Computational Statistics

Lab 4

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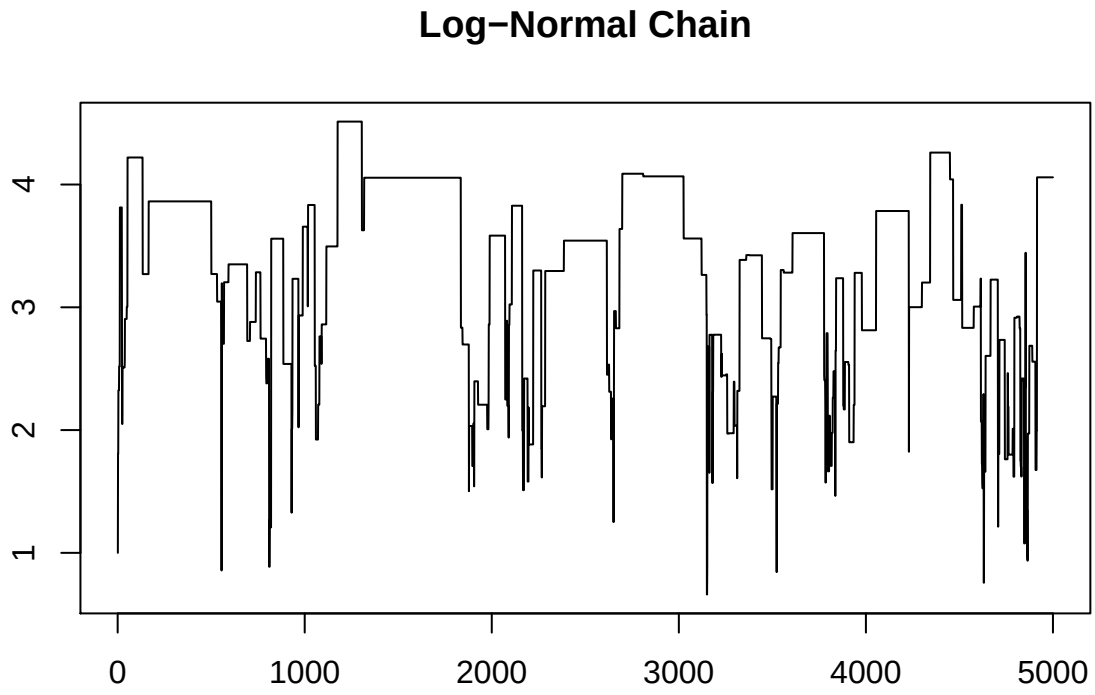
Question 1

```
targetdensity <- function(x) {
    x^5 * exp(-x)
}

lognormalfuncs <- list(propsample=function(x) { rlnorm(1, meanlog=x, sdlog=1) },
                       propdensity=function(x, y) { dlnorm(x, meanlog=y, sdlog=1) },
                       targdensity=targetdensity)

chisquarefuncs <- list(propsample=function(x) { rchisq(1, df=floor(x + 1)) },
                       propdensity=function(x, y) { dchisq(x, df=floor(y + 1)) },
                       targdensity=targetdensity)

metropolis_hastings <- function(X0, iters, funcs) {
    x <- X0
    values <- rep(0, iters)

    alpha <- function(x, y) {
        numerator <- funcs$targdensity(y) * funcs$propdensity(x, y)
        denominator <- funcs$targdensity(x) * funcs$propdensity(y, x)
        numerator / denominator
    }

    for (i in 1:iters) {
        y <- funcs$propsample(x)
        u <- runif(1)

        if (u < alpha(x, y)) {
            x <- y
        }

        values[i] <- x
    }

    values
}

iters <- 5000
X0 <- 1

actual <- rgamma(iters, shape=6, rate=1)
```

