Approaching Big Data Using dplyr

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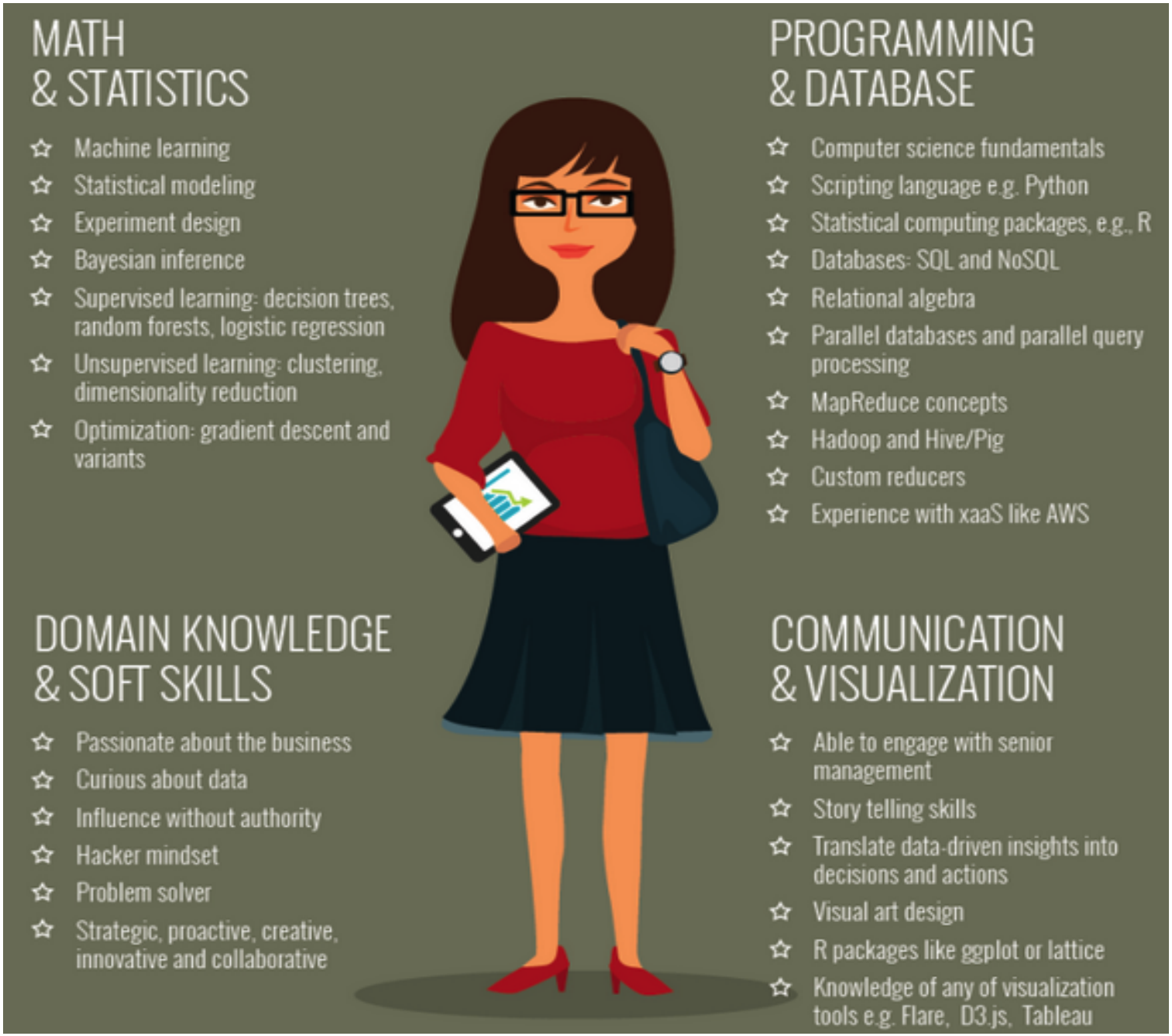
Slides and R Code can be downloaded from
`https://github.com/steviep42/NURS_741`



http://www.marketingdistillery.com/2014/11/29/is-data-science-a-buzzword-modern-data-scientist-defined/

