Metropolis-Hastings

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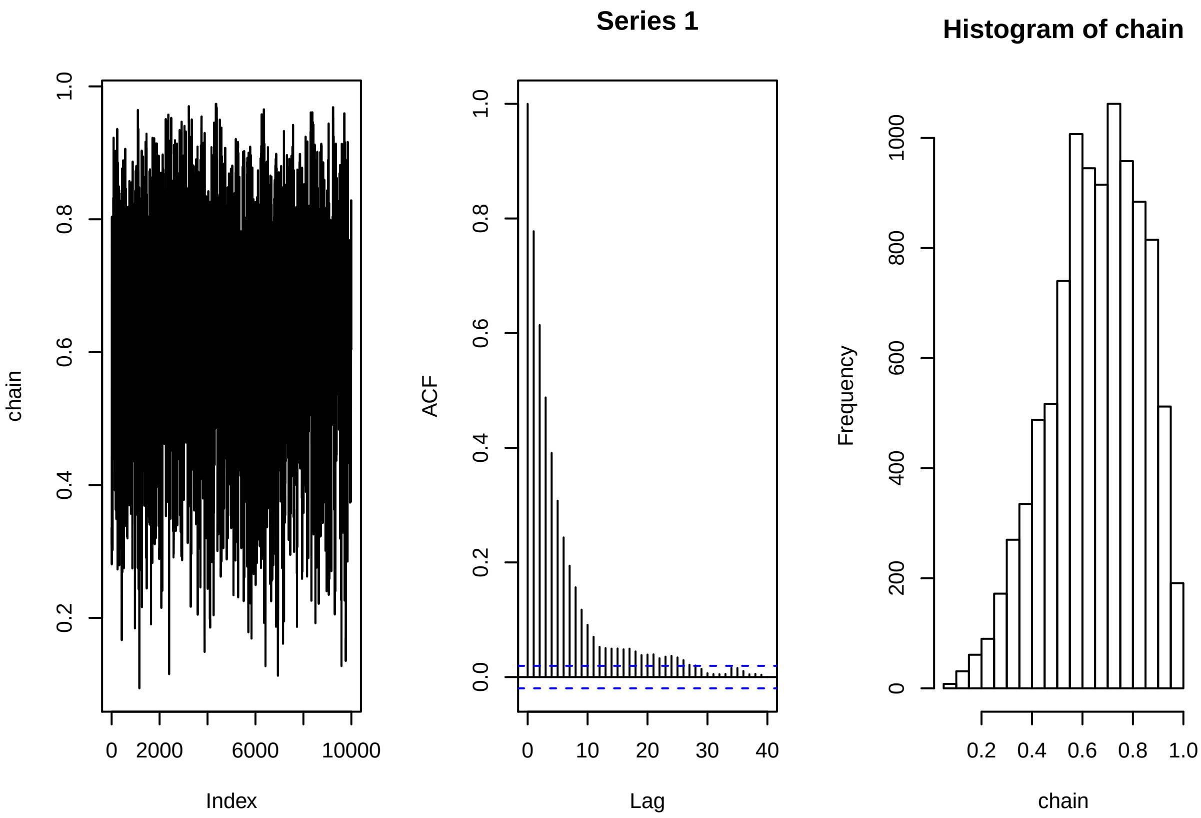
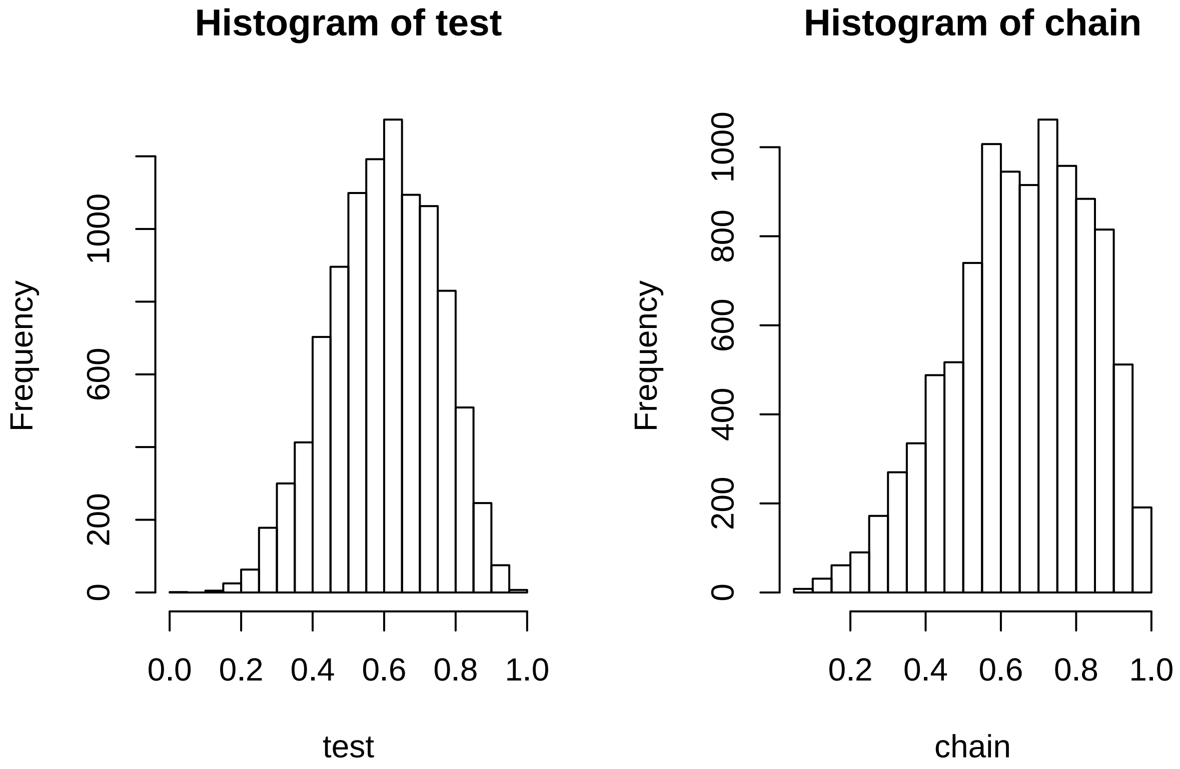
```r
a <- 6
b <- 4

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

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

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

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 = dbeta(proposal,a,b)/dbeta(chain[i,],a,b)
    if (runif(1) < probab){
      chain[i+1,] = proposal
    }else{
      chain[i+1,] = chain[i,]
    }
  }
  return(chain)
}

