Q1:

```
mean=10.4

sd=2.4

norm_17<-rnorm(n=17,mean,sd)

norm_30<-rnorm(n=30,mean,sd)

norm_300<-rnorm(n=300,mean,sd)

norm_3000<-rnorm(n=3000,mean,sd)
```

Q2:

```
png(filename=here("eco_634_2021","lab_04_hist_01.png"),width=1500,height=1600,units="p" ",res=180)
par(mfrow=c(2,2))
hist(norm_17,main="Hist.of 17 normally distributed random pnts.")
hist(norm_30,main = "Hist. of 30 normally distr. random pnts.")
hist(norm_300,main ="Hist. of 300 normally distr. random pnts.")
hist(norm_3000,main ="Hist. of 3000 normally distr. random pnts.")
dev.off()
```

Q3: Upload figure

Q4: With increased sample size the distribution appears more normal. The histograms with smaller samples are more prone variation from the mean. This is representative in my histograms as the histogram with the smallest sample size (17) looks the least normally distributed (around the mean) than the histogram with a sample of 3000. The histogram with a sample size of 30 and 300 appear progressively more normal.

Q5: This occurs because histograms with larger sample sizes are less prone to variation from the mean. As sample size increases, the distribution appears more normal. More representatives are provide a better picture of the distribution.

Q6: The parameters and their values for the standard normal distribution are the mean and the standard deviation. The values for the histograms we just made were mean=10.4, and sd=2.4.

Q7:

```
x = seq(-20, 20, length.out = 1000)

y = dnorm(x,mean=10.4,sd=2.4)

svg(filename=here("eco_634_2021","norm_1.svg"),width=7,height=9)

plot(x, y, type = "l", xlim = c(0, 20),main="normal distribution with a mean 10.4 and sd 2.4")

abline(h = 0)

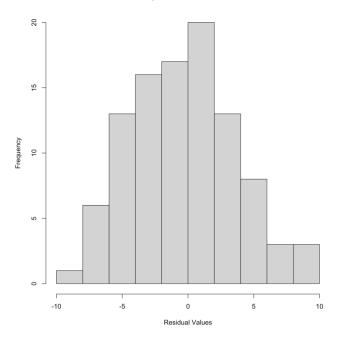
dev.off()
```

Q8: Upload figure

```
Q9:
#create the dataset
set.seed(100)
 n pts = 100
 x min = -10
 x_max = 10
 x = runif(n = n_pts, min = x_min, max = x_max)
 dat = data.frame(x = x, y observed = rpois(n pts,15))
#this is the code to make the figure
#create color
 mycol < -rgb(100, 80, 20, max = 100, alpha = 50)
 mycol2 < -rgb(20, 60, 20, max = 100, alpha = 80)
 mycol3<- rgb(100,0,80,max=100,alpha=25)
png(filename=here("eco_634_2021","lab_04_q_10.png"),width=1500,height=1600,units="px",r
es = 180)
par(mfrow = c(2, 2))
#scatterplot
plot(dat,cex=0.8,col=mycol,pch=19)
plot(dat,cex=2,col=mycol2,pch=18)
#histogram
hist(dat$x,col=mycol3)
#boxplot
boxplot(dat)
dev.off()
Q10: Upload figure
Q11:
#create the dataset
set.seed(100)
n pts = 100
x min = -10
x max = 10
x = runif(n = n pts, min = x min, max = x max)
dat = data.frame(x = x, y_observed = rpois(n_pts,15))
#create the figure (with custom color)
mycol < -rgb(100, 80, 20, max = 100, alpha = 50)
png(filename=here("eco_634_2021","lab_04_q_12.png"),width=1500,height=1600,units="px",r
es=180)
plot(dat,cex=0.8,col=mycol,pch=19)
guess x<-0
guess y<-15
```

```
guess slope<-0.2
x = runif(n = n, min = 1, max = 10)
#line point slope<-Vectorize(line point slope)
curve(line_point_slope(x,guess_x,guess_y,guess_slope),add=T)
dev.off()
Q12: Upload Image
Q13:
#create the dataset
set.seed(100)
n pts = 100
x min = -10
x max = 10
x = runif(n = n_pts, min = x_min, max = x_max)
dat = data.frame(x = x, y_observed = rpois(n_pts,15))
#column of predicted y-values
dat$y predicted<-line point slope(dat$x,guess x,guess y,guess slope)
#column of residuals
dat$resids<-dat$y predicted-dat$y observed
Q14: Upload two figures, one of the histogram one of the scatterplot.
#histogram of the models residuals
png(filename=here("eco_634_2021","lab_04_q_14_histogram.png"),width=1500,height=1600,
units="px",res=180)
hist(dat$resids,main="Histogram of Model Residuals",xlab="Residual Values",
ylab="Frequency")
dev.off()
#scatterplot of the models predicted values on x and residuals on y
png(filename=here("eco 634 2021","lab 04 q 14 scatterplot.png"),width=1500,height=1600,
units="px",res=180)
plot(dat$y predicted,dat$resids,xlab="predicted y values",ylab="residual
values",main="Residual Scatterplot")
dev.off()
```

Histogram of Model Residuals



Residual Scatterplot