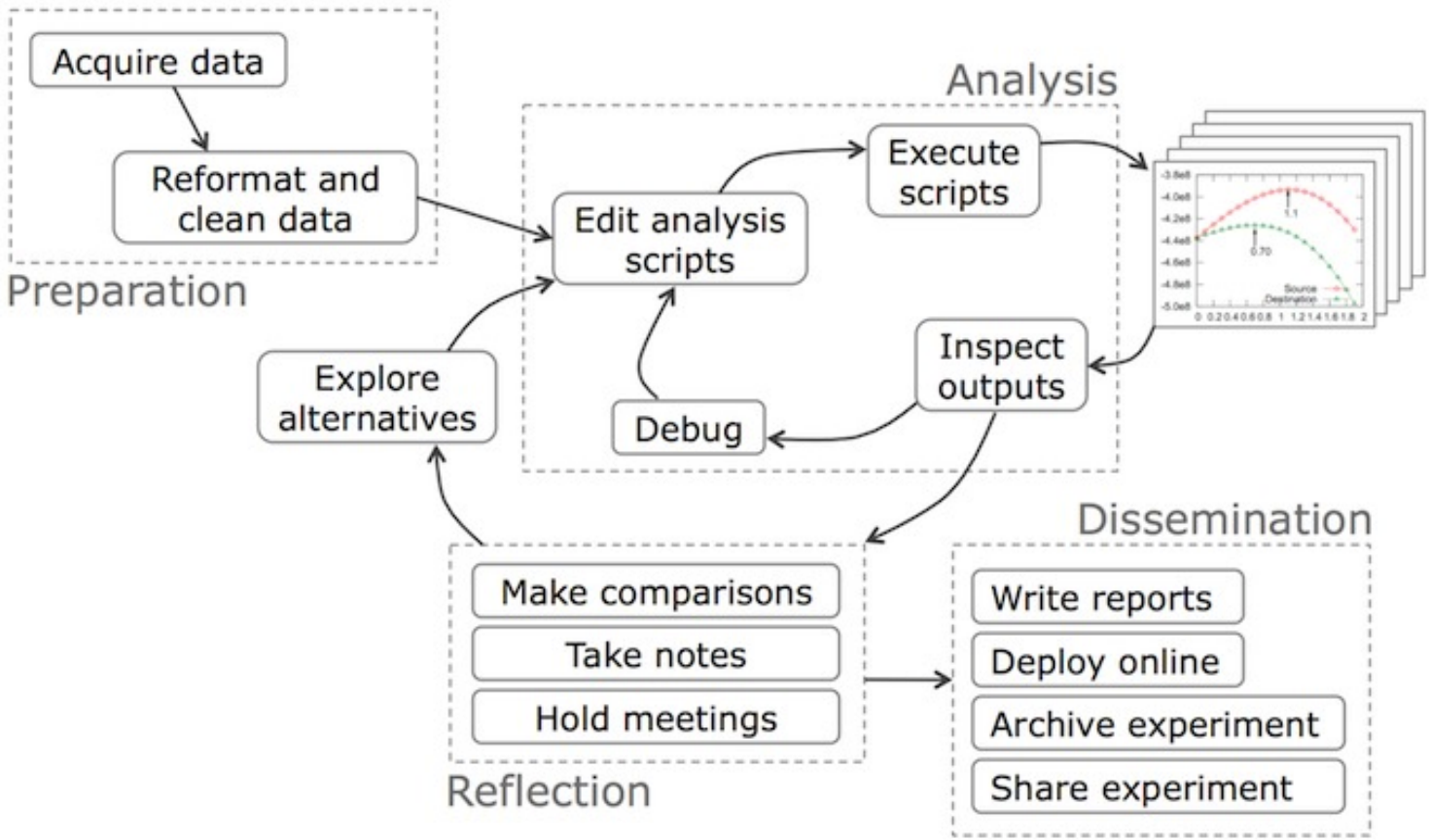
Solutions

Cheating is Good ! Well no not really. What I meant to say was that *Cheat Sheets* are good !

`https://www.rstudio.com/resources/cheatsheets/`

- Data Import
- Data Transformation
- R Markdown
- RStudio
- Shiny
- Data Visualization
- Package Development
- Advanced R
- Regular Expressions

Data Science Workflow



https://cacm.acm.org/blogs/blog-cacm/169199-data-science-workflow-overview-and-challenges/fulltext

Data Science Workflow

The acquisition and preparation of data can take up a lot of time and energy and usually does because data can:

- Come from many sources (spreadhseets, lab instruments, URLs, databases, APIs
- Have different formats (.CSV, XML, JSON, CDF, SQL, HTML, TEXT)
- Come from lab instruments like Genomic Sequencing Machines
- Require different packages to parse and clean
- Be "dirty" because of missing and/or improbable values
- Require merging from different sources into a more manageable format (e.g. data frame or data base)

Data Science Workflow

Need to track the point of origin ("provenance") for all data to:

- Reference sources accordingly in subsequent publications
- Insure that data is up to date
- Insure that it can be re-downloaded to execute updated experiments
- Enable reproducibility by other users

Managing data can be challenging after downloading. One must:

- Develop reasonable naming conventions
- Create an intelligent folder structure for reference and storage
- Make it easy to add newly generated data that fits existing conventions
- Consider using Databases if multi-user access is required

This is all too much ! The stress !

Motivations

Data frames are an excellent way to host data:

- Intutive, Easy to Subset and Interrogate
- Import tools like **read.csv** give you a data frame

```
head(mtcars,2)
              mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4      21   6  160 110  3.9 2.620 16.46  0  1    4    4
Mazda RX4 Wag  21   6  160 110  3.9 2.875 17.02  0  1    4    4

# Find all rows where MPG > 30 MPG

mtcars[mtcars$mpg > 30.0,]
                mpg cyl disp  hp drat    wt  qsec vs am gear carb
Fiat 128       32.4   4 78.7  66 4.08 2.200 19.47  1  1    4    1
Honda Civic    30.4   4 75.7  52 4.93 1.615 18.52  1  1    4    2
Toyota Corolla 33.9   4 71.1  65 4.22 1.835 19.90  1  1    4    1
Lotus Europa   30.4   4 95.1 113 3.77 1.513 16.90  1  1    5    2
```

Motivations

You can easily read data straight off the Internet. This results in a Data frame

```
# This data relates to attributes of some Wines. Let's read it
# from my Github. The URL is long so I create it in steps

str1 <- "https://raw.githubusercontent.com/steviep42/youtube/"

url  <- paste0(str1,"master/YOUTUBE.DIR/wines.csv")

my.wines <- read.csv(url, header=TRUE, stringsAsFactors=FALSE)

str(my.wines)

'data.frame': 5 obs. of  8 variables:
 $ Wine   : Factor w/ 5 levels "Wine_1","Wine_2",..: 1 2 3 4 5
 $ Hedonic: int  14 10 8 2 6
 $ Meat   : int  7 7 5 4 2
 $ Dessert: int  8 6 5 7 4
 $ Price  : int  7 4 10 16 13
 $ Sugar  : int  7 3 5 7 3
 $ Alcohol: int  13 14 12 11 10
 $ Acidity: int  7 7 5 3 3
```

Motivations

There are different ways to interrogate a data frame:

```
# Find all cars with automatic transmission and MPG > 20

subset(mtcars, mpg > 20 & am == 0)
                mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Hornet 4 Drive 21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
Merc 240D      24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2
Merc 230       22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2
Toyota Corona  21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1

# Same as

mtcars[mtcars$mpg > 20 & mtcars$am == 0,]
                mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Hornet 4 Drive 21.4   6 258.0 110 3.08 3.215 19.44  1  0    3    1
Merc 240D      24.4   4 146.7  62 3.69 3.190 20.00  1  0    4    2
Merc 230       22.8   4 140.8  95 3.92 3.150 22.90  1  0    4    2
Toyota Corona  21.5   4 120.1  97 3.70 2.465 20.01  1  0    3    1
```

Motivations

There are various aggregation commands

```
# Look at the average MPG and Wt for each Transmission type

mtcars$am <- factor(mtcars$am,labels=c("Auto","Manual"))
aggregate(cbind(mpg,wt)~am,mtcars,mean)
  am      mpg       wt
1  0 17.14737 3.768895
2  1 24.39231 2.411000

# We can supply our own Function

myfunc <- function(x) {
  return(c(avg=mean(x),variance=var(x)))
}

aggregate(cbind(mpg,wt)~am, mtcars, myfunc)
      am  mpg.avg mpg.variance    wt.avg wt.variance
1   Auto 17.14737     14.69930 3.7688947   0.6043510
2 Manual 24.39231     38.02577 2.4110000   0.3806663
```

Motivations

But R was written at a time when data was not so BIG. You could fit data into the memory of your desktop and/or laptop.

- R tries to load everything into RAM
- Do you really need to see all rows of a data frame ?
- Experimental data types can be HUGE (many GB or even TB)
- What about accessing databases ? (Oracle, MySQL, etc)
- There are multiple ways to interrogate or transform data frames
- Is there a "best practice" approach ?