startvalue <- runif(1, 0, 1)
chain=metropolis_MCMC(startvalue, 10000, c=1)

test <- rbeta(10000, 6, 4)

# Performance of the sampler: c = 1
par(mfrow=c(1,3))
plot(chain, type='l')
acf(chain); hist(chain)
```



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

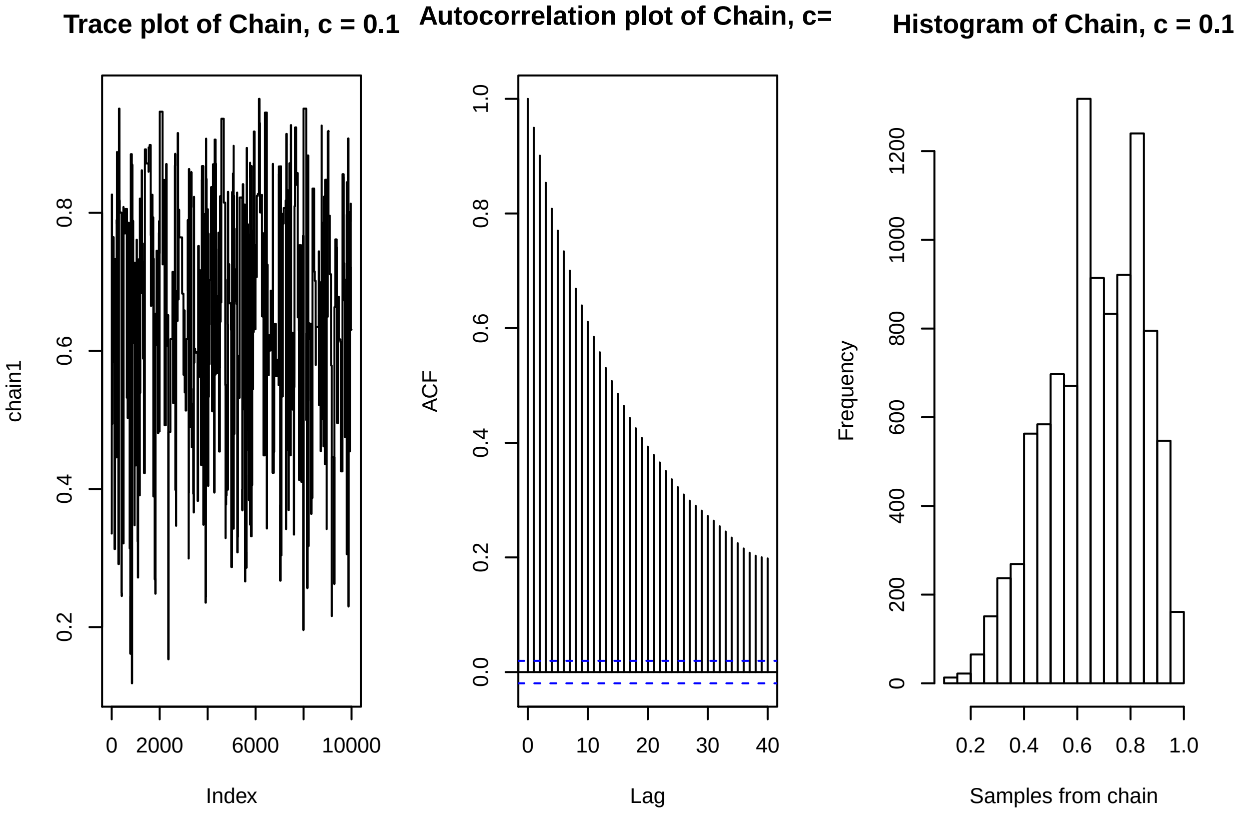


```r
ks.test(chain, test)
```

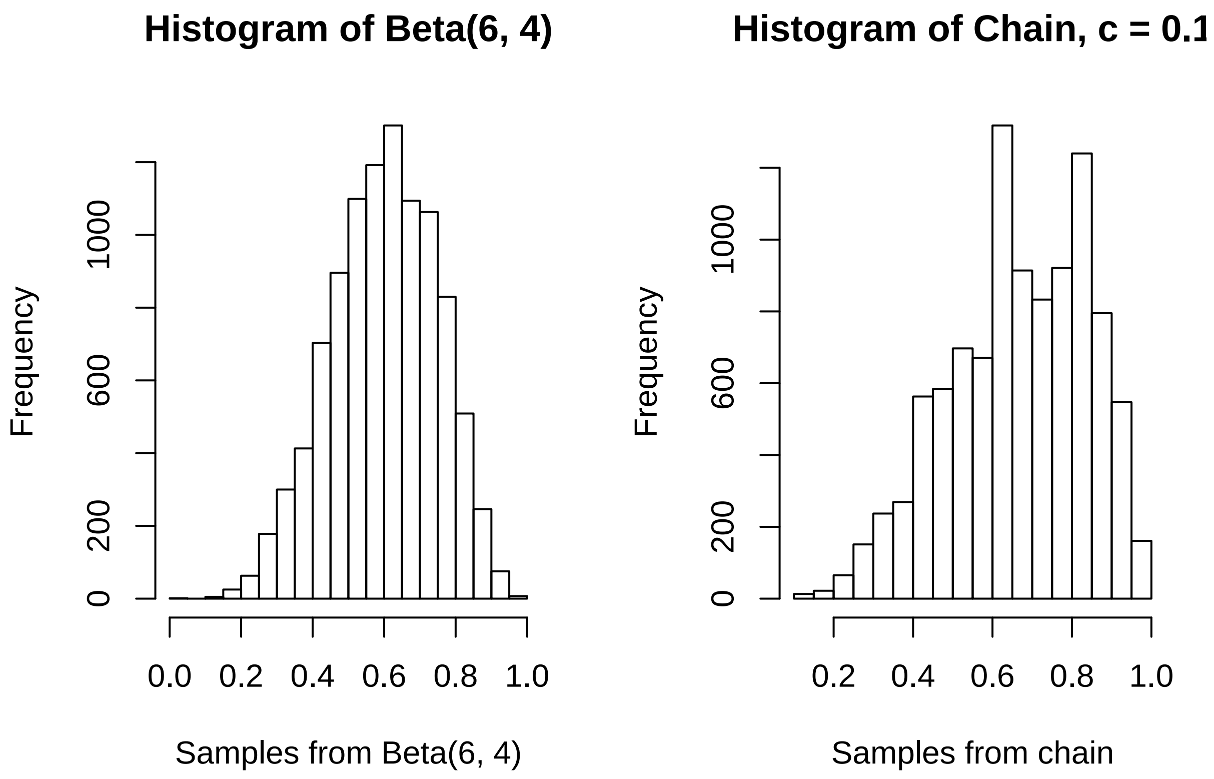
```
## Warning in ks.test(chain, test): p-value will be approximate in the
## presence of ties
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  chain and test
