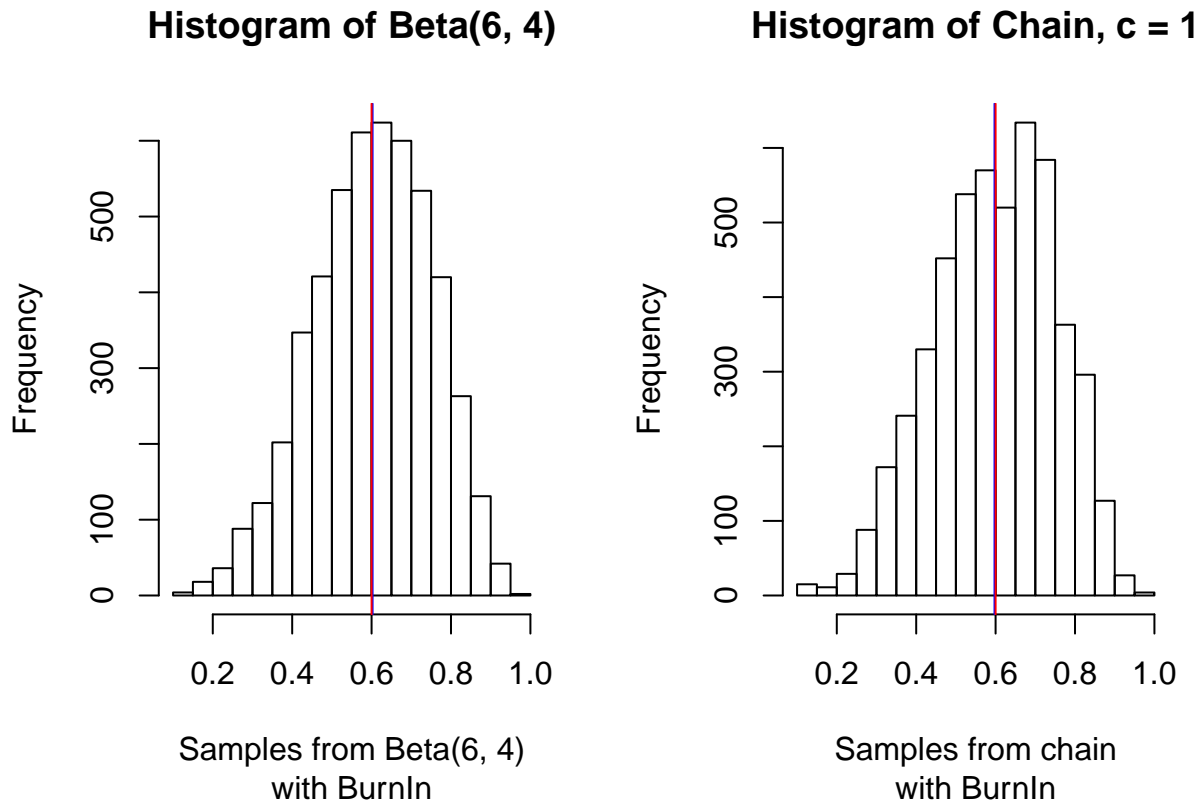
# Performance of the sampler: c = 1 with BurnIn
par(mfrow=c(1,3))
test2 <- test[5001:10000]
burnIn = 5000
acceptance = 1-mean(duplicated(chain[-(1:burnIn),]))
plot(chain[-(1:burnIn),1], type='l', main = "Trace plot of Chain, c = 1")
abline(h=0.6, col="red")
acf(chain[-(1:burnIn),1], main = "Autocorrelation plot of Chain, c = 1")
hist(chain[-(1:burnIn),1], xlab = "Samples from chain", main = "Histogram of Chain, c = 1")
```



Here, we evaluate the performance of the sampler when  $c = 1$  without burn in. The first plot is the trace plot, showing the trace of our chain. We can check that the trace plot does not have any trends, and it is well bounded.

/# The auto correlation

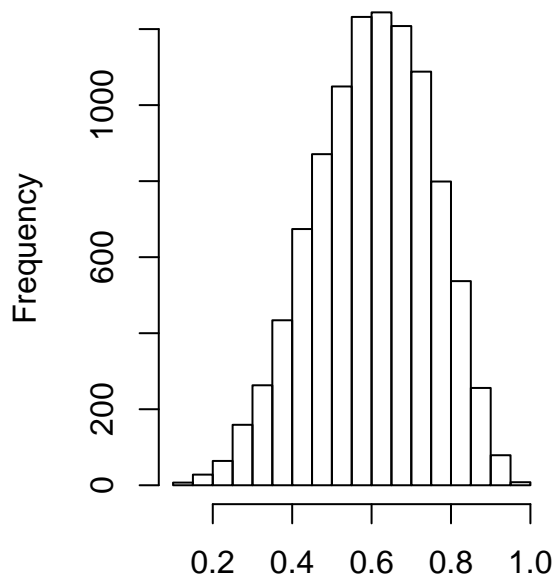
```
# Histogram of the target distribution Beta(6,4) vs. the Chain with burnIn
par(mfrow=c(1,2))
hist(test2, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",
     sub = "with BurnIn")
abline(v=mean(test2), col="blue")
abline(v=0.6, col="red")
hist(chain[-(1:burnIn),1], xlab = "Samples from chain", main = "Histogram of Chain, c = 1",
     sub = "with BurnIn")
abline(v = mean(chain[-(1:burnIn),1]), col="blue")
