

# **PSY 503: Foundations of Statistical Methods in Psychological Science**

**LAB: Joins, Broom,  
Regression Intro**

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Zoom & 311 PSH (Princeton University)

1st October, 2025

# ID / Primary key

Customers			
	ID	Company	First Name
[+]	1	Company A	Anna
[+]	2	Company B	Antonio
[+]	3	Company C	Thomas

Orders			
	Order ID	Customer ID	Employee
[+]	44		1 Nancy Freehafer
[+]	71		1 Nancy Freehafer
[+]	36		3 Mariya Sergienko

# ID / Primary key

- a column that is distinct for each record
  - SSN
  - Princeton NetID
  - Username
  - , etc.

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  - E.g.
    - Govt Source A: COVID-19 daily case counts by region
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  - **Join:** For analyzing the correlation between vaccination rates and case numbers

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# ID / Primary key

- a column that is distinct for each record
  - SSN
  - Princeton NetID
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  - , etc.
- Seldom are all necessary data in a single dataset
  - E.g. Psychology experiment
    - A: Demographic information
    - B: Cognitive Tests data
  - **Join:** To get the complete picture and to look at association with demographic information

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# Joins

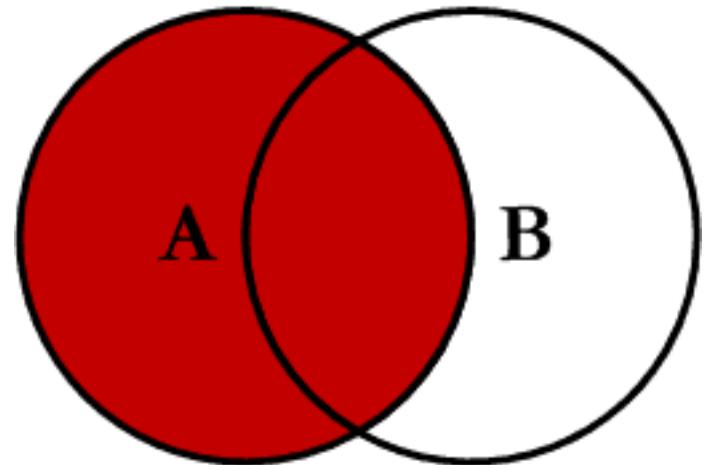
- Different ways to merge dataframes
- Around one or more identifying variables
- Interface:
  - Input: Two dataframes
  - Output: One dataframe

# Joins

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- Around one or more identifying variables
- Interface:
  - Input: Two dataframes
  - Output: One dataframe  
(different join types keep different rows)

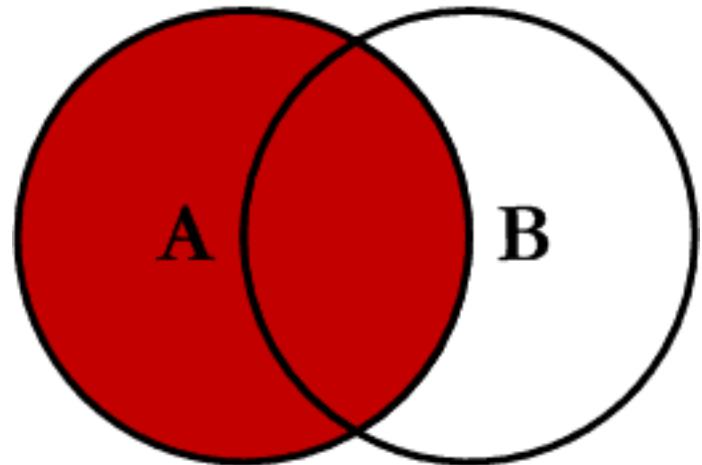
# Left Join

- Keep all of Left Data



# Left Join

- Keep all of Left Data
- Result has same number of rows as Data on the Left



# Left Join

LEFT

JOIN

- Keep all of Left Data
- Result has same number of rows as Data on the Left



# Left Join (Exercise)

```
```{r}
# Create sample dataframe A
df_a <- tibble(
  ID = c(1, 2, 3, 4, 5),
  Name = c("Alice", "Bob", "Charlie", "David", "Eve"),
  Age = c(25, 30, 35, 40, 45)
)