Solutions

If you data is biological or genomic in nature it is quite possible that there are specialized packages available to help you manage these files

- R BioConductor has many such tools

`https://www.bioconductor.org/`

Solutions

For more general forms of data see the CRAN Task View that lists packages by research domain. Here is a subset of packages

- CRAN Task Views

Bayesian	Bayesian Inference
ChemPhys	Chemometrics and Computational Physics
ClinicalTrials	Clinical Trial Design, Monitoring, and Analysis
Cluster	Cluster Analysis & Finite Mixture Models
DifferentialEquations	Differential Equations
Distributions	Probability Distributions
Econometrics	Econometrics
Environmetrics	Analysis of Ecological and Environmental Data
ExperimentalDesign	Design of Experiments (DoE) & Analysis of Experimental Data
ExtremeValue	Extreme Value Analysis
Finance	Empirical Finance
Genetics	Statistical Genetics

`https://cran.r-project.org/web/views/`

Solutions

Data can be so large that we have to "split" the data across multiple computers (aka "nodes")

Assume N = 1,000,000

	Col 1	Col 2	..	Col X
Row 1				
Row 2				
..				
..				
Row N				

	Col 1	Col 2	..	Col X
Row 1				
Row 2				
..				
Row 100,000				

Node 1

	Col 1	Col 2	..	Col X
Row 100,001				
..				
Row 200,000				

Node 2

.....

.....

	Col 1	Col 2	..	Col X
Row 900.001				
..				
Row 1,000,000				

Node 10

Solutions

But we don't want to have to (re)learn alot to be productive !

Assume N = 1,000,000

	Col 1	Col 2	..	Col X
Row 1				
Row 2				
..				
..				
Row N				

	Col 1	Col 2	..	Col X
Row 1				
Row 2				
..				
Row 100,000				

Node 1

	Col 1	Col 2	..	Col X
Row 100,001				
..				
Row 200,000				

Node 2

.....

.....

	Col 1	Col 2	..	Col X
Row 900.001				
..				
Row 1,000,000				

Node 10

Solutions

Some solutions for handling large and unwieldy data

- The data.table package
  - Handles large files well
  - Combines aggregation with subsetting
- Use SQL to query databases
  - Very flexible
  - Requires knowledge of SQL
- Use Apache Spark (a Distributed data frame usually on the cloud)
  - Handles HUGE (multi-terabyte) data frames
  - Requires a HUGE computer or use of Amazon
  - Has an R interface

dplyr

dplyr is an add on package designed to efficiently transform and summarize tablular data such as data frames. The package has a number of functions ("verbs") that perform a number of data manipulation tasks:

- Filtering rows
- Select specific columns
- Re-ordering or arranging rows
- Summarizing and aggregating data

One of the unique strengths of **dplyr** is that it implements what is known as a Split-Apply-Combine technique that we will explore in this session.

The dyplr function can also be used with the **magrittr** package for setting up workflows or pipelines to process data.

tidyverse

- **dplyr** is part of the tidyverse which is a "collection of R packages that share common philosphies and are designed to work together"
- The best place to learn the complete philsophy of the tidyverse is the "R for Data Science" book. `http://r4ds.had.co.nz/`
- Summary of tidyverse functions:
  - **readr** for importing data from files
  - **tibble** a modern iteration on data frames
  - **tidyr** functions to rearrange data for analysis
  - **dplyr** functions to filter, arrange, susbet, modify and aggregate data frames
  - **ggplot2** a system for declaratively creating graphics, based on The Grammar of Graphics

tidyverse

- The tidyverse was written mostly by the same person, Hadley Wickham, who has insured that thee programs work together smoothly
- These packages do not overwrite any of the native R commands. So there are no collisions between existing and new commands
- Once you learn the philosophy behind a given package it becomes much easier than trying to piece together individual native R commands
- Do not feel obligated to learn them all at once. Start with say **ggplot2** and **dplyr** and use the others as needed
- We'll focus on **dplyr** for this session

dplyr

- **dplyr** is designed to work with data frames but it can also connect to relational databases that are locally or remotely available.
- Access to data frames or databases can be accomplished as before so older code will not break
- But you should use the "verbs" provided by dplyr since they simplify things (in my opinion)
- Relative to databases use the "verbs" provided with dplyr that in turn are translated into appropriate SQL statements to interact with the databases.

How to Install dplyr ?

```
# install the package

install.packages("dplyr")

# Get's the equivalent to data.table's fread package
install.packages("readr")

# Loads the package

library(dplyr)

# Launches a browser to explore

browseVignettes(package = "dplyr")
```

dplyr

This slide deck references "Becoming a data ninja with dplyr" `https://speakerdeck.com/dpastoor/becoming-a-data-ninja-with-dplyr` and the dplyr tutorial `http://genomicsclass.github.io/book/pages/dplyr_tutorial.html`

dplyr - data frames

- A data frame is a set of columns. Every column is same length but of possibly different types.
- It has characteristics of both a matrix, (each row is the same data type),
- Each column can be a different data type
- Bracket notation offers a convenient way to search through the data drame

dplyr - data frames

```
head(mtcars,12)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160.0	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160.0	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258.0	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360.0	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225.0	105	2.76	3.460	20.22	1	0	3	1
Duster 360	14.3	8	360.0	245	3.21	3.570	15.84	0	0	3	4
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Merc 280	19.2	6	167.6	123	3.92	3.440	18.30	1	0	4	4
Merc 280C	17.8	6	167.6	123	3.92	3.440	18.90	1	0	4	4
Merc 450SE	16.4	8	275.8	180	3.07	4.070	17.40	0	0	3	3

dplyr - data frames

There are some common activites associated with a data frame:

- filter - find observations satisfying some condition(s)
- select - selecting specific columns by name
- mutate - adding new columns or changing existing ones
- arrange - reorder or sort the rows
- summarize - do some aggregation or summary by groups

dplyr - data frames

```
df <- data.frame(id = 1:5,
                 gender = c("MALE","MALE","FEMALE","MALE","FEMALE"),
                 age = c(70,76,60,64,68))
```

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

Filter

```
filter(df,gender == "FEMALE")
  id gender age
1  3 FEMALE  60
2  5 FEMALE  68
```

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

ID	GENDER	AGE
3	FEMALE	60
5	FEMALE	68

Filter