abline(v=0.6, col="red")
```



In addition, we can compare the target distribution Beta(6,4) with the histogram of the chain as we can see above. The red line indicates the real mean of the distribution, which is  $\frac{6}{4+6} = 0.6$ . We can check that both histogram looks similar and the mean of the chain is 0.5972699 which is very close to 0.6. This is after we remove some redundant moves from the chain using BurnIn. However, we can still compare the distribution of Beta(6,4) with the whole chain without BurnIn.

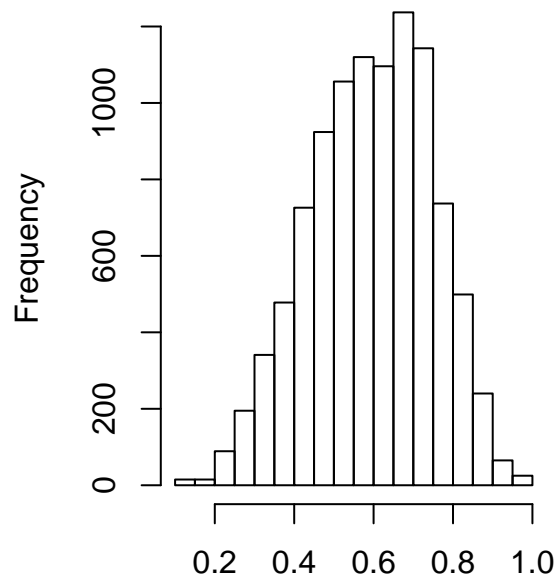
```
# Histogram of the chain vs. the target distribution Beta(6,4) without BurnIn
par(mfrow=c(1,2))
hist(test, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",
     sub = "without BurnIn")
hist(chain, xlab = "Samples from Chain", main = "Histogram of Chain, c = 1",
     sub = "without BurnIn")
```

### Histogram of Beta(6, 4)



Samples from Beta(6, 4)  
without BurnIn

### Histogram of Chain, c = 1



Samples from Chain  
without BurnIn

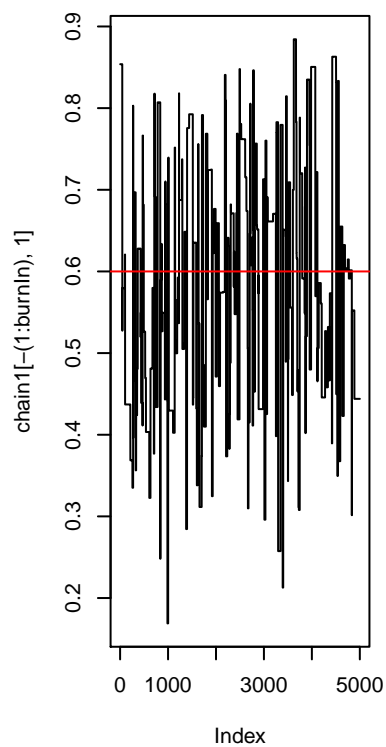
```
# Kolmogorov-Smirnov statistic
chainks <- sort(chain[-(1:burnIn),1])
ks.test(chainks, "pbeta", 6, 4)
```