df_a
```

A tibble: 5 × 3

	ID	Name	Age
	<dbl>	<chr>	<dbl>
1	1	Alice	25
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1	Alice	25
2	Bob	30
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4	David	40
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```
```{r}
# Create sample dataframe B
df_b <- tibble(
  ID = c(2, 4, 6, 8),
  City = c("New York", "Los Angeles", "Chicago",
  "Houston"),
  Salary = c(50000, 60000, 55000, 65000)
)

df_b
```

A tibble: 4 × 3

ID	City	Salary
<dbl>	<chr>	<dbl>
2	New York	50000
4	Los Angeles	60000
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# Left Join (Exercise)

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ID	Name	Age
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1	Alice	25
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```{r}
# Perform left join
result <- df_a %>%
  left_join(df_b, by = "ID")

result
```

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```{r}
# Perform left join
result <- df_a %>%
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result
```

A tibble: 5 × 5

ID	Name	Age	City	Salary
<dbl>	<chr>	<dbl>	<chr>	<dbl>
1	Alice	25	NA	NA
2	Bob	30	New York	50000
3	Charlie	35	NA	NA
4	David	40	Los Angeles	60000
5	Eve	45	NA	NA

```
```{r}
# Create sample dataframe B
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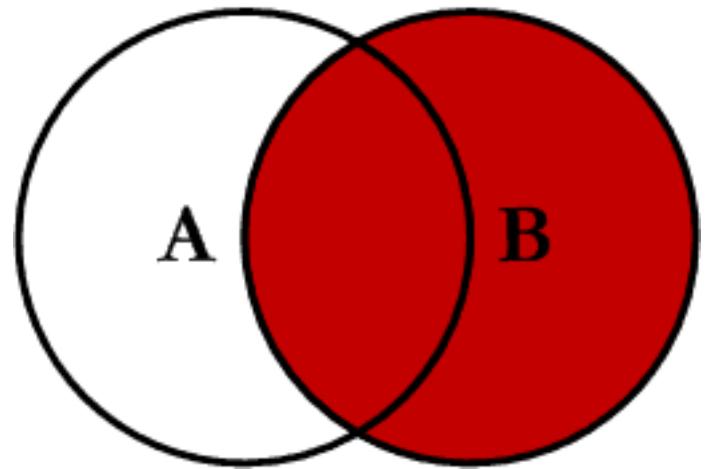
df_b
```

A tibble: 4 × 3

ID	City	Salary
<dbl>	<chr>	<dbl>
2	New York	50000
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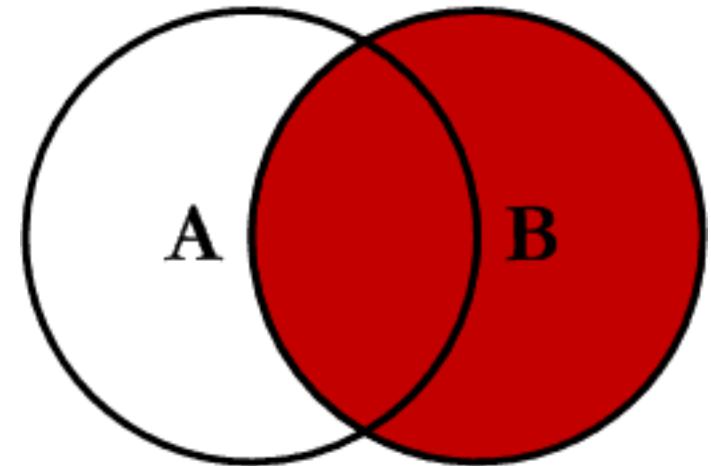
# Right Join

