

CDT Module 1 - R Review

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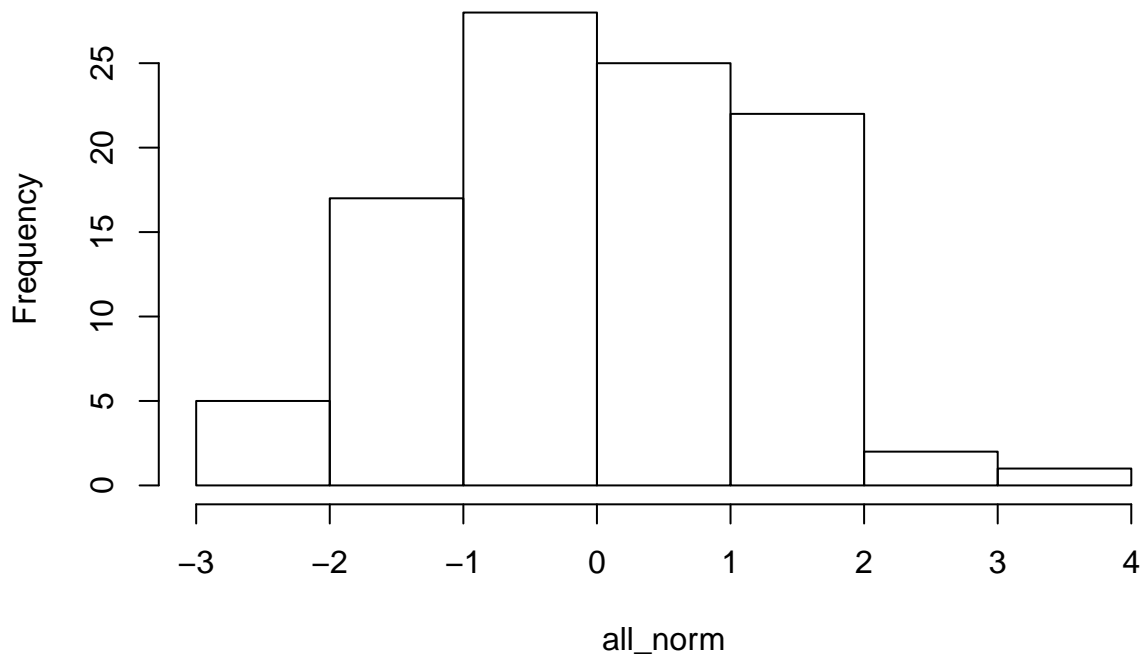
9/19/2018

1. Vectors

- Generate 100 standard normal random variables, and keep only the ones which are greater than 1.
Don't use a loop!

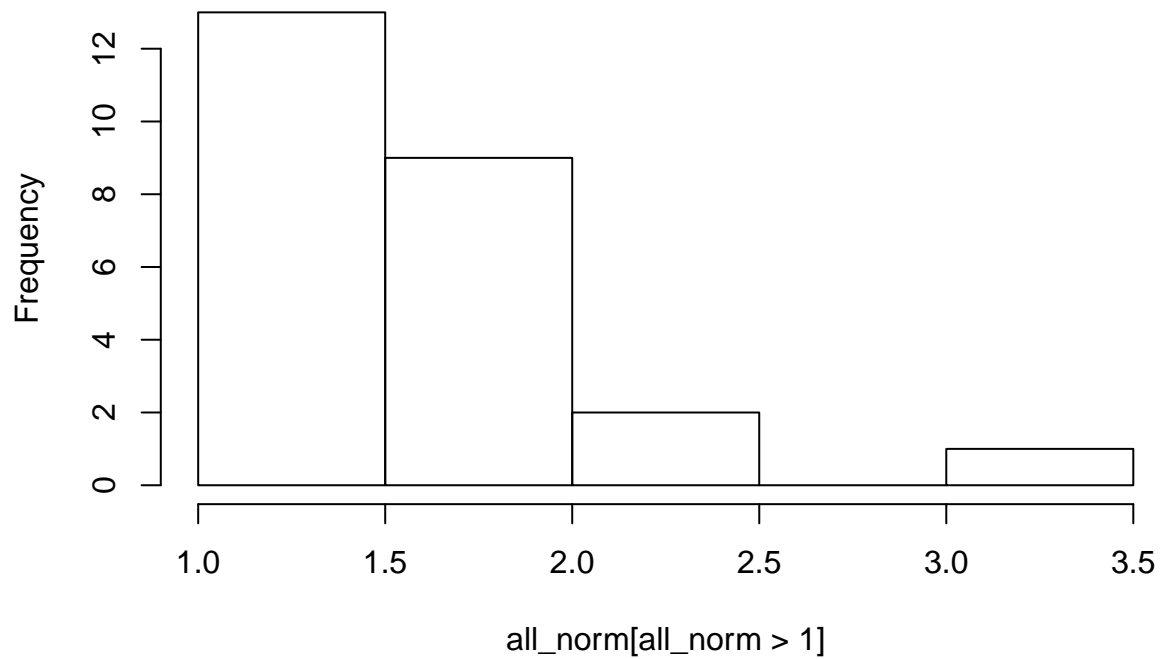
```
all_norm = rnorm(100)
hist(all_norm)
```