```
## Warning in ks.test(chainks, "pbeta", 6, 4): ties should not be present for
## the Kolmogorov-Smirnov test
```

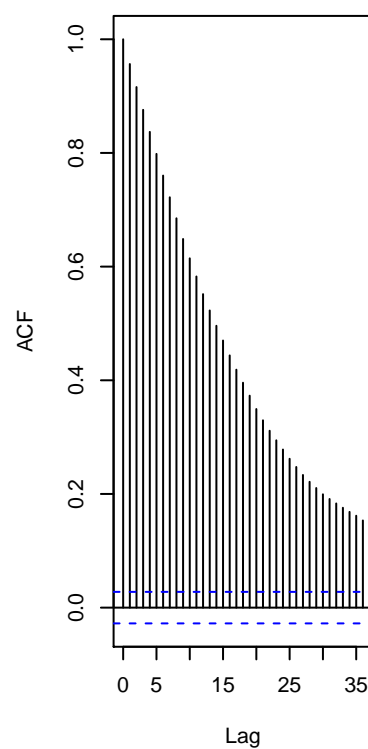
```
##
## One-sample Kolmogorov-Smirnov test
##
## data: chainks
## D = 0.028784, p-value = 0.0005038
## alternative hypothesis: two-sided
```

```
set.seed(1)
# Performance of the sampler: c = 0.1
chain1=metropolis_MCMC(startvalue, 10000, c=0.1)
par(mfrow=c(1,3))
acceptance1 = 1-mean(duplicated(chain1[-(1:burnIn),]))
plot(chain1[-(1:burnIn),1], type='l', main = "Trace plot of Chain, c = 0.1")
abline(h=0.6, col="red")
acf(chain1[-(1:burnIn),1], main = "Autocorrelation plot of Chain, c = 0.1")
hist(chain1[-(1:burnIn),1], xlab = "Samples from chain",
     main = "Histogram of Chain, c = 0.1")
```

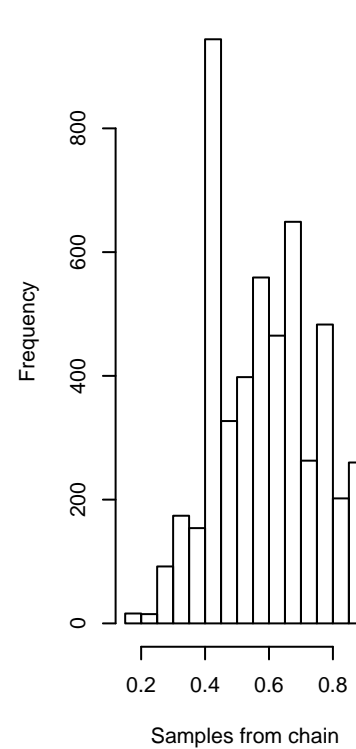
Trace plot of Chain, c = 0.1



Autocorrelation plot of Chain, c =

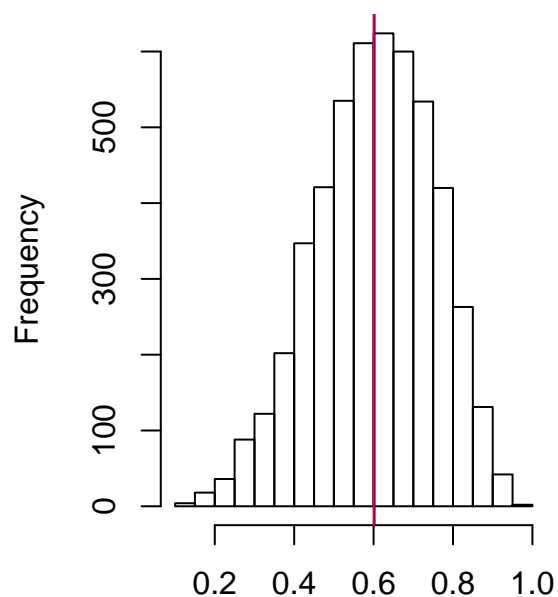


Histogram of Chain, c = 0.1



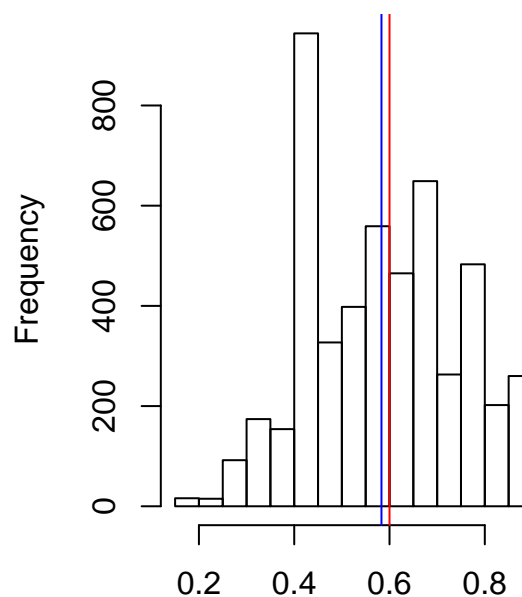
```
# Histogram of the target distribution Beta(6,4) vs. the Chain after burnIn
par(mfrow=c(1,2))
hist(test2, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",
