

# dplyr, tidyr, and ggplot2

Intro to the *tidyverse*

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## Part 1: dplyr and tidyr

# Data manipulation in base R

```
#Changes species to factor
plants$Species <- as.factor(plants$Species)
#Changes plant code to factor
plants$Plant.Code <- as.factor(plants$Plant.Code)
#Changes Seed to factor
seeds$Seed <- as.factor(seeds$Seed)
#Changes plant code to factor
seeds$Plant.Code <- as.factor(seeds$Plant.Code)
#Selects Flower, Code, Total.Germ columns
germ <- germ[,c('Flower', 'Code', 'Total.Germ')]

#Sets numerics
plants[,c(3:9)] <- as.numeric(unlist(plants[,c(3:9)]))
#Sets Dates
seeds$Collection.Date <- as.Date(seeds$Collection.Date, origin='2012-01-01')
```

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```

- One line of code per column - lots of typing
- Lots of \$\$\$s
- Lots of room for errors

# Data manipulation using dplyr/tidyr

```
library(tidyverse)
#Convert factors in plants df
plants <- plants %>% mutate(across(c(Species,Plant.Code)),factor)
#Convert factors in seeds df
seeds <- seeds %>% mutate(across(c(Seed,Plant.Code)),factor)
#Select Flower, Code, and Total.Germ columns in germ df
germ <- germ %>% select(Flower,Code,Total.Germ)

#Change columns 3:9 to numeric
plants <- plants %>% mutate(across(c(3:9)),as.numeric)
#Convert Collection.Date to Date format
seeds <- seeds %>%
  mutate(Collection.Date=as.Date(Collection.Date,origin='2012-01-01'))
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- More compact, less typing



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- Easier to read

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#Convert Collection.Date to Date format
seeds <- seeds %>%
  mutate(Collection.Date=as.Date(Collection.Date,origin='2012-01-01'))
```

- More compact, less typing
- Easier to read
- Faster (matters for large datasets)

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**Start with small, simple tasks, and work your way up to larger, complicated ones**



## Things to learn today:

- Basic syntax and table verbs



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- Piping



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- Reshaping



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- Grouping



## Things to learn today:

- Basic syntax and table verbs
- Piping
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- Exercise!



## Basic Syntax

Both `dplyr` and `tidyr` work with data frames or tibbles

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# Basic Syntax

Both dplyr and tidyr work with data frames or tibbles

- data frame: similar to matrix, but with different data types for each column
- tibble: “compact” data frame, with some annoying features removed

```
head(iris) #Regular data frame
```

##	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

# Basic Syntax

```
as_tibble(iris) #This is usually done automatically
```

```
## # A tibble: 150 x 5
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>
## 1         5.1         3.5         1.4         0.2 setosa
## 2         4.9         3         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         3.6         1.4         0.2 setosa
## 6         5.4         3.9         1.7         0.4 setosa
## 7         4.6         3.4         1.4         0.3 setosa
## 8         5         3.4         1.5         0.2 setosa
## 9         4.4         2.9         1.4         0.2 setosa
## 10        4.9         3.1         1.5         0.1 setosa
## # i 140 more rows
```



## Basic verbs - subsetting

- **select:** returns only columns that you want

##	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
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```
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## 1          5.1          3.5          1.4          0.2   setosa
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## 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
```

- Select Petal.Length, Petal.Width, and Species columns

```
irisTemp <- select(iris, Petal.Length, Petal.Width, Species)
```

```
##   Petal.Length Petal.Width Species
## 1          1.4          0.2   setosa
## 2          1.4          0.2   setosa
## 3          1.3          0.2   setosa
## 4          1.5          0.2   setosa
## 5          1.4          0.2   setosa
## 6          1.7          0.4   setosa
```

## Basic verbs - subsetting

- Helper functions for **select**: *colon* operator

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
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##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
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## 3         4.7         3.2         1.3         0.2   setosa
```

- Get all columns between Petal.Length and Species

```
irisTemp <- select(iris,Petal.Length:Species)
```

```
##   Petal.Length Petal.Width Species
## 1         1.4         0.2   setosa
## 2         1.4         0.2   setosa
## 3         1.3         0.2   setosa
```

## Basic verbs - subsetting

- Helper functions for **select**: `-`, and *contains*

```
## 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
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```
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```

- `-`: selects all columns EXCEPT the one(s) specified

```
irisTemp <- select(iris,-Species)
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1           5.1           3.5           1.4           0.2
## 2           4.9           3.0           1.4           0.2
## 3           4.7           3.2           1.3           0.2
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## 2           4.9           3.0           1.4           0.2
## 3           4.7           3.2           1.3           0.2
```

- Some common selection helpers:
  - `contains()` contains a string
  - `starts_with()` column name starts with a string

## Basic verbs - subsetting

- **filter**: returns only rows that you want

##	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

## Basic verbs - subsetting

- **filter**: returns only rows that you want

```
##   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
```

- Chooses rows where Species is *versicolor*

```
irisTemp <- filter(iris, Sepal.Length < 5, Species == 'versicolor')
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 1         4.9         2.4         3.3         1   versicolor
```

## Basic verbs - subsetting

- **filter**: returns only rows that you want

```
## 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
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- Some common logical operators:

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## Sepal.Length Sepal.Width Petal.Length Petal.Width Species
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- Some common logical operators:
  - == equal to, != not equal to

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##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.2   setosa
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## 4         4.6         3.1         1.5         0.2   setosa
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##   Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 1         4.9         2.4         3.3         1   versicolor
```

- Some common logical operators:
  - == equal to, != not equal to
  - < less than, > greater than
  - & AND, | OR

## Basic verbs - make new variables

- **mutate**: add new columns or alter existing ones

```
##   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
```



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## 2         4.9         3.0         1.4         0.2   setosa
## 3         4.7         3.2         1.3         0.2   setosa
```

- Squares the Petal.Width column

```
irisTemp <- mutate(iris,Petal.Width=Petal.Width^2)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1         5.1         3.5         1.4         0.04   setosa
## 2         4.9         3.0         1.4         0.04   setosa
## 3         4.7         3.2         1.3         0.04   setosa
```

## Basic verbs - make new variables

- **across**: uses the function on a number of columns. Must be used *inside* verbs like *mutate*

```
## 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
```

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```
##   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
```

- Squares the Sepal.Length and Petal.Width columns

```
irisTemp <- mutate(iris, across(c(Sepal.Length, Petal.Width), ~.^2))
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1        26.01         3.5         1.4         0.04   setosa
## 2        24.01         3.0         1.4         0.04   setosa
## 3        22.09         3.2         1.3         0.04   setosa
```

## Basic verbs - make new variables

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```
##   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
```

- Squares the Sepal.Length and Petal.Width columns

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```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1        26.01         3.5         1.4         0.04   setosa
## 2        24.01         3.0         1.4         0.04   setosa
## 3        22.09         3.2         1.3         0.04   setosa
```

- `~` is called a lambda (similar to a function)

## Basic verbs - make new variables

- **across**: uses the function on a number of columns. Must be used *inside* verbs like *mutate*

```
##   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
```

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```
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```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1        26.01         3.5         1.4         0.04   setosa
## 2        24.01         3.0         1.4         0.04   setosa
## 3        22.09         3.2         1.3         0.04   setosa
```

- `~` is called a lambda (similar to a function)
- `.` means “input data from column X”, so...