```
filter(df, id %in% c(1,3,5))
  id gender age
1  1   MALE  70
2  3 FEMALE  60
3  5 FEMALE  68
```

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

ID	GENDER	AGE
1	MALE	70
3	FEMALE	60
5	FEMALE	68

Mutate

Mutate is used to add or remove columns in a data frame

```
mutate(df,meanage = mean(age))
  id gender age meanage
1  1   MALE  70     67.6
2  2   MALE  76     67.6
3  3 FEMALE  60     67.6
4  4   MALE  64     67.6
5  5 FEMALE  68     67.6
```

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

ID	GENDER	AGE	MEANWT
1	MALE	70	67.6
2	MALE	76	67.6
3	FEMALE	60	67.6
4	MALE	64	67.6
5	FEMALE	68	67.6

Mutate

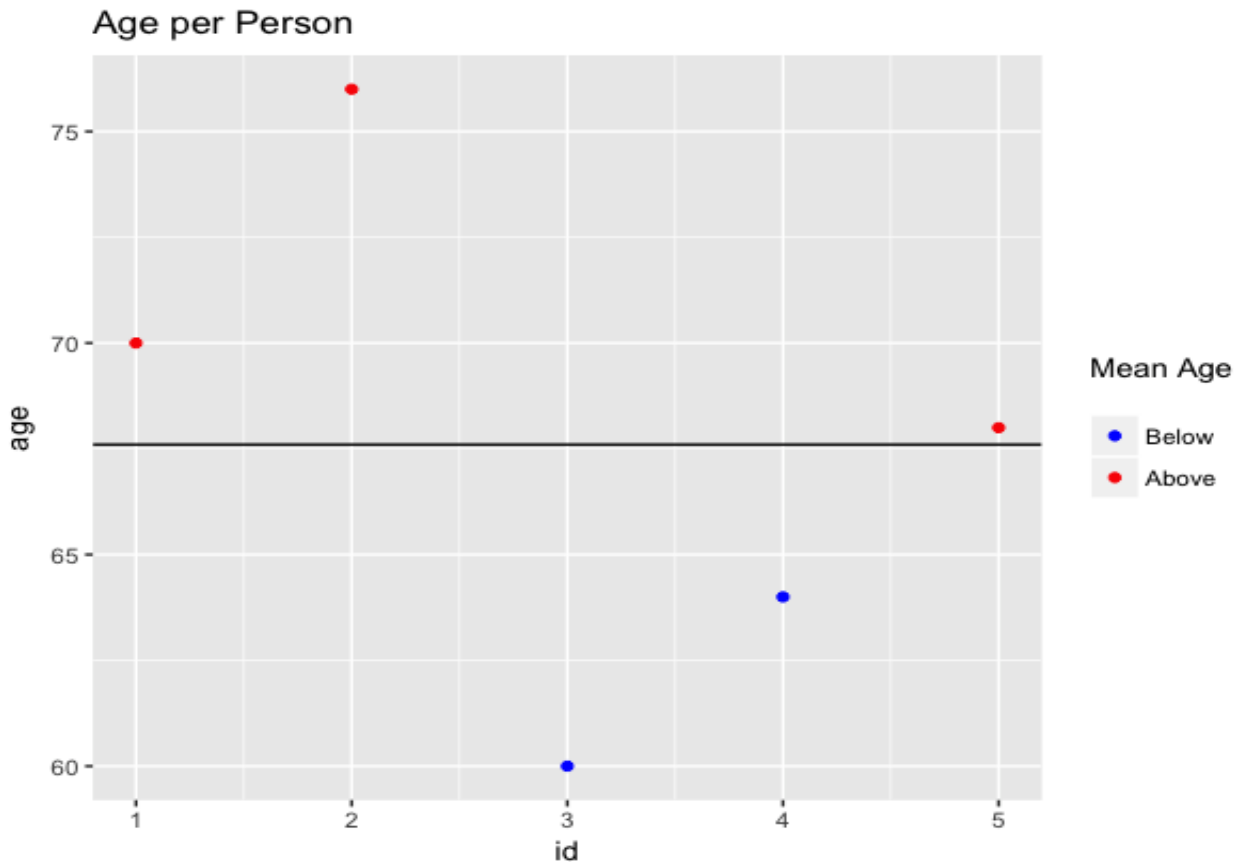
Here we create a new column designed to tell us if a given observation has an age that is greater than or equal to the average age.

We create a variable called old_young and assing a value of "Y" if the are above the mean age and a value of "N" if they are not.

```
mutate(df,old_young=ifelse(df$age>=mean(df$age),"Y","N"))
  id gender age old_young
1  1   MALE  70         Y
2  2   MALE  76         Y
3  3 FEMALE  60         N
4  4   MALE  64         N
5  5 FEMALE  68         Y
```

Mutate

```
tmp <- mutate(df, color = ifelse(age > mean(age),"red","blue"))
ggplot(tmp,aes(x=id,y=age)) +
      geom_point(aes(color=color)) +
      geom_hline(aes(yintercept=mean(age))) +
      labs(title="Age per Person",color="Mean Age\n") +
      scale_color_manual(labels = c("Below", "Above"), values = c("blue", "red"))
```



Arrange

Use arrange for sorting the data frame by a column(s)

```
# Sort df by age from highest to lowest

arrange(df, desc(age))
  id gender age
1  2   MALE  76
2  1   MALE  70
3  5 FEMALE  68
4  4   MALE  64
5  3 FEMALE  60

# Sort df by gender (alphabetically) and then by age
# from highest to lowest

arrange(df, gender,desc(age))
  id gender age
1  5 FEMALE  68
2  3 FEMALE  60
3  2   MALE  76
4  1   MALE  70
5  4   MALE  64
```

Select

Select allows us to select groups of columns from a data frame

```
select(df,gender,id,age)  # Reorder the columns
  gender id age
1   MALE  1  70
2   MALE  2  76
3 FEMALE  3  60
4   MALE  4  64
5 FEMALE  5  68

select(df,-age)   # Select all but the age column
  id gender
1  1   MALE
2  2   MALE
3  3 FEMALE
4  4   MALE
5  5 FEMALE

select(df,id:age)  # Can use : to select a range
  id gender age
1  1   MALE  70
2  2   MALE  76
3  3 FEMALE  60
4  4   MALE  64
5  5 FEMALE  68
```

Select

You can select by regular expressions or numeric paterns

