Quick Intro to R

Contents

Welcome to R

In this very brief introduction to R, we work up to a few examples from two popular packages: *dplyr* for data wrangling and *ggplot2* for plotting. Additionally, we give two examples of some common statistical models. We will use this code later in a Shiny application. These topics comprise some of R's greatest strengths: + Data wrangling + Plotting/visuals + Statistical model fitting + Interactive applications (Shiny) + All in a fantastic GUI (RStudio)

Objects

Scalars

```
1 + 1
```

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

```
a <- 1 + 1
```

Vectors

We show various ways to make similar numeric vectors:

```
v1 <- 1:3
v2 <- c(1, 2, 3)
v3 <- seq(1, 3, by = 1)
v4 <- seq(1, 3, length.out = 3)
v1
```

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

```
v2
```

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

```
v3
```

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

```
v4
```

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

```
v1*v2
```

```
## [1] 1 4 9
```

Character and factor vectors

```
c1 <- c("one", "two", "three", "one", "two", "three")
c1
```

```
## [1] "one"   "two"   "three" "one"   "two"   "three"
```

```
f1 <- factor(c("one", "two", "three", "one", "two", "three"))
f1
```

```
## [1] one   two   three one   two   three
## Levels: one three two
```

Matrices

```
m1 <- matrix(data = c(1, 2, 3, 4, 5, 6, 7, 8, 9),
             nrow = 3,
             ncol = 3,
             byrow = FALSE)

m2 <- matrix(data = rnorm(n = 9, mean = 0, sd = 1),
             nrow = 3,
             ncol = 3,
             byrow = TRUE)
m1 * m2
```

```
##              [,1]      [,2]        [,3]
## [1,] -0.363134266  3.782423 -10.6122878
## [2,] -0.005303108  4.341679  -0.2117668
## [3,] -3.122262923 -8.300383  -9.2579059
```

```
m1 %*% m2
```

```
##            [,1]      [,2]       [,3]
## [1,]  -7.659021 -5.264830  -8.822518
## [2,]  -9.065561 -4.834286 -11.393686
## [3,] -10.472101 -4.403741 -13.964854
```

Data frame objects

```
d <- data.frame(A = 1:4,
                B = c("red", "blue", "yellow", "green"))
class(d)
```

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

```
class(iris)
```

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

```
summary(iris)
```

```
##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
##        Species
##  setosa    :50
##  versicolor:50
##  virginica :50
##
##
##
```

```
str(iris)
```

```
## 'data.frame':    150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
##  $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

```
head(iris)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1         3.5          1.4         0.2  setosa
## 2          4.9         3.0          1.4         0.2  setosa
## 3          4.7         3.2          1.3         0.2  setosa
## 4          4.6         3.1          1.5         0.2  setosa
## 5          5.0         3.6          1.4         0.2  setosa
## 6          5.4         3.9          1.7         0.4  setosa
```

Reading and writing data

CSV

```
write.csv(x = iris,
          file = "iris.csv",
          row.names = F)
mattysdf <- read.csv(file = "iris.csv")
```

RDS

```
saveRDS(object = iris,
        file = "iris.RDS")
mattysdf <- readRDS("iris.RDS")
```

Data wrangling

We turn to our favorite data wrangling package, dplyr.

```
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

Select specific columns

```
mattysdf %>%
  select(Petal.Length, Species) %>%
  head(5)
```

```
##   Petal.Length Species
## 1          1.4  setosa
## 2          1.4  setosa
## 3          1.3  setosa
## 4          1.5  setosa
## 5          1.4  setosa
```

Filter to specific rows

```
mattysnewdf <- mattysdf %>%
  filter(Species == "versicolor")
```

"Mutate" on new columns

```
mattysnewdf2 <- mattysdf %>%
  mutate(Sepal.Area = Sepal.Width*Sepal.Length,
         Petal.Area = Petal.Width*Petal.Length)
```

Pivot table

```
mattysnewdf2 %>%
  group_by(Species) %>%
  summarize(Sepal.Area.mean = mean(Sepal.Area),
            Sepal.Area.sd = sd(Sepal.Area),
            Petal.Area.mean = mean(Petal.Area),
            Petal.Area.sd = sd(Petal.Area))
```