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- Squares the Sepal.Length and Petal.Width columns

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```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1        26.01         3.5         1.4         0.04   setosa
## 2        24.01         3.0         1.4         0.04   setosa
## 3        22.09         3.2         1.3         0.04   setosa
```

- `~` is called a lambda (similar to a function)
- `.` means “input data from column X”, so...
- `~.^2` means “square anything in these named column

## Basic verbs - make new variables

- **rename & transmute**

##	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

## Basic verbs - make new variables

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```
## 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
```

- Renames Petal.Length to PLength

```
irisTemp <- rename(iris, PWidth=Petal.Width, PLength=Petal.Length)
```

```
## Sepal.Length Sepal.Width PLength PWidth 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
```



## Basic verbs - make new variables

- **rename & transmute**

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## 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
```

- Renames Petal.Length to PLength

```
irisTemp <- rename(iris, PWidth=Petal.Width, PLength=Petal.Length)
```

```
## Sepal.Length Sepal.Width PLength PWidth 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
```

- Same as *mutate* but drops other columns

```
irisTemp2 <- transmute(iris, P.Width2=(Petal.Width^2))
```

```
## P.Width2
## 1      0.04
## 2      0.04
## 3      0.04
```

## Mini-summary

- **select**: subset columns

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- **filter**: subset rows
- **mutate**: add new columns, or alter existing
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- **rename**: changes column names
- **across**: applies function across multiple columns
  - Used *inside of* table verbs



## First challenge

Using the iris dataset (type  
`data(iris)`):

- Filter only rows with “virginica”

Goal:

##	Species	P.Area	S.Area
## 1	virginica	15.00	20.79
## 2	virginica	9.69	15.66
## 3	virginica	12.39	21.30
## 4	virginica	10.08	18.27
## 5	virginica	12.76	19.50
## 6	virginica	13.86	22.80
## 7	virginica	7.65	12.25
## 8	virginica	11.34	21.17
## 9	virginica	10.44	16.75
## 10	virginica	15.25	25.92

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## First challenge

Using the iris dataset (type  
`data(iris)`):

- Filter only rows with “virginica”
- Make 2 new “area” columns, which are length  $\times$  width of Petals and Sepals
- Get rid of all columns except “Species” + 2 new columns

Goal:

##	Species	P.Area	S.Area
## 1	virginica	15.00	20.79
## 2	virginica	9.69	15.66
## 3	virginica	12.39	21.30
## 4	virginica	10.08	18.27
## 5	virginica	12.76	19.50
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## Piping - %>%

This is where the tidyverse becomes *very* useful

- Takes data from one verb and passes it to the next one.

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- Takes data from one verb and passes it to the next one.
- Lets you string together complex operations:

```
irisTemp <- select(iris, Sepal.Length, Species) %>% #Selects Sepal.Length & Species  
  filter(Sepal.Length>5, Species=='versicolor') %>% #Filters using dataframe from above  
  mutate(SLength2=Sepal.Length^2) #Mutates using dataframe from above
```

##	Sepal.Length	Species	SLength2
## 1	7.0	versicolor	49.00
## 2	6.4	versicolor	40.96
## 3	6.9	versicolor	47.61
## 4	5.5	versicolor	30.25
## 5	6.5	versicolor	42.25
## 6	5.7	versicolor	32.49

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## Reshaping - i.e. “data gymnastics”

- This is very tedious to do in base R and Excel
- Reshaping operations in `tidyr` make this much easier
- Main commands:
  - ① `pivot_longer` - gather columns into rows ('long format')
  - ② `pivot_wider` - spread rows into columns ('wide format')

## Reshaping - *pivot\_longer*: columns to rows

Here's some data in both **wide** and **long** format:

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Here's some data in both **wide** and **long** format:

**wide** format: data for each “unit” listed  
in multiple columns

```
##   bat weight height wings
## 1   a      1     2.5     2
## 2   b      2     4.0     2
## 3   c      3     5.5     2
```

## Reshaping - *pivot\_longer*: columns to rows

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**wide** format: data for each “unit” listed  
in multiple columns

##	bat	weight	height	wings
## 1	a	1	2.5	2
## 2	b	2	4.0	2
## 3	c	3	5.5	2

**long** format: data listed in single column,  
plus an ID column

##	#	A	tibble: 9 x 3
##	bat	name	value
##	<chr>	<chr>	<dbl>
## 1	a	weight	1
## 2	a	height	2.5
## 3	a	wings	2
## 4	b	weight	2
## 5	b	height	4
## 6	b	wings	2
## 7	c	weight	3
## 8	c	height	5.5
## 9	c	wings	2

## Reshaping - *pivot\_longer*: columns to rows

Change wide dataframe to long dataframe:

```
(longBats <- bats %>% pivot_longer(cols=weight:wings, #Columns to be made into 2  
                                names_to='trait', #Name of "naming" column  
                                values_to='meas')) #Name of "value" column
```

```
## # A tibble: 9 x 3  
##   bat   trait   meas  
##   <chr> <chr>   <dbl>  
## 1 a     weight    1  
## 2 a     height   2.5  
## 3 a     wings     2  
## 4 b     weight    2  
## 5 b     height    4  
## 6 b     wings     2  
## 7 c     weight    3  
## 8 c     height   5.5  
## 9 c     wings     2
```

## Reshaping - *pivot\_wider*: rows to columns

Change long dataframe to wide (reverse of *pivot\_longer*)

```
longBats %>% pivot_wider(names_from=trait, #Names of new columns  
                        values_from=meas) #Values to go into new columns
```

```
## # A tibble: 3 x 4  
##   bat   weight height wings  
##   <chr>   <dbl>   <dbl> <dbl>  
## 1 a         1     2.5     2  
## 2 b         2     4       2  
## 3 c         3     5.5     2
```

*#Note: this must have unique row identifiers*



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- `pivot_wider`: reshapes data into *wide* form

# Exercises!

Using the *CO2* dataset:

- Select only *non-chilled* plants from *Quebec*

Goal:

```
## # A tibble: 7 x 4
##   conc    Qn1    Qn2    Qn3
##   <dbl> <dbl> <dbl> <dbl>
## 1    95    16   13.6   16.2
## 2   175   30.4   27.3   32.4
## 3   250   34.8   37.1   40.3
## 4   350   37.2   41.8   42.1
## 5   500   35.3   40.6   42.9
## 6   675   39.2   41.4   43.9
## 7  1000   39.7   44.3   45.5
```

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Using the *CO2* dataset:

- Select only *non-chilled* plants from *Quebec*
- Pipe data frame to next command

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Using the *CO2* dataset:

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- Change the uptake dataset from long to wide format (each plant should have its own column), with a column at the beginning showing concentration

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## 1    95    16   13.6   16.2
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Using the *CO2* dataset:

- Select only *non-chilled* plants from *Quebec*
- Pipe data frame to next command
- Change the uptake dataset from long to wide format (each plant should have its own column), with a column at the beginning showing concentration
- Hint: *filter* rows and *select* columns you need, then *pivot\_wide* to wide format

Goal:

```
## # A tibble: 7 x 4
##   conc    Qn1    Qn2    Qn3
##   <dbl> <dbl> <dbl> <dbl>
## 1    95    16   13.6   16.2
## 2   175   30.4   27.3   32.4
## 3   250   34.8   37.1   40.3
## 4   350   37.2   41.8   42.1
## 5   500   35.3   40.6   42.9
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- For example, what is the average of each species' *Petal.width*?
- This can be done in base R:

```
with(iris,tapply(Petal.Width,Species,mean)) #Using tapply
```

```
##      setosa versicolor  virginica  
##      0.246      1.326      2.026
```

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- For example, what is the average of each species' *Petal.width*?
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with(iris,tapply(Petal.Width,Species,mean)) #Using tapply
```

```
##      setosa versicolor  virginica  
##      0.246      1.326      2.026
```

```
aggregate(Petal.Width~Species,data=iris,mean) #Using aggregate
```

```
##      Species Petal.Width  
## 1      setosa      0.246  
## 2 versicolor      1.326  
## 3  virginica      2.026
```

# Grouping

- How can this be done in dplyr and tidyr?

```
iris %>% group_by(Species) %>% #Group by species  
  summarize(meanPWidth=mean(Petal.Width), #Mean of Petal.Width  
            sdPWidth=sd(Petal.Width)) #SD of Petal.Width
```

```
## # A tibble: 3 x 3  
##   Species    meanPWidth sdPWidth  
##   <fct>      <dbl>    <dbl>  
## 1 setosa      0.246     0.105  
## 2 versicolor 1.33      0.198  
## 3 virginica  2.03      0.275
```

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```

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## # A tibble: 3 x 3
##   Species    meanPWidth sdPWidth
##   <fct>         <dbl>    <dbl>
## 1 setosa         0.246     0.105
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```

- Apply *grouping*, then use `summarize` function

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```

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## # A tibble: 3 x 3
##   Species    meanPWidth sdPWidth
##   <fct>         <dbl>    <dbl>
## 1 setosa         0.246     0.105
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```

- Apply *grouping*, then use `summarize` function
  - Breaks dataframe into “mini-dataframes” before applying the function



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- How can this be done in dplyr and tidyr?

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iris %>% group_by(Species) %>% #Group by species
  summarize(meanPWidth=mean(Petal.Width), #Mean of Petal.Width
            sdPWidth=sd(Petal.Width)) #SD of Petal.Width
```

```
## # A tibble: 3 x 3
##   Species    meanPWidth sdPWidth
##   <fct>      <dbl>    <dbl>
## 1 setosa      0.246     0.105
## 2 versicolor 1.33      0.198
## 3 virginica  2.03      0.275
```

- Apply *grouping*, then use *summarize* function
  - Breaks dataframe into “mini-dataframes” before applying the function
- Data frame can be fed into other functions after summarizing

## Grouping - Examples

```
iris %>% group_by(Species) %>% #Group by species
  summarize(count=n(), #Number of rows
            med=median(Petal.Width), #Median
            iqr=IQR(Petal.Width)) #Inter-quartile range
```

```
## # A tibble: 3 x 4
##   Species    count  med   iqr
##   <fct>    <int> <dbl> <dbl>
## 1 setosa      50   0.2   0.1
## 2 versicolor  50   1.3   0.3
## 3 virginica   50    2    0.5
```

- *n* is empty, because it shows the number of rows of the grouped “mini-dataframe”

## Grouping - Examples

- Also useful for applying functions to subsets of data, *without* summarizing

```
iris %>% group_by(Species) %>%  
  mutate(ID=1:n()) %>% #Makes ID column, with numbers 1-N  
  filter(ID<4) #Selects ID 1-3 from each group
```

```
## # A tibble: 9 x 6  
## # Groups:   Species [3]  
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species      ID  
##      <dbl>         <dbl>         <dbl>         <dbl> <fct>    <int>  
## 1         5.1         3.5         1.4         0.2 setosa      1  
## 2         4.9         3         1.4         0.2 setosa      2  
## 3         4.7         3.2         1.3         0.2 setosa      3  
## 4         7         3.2         4.7         1.4 versicolor  1  
## 5         6.4         3.2         4.5         1.5 versicolor  2  
## 6         6.9         3.1         4.9         1.5 versicolor  3  
## 7         6.3         3.3         6         2.5 virginica   1  
## 8         5.8         2.7         5.1         1.9 virginica   2  
## 9         7.1         3         5.9         2.1 virginica   3
```

# Grouping

- Another way of doing the same thing

```
iris %>% group_by(Species) %>%  
  slice(1:3) #Selects rows 1-3 from each group
```

```
## # A tibble: 9 x 5  
## # Groups:   Species [3]  
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species  
##           <dbl>         <dbl>         <dbl>         <dbl> <fct>  
## 1           5.1           3.5           1.4           0.2 setosa  
## 2           4.9           3            1.4           0.2 setosa  
## 3           4.7           3.2           1.3           0.2 setosa  
## 4           7            3.2           4.7           1.4 versicolor  
## 5           6.4           3.2           4.5           1.5 versicolor  
## 6           6.9           3.1           4.9           1.5 versicolor  
## 7           6.3           3.3           6             2.5 virginica  
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```

```
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## # Groups:   Species [3]  
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species  
##         <dbl>         <dbl>         <dbl>         <dbl> <fct>  
## 1          5.1          3.5          1.4          0.2 setosa  
## 2          4.9          3           1.4          0.2 setosa  
## 3          4.7          3.2          1.3          0.2 setosa  
## 4           7          3.2          4.7          1.4 versicolor  
## 5          6.4          3.2          4.5          1.5 versicolor  
## 6          6.9          3.1          4.9          1.5 versicolor  
## 7          6.3          3.3          6           2.5 virginica  
## 8          5.8          2.7          5.1          1.9 virginica  
## 9          7.1          3           5.9          2.1 virginica
```

- You can use most of the subset and window functions across groups

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Using the *InsectSprays* dataset:

- Find the mean and SD of counts for each type of spray

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- Reshape dataframe so that each spray has its own column, with mean and SD in separate rows
- Hint: get summary stats (mean, SD), then `pivot_longer`, and finally `pivot_wider`