Histogram of all_norm



```
hist(all_norm[all_norm > 1])
```

Histogram of all_norm[all_norm > 1]

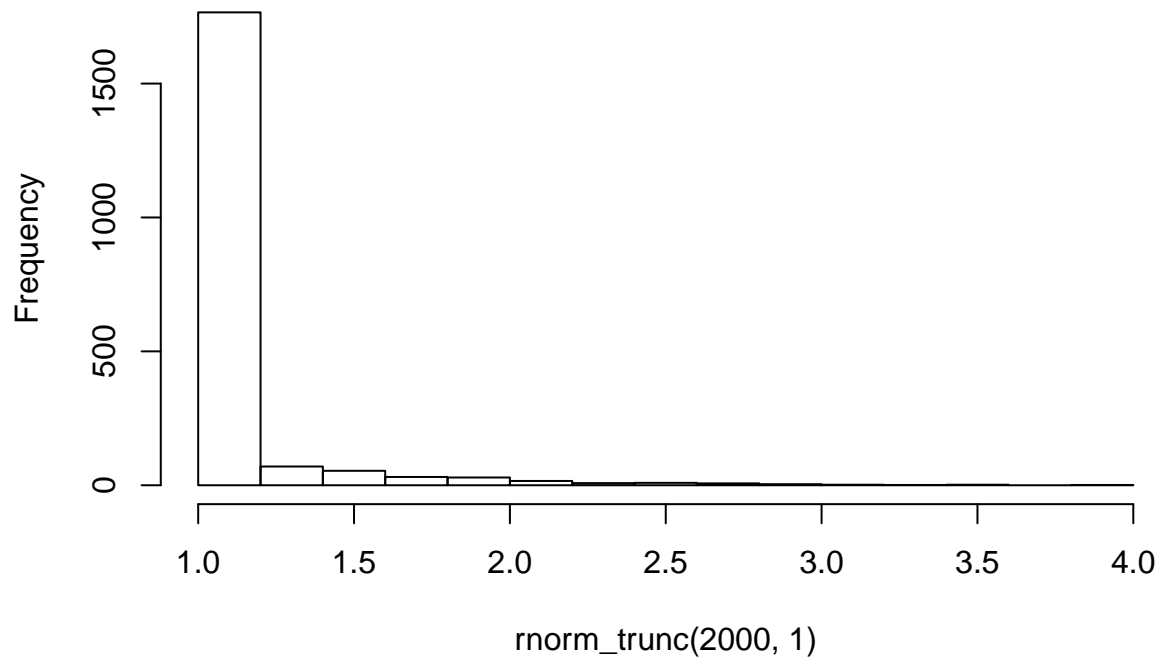


- b. Write a function which takes two arguments `n` and `min`, and returns `n` independent random variables from a standard normal distribution truncated below by `min`. Let `min` default to 0.

```
rnorm_trunc = function(n, min = 0){  
  X = rnorm(n)  
  X = unlist(lapply(X, max, min))  
  return(X)  
}
```

```
hist(rnorm_trunc(2000, 1))
```

