#### Untitled

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1

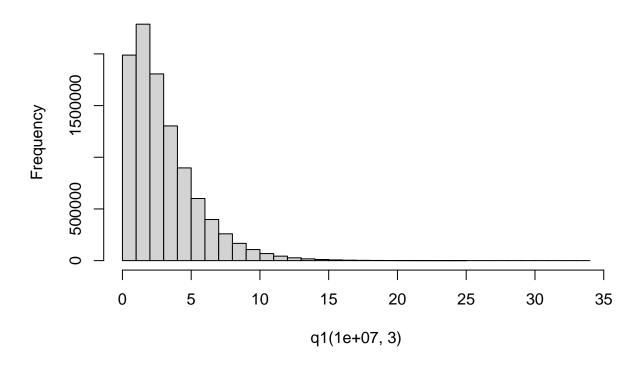
```
df <- c(1)
q1<-
  function (n,k){
    df <- c(1)
    for (b in seq(n)){
        a <- 0
        for( x in seq(k)){
        a = a + (rnorm(1))^2
        }
        df[b] = a
    }
  return(df)
}</pre>
```

2

By function in #1

```
set.seed(1001)
hist(q1(10000000,3), main="Histogram of function from #1")
```

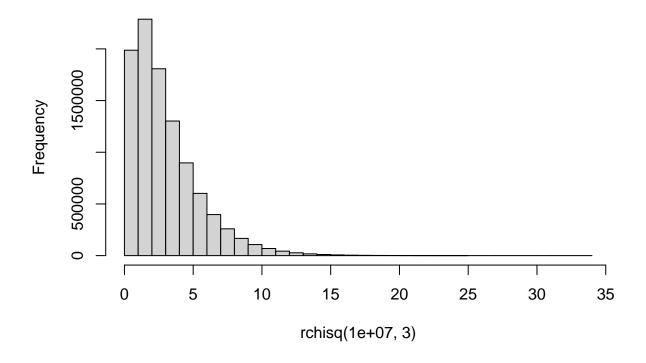
### Histogram of function from #1



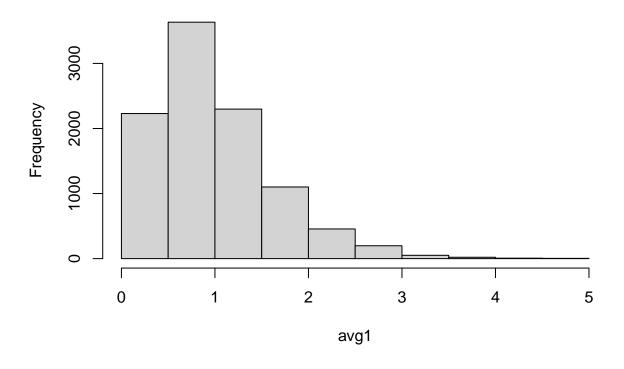
#### By function rchisq()

```
set.seed(8289)
hist(rchisq(10000000,3), main="Histogram of rchisq()")
```

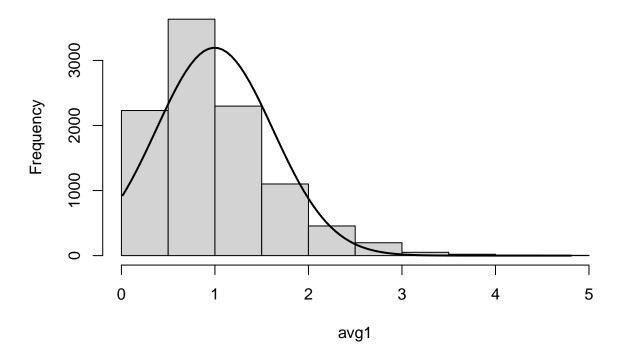
### Histogram of rchisq()



```
set.seed(8289)
avg1=c(0)
for(x in seq(10000)){
   avg1[x] = mean(rchisq(5,1))
}
x2 <- seq(min(avg1), max(avg1), length = 100)
fun <- dnorm(x2, mean = mean(avg1), sd = sd(avg1))
y2<-fun* diff(hist(avg1)$mids[1:2])*length(avg1)</pre>
```