- Keeps all of Right Data



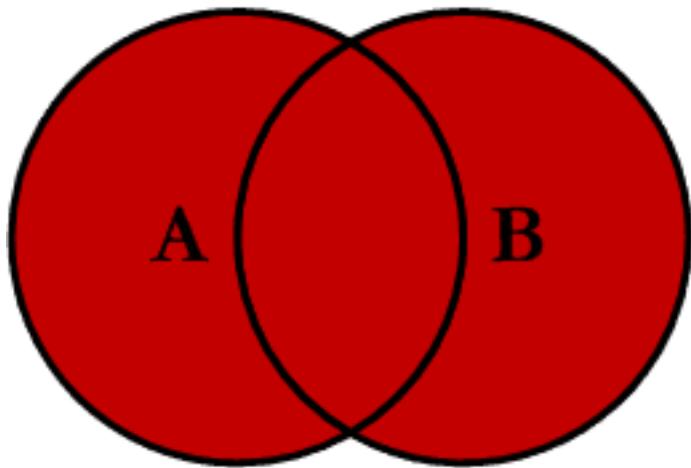
# Right Join

- Keeps all of Right Data
- Same as left join with the sides of the data swapped
- Rarely used. Left join is the norm.  
(Best to ignore this command)



# Full Join

- Keep all of Left and Right data
  - Even the ones where there is no overlap



# Full Join (Exercise)

```
```{r}
# Create sample dataframe A
df_a <- tibble(
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)

df_a
```

A tibble: 5 × 3

	ID	Name	Age
	<dbl>	<chr>	<dbl>
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df_a
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A tibble: 5 × 3

ID	Name	Age
<dbl>	<chr>	<dbl>
1	Alice	25
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df_b
```

A tibble: 4 × 3

ID	City	Salary
<dbl>	<chr>	<dbl>
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A tibble: 5 × 3

ID	Name	Age
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1	Alice	25
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```
```{r}
# Perform right join
result <- df_a %>%
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result
```

```
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```{r}
# Perform right join
result <- df_a %>%
  full_join(df_b, by = "ID")
```

result

A tibble: 7 × 5

ID	Name	Age	City	Salary
<dbl>	<chr>	<dbl>	<chr>	<dbl>
1	Alice	25	NA	NA
2	Bob	30	New York	50000
3	Charlie	35	NA	NA
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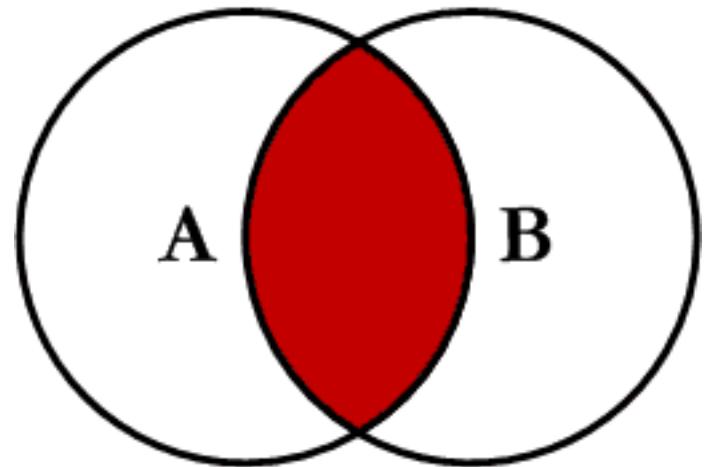
df\_b

A tibble: 4 × 3

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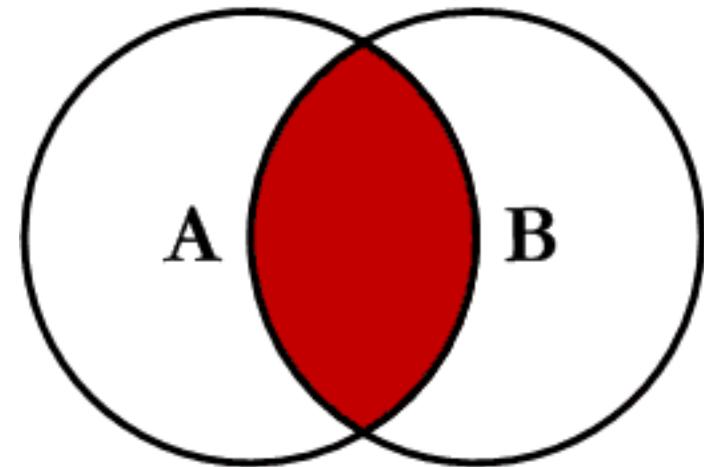
# Inner Join

- Keep only data where id is present in both left and right datasets.