```
## # A tibble: 2 x 7
##   stat      A      B      C      D      E      F
##   <chr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 mean  14.5  15.3   2.08  4.92   3.5   16.7
## 2 sd     4.72  4.27   1.98  2.50   1.73   6.21
```

Happy data wrangling! Yee-haw!



## Part 2: ggplot2

# Motivation

What is ggplot2?

- ggplot philosophy

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## Philosophy:

- Data input centered around `data.frames` or `tibbles`

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- Data input centered around `data.frames` or `tibbles`
- Data display centered around `geoms` (geometric objects)



## What is ggplot2?

- Updated version of `ggplot` (older R package)
- Implementation of Wilkinson's *grammar of graphics*
- Elements: data, transformations, elements, scale, guide, coordinates
- Describes a [layered approach to building graphics](#) beyond formulaic plots (e.g. “boxplot”, “scatterplot”)
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- Data display centered around `geoms` (geometric objects)
- Columns from data frames are mapped into `geoms` using `aesthetics`
- `geoms` are displayed according to `themes`

## Simple example - scatterplot

```
data(mtcars) # mtcars dataset (built into R)
```

##		mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
##	Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
##	Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
##	Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
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##	Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2

```
ggplot(data = mtcars, aes(x = disp, y = mpg))+  
  geom_point() # Display data using points
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## Simple example - scatterplot

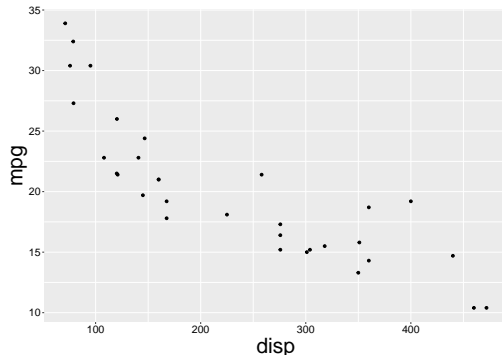
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Top line of code says:

- data from `mtcars` dataframe



# Simple example - scatterplot

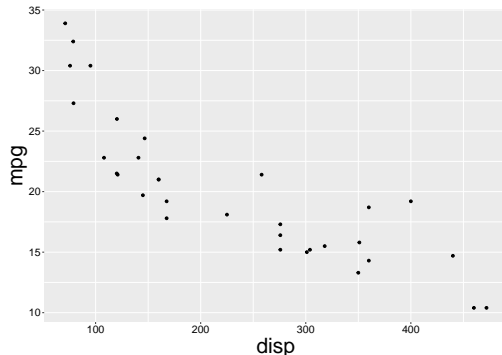
```
data(mtcars) # mtcars dataset (built into R)
```

```
##           mpg cyl  disp  hp  drat    wt  qsec vs  am  gear  carb
## Mazda RX4      21.0   6  160 110 3.90 2.620 16.46  0   1    4    4
## Mazda RX4 Wag  21.0   6  160 110 3.90 2.875 17.02  0   1    4    4
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Top line of code says:

- data from mtcars dataframe
- aes = aesthetics from dataframe



## Simple example - scatterplot

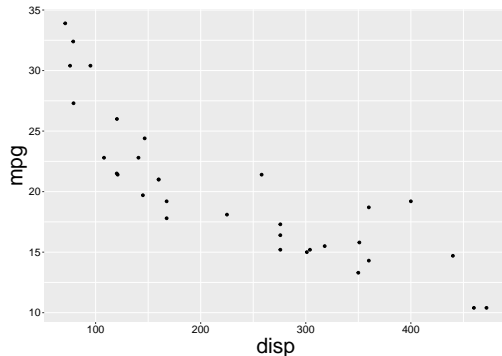
```
data(mtcars) # mtcars dataset (built into R)
```

##	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
## Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
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ggplot(data = mtcars, aes(x = disp, y = mpg))+  
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```

Top line of code says:

- data from `mtcars` dataframe
- `aes` = aesthetics from dataframe
- map `disp` to x-axis, `mpg` to y-axis



## Simple example - bar plot

```
data(mtcars) # mtcars dataset (built into R)
```

##		mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
##	Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
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```
ggplot(data = mtcars, aes(x = factor(gear)))+  
  geom_bar()  
# Display number of data points for each  
# factor level
```

## Simple example - bar plot

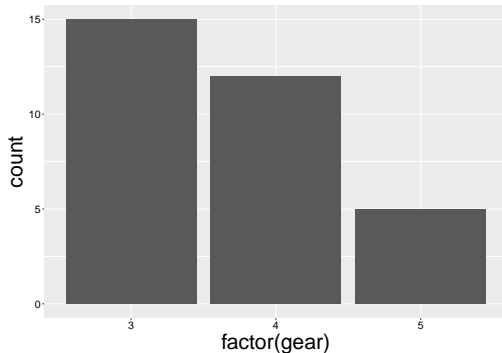
```
data(mtcars) # mtcars dataset (built into R)
```

```
##           mpg  cyl  disp  hp  drat    wt   qsec  vs  am  gear  carb
## Mazda RX4      21.0   6  160 110 3.90 2.620 16.46  0   1    4    4
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Top line of code says:

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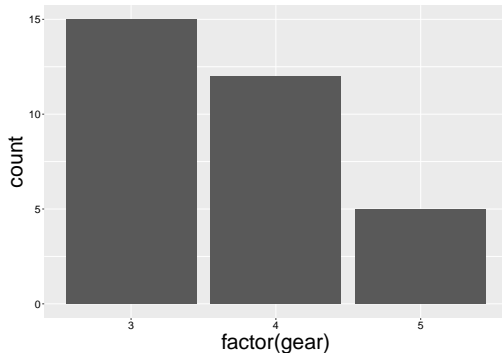
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```
ggplot(data = mtcars, aes(x = factor(gear)))+  
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# Display number of data points for each  
# factor level
```

Top line of code says:

- map gear to x-axis (first converted to a factor)
- Automatically uses `stat='count'` to group data according to factor



## Simple example - histogram

```
data(mtcars) # mtcars dataset (built into R)
```

##		mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
##	Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
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##	Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2

```
ggplot(data = mtcars, aes(x = disp))+  
  # Group disp into bins, and display  
  #   count in each bin  
  geom_histogram()
```