```
library(ggplot2)
data(diamonds)
names(diamonds)
 [1] "carat"   "cut"     "color"   "clarity" "depth"   "table"   "price"
 [8] "x"       "y"       "z"

head(select(diamonds,starts_with("c")))
  carat       cut color clarity
1  0.23     Ideal     E     SI2
2  0.21   Premium     E     SI1
3  0.23      Good     E     VS1
4  0.29   Premium     I     VS2
5  0.31      Good     J     SI2
6  0.24 Very Good     J    VVS2

head(select(diamonds,ends_with("t")))
  carat       cut
1  0.23     Ideal
2  0.21   Premium
3  0.23      Good
4  0.29   Premium
5  0.31      Good
6  0.24 Very Good
```

Select

You can select by regular expressions or numeric paterns

```
testdf <- expand.grid(m_1=seq(60,70,10),age=c(25,32),m_2=seq(50,60,10))

head(testdf, 4)
  m_1 age m_2
1  60  25  50
2  70  25  50
3  60  32  50
4  70  32  50

head( select(testdf,matches("_")) ,2)
  m_1 m_2
1  60  50
2  70  50

head( select(testdf,contains("_"), 2)
  m_1 m_2
1  60  50
2  70  50

head( select(testdf,num_range("m_",1:2)), 2)
  m_1 m_2
1  60  50
2  70  50
```

group_by

group_by let's you organize a data frame by some factor or grouping variable

```
df
  id gender age
1  1   MALE  70
2  2   MALE  76
3  3 FEMALE  60
4  4   MALE  64
5  5 FEMALE  68

group_by(df,gender)   # Hmm. Did this really do anything ?

Source: local data frame [5 x 3]
Groups: gender

  id gender age
1  1   MALE  70
2  2   MALE  76
3  3 FEMALE  60
4  4   MALE  64
5  5 FEMALE  68
```

group_by

group_by let's you organize a data frame by some factor or grouping variable

```
df
  id gender age
1  1   MALE  70
2  2   MALE  76
3  3 FEMALE  60
4  4   MALE  64
5  5 FEMALE  68

gdf <- group_by(df,gender)    # Hmm. Did this really do anything ?

Source: local data frame [5 x 3]
Groups: gender

  id gender age
1  1   MALE  70
2  2   MALE  76
3  3 FEMALE  60
4  4   MALE  64
5  5 FEMALE  68
```

Summarize

```
summarize(group_by(df,gender),total=n())
Source: local data frame [2 x 2]

  gender total
1 FEMALE     2
2   MALE     3
```

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

GENDER	TOTAL
FEMALE	2
MALE	3

Summarize

```
summarize(group_by(df,gender),av_age=mean(age))
Source: local data frame [2 x 2]

  gender av_age
1 FEMALE     64
2   MALE     70
```

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

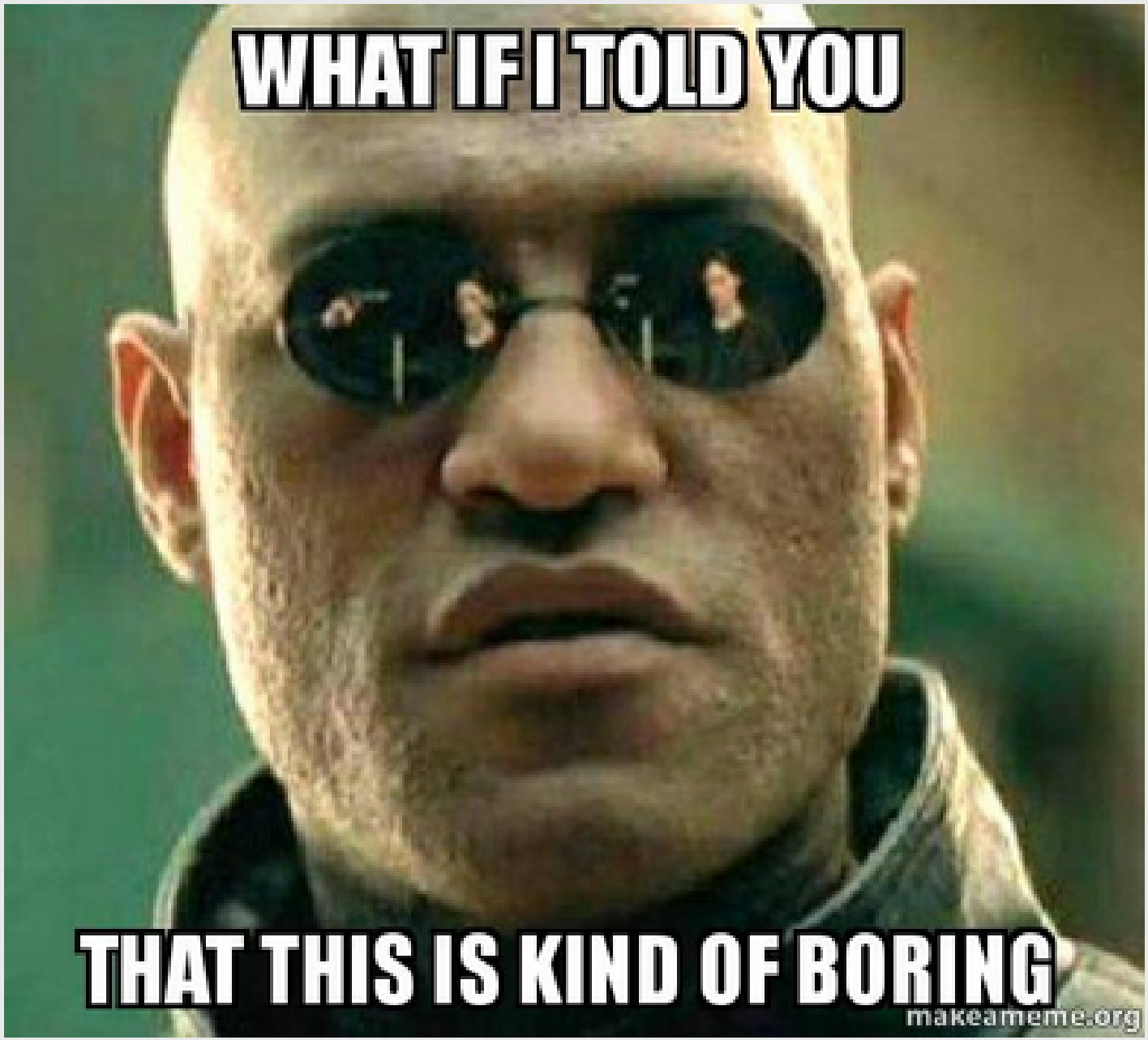
GENDER	AV_AGE
FEMALE	64
MALE	70

Summarize

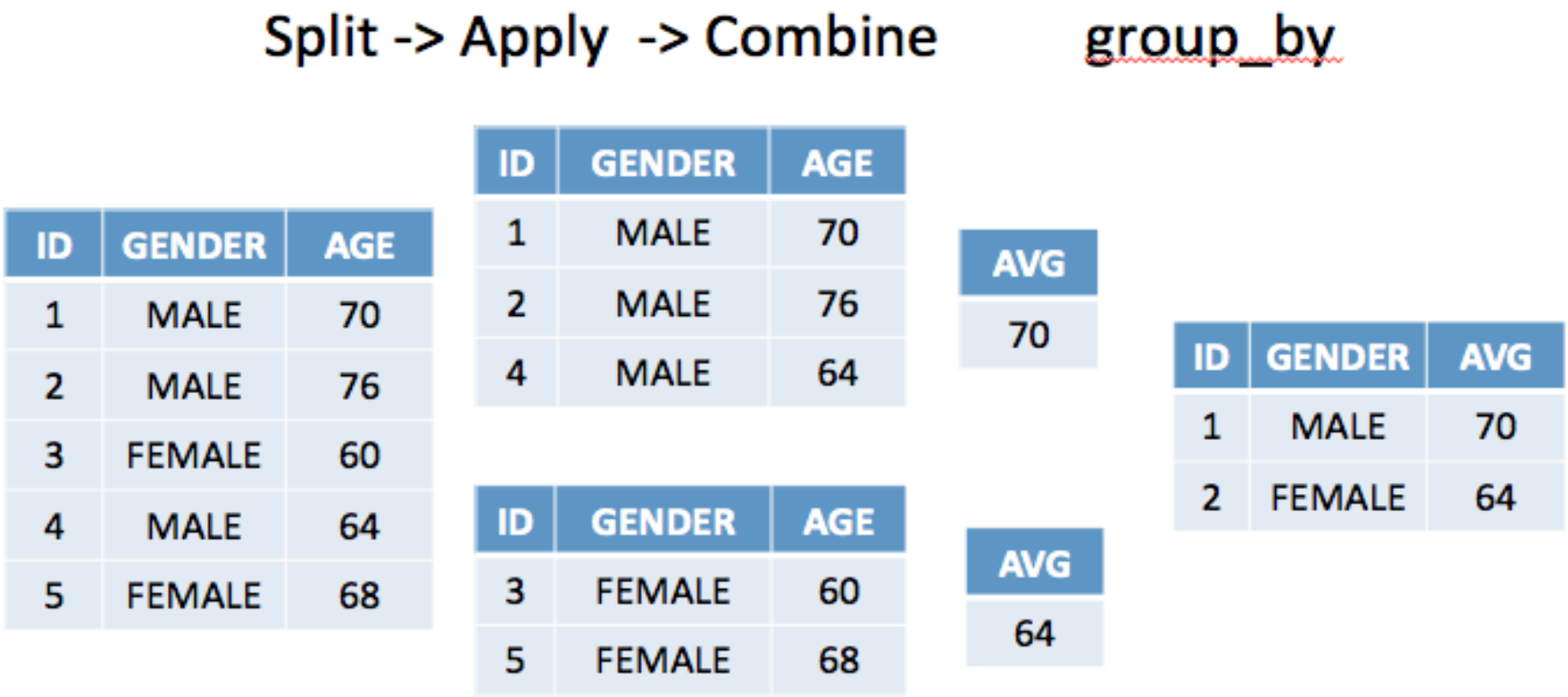
```
summarize(group_by(df,gender),av_age=mean(age),total=n())
Source: local data frame [2 x 3]