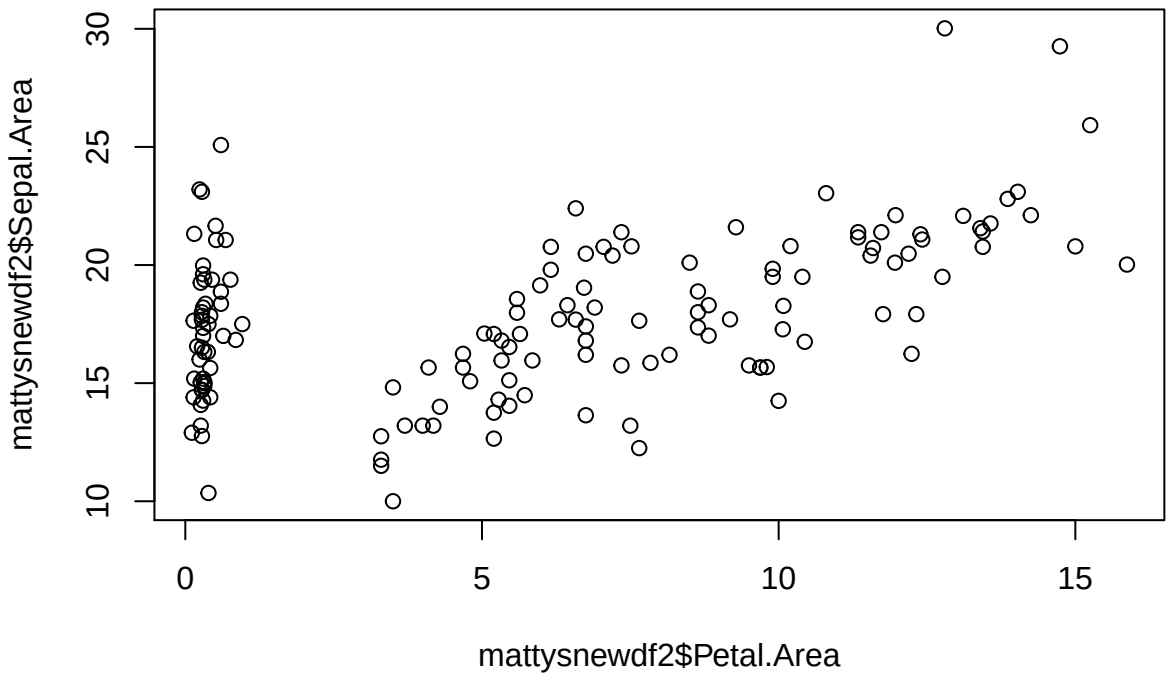
```
## # A tibble: 3 x 5
##      Species Sepal.Area.mean Sepal.Area.sd Petal.Area.mean Petal.Area.sd
##       <fctr>           <dbl>         <dbl>           <dbl>         <dbl>
## 1     setosa         17.2578      2.933775          0.3656     0.1811546
## 2 versicolor         16.5262      2.866882          5.7204     1.3684029
## 3  virginica         19.6846      3.458783         11.2962     2.1574124
```

