# Statistics II

## Week 2: **Causes & Effects**

# Content for Today

1. Brief review of core concepts from lecture
2. Creating plots with `ggplot2`
3. Creating and plotting simulated data
4. Plotting DAGs with `ggdag`

# Lecture Review

# Potential Outcomes Framework

**Key concept:** Every individual in a sample could *theoretically* be exposed to two states with different potential outcomes. However, we can only ever observe one state. The other will always be a counterfactual, meaning we cannot observe causal effects at the individual level.

Therefore, we look at averages:

**ATE:** Expected mean value for those in the treatment group minus the expected mean value for those same individuals, had they not been treated.

**NATE:** The difference in the sample means on the observed outcome variable Y for the observed treatment and control groups

# Potential Outcomes Framework

**For example:** If we compared the earnings of those who went to university with those who did not, the NATE of education would be the difference between the two group means.

This is naive because it does not consider the counterfactual - how much would the group with university have made without it?

# Estimating Bias

We can define the ATE as a weighted average of the ATT and ATC:

**ATT**: The expected mean for those in the treatment group *with* treatment, minus the expected mean of those in the treatment group *without* treatment.

**ATC**: The expected mean for those in the control group *with* treatment, minus the expected mean of those in the control group *without* treatment.

$$\mathrm{ATE} = \pi \mathrm{ATT} + (1 - \pi)\mathrm{ATC}$$

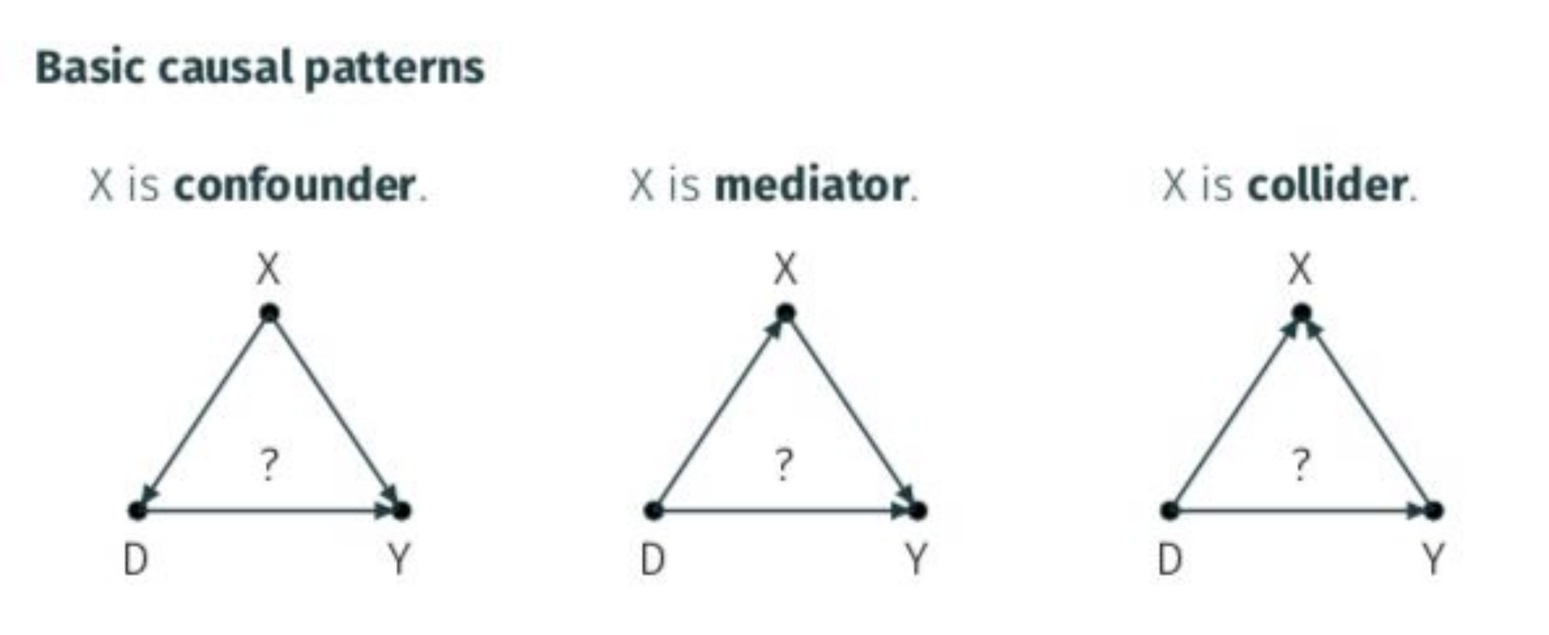
Where $\pi$ is the proportion of subjects under treatment