      sub = "with BurnIn")
abline(v=mean(test2), col="blue")
abline(v=0.6, col="red")
hist(chain1[-(1:burnIn),1], xlab = "Samples from chain",
      main = "Histogram of Chain, c = 0.1", sub = "with BurnIn")
abline(v = mean(chain1[-(1:burnIn),1]), col="blue")
abline(v=0.6, col="red")
```

### Histogram of Beta(6, 4)



Samples from Beta(6, 4)  
with BurnIn

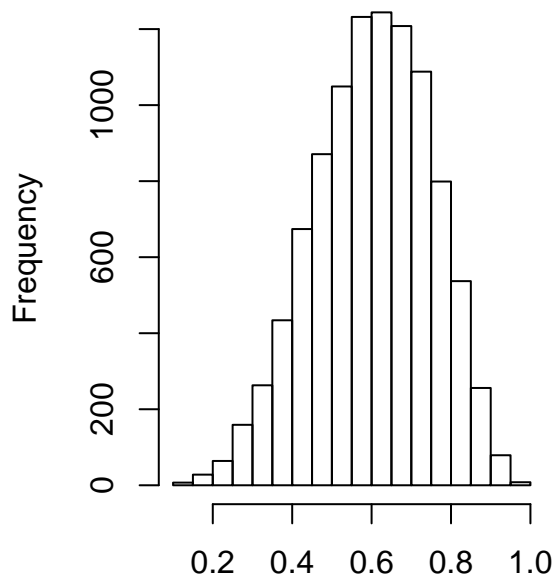
### Histogram of Chain, c = 0.1



Samples from chain  
with BurnIn

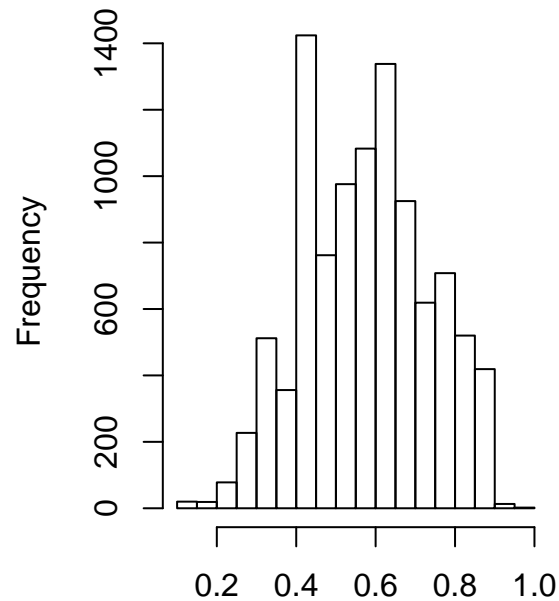
```
# Comparing the histogram of the chain with the target distribution Beta(6,4)
par(mfrow=c(1,2))
hist(test, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",
      sub = "without BurnIn")
hist(chain1, xlab = "Samples from chain", main = "Histogram of Chain, c = 0.1",
      sub = "without BurnIn")
```

### Histogram of Beta(6, 4)



Samples from Beta(6, 4)  
without BurnIn

### Histogram of Chain, c = 0.1



Samples from chain  
without BurnIn

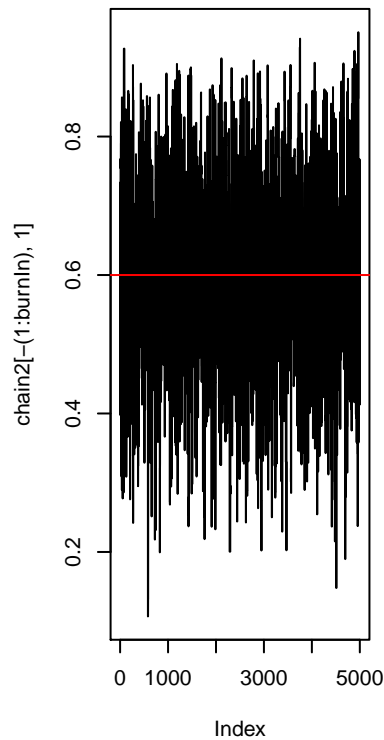
```
# Kolmogorov-Smirnov statistic
chain1ks <- sort(chain1[-(1:burnIn),1])
ks.test(chain1ks, "pbeta", 6, 4)
```