## Simple example - histogram

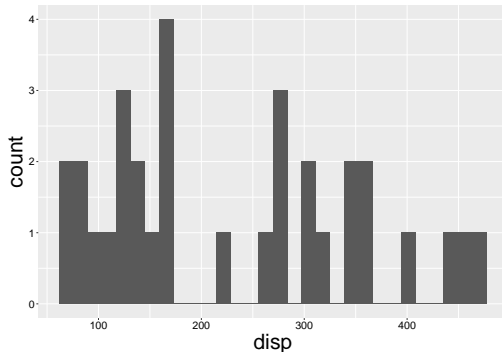
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data(mtcars) # mtcars dataset (built into R)
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##	Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
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Top line of code says:

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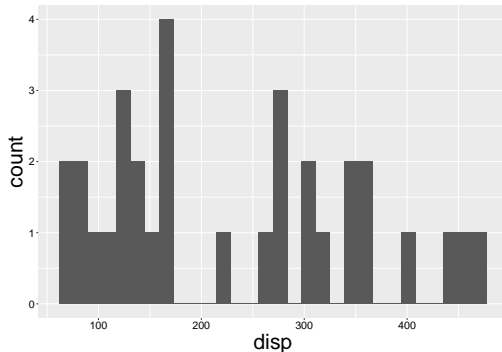
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```
ggplot(data = mtcars, aes(x = disp))+  
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Top line of code says:

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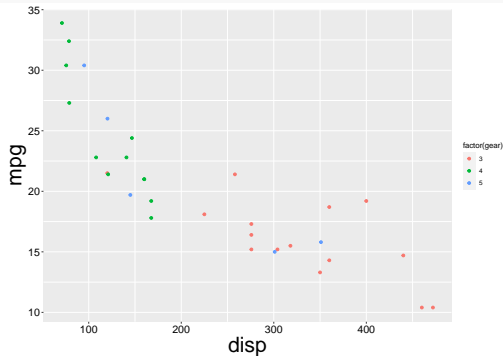
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Maps colour to gear

```
ggplot(data=mtcars, aes(x=disp, y=mpg)) +  
  geom_point(aes(col=factor(gear)))
```



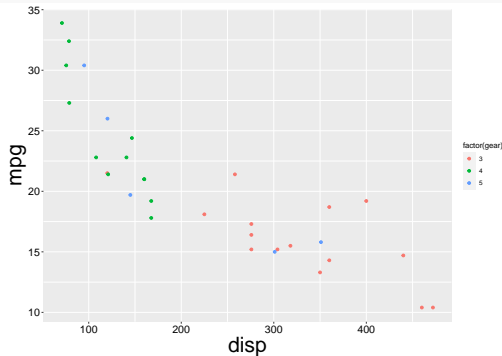


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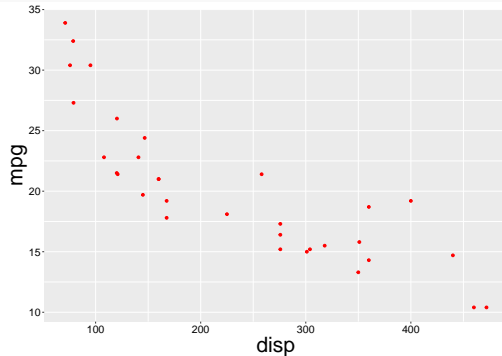
## Maps colour to gear

```
ggplot(data=mtcars, aes(x=displacement, y=mpg)) +  
  geom_point(aes(col=factor(gear)))
```



## Sets colour as red

```
ggplot(data=mtcars, aes(x=displacement, y=mpg)) +  
  geom_point(colour='red')
```



## What if I want different colours?

- Default colour themes are pretty bad.  
Change them with  
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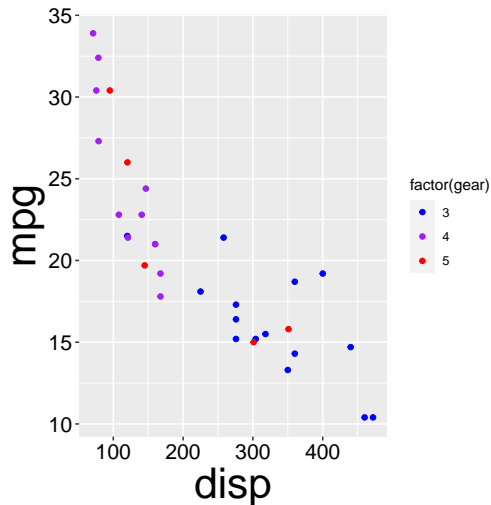
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```
ggplot(data=mtcars, aes(x=displacement, y=mpg)) +  
  geom_point(aes(col=factor(gear))) +  
  scale_colour_manual(  
    values=c('blue', 'purple', 'red')  
  )
```

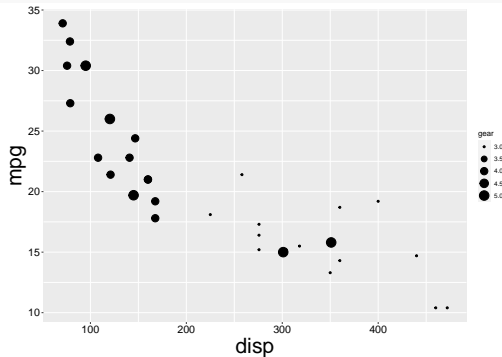


# Sizes in plots

- Sizes of things can also be *mapped* (via aes) or *set* (outside of aes), similar to colours. You can alter mapped sizes using `scale_size`

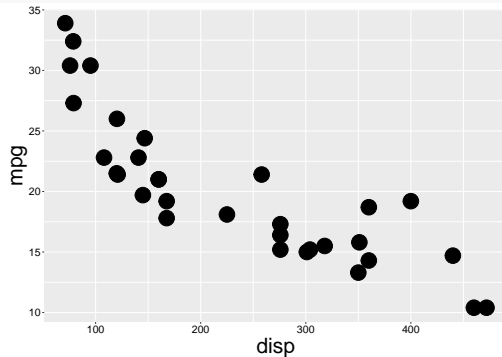
Maps gear to size:

```
ggplot(data=mtcars, aes(x=disp, y=mpg)) +  
  geom_point(aes(size=gear))
```



Sets size at 10:

```
ggplot(data=mtcars, aes(x=disp, y=mpg)) +  
  geom_point(size=10)
```



## Change plot theme

- theme controls almost all non-data elements of plots



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- Made up of *elements*:  
`element_line()`, `element_text()`,  
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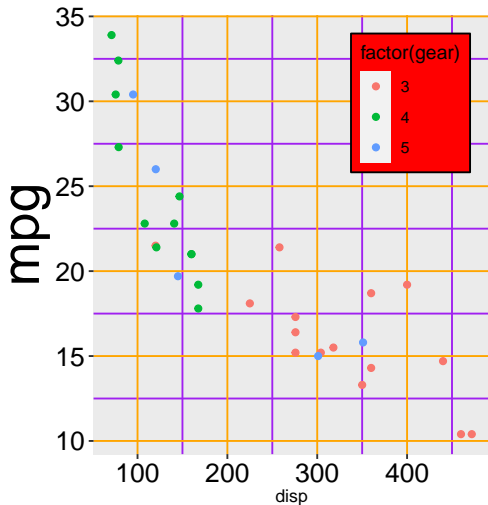
- theme controls almost all non-data elements of plots
- Made up of *elements*:  
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## Change plot theme

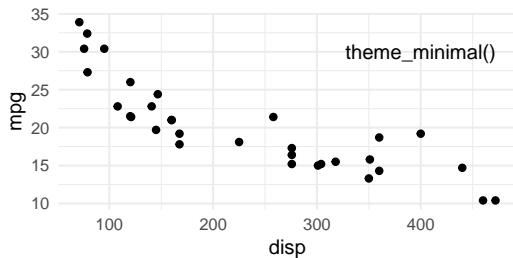
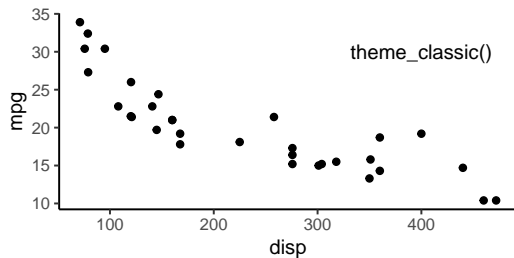
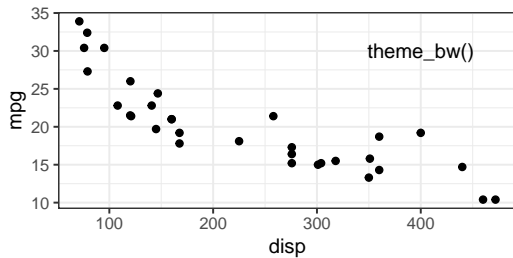
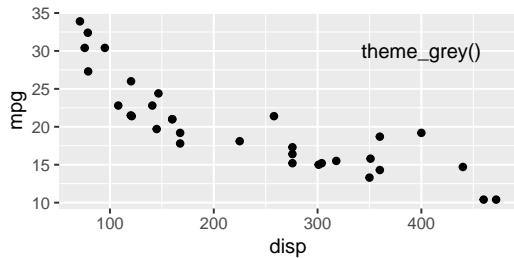
- theme controls almost all non-data elements of plots
- Made up of *elements*:  
element\_line(), element\_text(),  
element\_rect()

```
ggplot(data=mtcars, aes(x=disp, y=mpg)) +  
  # Maps gear to colour  
  geom_point(aes(col=factor(gear))) +  
  # Changes plot theme  
  theme(axis.title.x=element_text(size=10),  
        legend.background=element_rect(fill='red'),  
        legend.position=c(0.8, 0.8),  
        panel.grid.minor=element_line(colour='purple'),  
        panel.grid.major=element_line(colour='orange'))
```

- This plot is hideous, but it gives you the idea; use ?theme to see all options



# Preset themes



## Make your own themes!

- You can modify existing themes in order to create your own

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- Try using `theme_set()` at the start of your script to pre-set the theme for the rest of the script

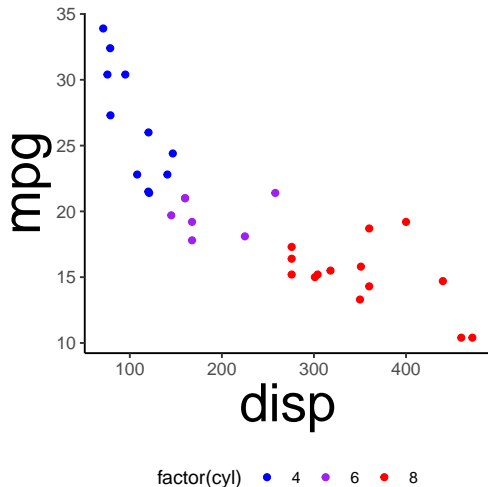
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```
myTheme <- theme_classic() + #Existing theme  
  #Makes axis text bigger  
  theme(axis.title=element_text(size=30),  
        axis.text=element_text(size=10),  
        legend.position='bottom')  
#Sets up this theme as "default"  
theme_set(myTheme)
```