  gender av_age total
1 FEMALE      64     2
2   MALE      70     3
```

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

GENDER	AV_AGE	TOTAL
FEMALE	64	2
MALE	70	3


WHAT IF I TOLD YOU
THAT THIS IS KIND OF BORING
makeameme.org

Split -> Apply -> Combine



Split -> Apply -> Combine

But do you really need dplyr to do this ? No but it makes it a lot easier

```
df
  id gender age
1  1   MALE  70
2  2   MALE  76
3  3 FEMALE  60
4  4   MALE  64
5  5 FEMALE  68

tapply(df$age,df$gender,mean)    # tapply function
FEMALE   MALE
    64     70

aggregate(age~gender,data=df,mean) # aggregate works also
 gender age
1 FEMALE  64
2   MALE  70

lapply(split(df,df$gender),function(x) mean(x$age)) # complicated
$FEMALE
[1] 64

$MALE
[1] 70
```

Split -> Apply -> Combine: Chaining

- Before moving forward let us consider the "pipe" operator that is included with the **magrittr** package. This is used to make it possible to "pipe" the results of one command into another command and so on.
- The inspiration for this comes from the UNIX/LINUX operating system where pipes are used all the time. So in effect using "pipes" is nothing new in the world of research computation.
- Warning: Once you get used to pipes it is hard to go back to not using them

Split -> Apply -> Combine: Chaining

- Loading the dplyr package also loads the necessary packages for supporting the piping capability
- Here we will select the age and id column from df and view the top 3 rows.

```
head(select(df, age, id),3)
```

```
  age id
1  70  1
2  76  2
3  60  3
```

Split -> Apply -> Combine: Chaining

Here we will select the age and id column from df and view the top 3 rows. Instead of nesting functions, the idea of of piping is to read the functions from left to right.

```
df %>% select(age, id) %>% head(3)
```

```
  age id
1  70  1
2  76  2
3  60  3
```

Split -> Apply -> Combine: Chaining

What about this ? We can chain together the output of one command to the input of another !

```
df %>% group_by(gender) %>% summarize(avg=mean(age))
Source: local data frame [2 x 2]

  gender avg
1 FEMALE  64
2   MALE  70

df %>% group_by(gender) %>% summarize(avg=mean(age),total=n())
Source: local data frame [2 x 3]

  gender avg total
1 FEMALE  64     2
2   MALE  70     3

df %>% filter(gender == "MALE") %>% summarize(med_age=median(age))
  med_age
1      70
```

Split -> Apply -> Combine: Chaining

What about this ? We can chain together the output of one command to the input of another !

```
df %>% filter(gender == "MALE") %>% summarize(med_age=median(age))
  med_age
1      70
```

df

ID	GENDER	AGE
1	MALE	70
2	MALE	76
3	FEMALE	60
4	MALE	64
5	FEMALE	68

filter

ID	GENDER	AGE
1	MALE	70
2	MALE	76
4	MALE	64

summarize

med_age
70

Split -> Apply -> Combine: Chaining

Using the built in mtcars dataframe filter out records where the wt is greater than 3.3 tons.

Then create a column called ab_be (Y or N) that indicates whether that observation's mpg is greater (or not) than the average mpg for the filtered set.

Then present the average mpg for each group

```
mtcars %>% filter(wt > 3.3)  %>%
         mutate(ab_be=ifelse(mpg > mean(mpg),"Y","N")  ) %>%
         group_by(ab_be) %>% summarize(mean_mpg=mean(mpg))
```

```
Source: local data frame [2 x 2]

  ab_be mean_mpg
1     N 13.77778
2     Y 18.10000
```

Split -> Apply -> Combine: Chaining

Using the built in mtcars dataframe filter out records where the wt is greater than 3.3 tons.