```
## Warning in ks.test(chain1ks, "pbeta", 6, 4): ties should not be present for
## the Kolmogorov-Smirnov test
```

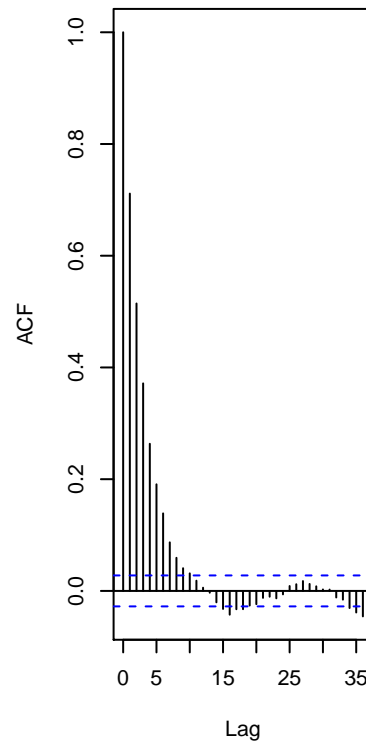
```
##
## One-sample Kolmogorov-Smirnov test
##
## data: chain1ks
## D = 0.11419, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```
set.seed(2)
# Performance of the sampler: c = 2.5
chain2=metropolis_MCMC(startvalue, 10000, c=2.5)
par(mfrow=c(1,3))
acceptance2 = 1-mean(duplicated(chain2[-(1:burnIn),]))
plot(chain2[-(1:burnIn),1], type='l', main = "Trace plot of Chain, c = 2.5")
abline(h=0.6, col="red")
acf(chain2[-(1:burnIn),1], main = "Autocorrelation plot of Chain, c = 2.5")
hist(chain2[-(1:burnIn),1], xlab = "Samples from chain",
     main = "Histogram of Chain, c = 2.5")
```

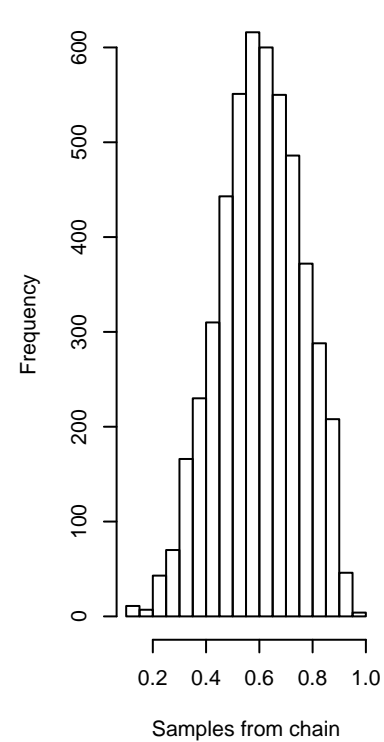
Trace plot of Chain, c = 2.5



Autocorrelation plot of Chain, c =



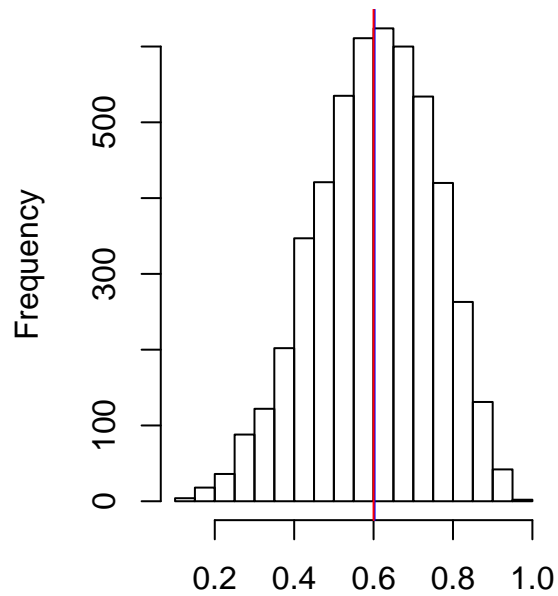
Histogram of Chain, c = 2.5