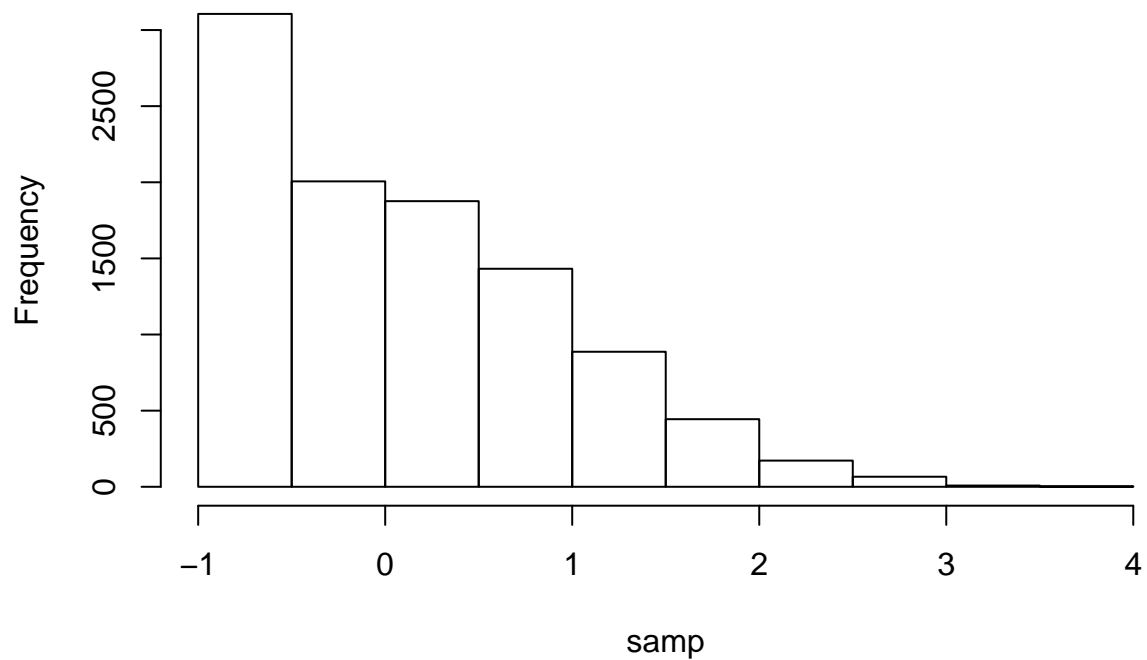
Histogram of rnorm_trunc(2000, 1)



c. Generate 10k truncated normals with min set at -1 and plot as histogram

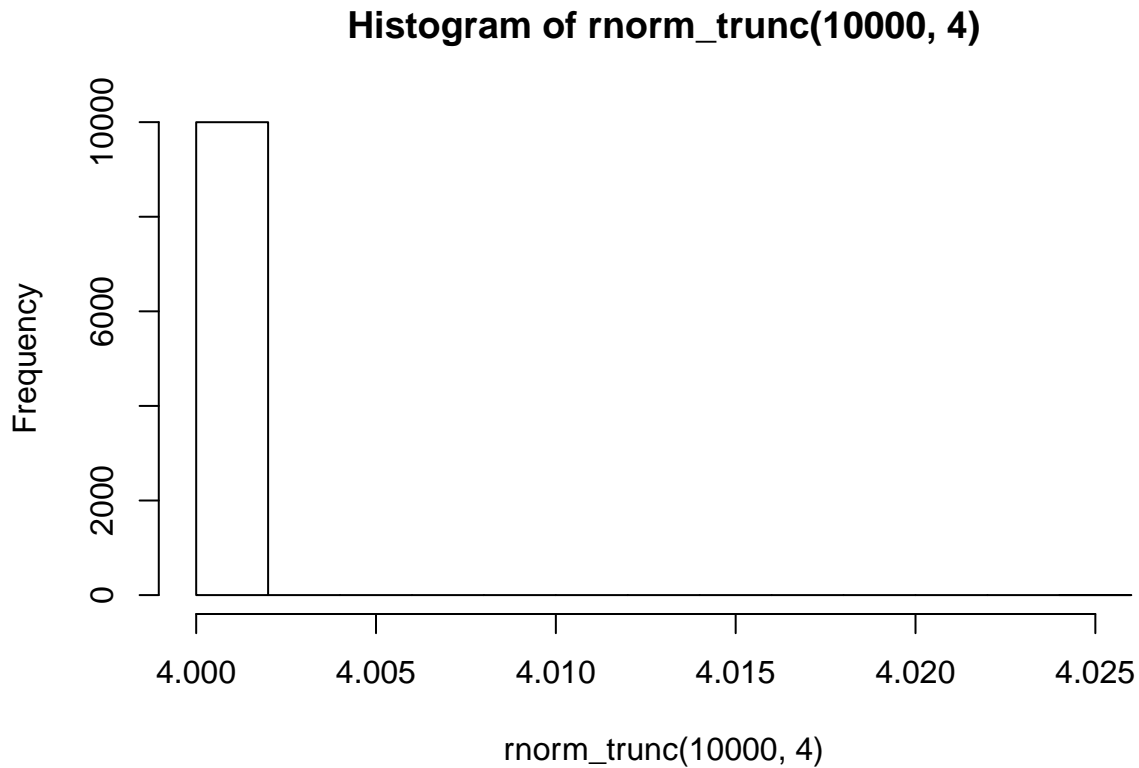
```
samp = rnorm_trunc(10000, -1)
hist(samp, breaks = 10)
```

