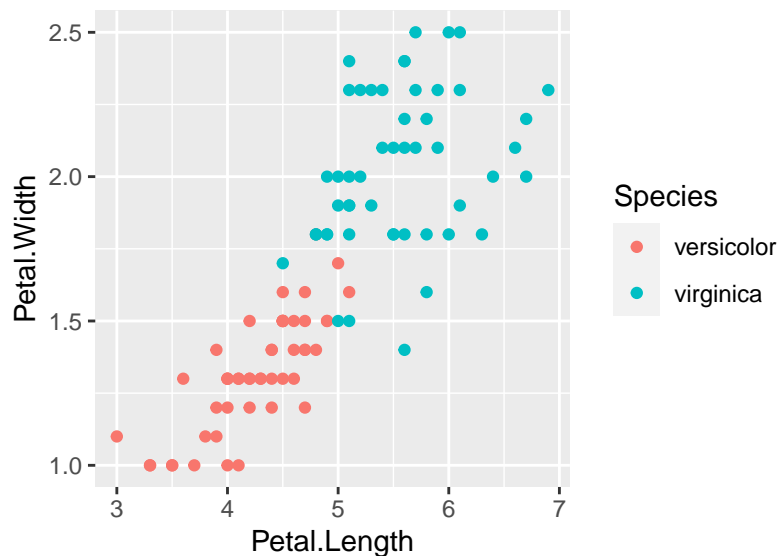


# Homework 3

due Feb 2, 2021

(Problems 1, 2) Recall `iris` data set.

1. Find the maximum value of the sum `Sepal.Length + Sepal.Width`. To which species does the sample with the maximum value you found above belong? *Hint*: you might want to start with defining a new variable `Sepal.Sum` using `mutate()`, for example.
2. Create the following plot. Note that `setosa` species do *not* show up. You do not need to adjust size or width/height ratio of the plot.



(Problems 3, 4, 5) Recall the `heights.txt` data we used in class with 1375 mother/daughter height pairs. The following code reads in the data set as `ht`.

```
ht <- read.table(file = "heights.txt", header = T, sep = " ")
```

3. Define an extra variable `FamilyID` for each family, like `Fam_1`, `Fam_2`, ..., `Fam_1375`, so that `head(ht)` and `tail(ht)` return the following, respectively.

```
##   Mheight Dheight FamilyID
## 1   59.7   55.1   Fam_1
## 2   58.2   56.5   Fam_2
## 3   60.6   56.0   Fam_3
## 4   60.7   56.8   Fam_4
## 5   61.8   56.0   Fam_5
## 6   55.5   57.9   Fam_6
```

```
##      Mheight Dheight FamilyID
## 1370    69.5    70.4  Fam_1370
## 1371    69.1    70.1  Fam_1371
## 1372    65.0    71.6  Fam_1372
## 1373    66.3    71.4  Fam_1373
## 1374    70.8    71.0  Fam_1374
## 1375    63.0    73.1  Fam_1375
```

4. In how many families, is mother taller than daughter?
5. Create the following box plot. *Hint:* you might want to start with transforming `ht` into a long form.