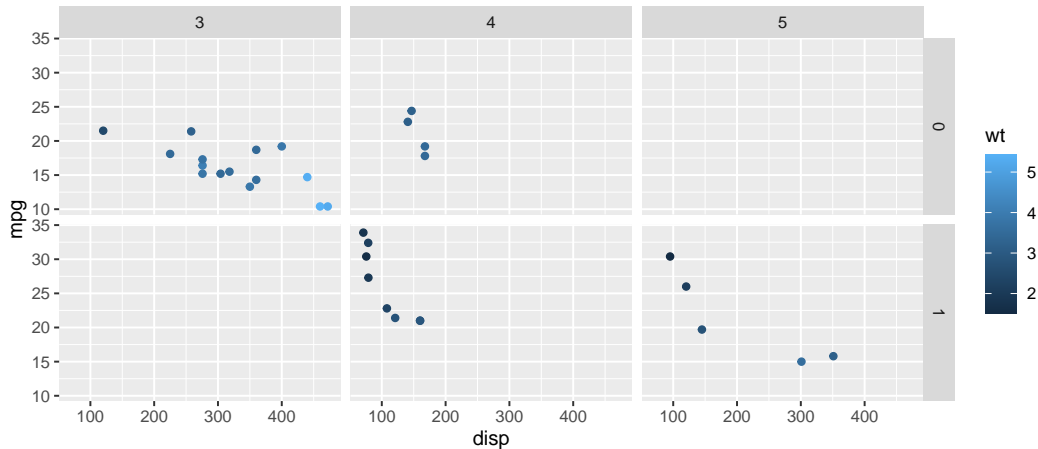




## Complex plots - facets

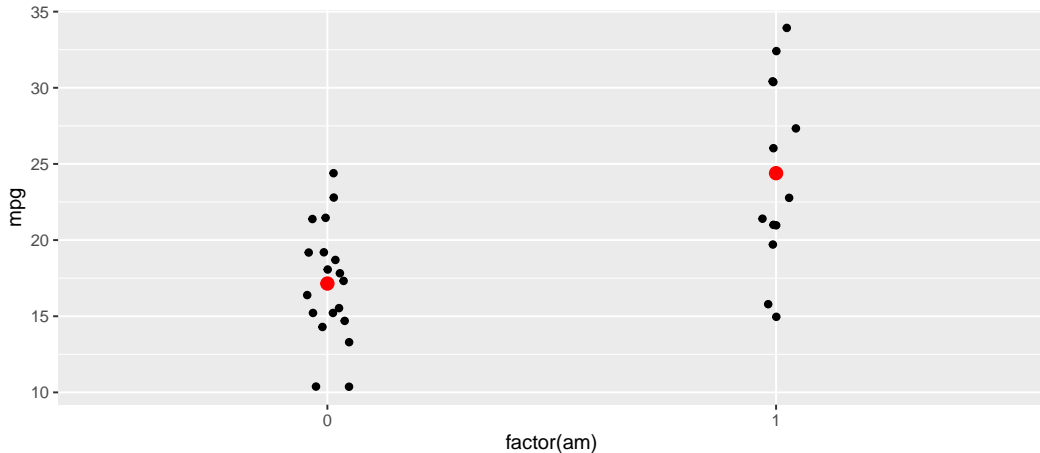
- You can break up the plot into smaller facets that are mapped to a given variable

```
ggplot(mtcars, aes(x=disp, y=mpg)) + geom_point(aes(col=wt)) +  
  facet_grid(factor(am) ~ factor(gear))
```



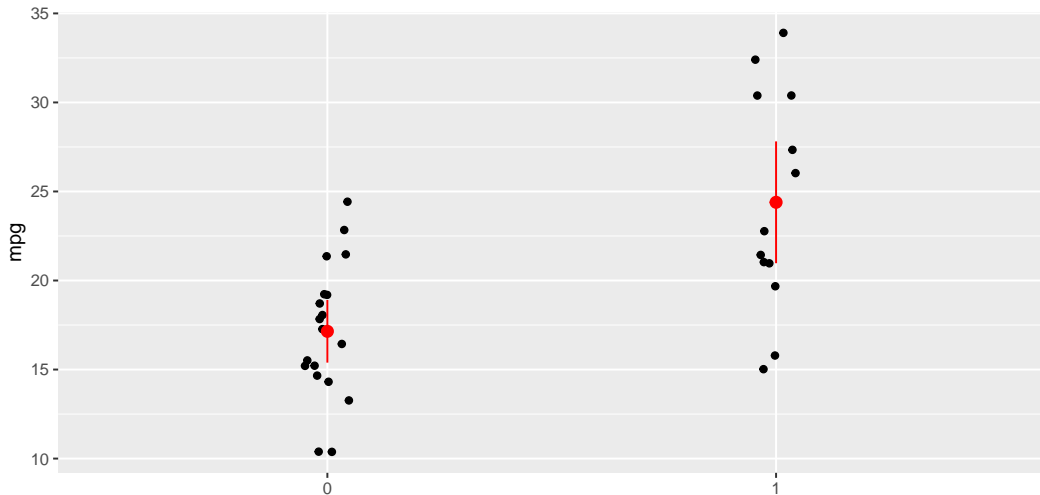
## Complex plots - summary statistics (mean)

```
ggplot(mtcars, aes(x=factor(am), y=mpg)) +  
  geom_point(position=position_jitter(width=0.05)) + #Adds noise to data in x-dimension  
  geom_point(stat='summary', fun=mean, col='red', size=3) #Mean only
```



## Complex plots - summary statistics (mean + SD)

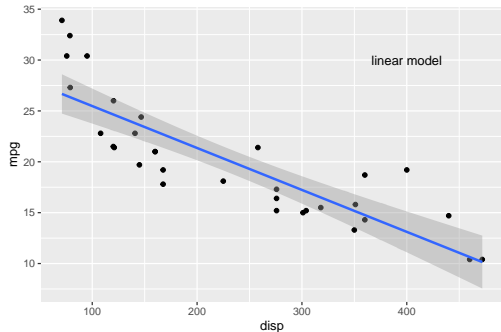
```
ggplot(arrange(mtcars, am, disp), aes(x=factor(am), y=mpg)) +  
  geom_point(position=position_jitter(width=0.05)) +  
  geom_pointrange(stat='summary', fun.data=mean_se,  
                 fun.args = list(mult = 2), col='red') #Mean + 2 SE
```



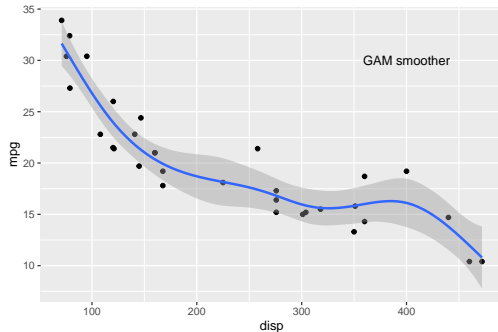
# Complex plots - smoothers

- You can add `lm` (or other model) predictions to your plots:

```
ggplot(mtcars, aes(x=displacement, y=mpg)) +  
  geom_point() +  
  geom_smooth(method='lm', formula=y~x)
```



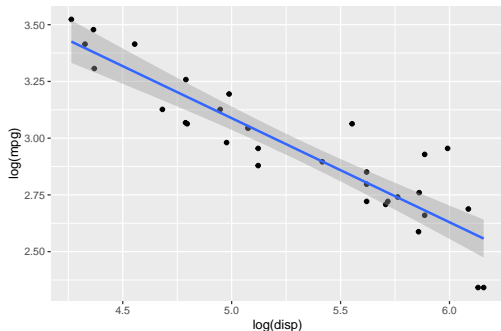
```
ggplot(mtcars, aes(x=displacement, y=mpg)) +  
  geom_point() +  
  geom_smooth(method='gam', formula=y~s(x))
```



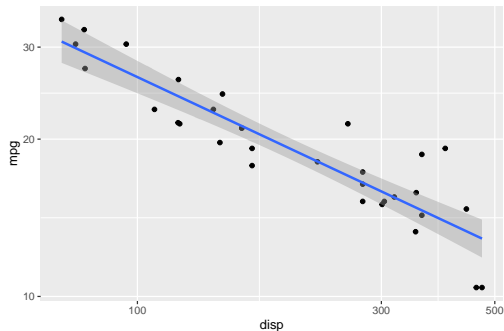
# Complex plots - transformations

- You can show transformed data OR you can transform the axes themselves using `scale_*_log10` (x or y axis)

```
ggplot(mtcars, aes(x=log(displacement), y=log(mpg))) +  
  geom_point() +  
  geom_smooth(method='lm', formula=y~x)  
# Harder to interpret, because people can't  
# usually do log(x) in their head
```



```
ggplot(mtcars, aes(x=displacement, y=mpg)) +  
  geom_point() +  
  geom_smooth(method='lm', formula=y~x) +  
  scale_x_log10() + scale_y_log10()  
# sqrt is also popular
```



## Things to remember:

- Simpler plots are often better. Try to keep it to 3 aesthetics per panel. Avoid 3D plots.