Histogram of samp



d. what happens if min is large?

```
hist(rnorm_trunc(10000,4))
```



Point here is that this method of rejection sampling is inefficient

2. Data

```
library(MASS)
data(hills)
summary(hills)
```

```
##      dist      climb      time
##  Min.   : 2.000   Min.   : 300   Min.   : 15.95
## 1st Qu.: 4.500   1st Qu.: 725   1st Qu.: 28.00
## Median : 6.000   Median :1000   Median : 39.75
## Mean   : 7.529   Mean   :1815   Mean   : 57.88
## 3rd Qu.: 8.000   3rd Qu.:2200   3rd Qu.: 68.62
## Max.   :28.000   Max.   :7500   Max.   :204.62
```

a. what sort of object is hills?

```
class(hills)
```

```
## [1] "data.frame"
```

b. how many columns?

```
ncol(hills)
```

```
## [1] 3
```

c. Change “Two Breweries” to “Three Breweries”

```

hills[which(rownames(hills) == 'Two Breweries'),]

##           dist climb   time
## Two Breweries    18  5200 170.25

row.names(hills)[which(rownames(hills) == 'Two Breweries')] <- 'Three Breweries'
hills[which(rownames(hills) == 'Two Breweries'),]

## [1] dist   climb time
## <0 rows> (or 0-length row.names)

hills[which(rownames(hills) == 'Three Breweries'),]

##           dist climb   time
## Three Breweries    18  5200 170.25

d. Find the mean time for races iwth a climb greater than 1000ft
with(hills[hills$climb > 1000,], mean(dist))

## [1] 10.41176

```

e. What sort of object is Orthodont? How is it different from hills?

```

library(nlme)
data(Orthodont)
head(Orthodont)

## Grouped Data: distance ~ age | Subject
##   distance age Subject Sex
## 1     26.0   8      M01 Male
## 2     25.0  10      M01 Male
## 3     29.0  12      M01 Male
## 4     31.0  14      M01 Male
## 5     21.5   8      M02 Male
## 6     22.5  10      M02 Male

#class(Orthodont)

```

It's grouped data.

```

head(methods(print))

## [1] "print.abbrev"      "print.acf"          "print.AES"          "print.anova"
## [5] "print.Anova"        "print.anova.lme"

#nlme:::print.groupedData(Orthodont)

```

3. Recursion

The n th Fibonacci number is defined by the recursion $F_n = F_{n-1} + F_{n-2}$ with $F_0 = F_1 = 1$

a. Write a recursive function with argument n which returns the n th Fibonacci number

```

fibonacci = function(n){
  if(n < 0) {
    #print(n)
    F_n = 0
  }else if(n <= 1){ #note this is different than the example given in Recall (they used <=2) - has to
    #print(n)

