

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",res=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",res=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()
```