```
# Histogram of the target distribution Beta(6,4) vs. the Chain after burnIn
par(mfrow=c(1,2))
hist(test2, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",
      sub = "with BurnIn")
abline(v=mean(test2), col="blue")
abline(v=0.6, col="red")
hist(chain2[-(1:burnIn),1], xlab = "Samples from chain",
      main = "Histogram of Chain, c = 2.5", sub = "with BurnIn")
abline(v = mean(chain2[-(1:burnIn),1]), col="blue")
abline(v=0.6, col="red")
```

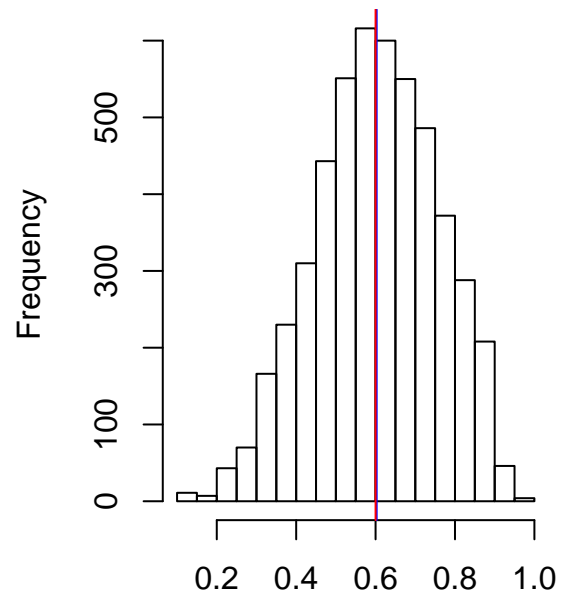


**Histogram of Beta(6, 4)**



**Samples from Beta(6, 4)  
with BurnIn**

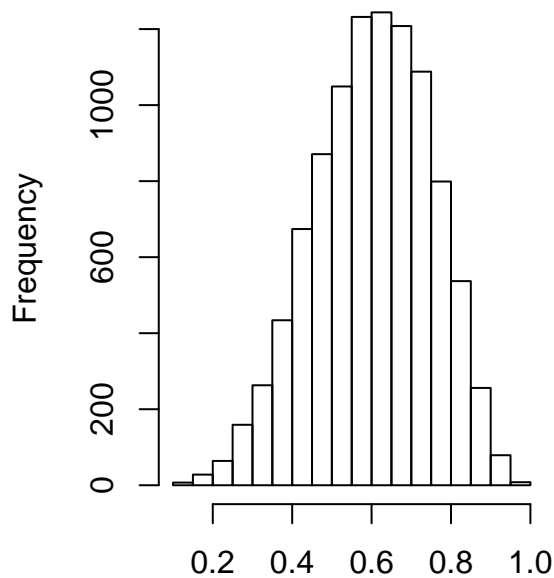
**Histogram of Chain, c = 2.5**



**Samples from chain  
with BurnIn**

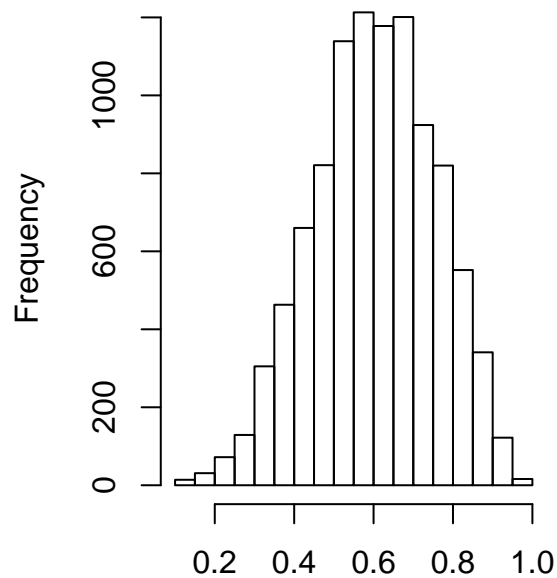
```
# Comparing the histogram of the chain with the target distribution Beta(6,4)
hist(test, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",
      sub = "without BurnIn")
hist(chain2, xlab = "Samples from chain", main = "Histogram of Chain, c = 2.5",
      sub = "without BurnIn")
```

### Histogram of Beta(6, 4)



Samples from Beta(6, 4)  
without BurnIn

### Histogram of Chain, c = 2.5



Samples from chain  
without BurnIn

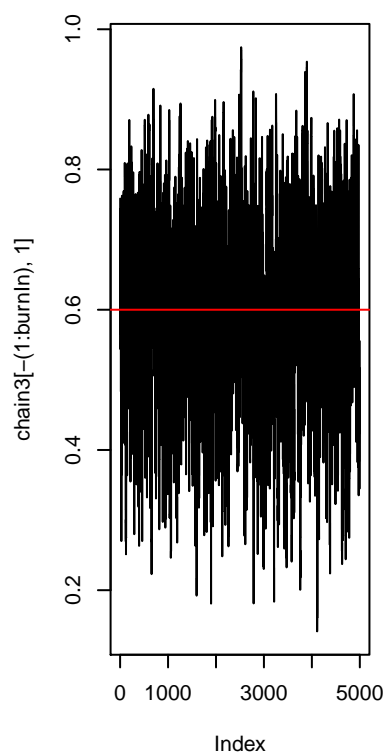
```
# Kolmogorov-Smirnov statistic
chain2ks <- sort(chain2[-(1:burnIn),1])
ks.test(chain2ks, "pbeta", 6, 4)
```