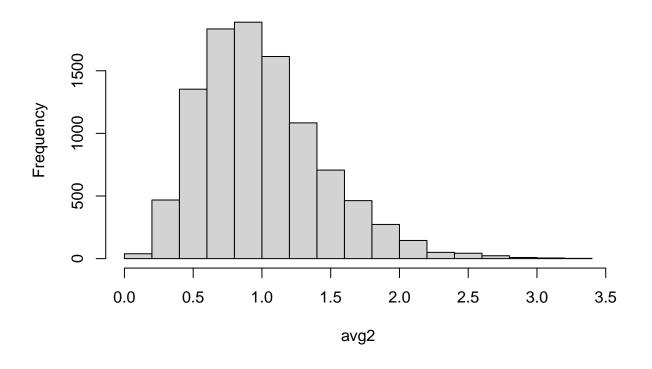


```
hist(avg1, main="Mean of Chi-sqr with n = 20")
lines(x2, y2, lwd = 2)
```

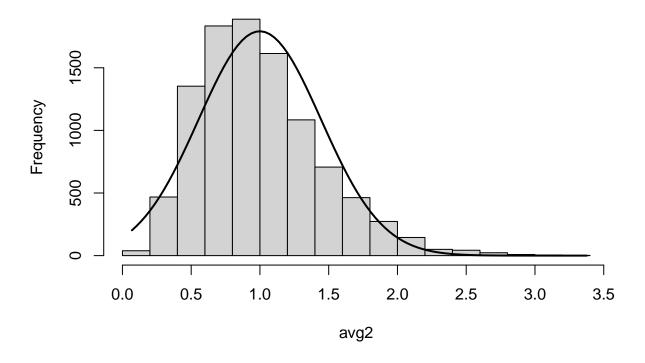


```
set.seed(8289)
avg2=c(0)
for(x in seq(10000)){
   avg2[x] = mean(rchisq(10,1))
}

x2 <- seq(min(avg2), max(avg2), length = 100)
fun <- dnorm(x2, mean = mean(avg2), sd = sd(avg2))
y2<-fun* diff(hist(avg2)$mids[1:2])*length(avg2)</pre>
```

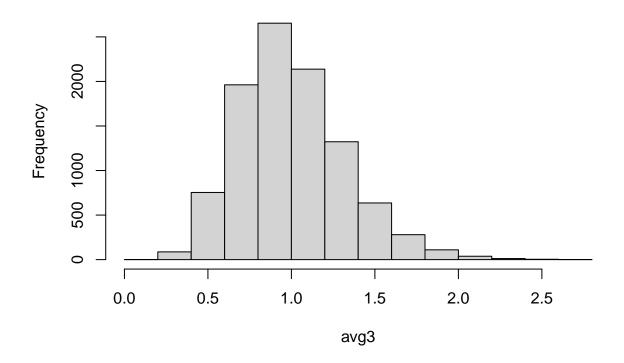


```
hist(avg2, main="Mean of Chi-sqr with n = 20")
lines(x2, y2, lwd = 2)
```

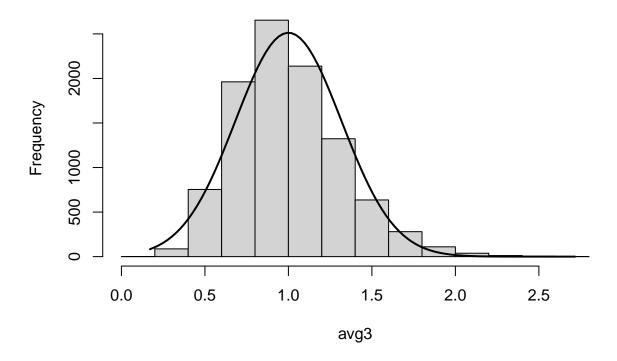


```
set.seed(8289)
avg3=c(0)
for(x in seq(10000)){
   avg3[x] = mean(rchisq(20,1))
}

x2 <- seq(min(avg3), max(avg3), length = 100)
fun <- dnorm(x2, mean = mean(avg3), sd = sd(avg3))
y2<-fun* diff(hist(avg3)$mids[1:2])*length(avg3)</pre>
```

