



Data Wrangling

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Load the iris dataset

```
data(iris)
colnames(iris)
```

```
## [1] "Sepal.Length" "Sepal.Width" "Petal.Length" "Petal.Width"
## [5] "Species"
```

```
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
```

Access the columns and rows

The i th entry in column j can be accessed using `[i,j]`

```
iris[3,2]    ### third entry in the second column
```

```
## [1] 3.2
```

Columns can also be accessed by name

```
head(iris$Sepal.Width)
```

```
## [1] 3.5 3.0 3.2 3.1 3.6 3.9
```

and indexed by entry as before

```
iris$Sepal.Width[3]
```

```
## [1] 3.2
```

Access items by a vector of indices

In addition, rather than just putting a single integer in `[]` (as in `iris$Sepal.Width[3]`), one can put a vector of indices in! Something like `iris$Sepal.Width[my_index_vector]`. Let's try this:

```
my_inds <- c(1,3,4)
iris$Sepal.Width[my_inds]
```

```
## [1] 3.5 3.2 3.1
```

```
iris$Sepal.Width[c(1,2,5)]
```

```
## [1] 3.5 3.0 3.6
```

```
iris$Sepal.Width[1:3]
```

```
## [1] 3.5 3.0 3.2
```

Access columns by name or number

Columns/variables can be accessed by number (Rather than by name):

```
head(iris$Sepal.Width)
```

```
## [1] 3.5 3.0 3.2 3.1 3.6 3.9
```

```
head(iris[,2])          ## Sepal.Width is second column
```

```
## [1] 3.5 3.0 3.2 3.1 3.6 3.9
```

An empty index (as above) means "give all the entries", so `iris[,2]` returns all of the entries in column 2 of the `iris` dataframe.

Manipulating Data with Base (aka Basic) R

There are two important commands we will go over: `which` and `by` (and others that we will not: eg. `apply`, `match`, `sort`, `order`, `max`, `which.max`).

The more important of these is `which`.

which()

which takes in a vector with 0 and 1 entries (or true and false) and returns a vector with the indices of the 1 or true entries

```
TF <- iris$Species == "versicolor"  
head(TF)
```

```
## [1] FALSE FALSE FALSE FALSE FALSE FALSE
```

```
head(which(TF))
```

```
## [1] 51 52 53 54 55 56
```

which()

```
head(iris[which(TF),])
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 51	7.0	3.2	4.7	1.4	versicolor
## 52	6.4	3.2	4.5	1.5	versicolor
## 53	6.9	3.1	4.9	1.5	versicolor
## 54	5.5	2.3	4.0	1.3	versicolor
## 55	6.5	2.8	4.6	1.5	versicolor
## 56	5.7	2.8	4.5	1.3	versicolor

Summarizing subsets

We can string commands together and use this to summarize subsets of our data

```
mean(iris$Sepal.Width[which(iris$Species == "versicolor")])
```

```
## [1] 2.77
```

```
short_sepal_ind <- which(iris$Sepal.Length < median(iris$Sepal.Length))  
mean(iris$Sepal.Width[short_sepal_ind])
```

```
## [1] 3.157534
```

```
short_sepal_versa_ind <- which((iris$Sepal.Length < median(iris$Sepal.Length)) &  
                               (iris$Species == "versicolor"))  
mean(iris$Sepal.Width[short_sepal_versa_ind])
```

```
## [1] 2.633333
```

Summarizing with `by()`

Rather than just summarizing for a single Species we may want to know mean Petal.Length for each species. `by` comes in handy here: It applies a summarizing function to subsets of our data defined by an index (or key):

```
by(iris$Sepal.Width, INDICES = iris$Species, FUN=mean)
```

```
## iris$Species: setosa
## [1] 3.428
## -----
## iris$Species: versicolor
## [1] 2.77
## -----
## iris$Species: virginica
## [1] 2.974
```

With enough typing, one can generally use these to do whatever one wishes.

A Better Way!

What I showed before generally ends up requiring a lot of code that is usually overly clever, and hard to read/manage.

A cleaner, easier way to do this: Use two packages written by Hadley Wickham, `tidyr` and `dplyr`.

The dplyr package

We will cover dplyr here. The 7 dplyr commands are:

- `select()`
- `filter()`
- `summarise()`
- `group_by()`
- `arrange()`
- `join()`
- `mutate()`

In addition there is a new operator `%>%` (piping operator) which is an easier-to-read way to combine functions.

```
suppressMessages(library(dplyr))
```

select()

select takes a dataframe, and grabs only some of the columns/features.