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- Result has same number of rows as overlapping *join by variable*.



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LEFT

A
B
F
H
K
L

JOIN

A
F
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F
G
L

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)

df_a
```
A tibble: 5 × 3
  ID   Name    Age
  <dbl> <chr>  <dbl>
1     1 Alice    25
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A tibble: 5 × 3

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A tibble: 4 × 3

ID	City	Salary
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```
```{r}
# Perform right join
result <- df_a %>%
  inner_join(df_b, by = "ID")

result
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A tibble: 4 × 3

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```
```{r}
# Perform right join
result <- df_a %>%
  inner_join(df_b, by = "ID")

result
```

A tibble: 2 × 5

ID	Name	Age	City	Salary
<dbl>	<chr>	<dbl>	<chr>	<dbl>
2	Bob	30	New York	50000
4	David	40	Los Angeles	60000

```
```{r}
# Create sample dataframe B
df_b <- tibble(
  ID = c(2, 4, 6, 8),
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)

df_b
```

A tibble: 4 × 3

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# Mutating Joins

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  - After the join, you have variables from both tables in the output.
  - number of rows change based on if there duplicates

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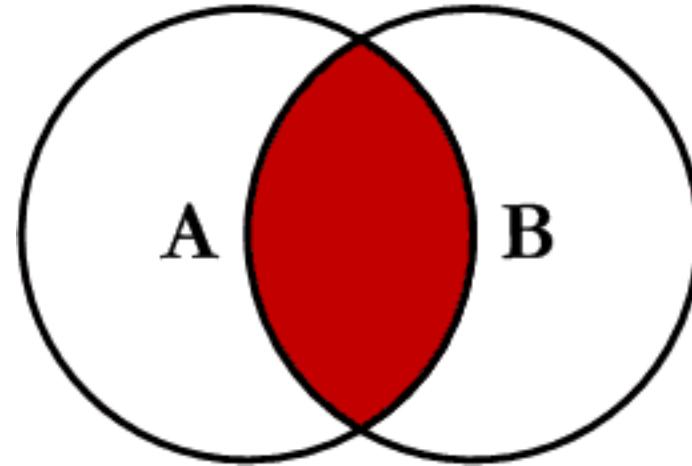
- “mutate” adds ***columns***
  - After the join, you have variables from both tables in the output.
- number of rows change based on if there duplicates
- Examples
  - inner join
  - left\_join
  - (right\_join)
  - full\_join

# Filtering joins

- No new columns are added
  - Output always has only columns from left(x) dataset
- `semi_join`
  - Keep rows in **x** that have matches in **y**
  - No duplication if multiple matches in **y**

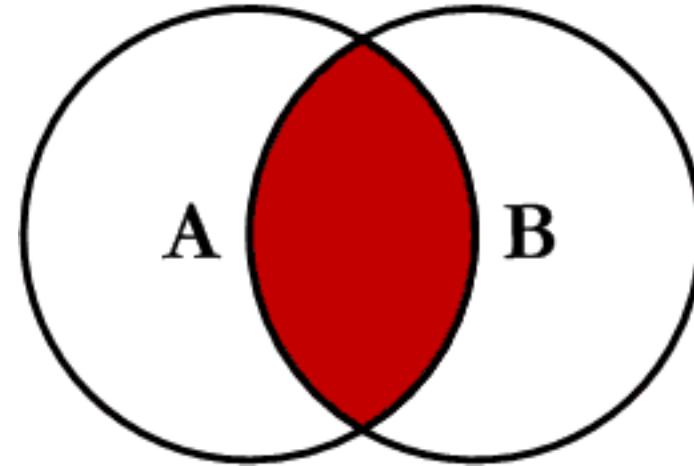
# Filtering joins

- No new columns are added
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- `semi_join`
  - Keep rows in `x` that have matches in `y`
  - No duplication if multiple matches in `y`
- `semi_join` vs `inner_join`?



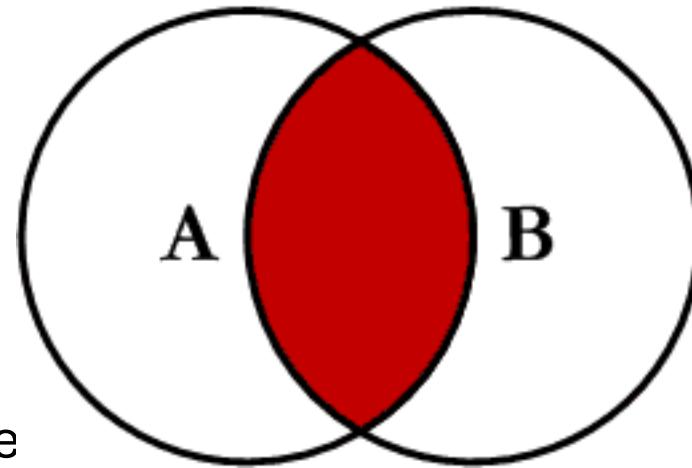
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  - No duplication if multiple matches in `y`