Plotting

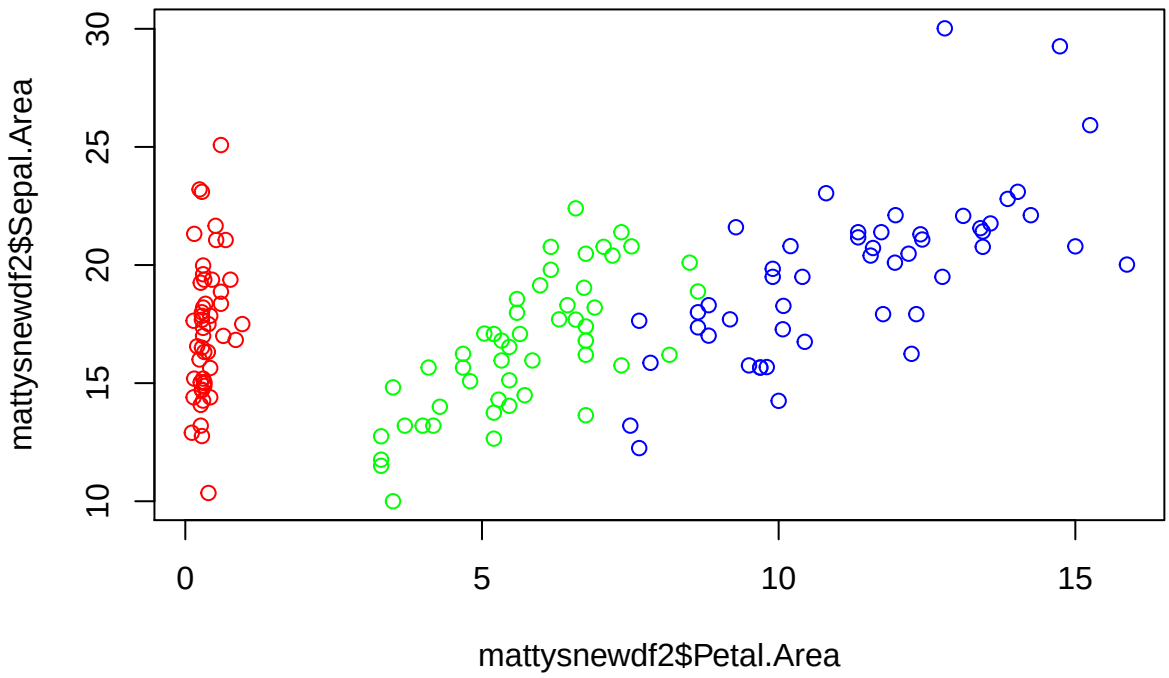
Base R

Scatter plot

```
plot(x = mattysnewdf2$Petal.Area,
     y = mattysnewdf2$Sepal.Area)
```

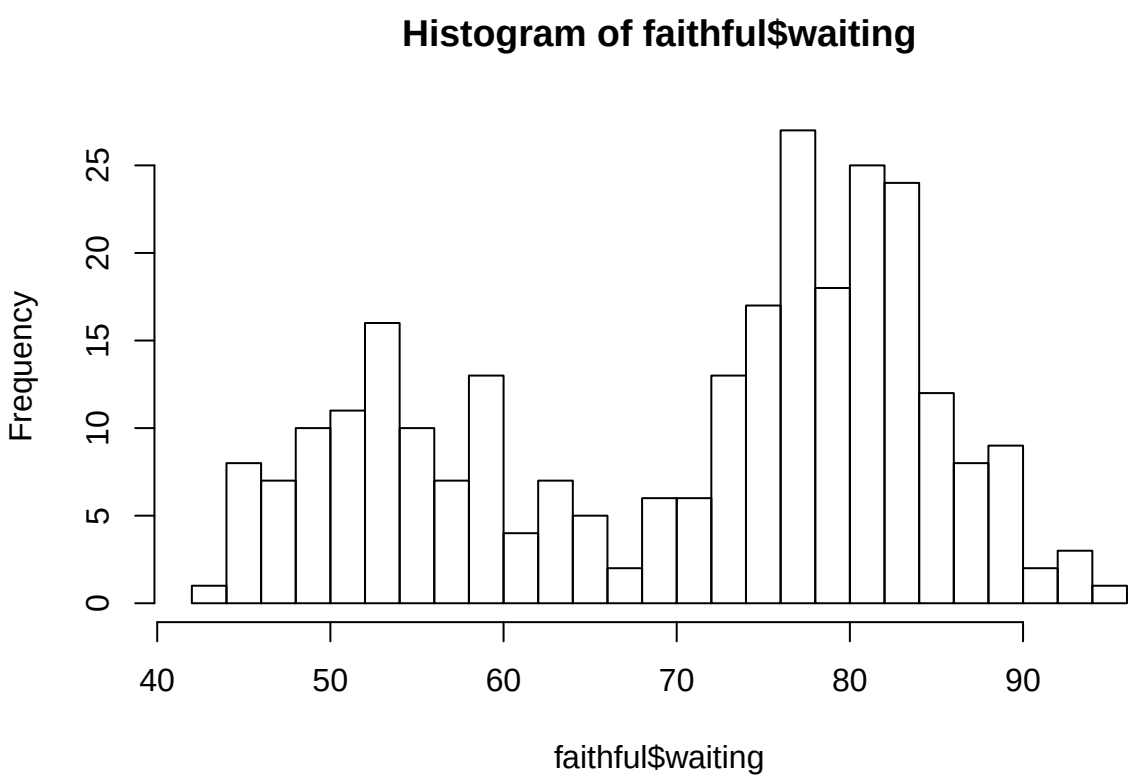



```
plot(x = mattysnewdf2$Petal.Area,
     y = mattysnewdf2$Sepal.Area,
     col = ifelse(mattysnewdf2$Species == "setosa", "red",
                  ifelse(mattysnewdf2$Species == "versicolor", "green", "blue")))
```