```
head(select(iris, Sepal.Width, Species))
```

```
##   Sepal.Width Species
## 1         3.5  setosa
## 2         3.0  setosa
## 3         3.2  setosa
## 4         3.1  setosa
## 5         3.6  setosa
## 6         3.9  setosa
```

```
head( iris %>% select(Sepal.Width, Species) )
```

```
##   Sepal.Width Species
## 1         3.5  setosa
## 2         3.0  setosa
## 3         3.2  setosa
## 4         3.1  setosa
## 5         3.6  setosa
## 6         3.9  setosa
```

select () with %>% "pipe"

```
iris %>% select(Sepal.Width, Species) %>% head()
```

```
##   Sepal.Width Species
## 1          3.5  setosa
## 2          3.0  setosa
## 3          3.2  setosa
## 4          3.1  setosa
## 5          3.6  setosa
## 6          3.9  setosa
```

Notice our use of the piping operator %>% (indicating that we "pipe" the `iris` data into the `select` function).

filter()

filter subsets rows of a dataframe by true/false vectors

```
head( filter( select(iris, Sepal.Width, Species), Species == "versicolor" ))
```

```
##   Sepal.Width   Species
## 1         3.2 versicolor
## 2         3.2 versicolor
## 3         3.1 versicolor
## 4         2.3 versicolor
## 5         2.8 versicolor
## 6         2.8 versicolor
```

filter() with %>%

```
iris %>%  
  select(Sepal.Width, Species) %>%  
  filter(Species == "versicolor") %>%  
  head()
```

```
##   Sepal.Width   Species  
## 1         3.2 versicolor  
## 2         3.2 versicolor  
## 3         3.1 versicolor  
## 4         2.3 versicolor  
## 5         2.8 versicolor  
## 6         2.8 versicolor
```

This is basically what we did using which in base-R

summarise()

summarise calculates a summary statistic on our manipulated data

```
iris %>%  
  select(Sepal.Width, Species) %>%  
  filter(Species == "versicolor") %>%  
  summarise(mean.sepal.width = mean(Sepal.Width))
```

```
##   mean.sepal.width  
## 1                2.77
```

group_by()

group_by groups our observations by a categorical variable (the first step of a by)

```
iris %>%  
  select(Sepal.Width, Species) %>%  
  group_by(Species) %>%  
  summarise(mean.sepal.width = mean(Sepal.Width))
```

```
## Source: local data frame [3 x 2]  
##  
##      Species mean.sepal.width  
##      (fctr)      (dbl)  
## 1    setosa      3.428  
## 2 versicolor    2.770  
## 3 virginica     2.974
```

This is a cleaner version of our by example from earlier.

arrange()

arrange orders our data by one of the features

```
head(iris %>%  
      select(Sepal.Width, Species) %>%  
      arrange(Sepal.Width))
```

```
##   Sepal.Width    Species  
## 1         2.0 versicolor  
## 2         2.2 versicolor  
## 3         2.2 versicolor  
## 4         2.2  virginica  
## 5         2.3     setosa  
## 6         2.3 versicolor
```

arrange()

This can be combined with previous commands:

```
iris %>%  
  select(Sepal.Width, Species) %>%  
  group_by(Species) %>%  
  arrange(Sepal.Width) %>%  
  head()
```

```
## Source: local data frame [6 x 2]  
## Groups: Species [1]  
##  
##   Sepal.Width Species  
##   (dbl)   (fctr)  
## 1      2.3  setosa  
## 2      2.9  setosa  
## 3      3.0  setosa  
## 4      3.0  setosa  
## 5      3.0  setosa  
## 6      3.0  setosa
```

arrange() and summarize()

... and can even be used on summaries.

```
iris %>%  
  group_by(Species) %>%  
  summarize(mean.sep.wid = mean(Sepal.Width),  
            mean.sep.len = mean(Sepal.Length)) %>%  
  arrange(mean.sep.wid)
```

```
## Source: local data frame [3 x 3]
```

```
##
```

```
##   Species mean.sep.wid mean.sep.len  
##   (fctr)      (dbl)      (dbl)  
## 1 versicolor      2.770      5.936  
## 2 virginica       2.974      6.588  
## 3 setosa         3.428      5.006
```

join()

Imagine we are analyzing patient information and have two datasets. Both datasets are on the same patients; one has clinical information on the patients, and another has lab information. `join()` allows us to combine these two datasets into one (even if patients are in different orders, so long as they have a unique identifier).

`join()` is particularly neat because it has options that allow it to flexibly work even if some patients don't have clinical information and others don't have lab information.

mutate()

mutate adds new features to our data. For example, we might want to work with the ratio of width-to-length:

```
iris %>% mutate(ratio.sep = Sepal.Width/Sepal.Length) %>% head()
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species ratio.sep
## 1          5.1         3.5         1.4         0.2   setosa 0.6862745
## 2          4.9         3.0         1.4         0.2   setosa 0.6122449
## 3          4.7         3.2         1.3         0.2   setosa 0.6808511
## 4          4.6         3.1         1.5         0.2   setosa 0.6739130
## 5          5.0         3.6         1.4         0.2   setosa 0.7200000
## 6          5.4         3.9         1.7         0.4   setosa 0.7222222
```

mutate()

```
iris %>%
  mutate(ratio.sep = Sepal.Width/Sepal.Length,
         ratio.pet = Petal.Width/Petal.Length,
         ratio.diff = ratio.sep - ratio.pet) %>%
  group_by(Species) %>%
  summarize(mean.sep.ratio = mean(ratio.sep),
            mean.pet.ratio = mean(ratio.pet),
            mean.ratio.diff = mean(ratio.diff))
```

Source: local data frame [3 x 4]

##

##	Species	mean.sep.ratio	mean.pet.ratio	mean.ratio.diff
##	(fctr)	(dbl)	(dbl)	(dbl)
## 1	setosa	0.6842483	0.1678683	0.51638002
## 2	versicolor	0.4676804	0.3111062	0.15657417
## 3	virginica	0.4533956	0.3667386	0.08665706

Some questions for you to work on!

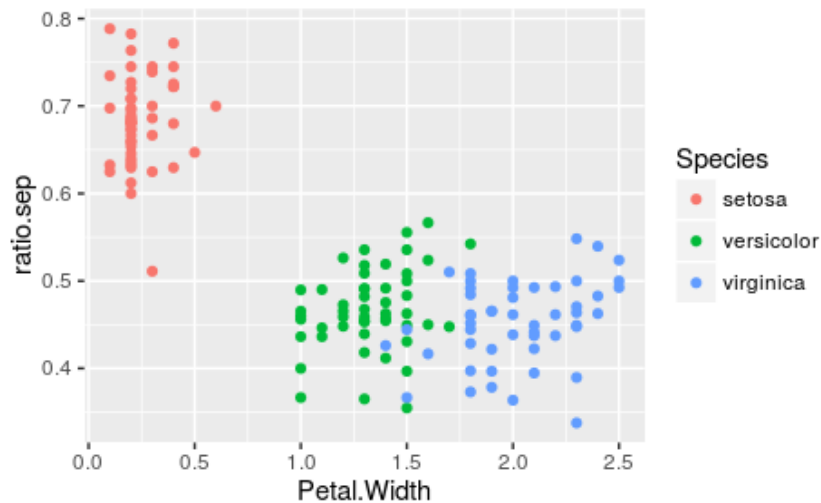
- How many flowers are there of each Species?
- How many flowers are there with Sepal.Width greater than the overall mean?
- Of the flowers with Sepal.Width greater than the overall mean, how many belong to each Species?
- For each Species, what is the mean Petal.Length for those flowers with Sepal.Length greater than the median Sepal.Length within their species?
- Is the ratio of Sepal.Length/Sepal.Width different for flowers with Petal.Length greater than the median vs those with Petal.Length less than the median? Is this different for different species?
- If you are particularly precocious, then you can answer the above graphically by piping your output into ggplot2

%>% into ggplot2

We can take our output and pipe directly into Hadley Wickham's plotting environment ggplot2.

```
library(ggplot2)
```

```
iris %>% mutate(ratio.sep = Sepal.Width/Sepal.Length) %>%  
  ggplot(., aes(x=Petal.Width, y=ratio.sep, color=Species)) + geom_point()
```



Another Dataset to play with

```
url <- "http://faculty.washington.edu/nrsimon/datasets/salary.txt"
salary_dat <- read.table(url)
names(salary_dat)
```

```
## [1] "V1" "V2" "V3" "V4" "V5" "V6" "V7" "V8" "V9" "V10" "V11"
```

oops!

Another Dataset to play with

```
salary_dat <- read.table(url, header = TRUE)
names(salary_dat)
```

```
## [1] "case"    "id"      "gender"  "deg"     "yrdeg"   "field"   "startyr"
## [8] "year"    "rank"    "admin"   "salary"
```

This data contains salary, rank, and gender information on faculty members in various fields at various times. Many faculty members have multiple entries in this data (id refers to the faculty member)

- Create a dataframe that has a single entry for each id which contains the gender the maximum salary for that id, and the rank at the time of that salary entry.
- Compare the average maximum salary between male and female professors
- Break this comparison down by rank
- Find the id of the female professor with the 10th smallest maximum salary among all female professors