# Estimating Bias

**Total bias of NATE** as an estimate of ATE is simply NATE − ATE

It is made up of the **baseline bias** (difference in average outcome without treatment for the treatment and control groups) and **differential treatment effect bias** (the difference in the average treatment effect between the treatment and control groups, weighted by the proportion of the population in the control group).

# Causal Graphs/DAGs



Basic causal patterns

X is **confounder**.

X is **mediator**.

X is **collider**.

# Causal Graphs/DAGs

**Back-door path**: Any path between the causal variable and the outcome variable that begins with an arrow that points into the causal variable.

Satisfying the **backdoor criterion** just means you closed all the backdoor paths.

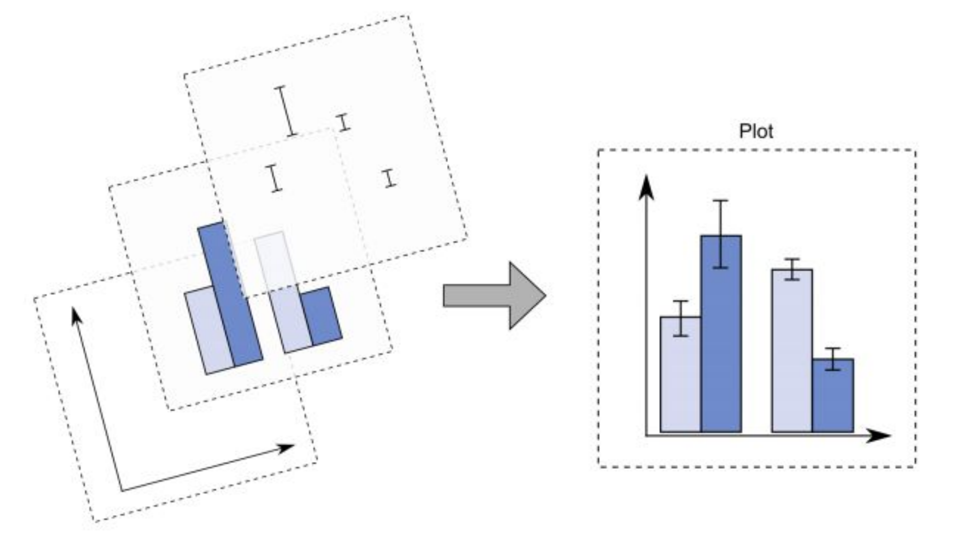
The key goal of a conditioning strategy is not to adjust for any particular confounder, but rather to remove the portion of the total association between D and Y that is non-causal.