- `anti_join`



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- No new columns are added
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- `semi_join`
  - Keep rows in **x** that have matches in **y**
  - No duplication if multiple matches in **y**
- `anti_join`
  - keeps only rows in **x** that **do not** have a match in **y**



**Semi Join**

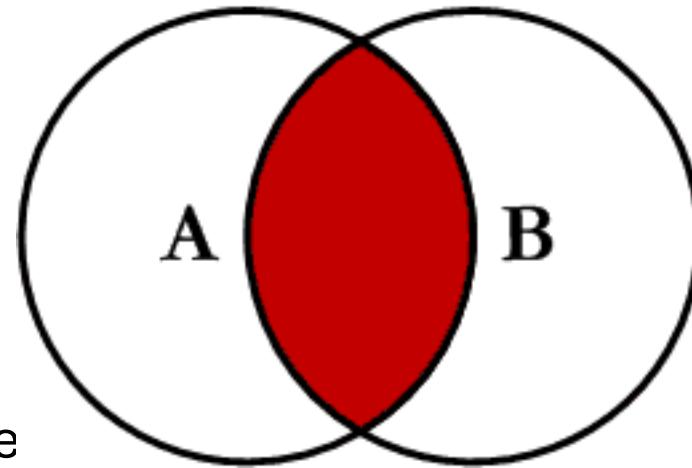


**Anti Join**



# Filtering joins

- No new columns are added
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- `semi_join`
  - Keep rows in **x** that have matches in **y**
  - No duplication if multiple matches in **y**
- `anti_join`
  - keeps only rows in **x** that **do not** have a match in **y**



**Semi Join**



**Anti Join**



Join	English
<b>Left join</b>	“Keep all of <b>x</b> , add what matches from <b>y</b> .”
<b>Right join</b>	“Keep all of <b>y</b> , add what matches from <b>x</b> (but really just swap and do a left join).”
<b>Inner join</b>	“Keep the overlap of both”
<b>Full join</b>	“Keep the union from both”
<b>Semi join</b>	“Keep the parts of <b>x</b> that have a match in <b>y</b> — <b>but don’t bring along y columns</b> ”
<b>Anti join</b>	“Keep the parts of <b>x</b> that have <b>no</b> match in <b>y</b> — <b>don’t worry about y columns</b> ”

# Common pitfalls

- join key isn't actually unique in one or both datasets
- If you don't specify “by =”
- NAs
  - losing information unintentionally [inner join]
  - unmatched cases get NAs in the new columns [left/full join]
    - *causing later issues*
- forgetting join direction matters

# Tips

- ensure uniqueness of your key in both tables, and use the appropriate join
- be explicit in “by =”
- validate and check results after joining.

# Broom

- Part of tidyverse
- “The broom package takes the messy output of built-in functions in R, such as `lm`, `nls`, or `t.test`, and turns them into tidy tibbles.”
- `broom` provides three verbs to make it convenient to interact with model objects:
  - `tidy()` summarizes information about model components
  - `glance()` reports information about the entire model
  - `augment()` adds informations about observations to a dataset

# tidy()

- “constructs a tibble that summarizes the model’s statistical findings. This includes coefficients and p-values for each term in a regression,...”