```

```

    F_n = 1
  }else{
    #print(n)
    F_n = Recall(n-1) + Recall(n-2)
  }
  F_n
}

fibonacci(2)    #evaluated 3 times

## [1] 2

fibonacci(0)    #evaluated 1 time

## [1] 1

fibonacci(1)    #evaluated 1 time

## [1] 1

fibonacci(3)    #evaluated 5 times

## [1] 3

fib_2 = function(n){

  f_n_minus_1 = 1
  f_n_minus_2 = 1

  if(n < 0){
    return(0)
  }else if(n <= 1){
    return(1)
  }else{
    #initialize f_i at the first lag
    f_i = f_n_minus_1

    for(i in 2:n){

      #save old value
      f_i_old = f_i

      #get new value of f_i
      f_i = f_n_minus_1 + f_n_minus_2

      #update lag counters
      f_n_minus_2 = f_n_minus_1
      f_n_minus_1 = f_i_old

      print(c(i, f_i, f_n_minus_1, f_n_minus_2))
    }
    return(f_i)
  }
}

fib_2(1)

## [1] 1

```

```
fib_2(2)
```

```
## [1] 2 2 1 1
```

```
## [1] 2
```

```
fib_2(3)
```

```
## [1] 2 2 1 1
```

```
## [1] 3 2 2 1
```

```
## [1] 2
```

```
fib_2(4)
```

```
## [1] 2 2 1 1
```

```
## [1] 3 2 2 1
```

```
## [1] 4 3 2 2
```

```
## [1] 3
```

```
fib_2(5)
```

```
## [1] 2 2 1 1
```

```
## [1] 3 2 2 1
```

```
## [1] 4 3 2 2
```

```
## [1] 5 4 3 2
```

```
## [1] 4
```