```
mtcars %>% filter(wt > 3.3)
```

```
    mpg cyl  disp  hp drat    wt  qsec vs am gear carb
1  18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2
2  18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
3  14.3   8 360.0 245 3.21 3.570 15.84  0  0    3    4
4  19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4
5  17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4
6  16.4   8 275.8 180 3.07 4.070 17.40  0  0    3    3
7  17.3   8 275.8 180 3.07 3.730 17.60  0  0    3    3
8  15.2   8 275.8 180 3.07 3.780 18.00  0  0    3    3
9  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4
10 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4
11 14.7   8 440.0 230 3.23 5.345 17.42  0  0    3    4
12 15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2
13 15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2
14 13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4
15 19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2
16 15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8
```

Split -> Apply -> Combine: Chaining

Create a column called ab_be (Y or N) that indicates whether that observation's mpg is greater (or not) than the average mpg for the filtered set.

```
mtcars %>% filter(wt > 3.3) %>%
             mutate(ab_be=ifelse(mpg > mean(mpg),"Y","N")  )
    mpg cyl  disp  hp drat    wt  qsec vs am gear carb ab_be
1  18.7   8 360.0 175 3.15 3.440 17.02  0  0    3    2     Y
2  18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1     Y
3  14.3   8 360.0 245 3.21 3.570 15.84  0  0    3    4     N
4  19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4     Y
5  17.8   6 167.6 123 3.92 3.440 18.90  1  0    4    4     Y
6  16.4   8 275.8 180 3.07 4.070 17.40  0  0    3    3     Y
7  17.3   8 275.8 180 3.07 3.730 17.60  0  0    3    3     Y
8  15.2   8 275.8 180 3.07 3.780 18.00  0  0    3    3     N
9  10.4   8 472.0 205 2.93 5.250 17.98  0  0    3    4     N
10 10.4   8 460.0 215 3.00 5.424 17.82  0  0    3    4     N
11 14.7   8 440.0 230 3.23 5.345 17.42  0  0    3    4     N
12 15.5   8 318.0 150 2.76 3.520 16.87  0  0    3    2     N
13 15.2   8 304.0 150 3.15 3.435 17.30  0  0    3    2     N
14 13.3   8 350.0 245 3.73 3.840 15.41  0  0    3    4     N
15 19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2     Y
16 15.0   8 301.0 335 3.54 3.570 14.60  0  1    5    8     N
```

Split -> Apply -> Combine: Chaining

Then present the average mpg for each group as defined by ab_be

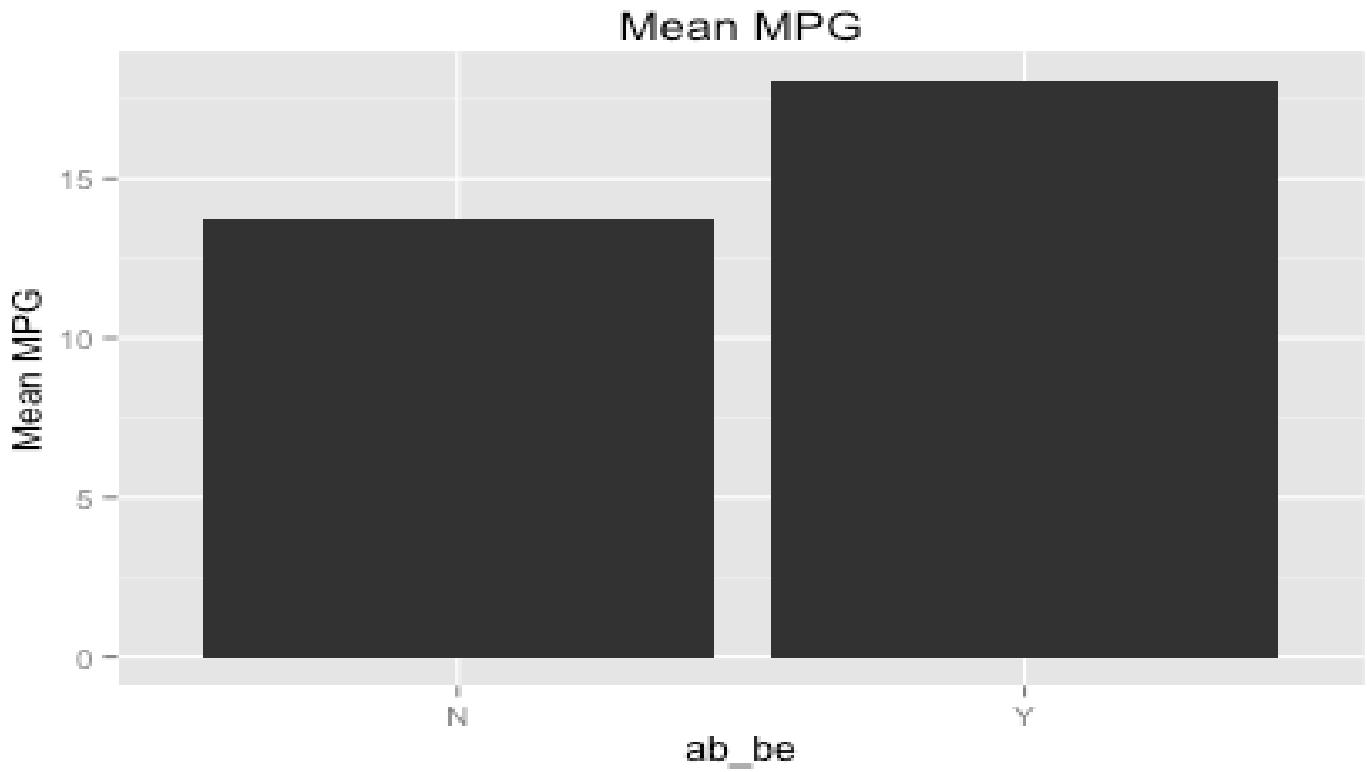
```
mtcars %>% filter(wt > 3.3)  %>%
         mutate(ab_be=ifelse(mpg > mean(mpg),"Y","N")  ) %>%
         group_by(ab_be) %>% summarize(mean_mpg=mean(mpg))
```