```
## Warning in ks.test(chain2ks, "pbeta", 6, 4): ties should not be present for
## the Kolmogorov-Smirnov test
```

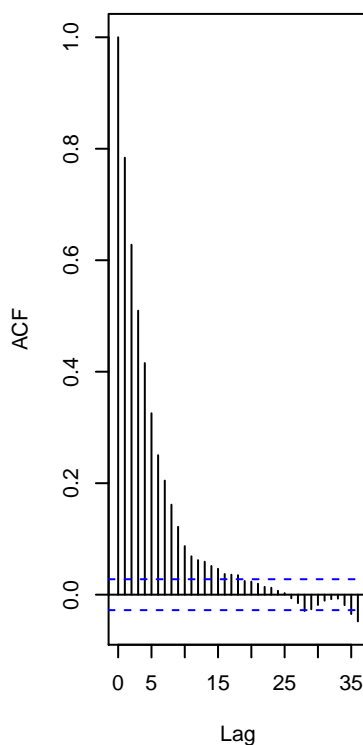
```
##
## One-sample Kolmogorov-Smirnov test
##
## data: chain2ks
## D = 0.03087, p-value = 0.0001451
## alternative hypothesis: two-sided
```

```
set.seed(3)
# Performance of the sampler: c = 10
chain3=metropolis_MCMC(startvalue, 10000, c=10)
par(mfrow=c(1,3))
acceptance3 = 1-mean(duplicated(chain3[-(1:burnIn),]))
plot(chain3[-(1:burnIn),1], type='l', main = "Trace plot of Chain, c = 10")
abline(h=0.6, col="red")
acf(chain3[-(1:burnIn),1], main = "Autocorrelation plot of Chain, c = 10")
hist(chain3[-(1:burnIn),1], xlab = "Samples from chain",
     main = "Histogram of Chain, c = 10")
```

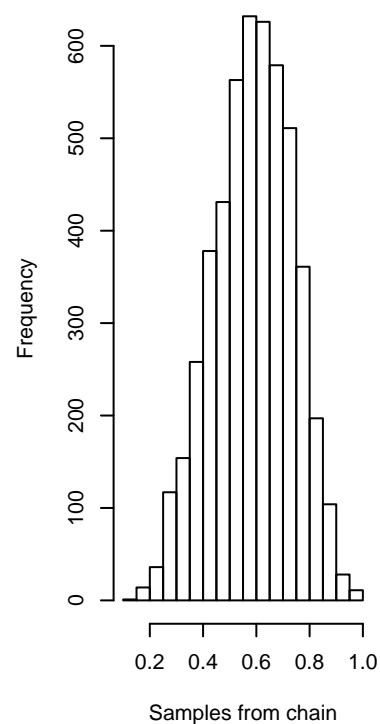
Trace plot of Chain, c = 10



Autocorrelation plot of Chain, c =



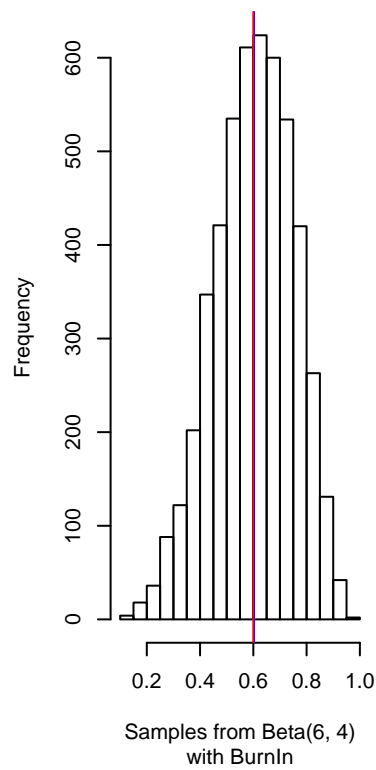
Histogram of Chain, c = 10



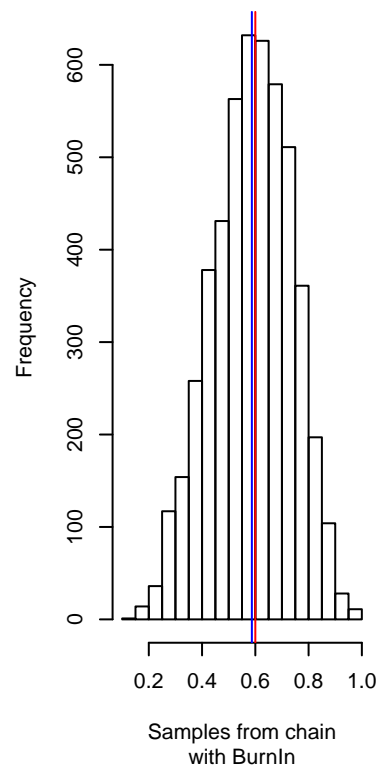
```
# Histogram of the target distribution Beta(6,4) vs. the Chain after burnIn
hist(test2, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",
     sub = "with BurnIn")
abline(v=mean(test2), col="blue")
abline(v=0.6, col="red")
hist(chain3[-(1:burnIn),1], xlab = "Samples from chain",
     main = "Histogram of Chain, c = 10", sub = "with BurnIn")
abline(v = mean(chain3[-(1:burnIn),1]), col="blue")
abline(v=0.6, col="red")

# Comparing the histogram of the chain with the target distribution Beta(6,4)
par(mfrow=c(1,2))
```

**Histogram of Beta(6, 4)**

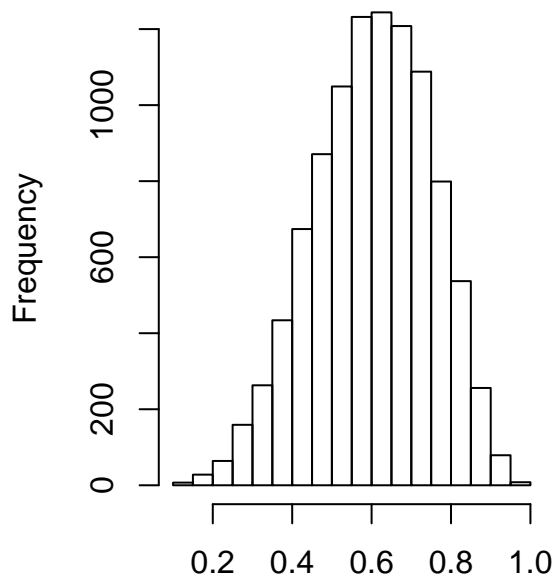


**Histogram of Chain, c = 10**



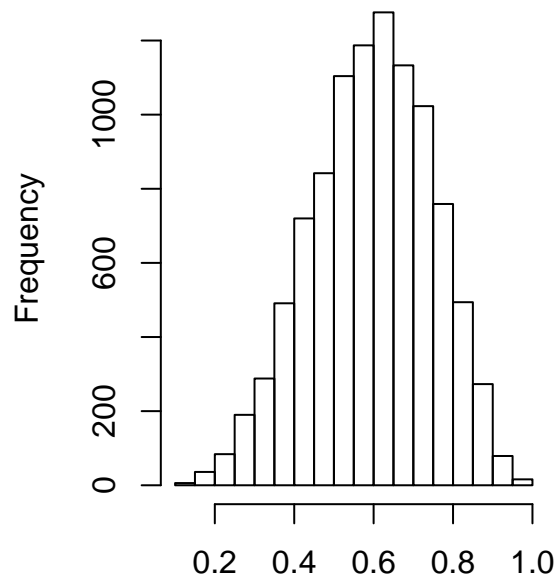
```
hist(test, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)",  
      sub = "without BurnIn")  
hist(chain3, xlab = "Samples from chain", main = "Histogram of Chain, c = 10",  
      sub = "without BurnIn")
```

### Histogram of Beta(6, 4)



Samples from Beta(6, 4)  
without BurnIn

### Histogram of Chain, c = 10



Samples from chain  
without BurnIn