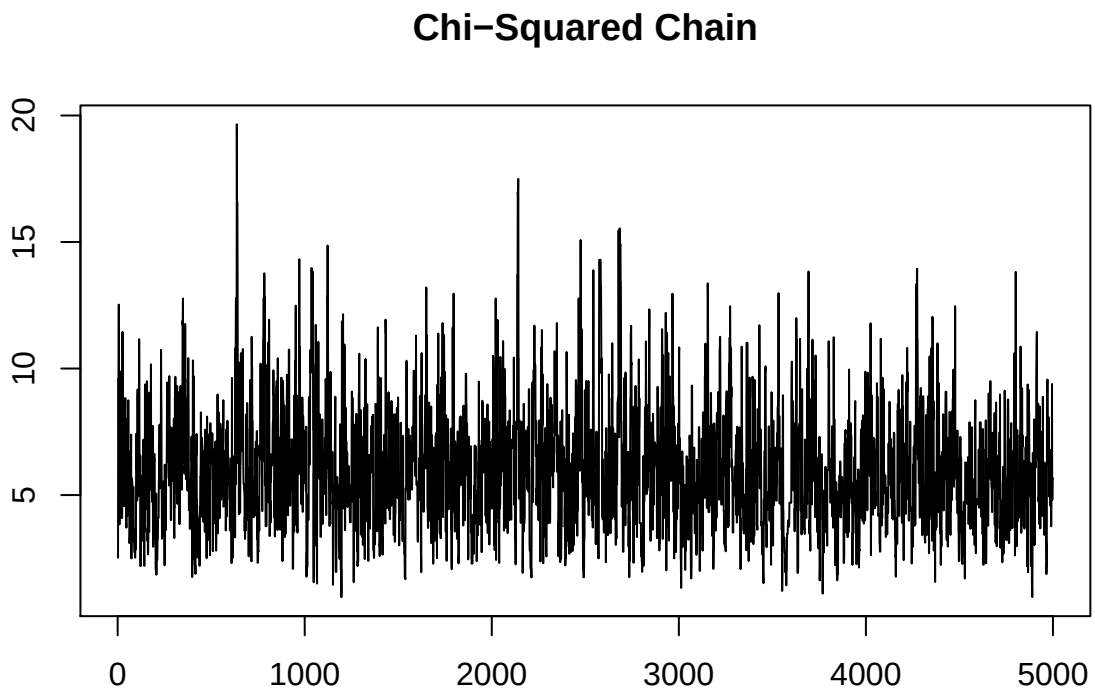
1.1

```
set.seed(123456)
lgnsamples <- metropolis_hastings(X0=X0, iters=iters, funcs=lognormalfuncs)
plot(lgnsamples, type="l", main="Log-Normal Chain", xlab="", ylab="")
```