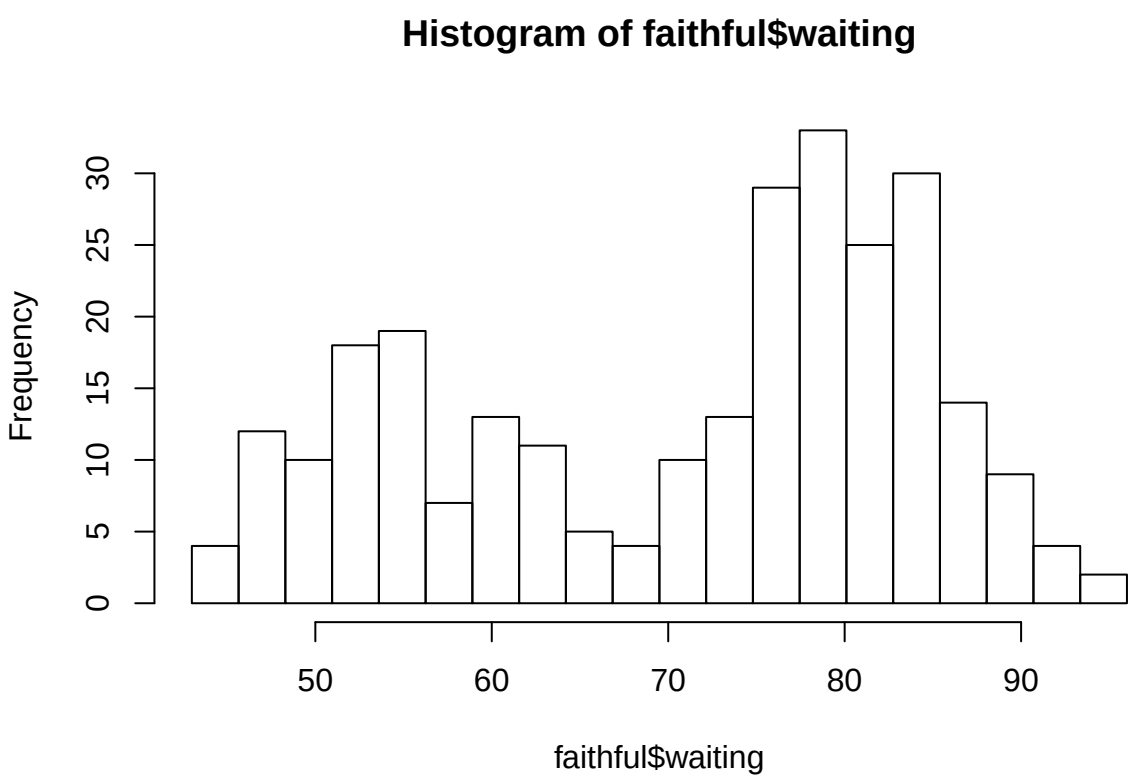


Histogram

```
hist(x = faithful$waiting,
     breaks = 20)
```




```
hist(x = faithful$waiting,
     breaks = seq(min(faithful$waiting), max(faithful$waiting), length.out = 20 + 1))
```