## D = 0.17386, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```r
par(mfrow=c(1,1))

# c = 0.1 / c - 2.5 / c = 10
chain1=metropolis_MCMC(startvalue, 10000, c=0.1)
chain2=metropolis_MCMC(startvalue, 10000, c=2.5)
chain3=metropolis_MCMC(startvalue, 10000, c=10)

# Putting burnIn in
burnIn = 5000
acceptance1 = 1-mean(duplicated(chain1[-(1:burnIn),]))
acceptance2 = 1-mean(duplicated(chain2[-(1:burnIn),]))
acceptance3 = 1-mean(duplicated(chain3[-(1:burnIn),]))

# Performance of the sampler: c = 0.1
par(mfrow=c(1,3))
plot(chain1, type='l', main = "Trace plot of Chain, c = 0.1")
acf(chain1, main = "Autocorrelation plot of Chain, c= 0.1")
hist(chain1, xlab = "Samples from chain", main = "Histogram of Chain, c = 0.1")
```



```r
# 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)")
hist(chain1, xlab = "Samples from chain", main = "Histogram of Chain, c = 0.1")
```

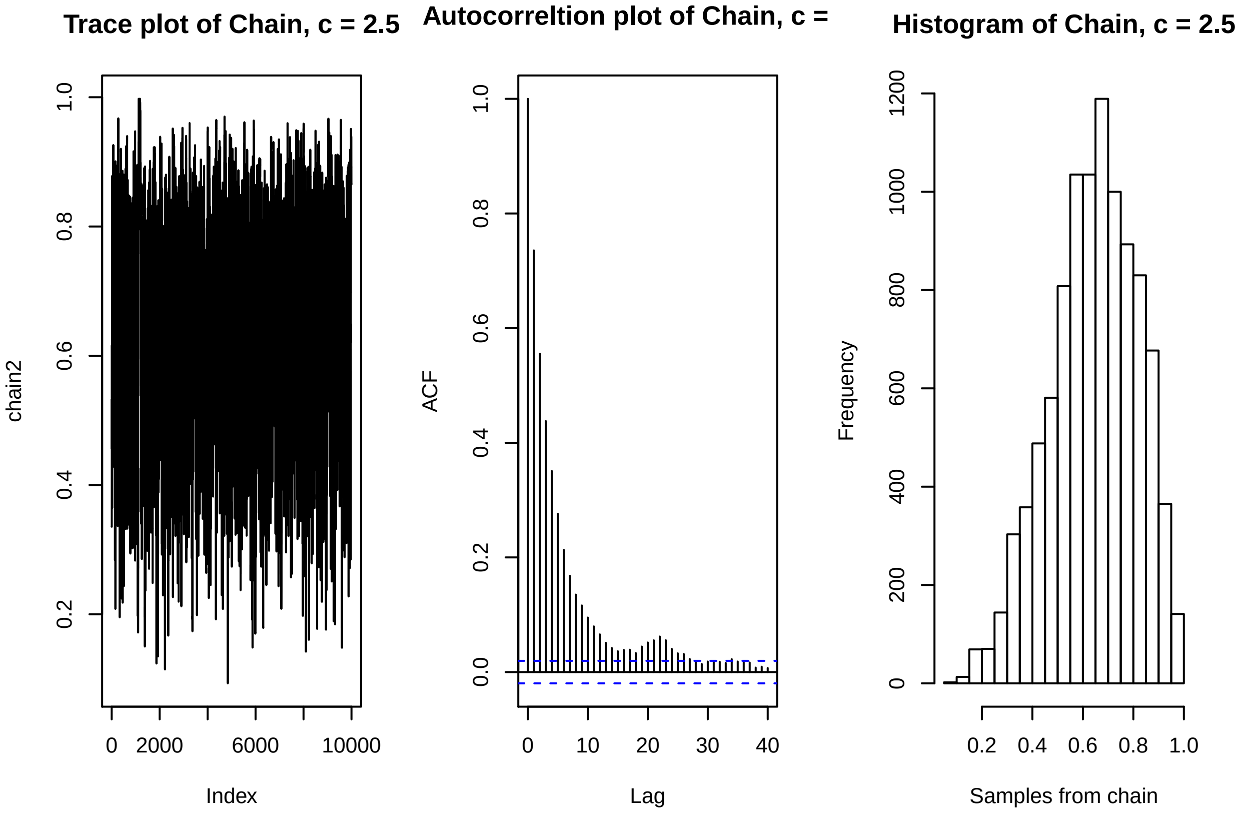


```r
ks.test(chain1, test)
```

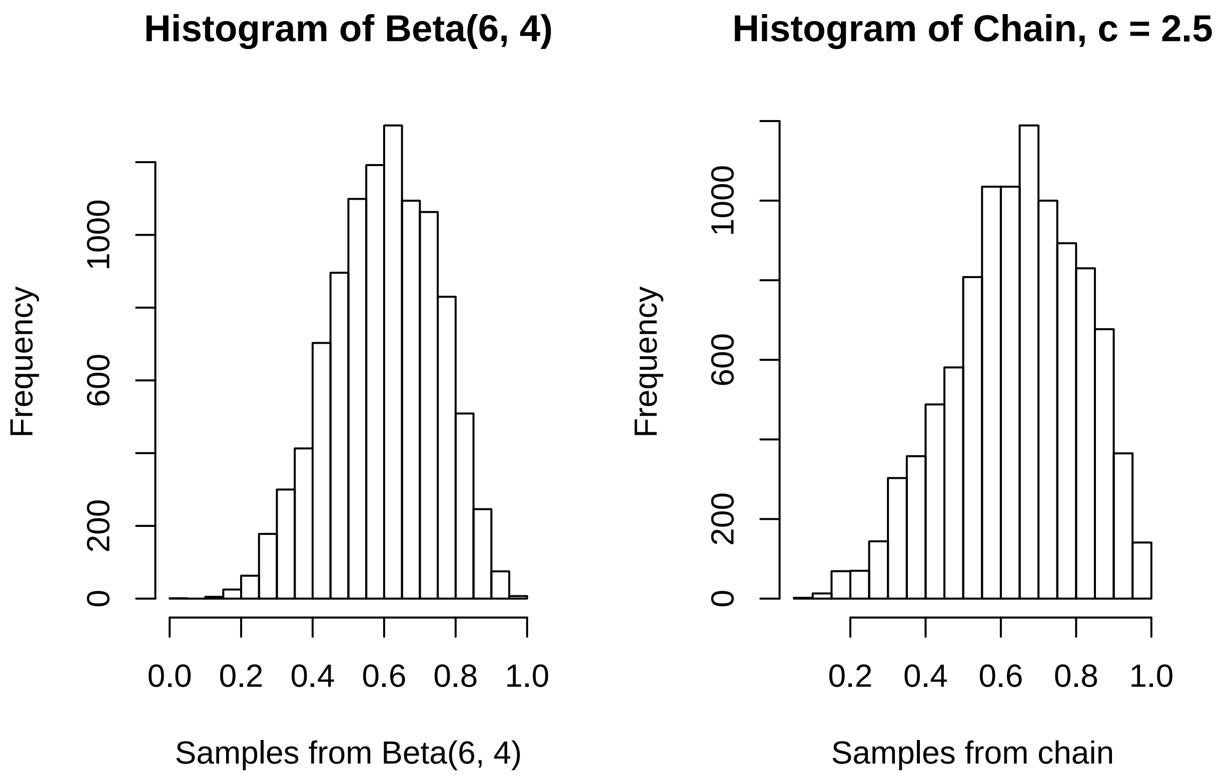
```
## Warning in ks.test(chain1, test): p-value will be approximate in the
## presence of ties
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  chain1 and test