4. MCMC

a. $X \sim \text{Gamma}(\alpha, \beta)$ $\alpha, \beta \sim \text{Exp}(1)$

```
#vector of data x
```

```
alpha_true = 1
```

```
beta_true = 2
```

```
x = rgamma(100, shape = alpha_true, rate = beta_true)
```

```
# evaluate the posterior distribution of alpha given a vector of data
```

```
posterior = function(x, alpha, beta){
```

```
  # get prior density
```

```
  prior_alpha = dexp(alpha, rate = 1, log = T) # alpha ~ exp(1)
```

```
  prior_beta = dexp(beta, rate = 1, log = T) # beta ~ exp(1)
```

```
  likelihood = dgamma(x, alpha, beta, log = T)
```

```
  posterior = prior_alpha + prior_beta + sum(likelihood)
```

```
  return(posterior)
```

```
}
```

```
posterior(x, alpha = 1.1, beta = 2.3)
```

```
## [1] -15.64293
```

```
posterior(x, alpha = 2, beta = 2)

## [1] -78.01093

b. single metropolis hastings step  $\alpha' = \alpha + \sigma Z_1$   $\beta' = \beta + \sigma Z_2$  where  $Z_1, Z_2$  are iid Standard Normal
 $q'(\alpha'|\alpha) N(\alpha, \sigma^2)$ 

step_MH = function(x, alpha, beta, sigma){

  alpha_prime = rnorm(n = 1, alpha, sigma)
  beta_prime = rnorm(n = 1, beta, sigma)

  a = exp(posterior(x, alpha = alpha_prime, beta = beta_prime) - posterior(x, alpha = alpha, beta = beta))
  u = runif(1)
  if(u < a){
    data.frame(alpha = alpha_prime, beta = beta_prime)
  }else{
    data.frame(alpha = alpha, beta = beta)
  }
}

step_MH(x, alpha = 1.1, beta = 2.3, sigma = 0.01)

##      alpha      beta
## 1 1.092917 2.30664

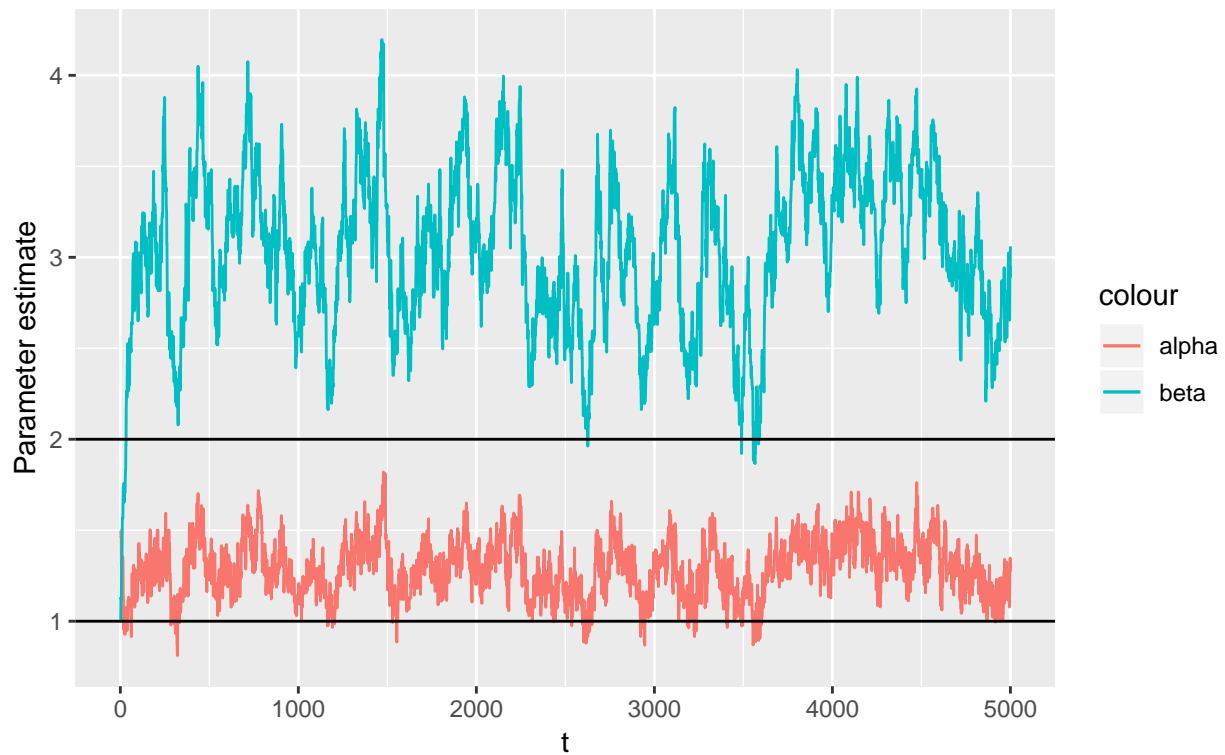
run_MH = function(N, x, alpha, beta, sigma){
  chains = data.frame(t = 0, alpha = alpha, beta = beta)
  for(t in 1:N){
    step = step_MH(x, alpha = chains[t,]$alpha, beta = chains[t,]$beta, sigma)
    chains[t+1, ] = c(t, step$alpha, step$beta)
  }
  return(chains)
}

chains = run_MH(5000, x = x, alpha = 1.5, beta = 1, sigma = 0.1)

ggplot(chains, aes(x = t, y = alpha)) + geom_line(aes(color = 'alpha')) + geom_line(aes(x = t, y = beta, color = 'beta'))
ggtitle(paste0("Metropolis-Hastings Sampling for Gamma(alpha, beta)\n", "alpha = ", alpha_true, ", beta = ", beta_true))
geom_hline(yintercept = alpha_true) +
geom_hline(yintercept = beta_true) +
ylab("Parameter estimate")
```


Metropolis–Hastings Sampling for Gamma(alpha, beta)