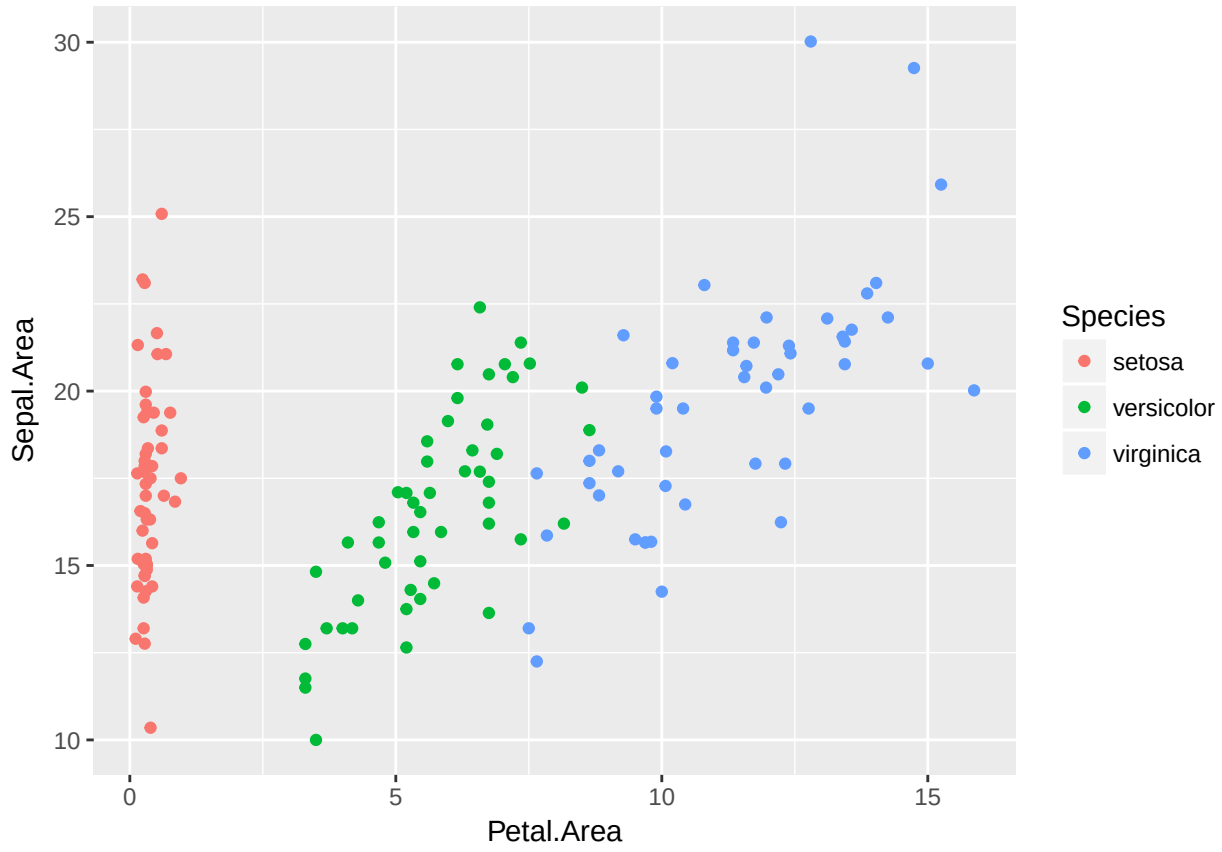


ggplot

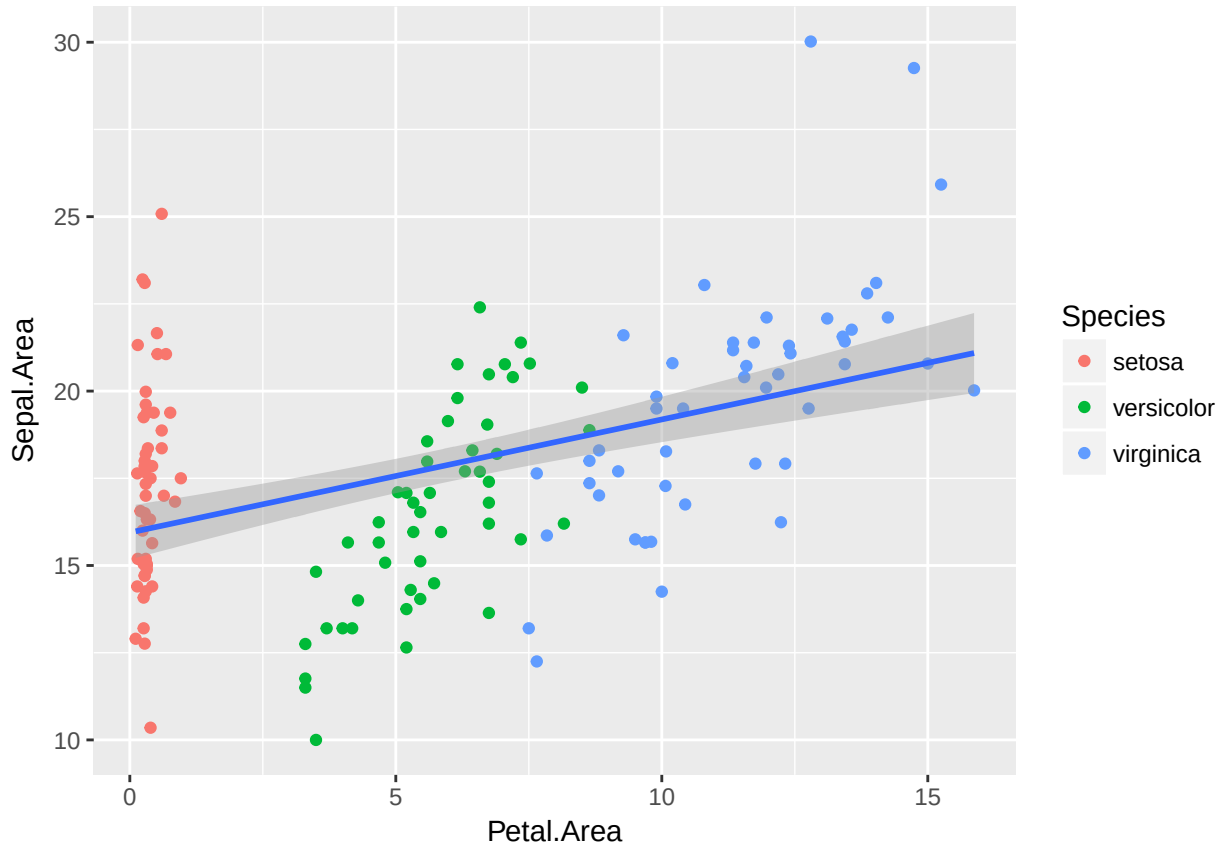
```
library(ggplot2)
```

Scatter plot

```
mattysnewdf2 %>%
  ggplot(mapping = aes(x = Petal.Area, y = Sepal.Area)) +
  geom_point(mapping = aes(color = Species))
```