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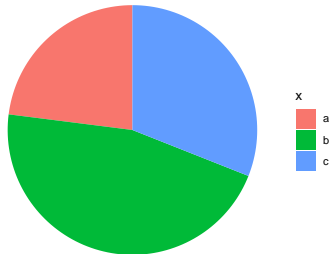
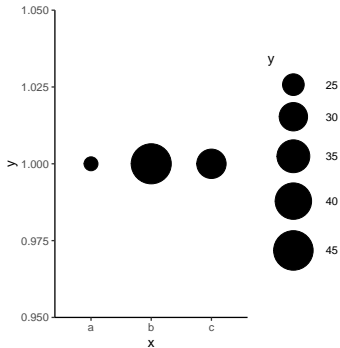
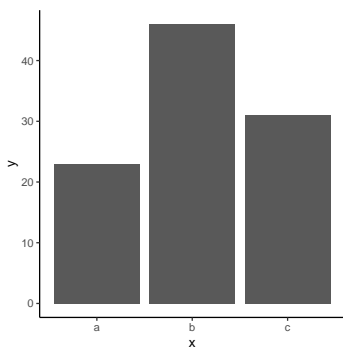
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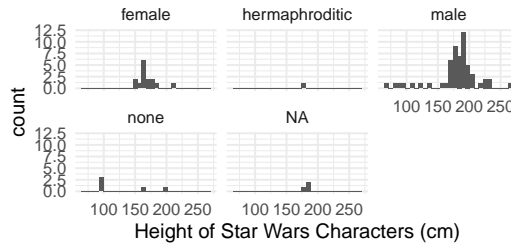
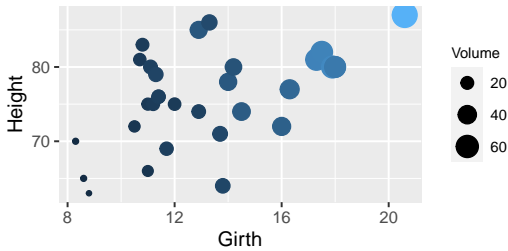
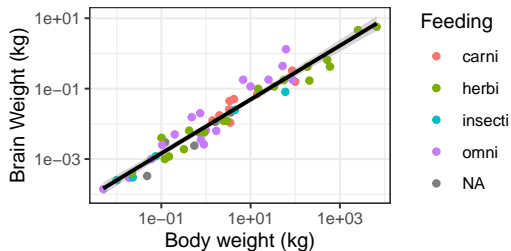
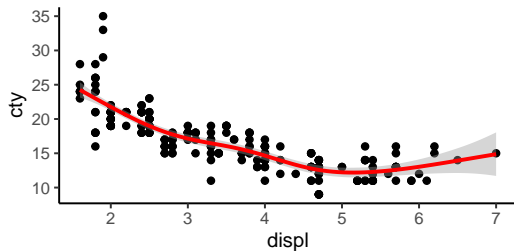
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## A challenger approaches:

Make these figures! Datasets are found in `mpg`, `msleep`, `trees`, and `starwars` (built into the `ggplot2` and `dplyr` packages)



## Final remarks

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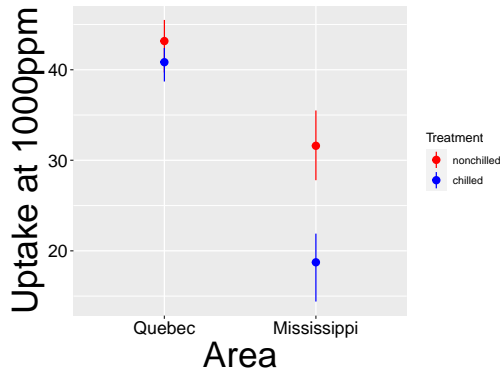
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- Example: filtered summary plot

```
#Code for dplyr begins here
CO2 %>% filter(conc==1000) %>%
  group_by(Type,Treatment) %>%
  summarize(meanUp=mean(uptake),
            maxUp=max(uptake),
            minUp=min(uptake)) %>%
#Code for ggplot begins here
ggplot(aes(x=Type,col=Treatment))+
  geom_pointrange(aes(y=meanUp,
                    ymax=maxUp,
                    ymin=minUp))+
  labs(x='Area',y='Uptake at 1000ppm')+
  scale_colour_manual(values=c('red','blue'))
```





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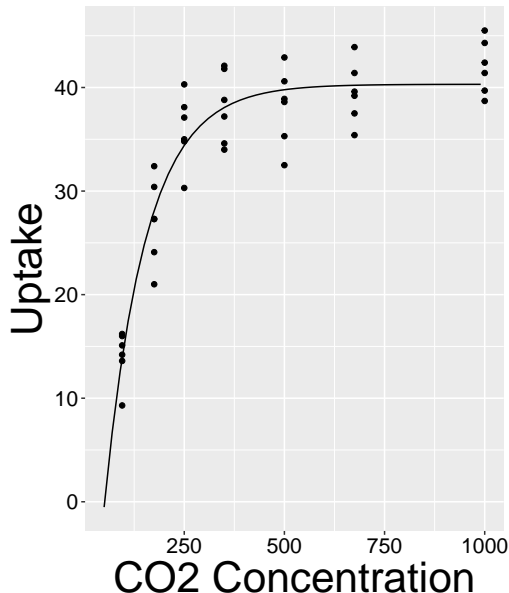
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- Example: nonlinear growth model

```
co2mod <- C02 %>%  
  filter(Type=='Quebec') %>%  
  #Code for nls begins here  
  nls(uptake~SSasymp(conc,A,B,C),  
      start=list(A=30,B=-15,C=-5),data=.)
```

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co2mod <- C02 %>%  
  filter(Type=='Quebec') %>%  
  #Code for nls begins here  
  nls(uptake~SSasymp(conc,A,B,C),  
      start=list(A=30,B=-15,C=-5),data=.)  
  
#Makes predictions along CO2 gradient  
data.frame(conc=seq(50,1000,20)) %>%  
  mutate(predUp=predict(co2mod,newdata=.) ) %>%  
  #Code for ggplot begins here  
  ggplot(aes(conc,predUp))+  
  geom_line()+ #Data from prediction line  
  #CO2 data  
  geom_point(data=filter(C02,Type=='Quebec'),  
            aes(conc,uptake))+  
  labs(x='CO2 Concentration',y='Uptake')
```



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Using that dataset that you acquired:

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Using that dataset that you acquired:

- ① Get some summary statistics for your data (e.g. group means, SDs) using `dplyr`
- ② Make a “presentation quality” plot of some of your data
- ③ Make the ugliest, most unreadable plot in human history. A prize will be awarded for the worst!