alpha = 1, beta = 2

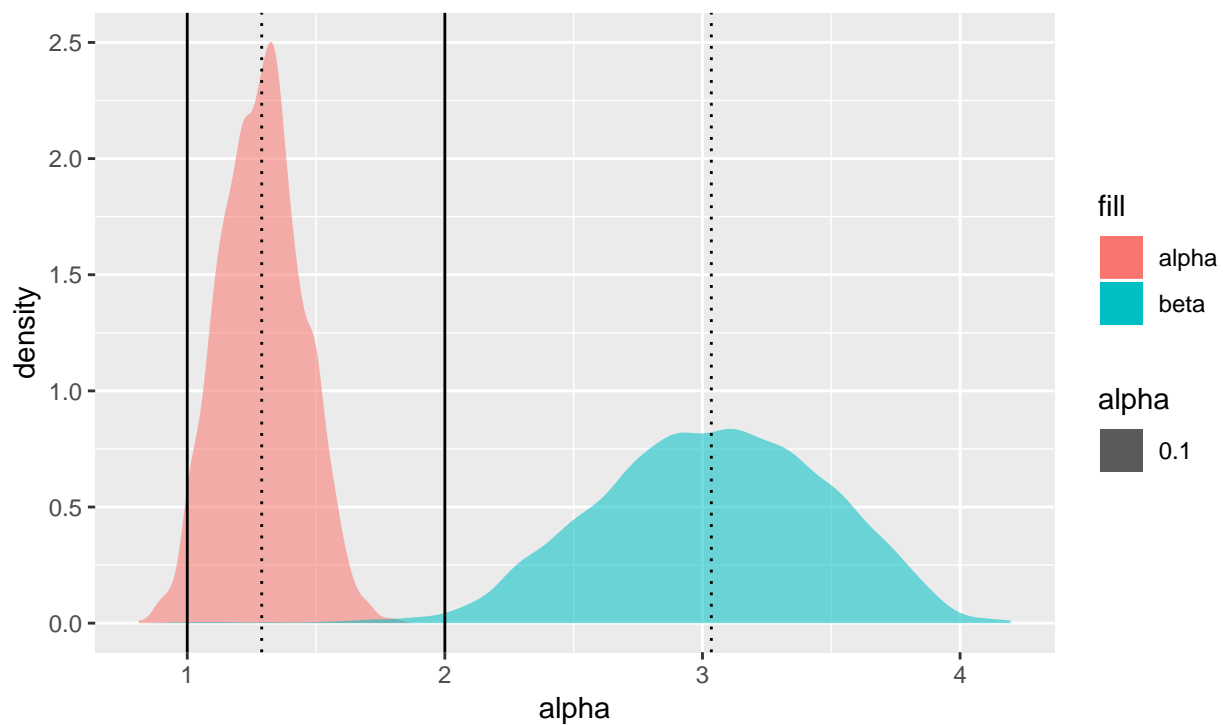


```
ggplot(chains) + stat_density(aes(x = alpha, fill = 'alpha', alpha = 0.1)) +
  stat_density(aes(x = beta, fill = 'beta', alpha = 0.1)) +
  geom_vline(xintercept = mean(chains$alpha), linetype = 'dotted') +
  geom_vline(xintercept = alpha_true) +
  geom_vline(xintercept = mean(chains$beta), linetype = 'dotted') +
  geom_vline(xintercept = beta_true) +
  ggtitle(paste0("M-H Sampling\nPosterior parameter distributions for Gamma(alpha, beta)\nT = ", nrow(chains)))
```

M-H Sampling

Posterior parameter distributions for Gamma(alpha, beta)

T = 5000



Let's see how this converges over time

```
Ts = seq(250, 5000, by = 250)

all_chains = lapply(Ts, FUN = run_MH, x = x, alpha = 1.5, beta = 1, sigma = 0.2)

all_chains = rbindlist(all_chains)
all_chains = as.data.table(all_chains)
all_chains[, N := rep(Ts, times = Ts + 1)]

all_chains[, .(mean(alpha), .N), N]
```