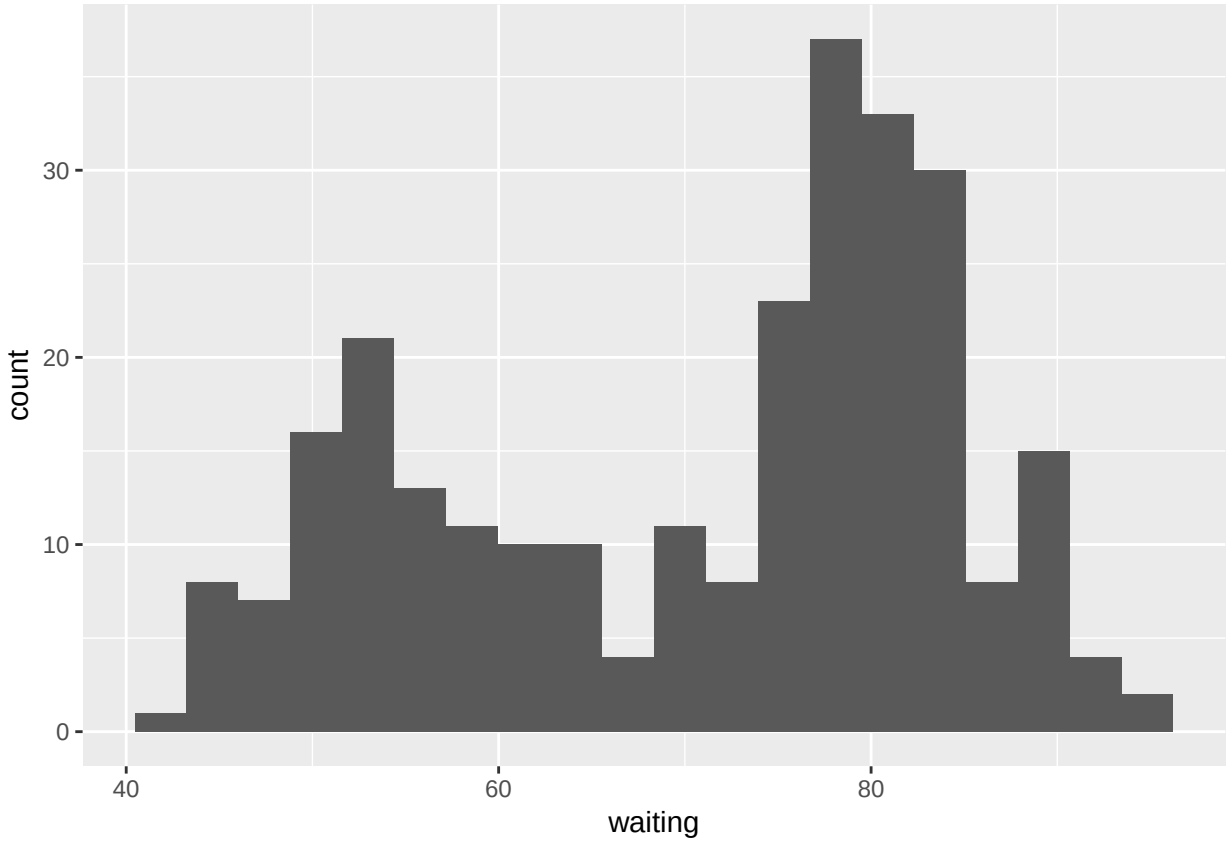



```
# More cooler scatter plot
mattysnewdf2 %>%
  ggplot(mapping = aes(x = Petal.Area, y = Sepal.Area)) +
  geom_point(mapping = aes(color = Species)) +
  geom_smooth(method = "lm")
```