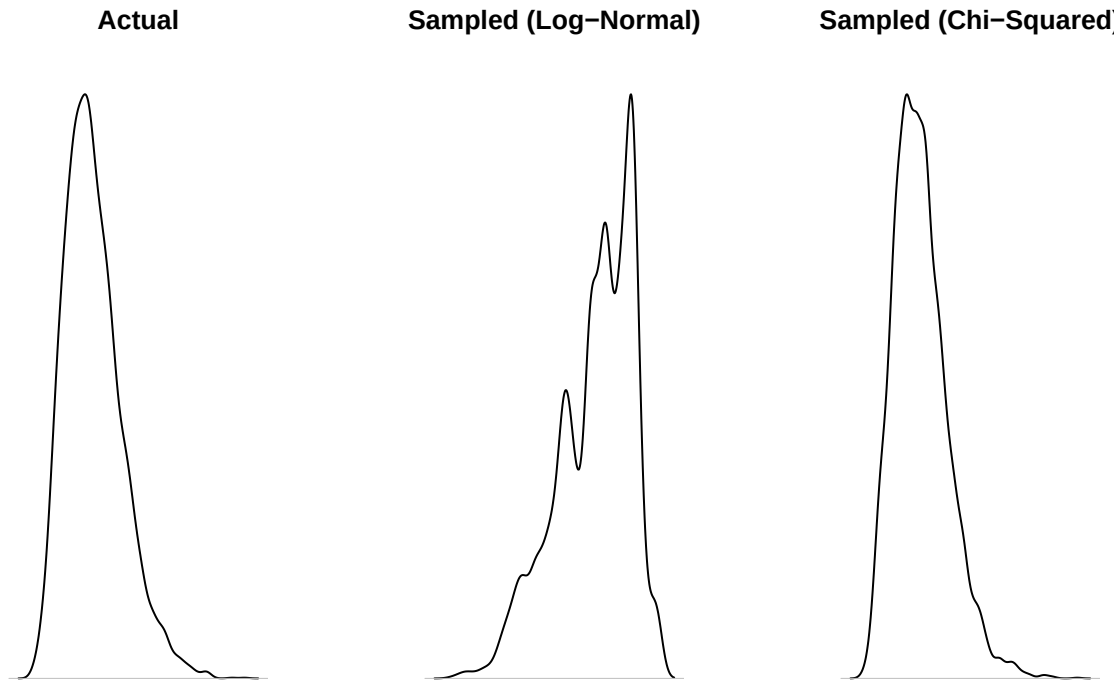


1.2

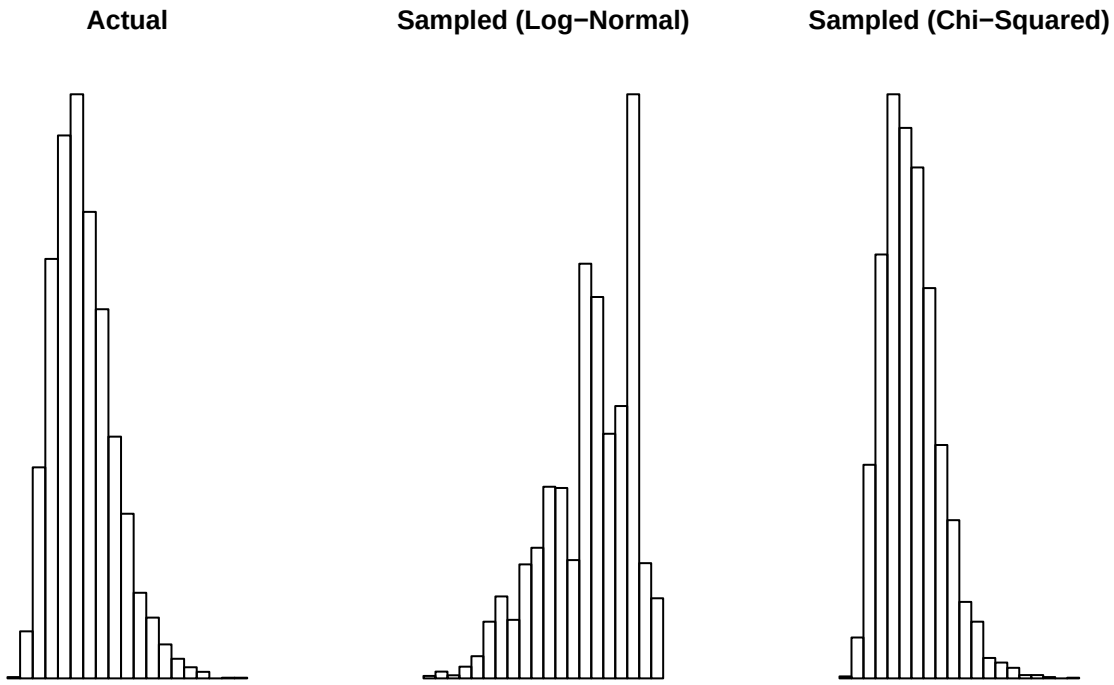
```
set.seed(123456)
chisamples <- metropolis_hastings(X0=X0, iters=iters, funcs=chisquarefuncs)
plot(chisamples, type="l", main="Chi-Squared Chain", xlab="", ylab="")
```




```
oldpar <- par(mfrow = c(1, 3))

plot(density(actual), main="Actual", xlab="", ylab="", axes=FALSE)
plot(density(lgnsamples), main="Sampled (Log-Normal)", xlab="", ylab="", axes=FALSE)
plot(density(chisamples), main="Sampled (Chi-Squared)", xlab="", ylab="", axes=FALSE)
```




```
oldpar <- par(mfrow = c(1, 3))

hist(actual, main="Actual", xlab="", ylab="", axes=FALSE)
hist(lgnsamples, main="Sampled (Log-Normal)", xlab="", ylab="", axes=FALSE)
hist(chisamples, main="Sampled (Chi-Squared)", xlab="", ylab="", axes=FALSE)
```



1.4

Geldman rubin

```
Geldman<-function(x){
  k <- nrow(x)
  n <- ncol(x)

  B <- (n / (k - 1)) * sum((rowMeans(x) - mean(x))^2)

  W <- sum((x - rowMeans(x))^2) / (k * (n - 1))

  VarV <- ((n - 1) / n) * W + B / n

  sqrtR <- sqrt(VarV / W)
  sqrtR
}

set.seed(123456)
resultMatrix <- do.call(rbind, lapply(1:10, FUN = function(x)
    metropolis_hastings(X0 = x, iters = iters, funcs = chisquarefuncs)))

GeldmanRes <- Geldman(resultMatrix)
GeldmanRes
```

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

We get a value of 1 which indicates that the chain has converged.