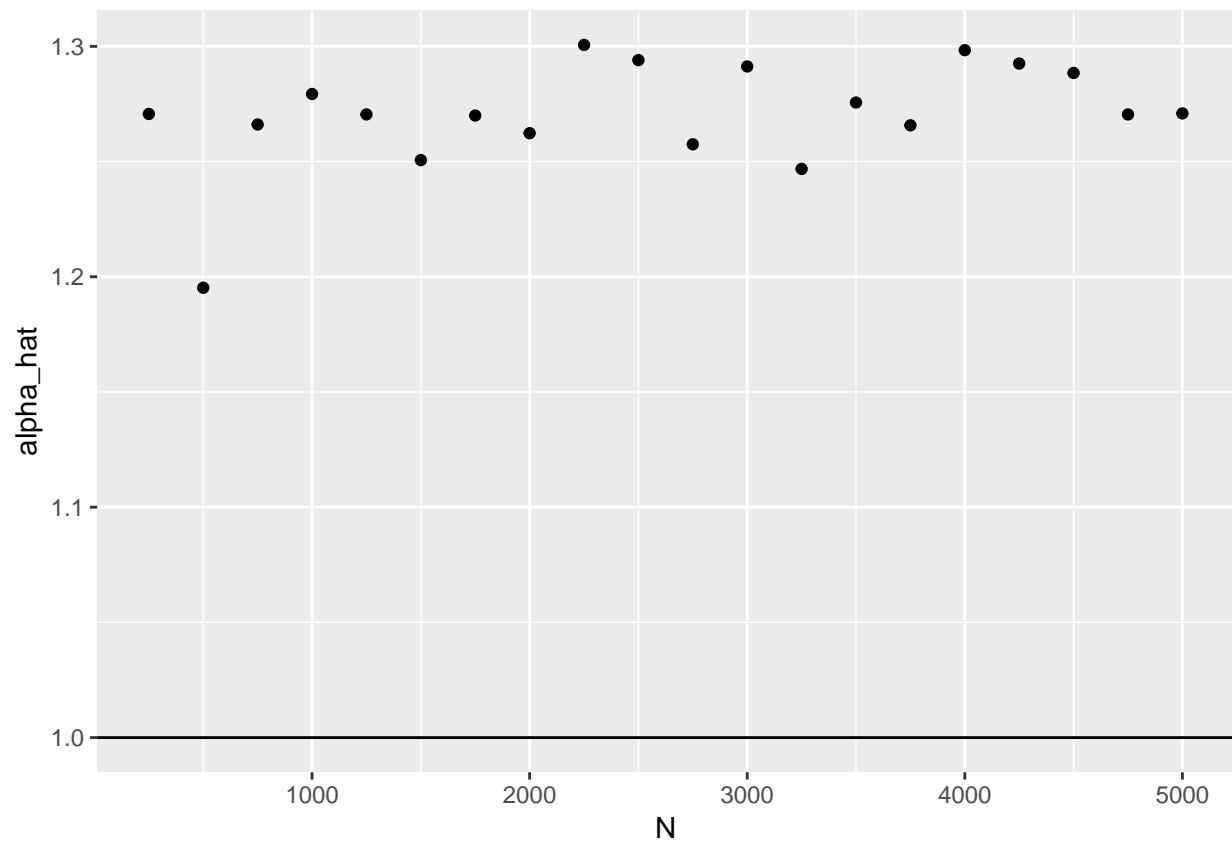
##	N	V1	N	
##	1:	250	1.270656	251
##	2:	500	1.195231	501
##	3:	750	1.266099	751
##	4:	1000	1.279338	1001
##	5:	1250	1.270465	1251
##	6:	1500	1.250645	1501
##	7:	1750	1.269973	1751
##	8:	2000	1.262321	2001
##	9:	2250	1.300630	2251
##	10:	2500	1.294036	2501
##	11:	2750	1.257512	2751
##	12:	3000	1.291271	3001
##	13:	3250	1.246820	3251
##	14:	3500	1.275628	3501

```
## 15: 3750 1.265723 3751
## 16: 4000 1.298344 4001
## 17: 4250 1.292533 4251
## 18: 4500 1.288440 4501
## 19: 4750 1.270453 4751
## 20: 5000 1.270900 5001
```

```
all_chains[, .(mean(beta), .N), N]
```

```
##      N      V1      N
## 1:  250 2.960724  251
## 2:  500 2.702690  501
## 3:  750 2.893831  751
## 4: 1000 2.991720 1001
## 5: 1250 2.978000 1251
## 6: 1500 2.898417 1501
## 7: 1750 2.963744 1751
## 8: 2000 2.933248 2001
## 9: 2250 3.083511 2251
## 10: 2500 3.045374 2501
## 11: 2750 2.926844 2751
## 12: 3000 3.048239 3001
## 13: 3250 2.915641 3251
## 14: 3500 2.997848 3501
## 15: 3750 2.981003 3751
## 16: 4000 3.078727 4001
## 17: 4250 3.079169 4251
## 18: 4500 3.031384 4501
## 19: 4750 2.965151 4751
## 20: 5000 2.984470 5001
```

```
ggplot(all_chains[, .(alpha_hat = mean(alpha)), N]) + geom_point(aes(x = N, y = alpha_hat)) + geom_hline
```



```
ggplot(all_chains[, .(beta_hat = mean(beta)), N]) + geom_point(aes(x = N, y = beta_hat)) + geom_hline(y
```