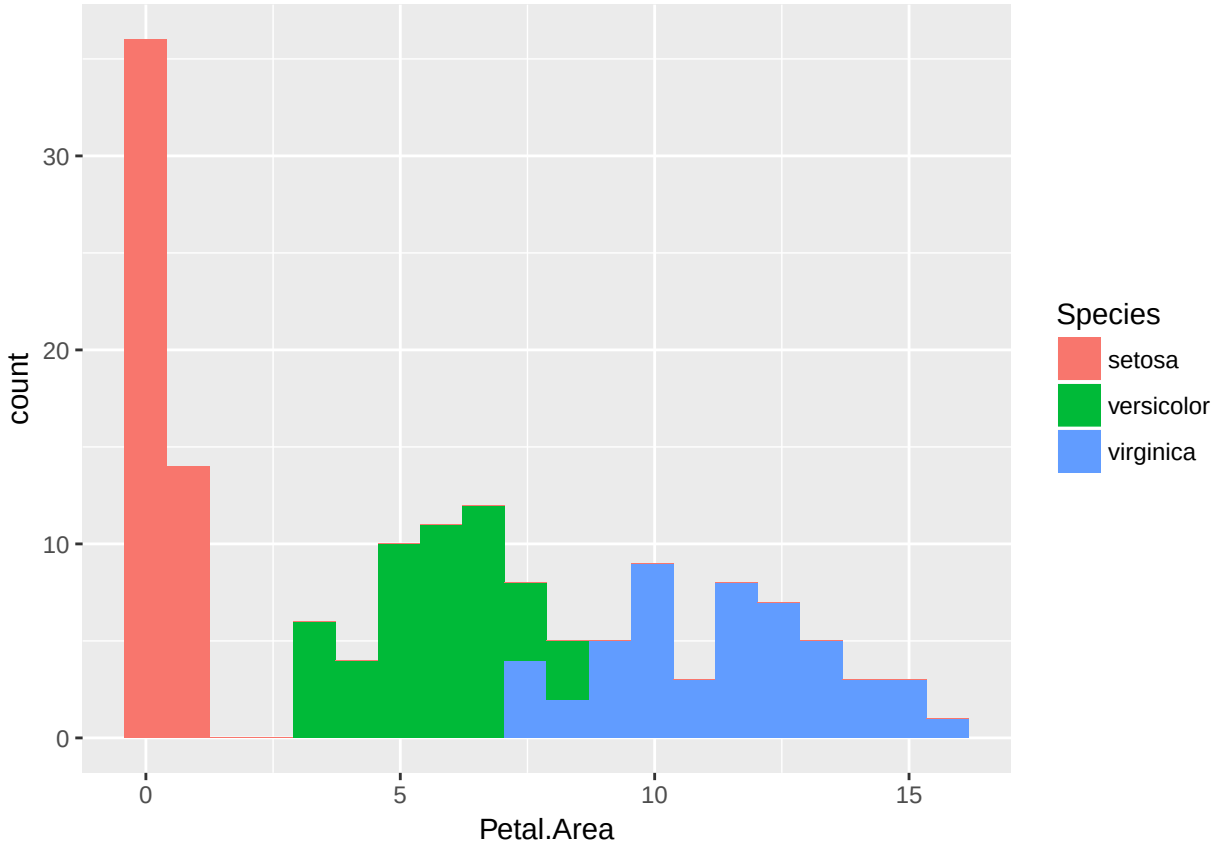


Histogram

```
faithful %>%
  ggplot(mapping = aes(x = waiting)) +
  geom_histogram(bins = 20)
```




```
# More betterer histogram
mattysnewdf2 %>%
  ggplot(mapping = aes(x = Petal.Area)) +
  geom_histogram(mapping = aes(fill = Species),
                 bins = 20)
```



Statistical models

R has a plethora of functions to create statistical models. Below we share two of the classics.

OLS

```
faithful.model <- lm(formula = eruptions ~ waiting,
                     data = faithful)
summary(faithful.model)
```

```
##
## Call:
## lm(formula = eruptions ~ waiting, data = faithful)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.29917 -0.37689  0.03508  0.34909  1.19329
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.874016   0.160143  -11.70   <2e-16 ***
## waiting      0.075628   0.002219   34.09   <2e-16 ***
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4965 on 270 degrees of freedom
## Multiple R-squared:  0.8115, Adjusted R-squared:  0.8108
## F-statistic:  1162 on 1 and 270 DF,  p-value: < 2.2e-16
```

Logistic GLM

```
iris.model <- glm(formula = versicolor ~ Sepal.Area + Petal.Area,
                  data = mattysnewdf2 %>%
                    mutate(versicolor = ifelse(Species == "versicolor", 1, 0)),
                  family = binomial(link = "logit"))
summary(iris.model)
```

```
##
## Call:
## glm(formula = versicolor ~ Sepal.Area + Petal.Area, family = binomial(link = "logit"),
##     data = mattysnewdf2 %>% mutate(versicolor = ifelse(Species ==
##         "versicolor", 1, 0)))
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5134  -0.9092  -0.6955   1.1504   2.0085
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  3.25729    1.12538   2.894 0.003799 **
## Sepal.Area  -0.25166    0.07117  -3.536 0.000406 ***
## Petal.Area   0.07684    0.04679   1.642 0.100513
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 190.95  on 149  degrees of freedom
## Residual deviance: 176.03  on 147  degrees of freedom
## AIC: 182.03
##
## Number of Fisher Scoring iterations: 4
```