1.5

```
cat("The estimated expected value by Log-Normal samples:", mean(lgnsamples))
```

```
## The estimated expected value by Log-Normal samples: 3.35
```

```
cat("The estimated expected value by Chi-Squared samples:", mean(chisamples))
```

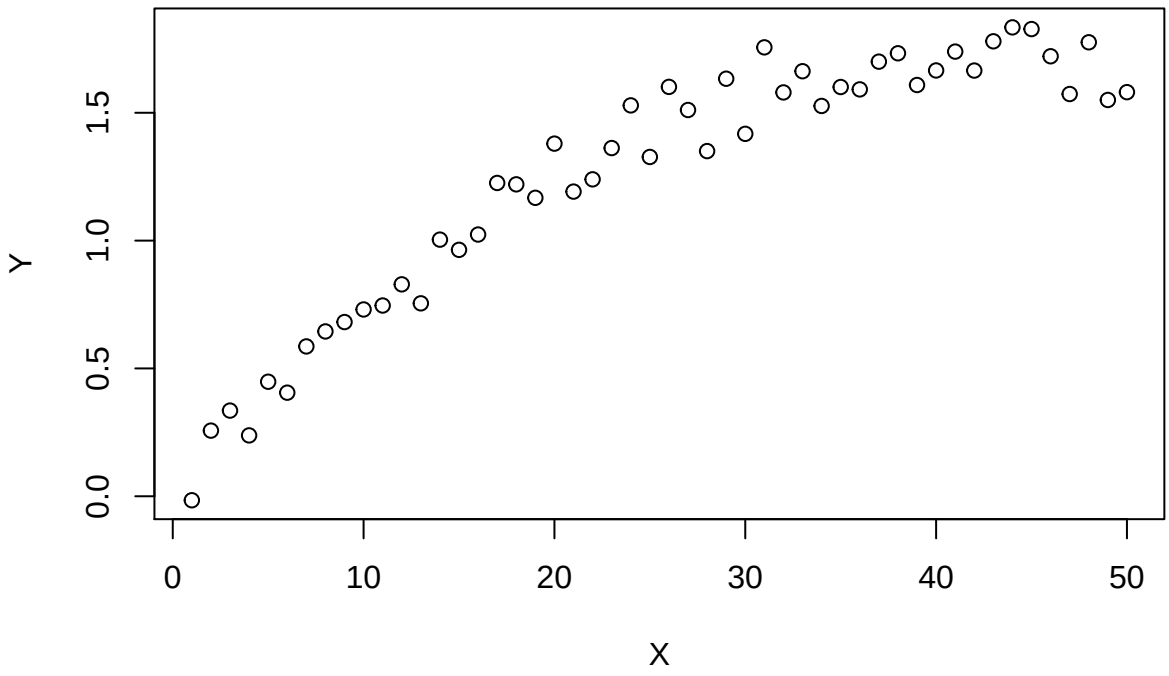
```
## The estimated expected value by Chi-Squared samples: 5.98
```

1.6

Since we know that the actual distribution is gamma with $\alpha = 6, \beta = 1$ and the expected value is defined as $\frac{\alpha}{\beta} = 6$. So we can see that the samples generated from metropolis-hasting algorithm using the chi-squared distribution as proposal have a very close estimate while using log-normal distribution does not.