```
Source: local data frame [2 x 2]

  ab_be mean_mpg
1     N 13.77778
2     Y 18.10000
```

Split -> Apply -> Combine: Chaining

This could then be chained to the ggplot command

```
mtcars %>% filter(wt > 3.3)  %>%
          mutate(ab_be=ifelse(mpg > mean(mpg),"Y","N")  ) %>%
          group_by(ab_be) %>% summarize(mean_mpg=mean(mpg)) %>%
          ggplot(aes(x=ab_be,y=mean_mpg)) + geom_bar(stat="identity") +
          ggtitle("Mean MPG") + labs(x = "ab_be", y = "Mean MPG")
```



dplyr additional commands

Other activities are possible

```
mtcars %>% sample_n(2) # Sample 2 records from a data frame

                  mpg cyl  disp  hp drat    wt  qsec vs am gear carb
Mazda RX4 Wag    21.0   6 160.0 110 3.90 2.875 17.02  0  1    4    4
Merc 280         19.2   6 167.6 123 3.92 3.440 18.30  1  0    4    4

# Sample 2 records from each cylinder group

mtcars %>% group_by(cyl) %>% do(sample_n(.,2))
Source: local data frame [6 x 11]
Groups: cyl

   mpg cyl  disp  hp drat    wt  qsec vs am gear carb
1 21.4   4 121.0 109 4.11 2.780 18.60  1  1    4    2
2 27.3   4  79.0  66 4.08 1.935 18.90  1  1    4    1
3 19.7   6 145.0 175 3.62 2.770 15.50  0  1    5    6
4 18.1   6 225.0 105 2.76 3.460 20.22  1  0    3    1
5 17.3   8 275.8 180 3.07 3.730 17.60  0  0    3    3
6 19.2   8 400.0 175 3.08 3.845 17.05  0  0    3    2
```

dplyr additional commands

Other activities are possible. You can use "do" to perform arbitrary computation, returning either a data frame or arbitrary objects which will be stored in a list. This is particularly useful when working with models

```
by_cyl <- group_by(mtcars, cyl)
models <- by_cyl %>% do(mod = lm(mpg ~ disp, data = .))

Source: local data frame [3 x 2]
Groups: <by row>

  cyl     mod
1   4 <S3:lm>
2   6 <S3:lm>
3   8 <S3:lm>

summarise(models, rsq = summary(mod)$r.squared)
Source: local data frame [3 x 1]

         rsq
1 0.64840514
2 0.01062604
3 0.27015777

# Here is a one liner that does the above
```

Joining data frames

```
idatime <- data.frame(id=rep(1:3,each=2),time=rep(0:1,each=3))
```

```
  id time
1  1    0
2  1    0
3  2    0
4  2    1
5  3    1
6  3    1
```

```
idawt <- data.frame(id=c(1,2,4),wt=c(110,130,115))
```

```
  id  wt
1  1 110
2  2 130
3  4 115
```

Inner joins - inner_join(x,y)

Will return all rows from x where there are matching values in y, and all columns from x and y

idatime

id	time
1	0
1	0
2	0
2	1
3	1
3	1

idawt

id	wt
1	110
2	130
4	115

inner_join(idatime, idawt)

id	time	wt
1	0	110
1	0	110
2	0	130
2	1	130

inner_join(idawt, idatime)

id	wt	time
1	110	0
1	110	0
2	130	0
2	130	1

Inner joins - inner_join(x,y)

Will return all rows from x where there are matching values in y, and all columns from x and y

```
inner_join(idatime,idawt)

Joining by: "id"
  id time  wt
1  1    0 110
2  1    0 110
3  2    0 130
4  2    1 130
```

Joining data frames - left_join(x,y)

return all rows from x, and all columns from x and y

idatime

id	time
1	0
1	0
2	0
2	1
3	1
3	1

idawt

id	wt
1	110
2	130
4	115

left_join(idatime, idawt)

id	time	wt
1	0	110
1	0	110
2	0	130
2	1	130
3	1	NA
3	1	NA

left_join(idawt, idatime)

id	wt	time
1	110	0
1	110	0
2	130	0
2	130	1
4	115	NA

Exercises

Now it is your turn. Let's do some exercises

```
load(dplyr)

url <- "https://raw.githubusercontent.com/steviep42/youtube/master/YOUTUBE.DIR/msleep_ggplot2.csv"

msleep <- read.csv(url)

names(msleep)
 [1] "name"         "genus"        "vore"         "order"        "conservation"
 [6] "sleep_total"  "sleep_rem"    "sleep_cycle"  "awake"        "brainwt"
[11] "bodywt"
```

Exercises

Remember - here are the following commands available to you from dplyr

- filter - find observations satisfying some condition(s)
- select - selecting specific columns by name
- mutate - adding new columns or changing existing ones
- arrange - reorder or sort the rows
- summarize - do some aggregation or summary by groups

Exercises

Here is a description of the columns / variables

COLUMN NAME	DESCRIPTION
name	common name
genus	taxonomic rank
vore	carnivore, omnivore or herbivore?
order	taxonomic rank
conservation	the conservation status of the mammal
sleep_total	total amount of sleep, in hours
sleep_rem	rem sleep, in hours
sleep_cycle	length of sleep cycle, in hours
awake	amount of time spent awake, in hours
brainwt	brain weight in kilograms
bodywt	body weight in kilograms

Exercises

Using the msleep data frame let's do the following activities and answer some questions. Try to use the chaining operator:

- Select the name and sleep_total columns
- Using the colon operator select all columns between name and order
- Select all columns that begin with "sl"
- Filter the data frame to find only rows with a sleep_total $>=$ 16
- Filter the rows for mammals that sleep a total of more than 16 hours and have a body weight of greater than 1 kilogram
- Arrange the data frame using the **order** column

Exercises

For these you will need to use the chaining operator:

- Select three columns from msleep, arrange the rows by the taxonomic order and then arrange the rows by sleep_total. Finally show the head of the final data frame
- Same as above, except here we filter the rows for mammals that sleep for 16 or more hours instead of showing the head of the final data frame
- Use the **mutate** function to create a new column called rem_proportion which is the ratio of rem sleep to total amount of sleep

Exercises

- Use the summarise() function: to compute the average number of hours of sleep, apply the mean() function to the column sleep_total and call the summary value avg_sleep.
- Group the msleep data frame by taxanomic order and then summarize the mean sleep total
- Same as above except summarize the mean, max, and min sleep total