Data Science for Environmental Health

Manipulating Data in R

Recap of Data Cleaning

- `is.na()`,`any(is.na())`, `all(is.na())`,`count()`, and functions from `naniar` like `gg_miss_var()` and `miss_var_summary` can help determine if we have `NA` values
- `miss_var_which()` can help you drop columns that have any missing values.
- `filter()` automatically removes `NA` values
- `drop_na()` can help you remove `NA` values
- `NA` values can change your calculation results
- think about what `NA` values represent - don't drop them if you shouldn't
- `replace_na()` will replace `NA values with a particular value

Recap of Data Cleaning

- `case_when()` can recode **entire values** based on conditions
  - remember `case_when()` needs `TRUE ~ variable` to keep values that aren't specified by conditions, otherwise will be `NA`
- `stringr` package has great functions for looking for specific **parts of values** especially `filter()` and `str_detect()` combined
  - also has other useful string manipulation functions like `str_replace()` and more!
  - `separate()` can split columns into additional columns
  - `unite()` can combine columns

[Cheatsheet]

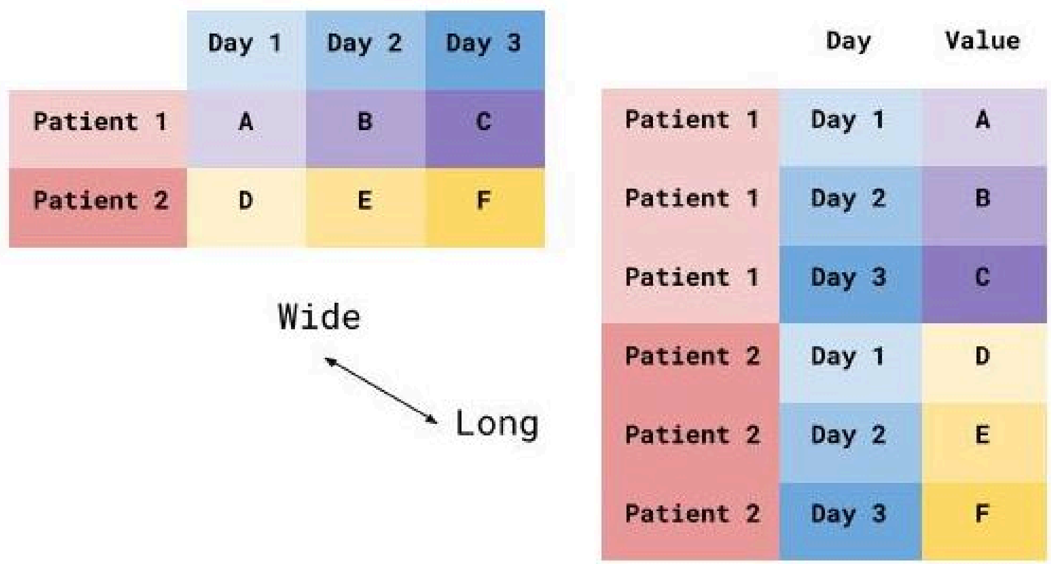
Manipulating Data

In this module, we will show you how to:

1. Reshape data from wide to long
2. Reshape data from long to wide
3. Merge Data/Joins

What is wide/long data?

Data is wide or long **with respect** to certain variables.



What is wide/long data?

Data is stored *differently* in the tibble.

Wide: has many columns

```
# A tibble: 1 × 4
  State   June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>            <dbl>         <dbl>           <dbl>
1 Alabama          0.516         0.514           0.511
```

Long: column names become data

```
# A tibble: 3 × 3
  State   name            value
  <chr>   <chr>           <dbl>
1 Alabama June_vacc_rate  0.516
2 Alabama May_vacc_rate   0.514
3 Alabama April_vacc_rate 0.511
```

What is wide/long data?

Wide: multiple columns per individual, values spread across multiple columns

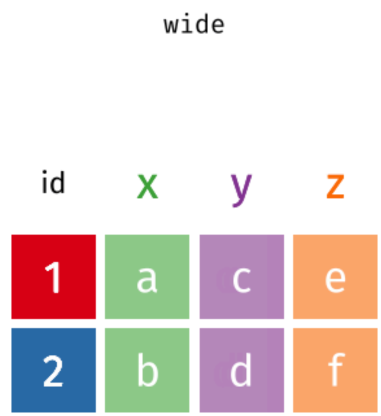
```
# A tibble: 2 × 4
  State   June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>            <dbl>         <dbl>           <dbl>
1 Alabama          0.516         0.514           0.511
2 Alaska           0.627         0.626           0.623
```

Long: multiple rows per observation, a single column contains the values

```
# A tibble: 6 × 3
  State   name            value
  <chr>   <chr>           <dbl>
1 Alabama June_vacc_rate  0.516
2 Alabama May_vacc_rate   0.514
3 Alabama April_vacc_rate 0.511
4 Alaska  June_vacc_rate  0.627
5 Alaska  May_vacc_rate   0.626
6 Alaska  April_vacc_rate 0.623
```

What is wide/long data?

https://github.com/gadenbuie/tidyexplain/blob/main/images/tidyr-pivoting.gif



Why do we need to switch between wide/long data?