Question 2

```
load("../data/chemical.RData")

chem <- data.frame(X = X , Y = Y)

plot(chem)
```



2.2

We have

$$\begin{aligned} p(\mu) &= p(\mu_1)p(\mu_2|\mu_1)\cdots p(\mu_n|\mu_{n-1}) \\ &= \frac{1}{\sqrt{(2\pi\sigma^2)^{n-1}}}\exp\left(-\frac{1}{2\sigma^2}\sum_{i=2}^{n}(\mu_i-\mu_{i-1})^2\right), \\ p(y|\mu) &= p(y_1|\mu_1)p(y_2|\mu_2)\cdots p(y_n|\mu_n) \\ &= \frac{1}{\sqrt{(2\pi\sigma^2)^{n}}}\exp\left(-\frac{1}{2\sigma^2}\sum_{i=1}^{n}(y_i-\mu_i)^2\right). \end{aligned}$$

2.3

The prosterior is then

$$
\begin{aligned}
p(\mu|y) &\propto p(y|\mu)p(\mu) \\
&\propto \exp\left(-\frac{1}{2\sigma^2}\left(\sum_{i=1}^{n}(y_i-\mu_i)^2+\sum_{i=2}^{n}(\mu_i-\mu_{i-1})^2\right)\right) \\
&\propto \exp\left(-\frac{2}{2\sigma^2}(\mu_1-(y_1+\mu_2)/2)^2-\frac{3}{2\sigma^2}\sum_{j=2}^{i}(\mu_j-(y_j+\mu_{j-1}+\mu_{j+1})/3)^2-\frac{2}{2\sigma^2}(\mu_n-(y_n+\mu_{n-1})/2)^2\right).
\end{aligned}
$$

This gives us

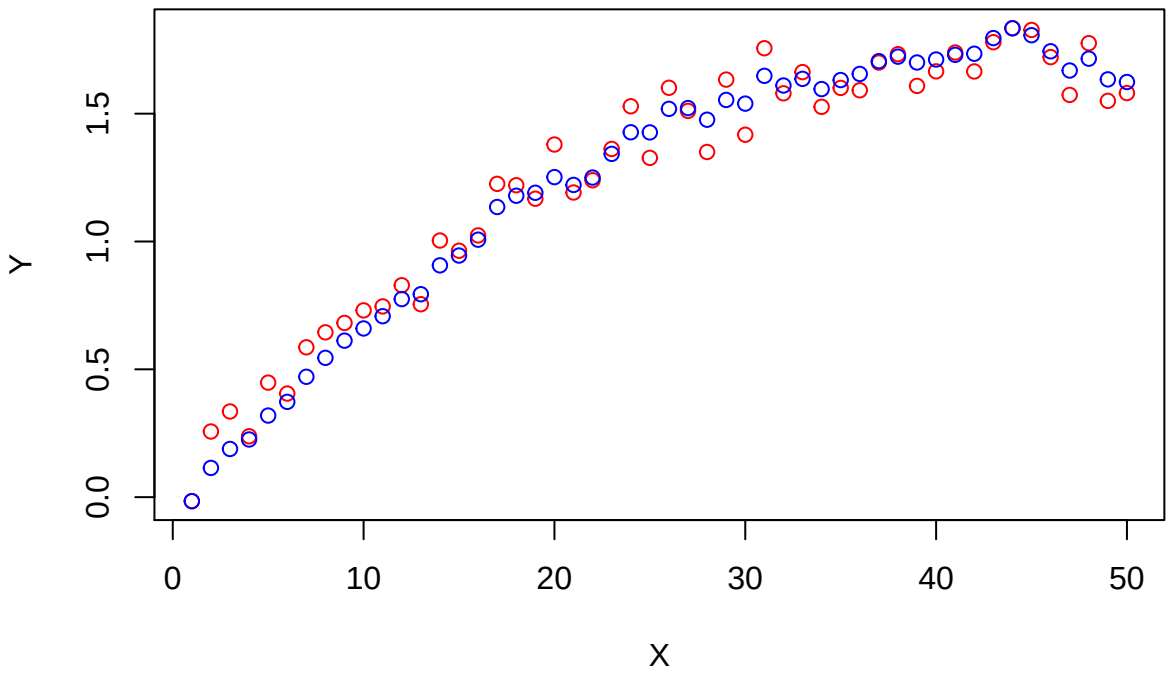
$$
\begin{aligned}
p(\mu_1|\mu_{-1},y) &\propto \exp\left(-\frac{2}{2\sigma^2}(\mu_1-(y_1+\mu_2)/2)^2\right), \\
p(\mu_i|\mu_{-i},y) &\propto \exp\left(-\frac{3}{2\sigma^2}(\mu_i-(y_i+\mu_{i-1}+\mu_{i+1})/3)^2\right) \text{ for } i=2,\ldots,n-1, \\
p(\mu_n|\mu_{-n},y) &\propto \exp\left(-\frac{2}{2\sigma^2}(\mu_n-(y_n+\mu_{n-1})/2)^2\right).
\end{aligned}
$$