## D = 0.20316, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```r
# Performance of the sampler: c = 2.5
par(mfrow=c(1,3))
plot(chain2, type='l', main = "Trace plot of Chain, c = 2.5")
acf(chain2, main = "Autocorreltion plot of Chain, c = 2.5")
hist(chain2, xlab = "Samples from chain", main = "Histogram of Chain, c = 2.5")
```



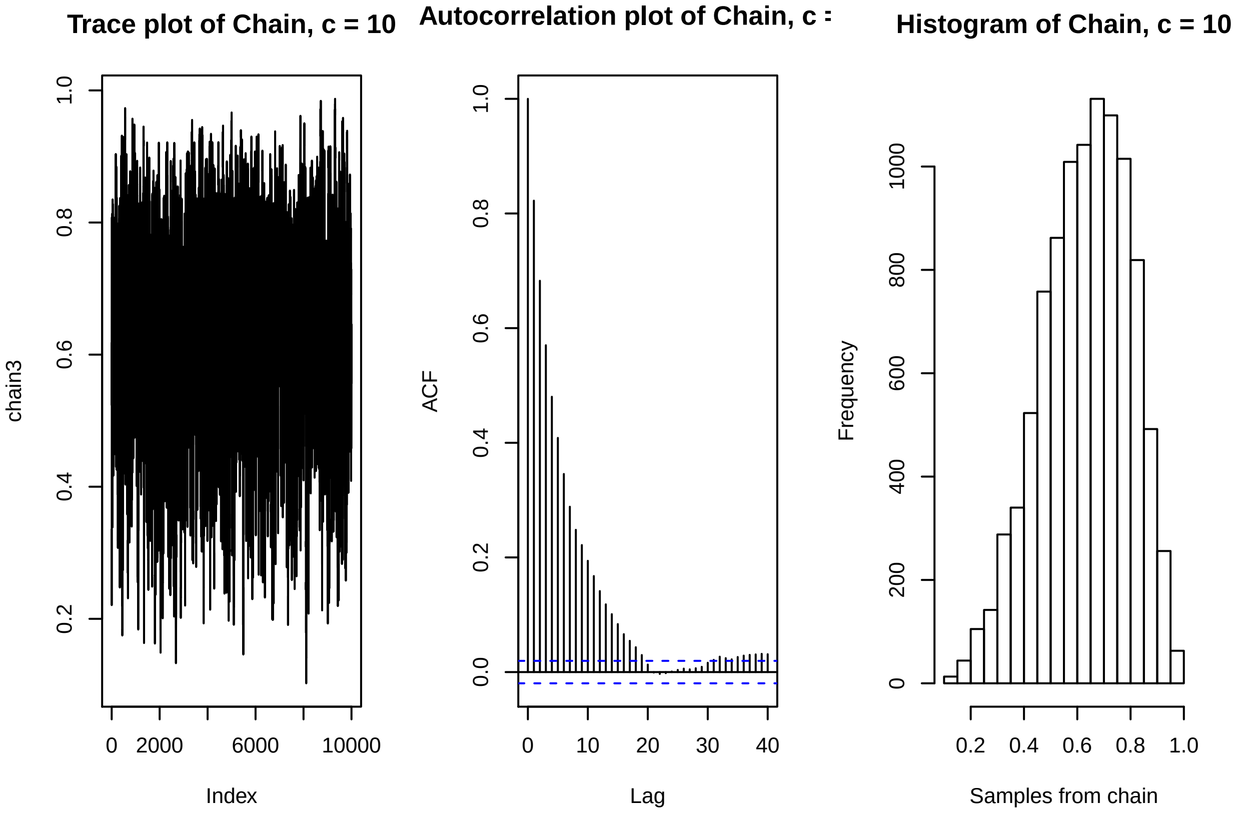
```
# Comparing the histogram of the chain with the target distribution Beta(6,4)
par(mfrow=c(1,2))
hist(test, xlab = "Samples from Beta(6, 4)", main = "Histogram of Beta(6, 4)")