# Questions?

# Plotting with `ggplot2`

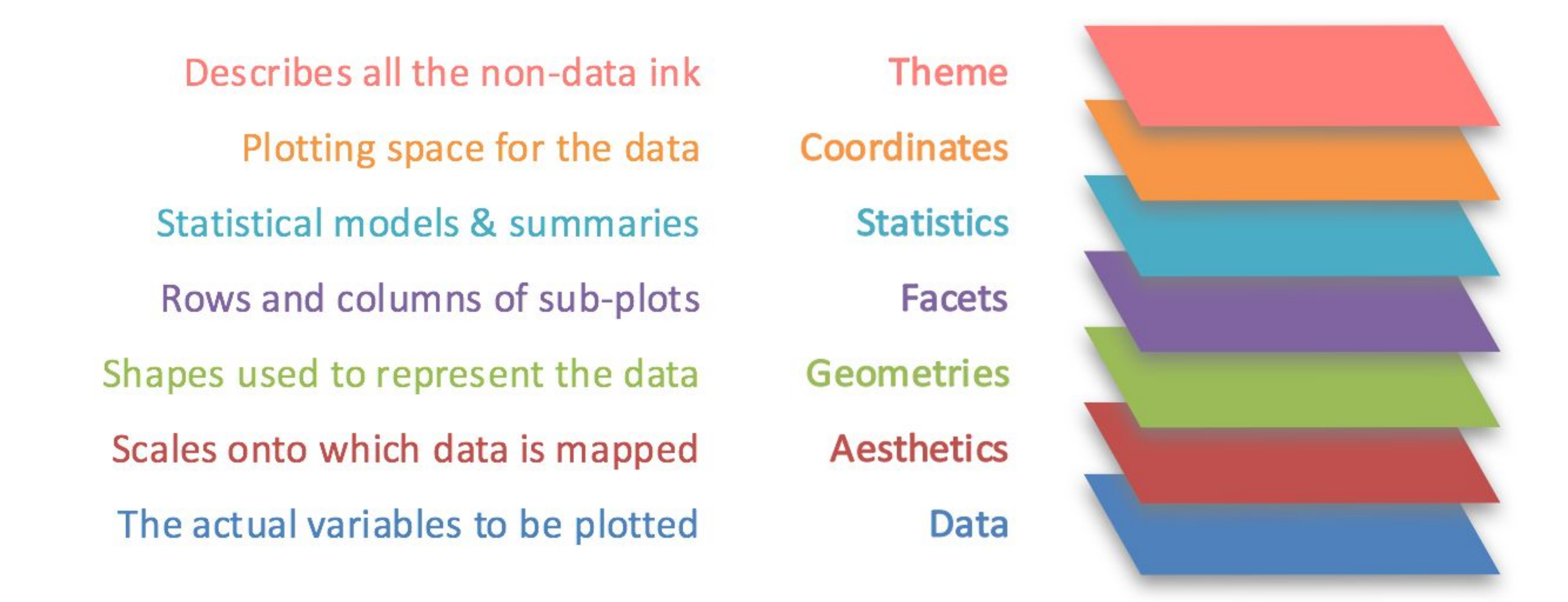
# ggplot2

In `ggplot2`, a graph is made up of a series of layers



Download the cheat sheet: [https://tinyurl.com/h5o9tfq](https://tinyurl.com/h5o9tfq)

# ggplot2



| | |
|---|---|
| Describes all the non-data ink | Theme |
| Plotting space for the data | Coordinates |
| Statistical models & summaries | Statistics |
| Rows and columns of sub-plots | Facets |
| Shapes used to represent the data | Geometries |
| Scales onto which data is mapped | Aesthetics |
| The actual variables to be plotted | Data |

# ggplot2

**Geometric objects** are the visual elements such as bars and points: **`geom()`**

- There are many kinds of geoms, such as scatterplots (`geom_point`) or barplots (`geom_bar`)

The appearance and location of these geoms (such as size and color) are controlled by the **aesthetics properties**: `aes()`

- The variables you want to plot are are referred to here.

```
myGraph <- ggplot(data,
                  aes(x = variable_for_x_axis,
                      y = variable_for_y_axis)) +
                  geom()
```