```
# Kolmogorov-Smirnov statistic
chain3ks <- sort(chain3[-(1:burnIn),1])
ks.test(chain3ks, "pbeta", 6, 4)
```

```
## Warning in ks.test(chain3ks, "pbeta", 6, 4): ties should not be present for
## the Kolmogorov-Smirnov test
```

```
##
## One-sample Kolmogorov-Smirnov test
##
## data: chain3ks
## D = 0.036698, p-value = 2.825e-06
## alternative hypothesis: two-sided
```

```
acceptance
```

```
## [1] 0.2637473
```

```
acceptance1
```

```
## [1] 0.04219156
```

```
acceptance2
```

```
## [1] 0.4169166
```

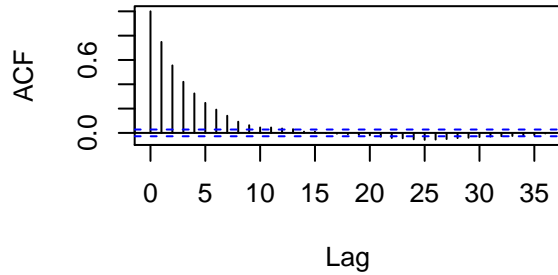
```
acceptance3
```

```
## [1] 0.675065
```

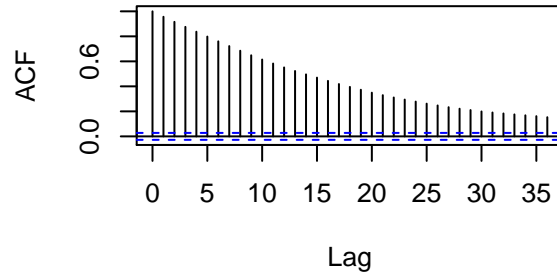
```
par(mfrow=c(2,2))
acf(chain[-(1:burnIn),1], main = "ACF for c = 1")
acf(chain1[-(1:burnIn),1], main = "ACF for c = 0.1")
```

```
acf(chain2[-(1:burnIn),1], main = "ACF for c = 2.5")
acf(chain3[-(1:burnIn),1], main = "ACF for c = 10")
```

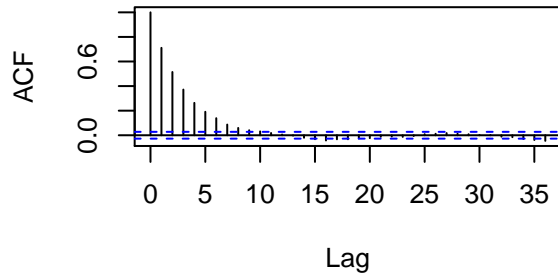
**ACF for c = 1**



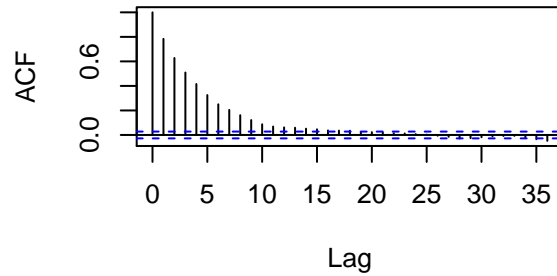
**ACF for c = 0.1**



**ACF for c = 2.5**



**ACF for c = 10**



Strong autocorrelation such as when  $c = 2.5$  or  $c = 10$  strong autocorrelation is related to higher p-value in the k-s test. We observe the strongest autocorrelation when  $c = 2.5$  compared to when  $c = 10$  or  $c = 0.1$ . In addition, p-value for the k-s test is highest when  $c = 2.5$  meaning the chain resembles  $\text{Beta}(6, 4)$  closest when  $c = 2.5$ . However, as the value of  $c$  increases, we observe that the acceptance rate increases. We can deduce from such observation that the proposal function may be different from  $\text{Beta}(6, 4)$  and high acceptance rate would actually make the samples drawn from the algorithm deviate from  $\text{Beta}(6, 4)$ , out target distribution. low dependence (i.e., low autocorrelation) - leads to better convergence toward stationary posterior - leads to lower uncertainty in results from posterior draws