2.4

```
posterior <- function(data, mus, index, sigmasq){
    if (index == 1){
        return(rnorm(1,
                     mean = (data[index] + mus[index + 1]) / 2,
                     sd = sqrt(sigmasq / 2)))
    }

    if (index == length(mus)){
        return(rnorm(1,
                     mean = (data[index] + mus[index - 1]) / 2,
                     sd = sqrt(sigmasq / 2)))
    }

    return(rnorm(1,
                 mean = (data[index] + mus[index - 1] + mus[index + 1]) / 3,
                 sd = sqrt(sigmasq / 3)))
}

gibbs <- function(data, tmax){
    d <- nrow(data)
    t <- 0

    mus <- matrix(0, nrow = tmax, ncol = d)
    sigmasq <- 0.2

    for (i in 1:tmax){
```

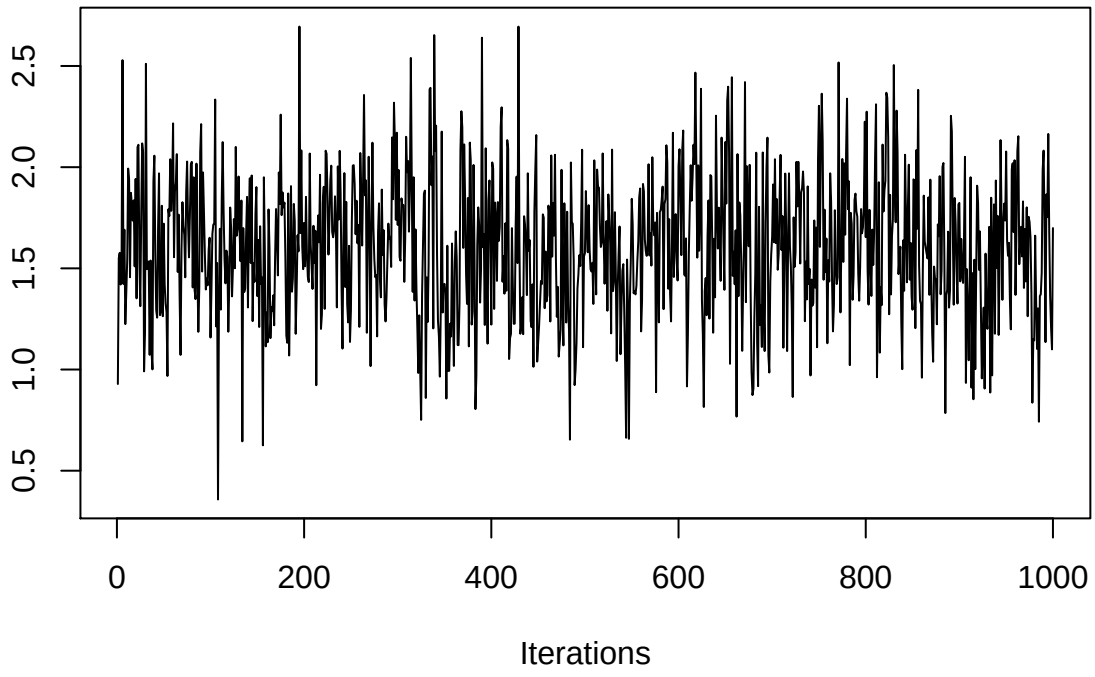
```
        for (j in 1:d){
            mus[i, j] <- posterior(data, mus[i, ], j, sigmasq)
        }

        if (i != tmax) {
            mus[i+1,] <- mus[i,]
        }
    }

    return(mus)
}
```

```
set.seed(123456)

d <- as.matrix(chem$Y)
mu <- gibbs(data = d, tmax = 1000)
emu <- colMeans(mu)

plot(chem, col="red", xlab="X", ylab="Y")
par(new = TRUE)
plot(chem$X, emu, col="blue", xlab="", ylab="", axes=FALSE)
```



2.5

```
library(coda)
traceplot(as.mcmc(mu[, 50]))
```



We can see that after roughly 600 iterations the value is more stable since it doesn't have those large spikes that occur in earlier iterations.