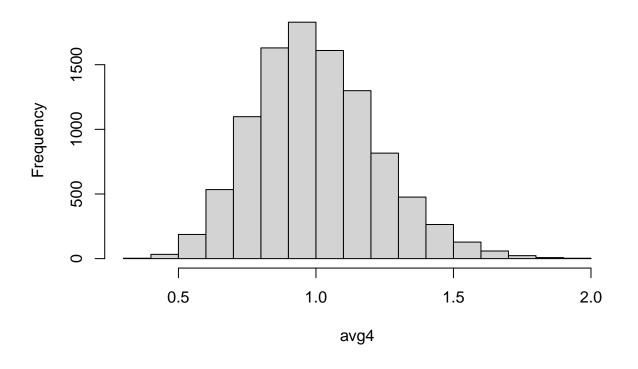


```
hist(avg3, main="Mean of Chi-sqr with n = 20")
lines(x2, y2, lwd = 2)
```

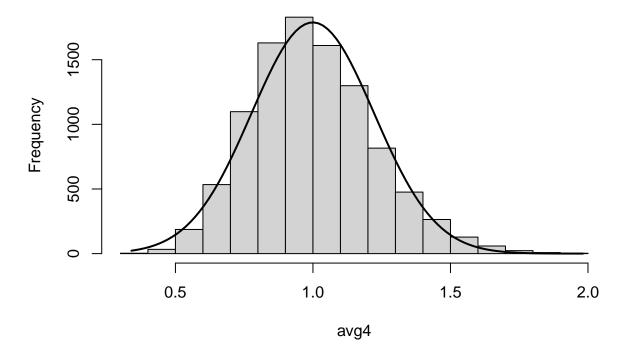


```
set.seed(8289)
avg4=c(0)
for(x in seq(10000)){
   avg4[x] = mean(rchisq(40,1))
}

x2 <- seq(min(avg4), max(avg4), length = 100)
fun <- dnorm(x2, mean = mean(avg4), sd = sd(avg4))
y2<-fun* diff(hist(avg4)$mids[1:2])*length(avg4)</pre>
```



```
hist(avg4, main="Mean of Chi-sqr with n = 20")
lines(x2, y2, lwd = 2)
```



#### Discussion

According to the LLNs, the sample average converage as the simple size n approaches to infinity (the sample average almost converge surely). From the abover progression we can tell that the histogram of sample mean for Chi-square distribution changed from very left-skewed to more and more central as sample size (n) increased from 5 to 40.

4

```
sig <- matrix(c(13.6, -14.5, -103.4, -14.5, 65.2, 154, -103.4, 154, 2702), 3, 3, byrow = TRUE)
error <- rnorm(1000,0,0.75^2)
mvn_gen <- function(n, mu, sigma, factorization = "Cholesky") {
    d <- length(mu)
    Z <- matrix(rnorm(n*d), nrow = n, ncol = d)
    if(factorization == "Cholesky") { Q <- chol(sigma) } else {
        if(factorization == "Spectral") {
            ev <- eigen(sigma)
            lambda <- ev$values
        P <- ev$vectors
        Q <- P %*% diag(sqrt(lambda)) %*% t(P) } else {
            stop("Arg factorization must be 'Cholesky' or 'Spectral'.")
        } }
        mu <- matrix(mu, nrow = d, ncol = 1)</pre>
```

```
J = matrix(1, nrow = n, ncol = 1)
X <- Z %*% Q + J %*% t(mu)
return(data.frame(X))
}
set.seed(1211)

mv <- mvn_gen(n = 1000, mu = c(0.5, 0.3, 10), sigma = sig, factorization = "Spectral")
Y = 71 - 0.28 *mv$X1 + 0.05*mv$X2 - 0.007*mv$X3+error
data2 <- cbind(mv,Y)

model<-lm(Y ~ X1 +X2 + X3 ,data = data2)</pre>
```

```
model%>%
  tidy() %>%
  kable()
```

term	estimate	std.error	statistic	p.value
(Intercept)	71.0014400	0.0192700	3684.55010	0
X1	-0.2790970	0.0065873	-42.36882	0
X2	0.0517965	0.0026530	19.52409	0
X3	-0.0069816	0.0004300	-16.23521	0