# ggplot2

## Types of Geoms:

Scatterplot: `geom_point()`

Histogram: `geom_histogram()`

Barplot: `geom_bar()`

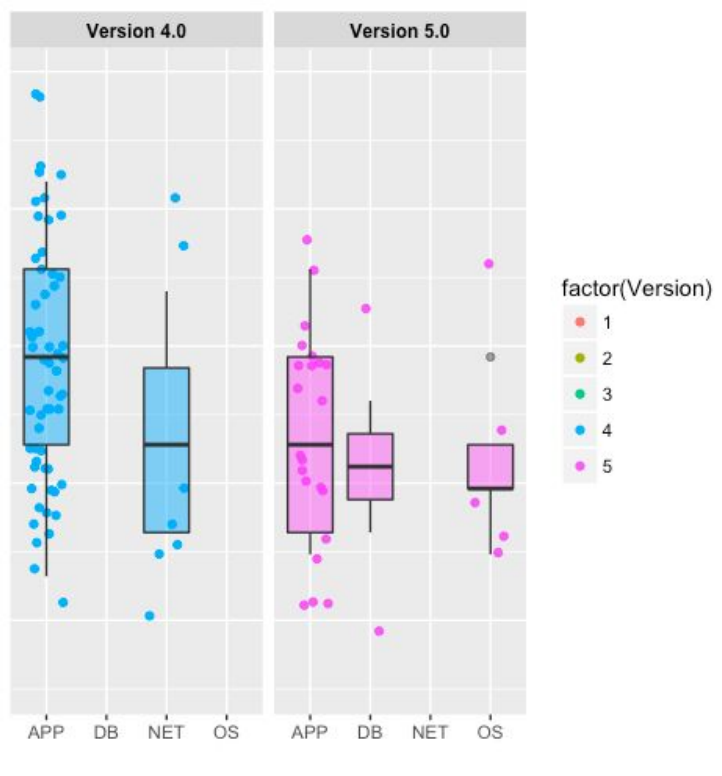
Boxplot: `geom_boxplot()`

Density: `geom_density()`

Adding a “linear regression” line:

```
geom_smooth(model = lm)
```

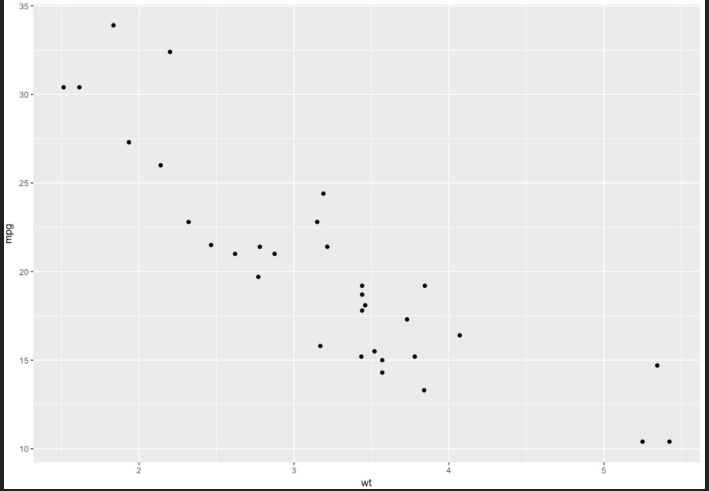
Or a combination of multiple.



# ggplot2

Using the build-in `mtcars` data frame, we can plot a basic scatterplot:

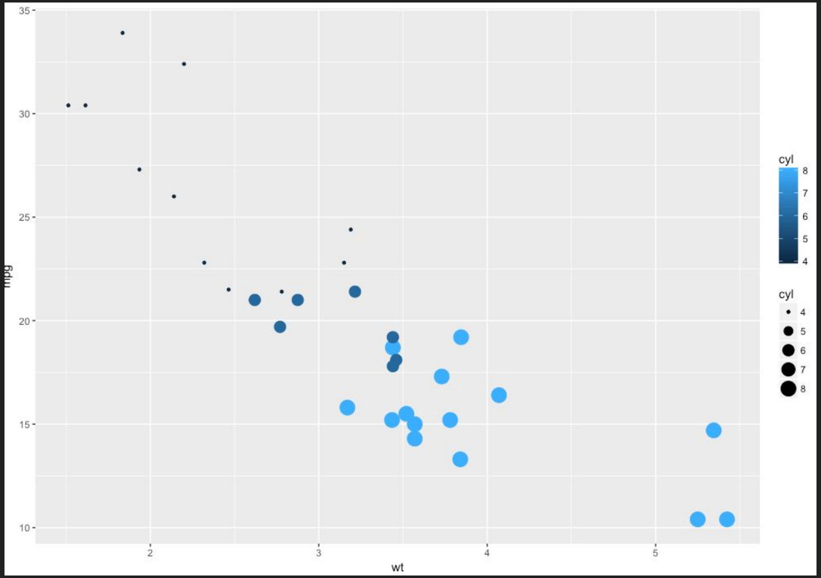
```
scatterplot <- ggplot(
    data = mtcars,
    aes(x = wt, y = mpg)) +
  geom_point()

print(scatterplot)
```



# ggplot2

From here we can add extra design elements, like changing the color and size of the points based on cylinder size:

```
scatterplot <- ggplot(
    data = mtcars,
    aes(x = wt,
        y = mpg,
        col = cyl,
        size = cyl)) +
  geom_point()
```



# ggplot2

## There are lots of other things we can do, too!

Change the transparency using `alpha` and a number from 0-1: ex. `alpha = 0.6`

Add a theme: ex. `geom_bar() + theme_bw()`

Add labels and titles: ex. `+ xlab('X label')+ ylab('Y label') + ggtitle(' Title')`

Change the size and shape of lines, points, etc.

Zoom in on a certain part of a graph

And more :)