```
lmfit <- lm(mpg ~ wt, mtcars)
lmfit

##
## Call:
## lm(formula = mpg ~ wt, data = mtcars)
##
## Coefficients:
## (Intercept)          wt
##           37.285      -5.344

summary(lmfit)

##
## Call:
## lm(formula = mpg ~ wt, data = mtcars)
##
## Residuals:
##    Min     1Q   Median     3Q    Max 
## -4.5432 -2.3647 -0.1252  1.4096  6.8727 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 37.2851    1.8776  19.858 < 2e-16 ***
## wt          -5.3445    0.5591  -9.559 1.29e-10 ***
## ---        
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Residual standard error: 3.046 on 30 degrees of freedom
## Multiple R-squared:  0.7528, Adjusted R-squared:  0.7446 
## F-statistic: 91.38 on 1 and 30 DF,  p-value: 1.294e-10
```

# tidy()

- “constructs a tibble that summarizes the model’s statistical findings. This includes coefficients and p-values for each term in a regression,...”

```
lmfit <- lm(mpg ~ wt, mtcars)  
lmfit
```

```
library(broom)  
tidy(lmfit)
```

```
## # A tibble: 2 × 5  
##   term      estimate std.error statistic  p.value  
##   <chr>        <dbl>     <dbl>      <dbl>    <dbl>  
## 1 (Intercept)  37.3      1.88     19.9  8.24e-19  
## 2 wt         -5.34     0.559     -9.56  1.29e-10
```

# augment()

- Instead of viewing the coefficients, you might be interested in the fitted values and residuals for each of the original points in the regression.
- For this, use `augment`, which augments the original data with information from the model:

```
lmfit <- lm(mpg ~ wt, mtcars)  
lmfit
```

```
augment(lmfit)
```

```
## # A tibble: 32 × 9  
##   .rownames     mpg      wt .fitted .resid    .hat .sigma .cooksD .std.resid  
##   <chr>     <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>  
## 1 Mazda RX4    21     2.62    23.3 -2.28  0.0433  3.07 1.33e-2 -0.766  
## 2 Mazda RX4...   21     2.88    21.9 -0.920 0.0352  3.09 1.72e-3 -0.307  
## 3 Datsun 710   22.8    2.32    24.9 -2.09  0.0584  3.07 1.54e-2 -0.706  
## 4 Hornet 4 D...  21.4    3.22    20.1  1.30  0.0313  3.09 3.02e-3  0.433  
## 5 Hornet Spo...  18.7    3.44    18.9 -0.200 0.0329  3.10 7.60e-5 -0.066  
## 6 Valiant       18.1    3.46    18.8 -0.693 0.0332  3.10 9.21e-4 -0.231  
## 7 Duster 360   14.3    3.57    18.2 -3.91  0.0354  3.01 3.13e-2 -1.31  
## 8 Merc 240D     24.4    3.19    20.2  4.16  0.0313  3.00 3.11e-2  1.39  
## 9 Merc 230      22.8    3.15    20.5  2.35  0.0314  3.07 9.96e-3  0.784  
## 10 Merc 280    19.2    3.44    18.9  0.300 0.0329  3.10 1.71e-4  0.100  
## # i 22 more rows
```

# glance()

- several summary statistics are computed for the entire regression, such as R<sup>2</sup> and the F-statistic. These can be accessed with the `glance` function

```
lmfit <- lm(mpg ~ wt, mtcars)  
lmfit
```

```
glance(lmfit)
```

```
## # A tibble: 1 × 12  
##   r.squared adj.r.squared sigma statistic p.value    df logLik     AIC  
##       <dbl>        <dbl> <dbl>    <dbl>    <dbl>    <dbl> <dbl> <dbl>  
## 1     0.753        0.745  3.05    91.4 1.29e-10      1 -80.0    166.  
## # i 4 more variables: BIC <dbl>, deviance <dbl>, df.residual <int>,  
## #   nobs <int>
```