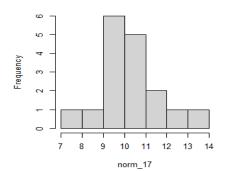
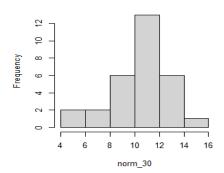
```
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ECO 634
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Lab 4: Uncertainty and Error
1.
norm_17 <- rnorm(n = 17, mean = 10.4, sd = 2.4)
norm 30 < -rnorm(n = 30, mean = 10.4, sd = 2.4)
norm_300 <- rnorm(n = 300, mean = 10.4, sd = 2.4)
norm_3000 < rnorm(n = 3000, mean = 10.4, sd = 2.4)
2.
par(mfrow = c(2,2))
hist(norm_17)
hist(norm_30)
hist(norm_300)
hist(norm_3000)
png(filename = here("lab_04_hist_01.png"), width = 1500, height = 1600,
  res = 120, units = "px")
3.
```

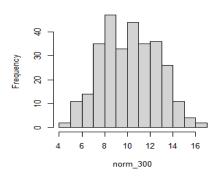
Normal Distribution of 17 points



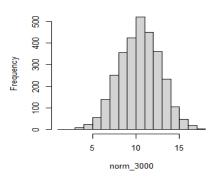
Normal Distribution of 30 points



Normal Distribution of 300 points



Normal Distribution of 3000 points

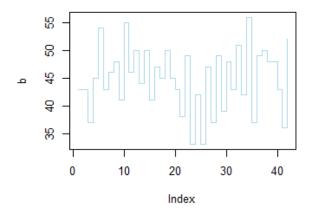


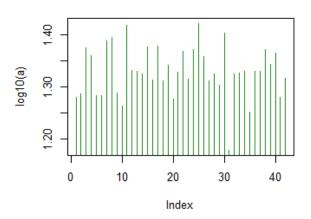
- 4. In the plots with lower #, the points aren't very *normal*-looking. The lower value plots seem skewed
- 5. The shapes of the distributions are different because when the sample size n is increased, the distributions become increasingly bell-shaped and normally distributed.
- 6. The parameters for the standard normal distribution are the mean and the standard deviation from the mean. The standard values are a mean of zero and a standard deviation of one.

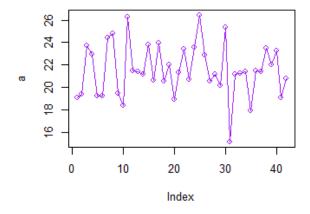
```
    x <- seq(0, 20, length.out = 1000)</li>
    y <- dnorm(x, mean=10.4, sd=2.4)</li>
    plot(x , y,
        type = "I",
        main = "Normal density distribution (mean = 10.4, sd = 2.4)")
    abline(v=10.4)
    9.
    set.seed(42)
    a <- rnorm(42, mean = 21, sd = 2)</li>
```

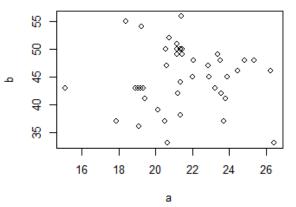
```
plot(log10(a),
type = "b",
cex = 2,
pch = 1,
col = c("blue", "red"))
```

10.









```
11.
n_pts = 10
x_min = 1
x_max = 10
```

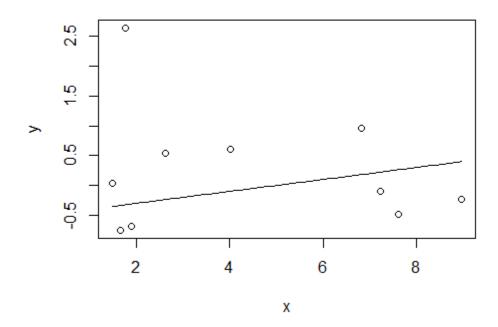
x_random = runif(n = n_pts, min = x_min, max = x_max) y_random = rnorm(n = n_pts)

guess_x <- 5 guess_y <- 0

```
guess_slope <- 0.1
plot(y~x, data = dat_random)
curve(line_point_slope(x, guess_x, guess_y, guess_slope), add = T)</pre>
```

12.

random datapoints + line

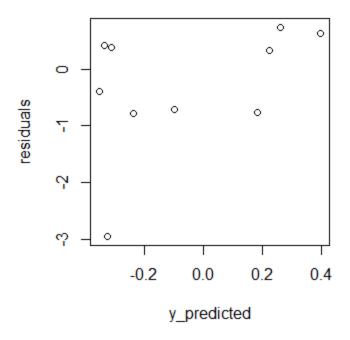


13. dat_random[,3] <- line_point_slope(dat_random\$x, guess_x, guess_y, guess_slope) names(dat_random)[3] <- "y_predicted"

```
residual <- (dat_random$y_predicted - dat_random$y) dat_random[ ,4] <- residual names(dat_random)[4] <- "residuals"
```

14.

Predicted Y-values vs residuals



Predicted model residuals