hist(chain2, xlab = "Samples from chain", main = "Histogram of Chain, c = 2.5")
```



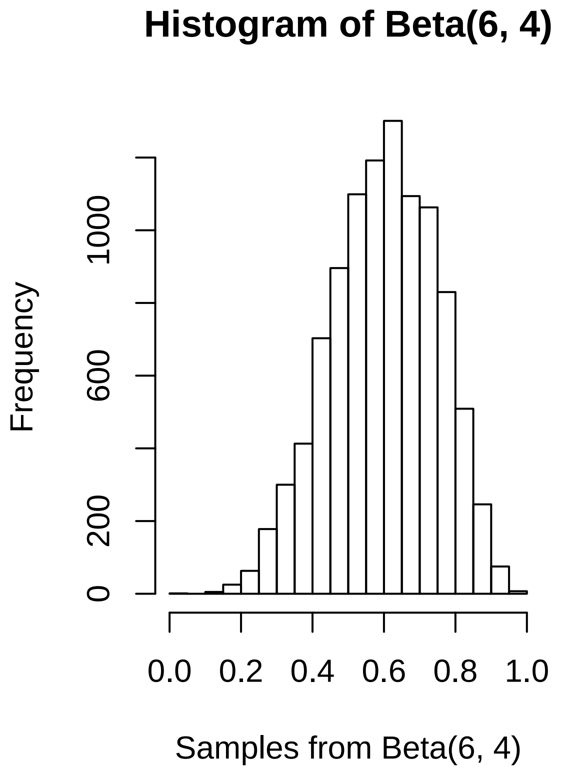
```r
ks.test(chain2, test)
```

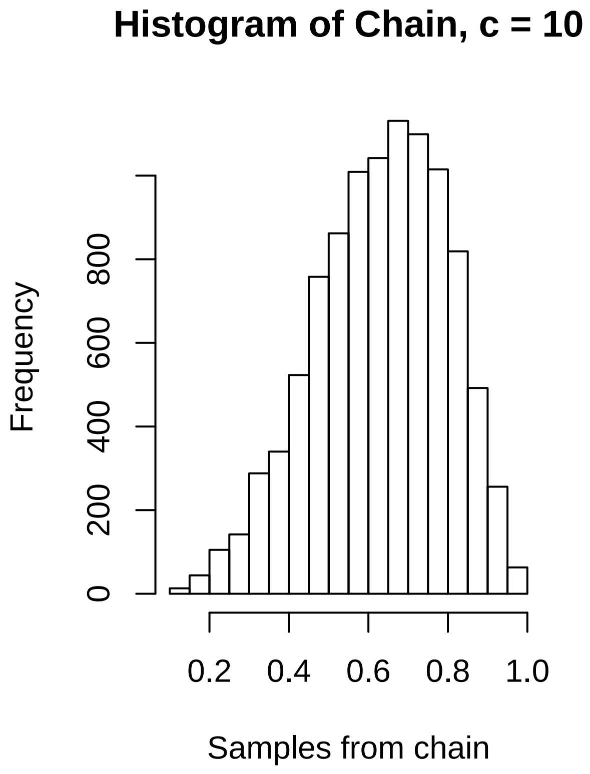
```
## Warning in ks.test(chain2, test): p-value will be approximate in the
## presence of ties

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  chain2 and test
## D = 0.12895, p-value < 2.2e-16
## alternative hypothesis: two-sided
```

```r
# Performance of the sampler: c = 10
par(mfrow=c(1,3))
plot(chain3, type='l', main = "Trace plot of Chain, c = 10")
acf(chain3, main = "Autocorrelation plot of Chain, c = 10")
hist(chain3, xlab = "Samples from chain", main = "Histogram of Chain, c = 10")
```



```r
# 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)")
hist(chain3, xlab = "Samples from chain", main = "Histogram of Chain, c = 10")
```





```
ks.test(chain3, test)
```

```
## Warning in ks.test(chain3, test): p-value will be approximate in the
## presence of ties
```

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  chain3 and test
## D = 0.10656, p-value < 2.2e-16
## alternative hypothesis: two-sided
```