Wide: **Easier for humans to read**

```
# A tibble: 2 × 4
  State   June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>            <dbl>         <dbl>           <dbl>
1 Alabama          0.516         0.514           0.511
2 Alaska           0.627         0.626           0.623
```

Long: **Easier for R to make plots & do analysis**

```
# A tibble: 6 × 3
  State   name            value
  <chr>   <chr>           <dbl>
1 Alabama June_vacc_rate  0.516
2 Alabama May_vacc_rate   0.514
3 Alabama April_vacc_rate 0.511
4 Alaska  June_vacc_rate  0.627
5 Alaska  May_vacc_rate   0.626
6 Alaska  April_vacc_rate 0.623
```

Pivoting using `tidyr` package

`tidyr` allows you to "tidy" your data. We will be talking about:

- `pivot_longer` - make multiple columns into variables, (wide to long)
- `pivot_wider` - make a variable into multiple columns, (long to wide)

The `reshape` command exists. Its arguments are considered more confusing, so we don't recommend it.

You might see old functions `gather` and `spread` when googling. These are older iterations of `pivot_longer` and `pivot_wider`, respectively.

pivot_longer...

Reshaping data from **wide to long**

`pivot_longer()` - puts column data into rows (`tidyr` package)

- First describe which columns we want to "pivot_longer"

```
{long_data} <- {wide_data} %>% pivot_longer(cols = {columns to pivot})
```

Reshaping data from **wide to long**

```
wide_vacc <- read_csv(
  file = "https://daseh.org/data/wide_vacc.csv")
```

```
wide_vacc
```

```
# A tibble: 1 × 3
  June_vacc_rate May_vacc_rate April_vacc_rate
           <dbl>         <dbl>           <dbl>
1          0.516         0.514           0.511
```

```
long_vacc <- wide_vacc %>% pivot_longer(cols = everything())
long_vacc
```

```
# A tibble: 3 × 2
  name            value
  <chr>           <dbl>
1 June_vacc_rate  0.516
2 May_vacc_rate   0.514
3 April_vacc_rate 0.511
```

Reshaping wide to long: Better column names

`pivot_longer()` - puts column data into rows (`tidyr` package)

- First describe which columns we want to "pivot_longer"
- `names_to =` new name for old columns
- `values_to =` new name for old cell values

```
{long_data} <- {wide_data} %>% pivot_longer(cols = {columns to pivot},
                                        names_to = {name for old columns},
                                        values_to = {name for cell values})
```

Reshaping data from **wide to long**

```
wide_vacc
```

```
# A tibble: 1 × 3
  June_vacc_rate May_vacc_rate April_vacc_rate
           <dbl>         <dbl>           <dbl>
1          0.516         0.514           0.511
```

```
long_vacc <- wide_vacc %>% pivot_longer(cols = everything(),
                                        names_to = "Month",
                                        values_to = "Rate")
long_vacc
```

```
# A tibble: 3 × 2
  Month            Rate
  <chr>           <dbl>
1 June_vacc_rate  0.516
2 May_vacc_rate   0.514
3 April_vacc_rate 0.511
```

Newly created column names are enclosed in quotation marks.

Data used: Nitrate exposure

Nitrate exposure by quarter for populations on public water systems in the state of Washington for 1999-2020.

https://daseh.org/data/Nitrate_Exposure_for_WA_Public_Water_Systems_byquarter_da

```
library(dasehr)
wide <- nitrate
head(nitrate)
```

```
# A tibble: 6 × 11
   year quarter pop_on_sampled_PWS `pop_0-3ug/L` `pop_>3-5ug/L` `pop_>5-10ug/L
  <dbl> <chr>                <dbl>         <dbl>          <dbl>           <dbl
1  1999 Q1                  106720         67775              0               3
2  1999 Q2                   85541         55476              0              21
3  1999 Q3                  559137        319252         231186              21
4  1999 Q4                   26995         25969            420
5  2000 Q1                   34793          5904              0               9
6  2000 Q2                  184521        157396              0               3
# ℹ 5 more variables: `pop_>10-20ug/L` <dbl>, `pop_>20ug/L` <dbl>,
#   `pop_on_PWS_with_non-detect` <dbl>, pop_exposed_to_exceedances <dbl>,
#   perc_pop_exposed_to_exceedances <dbl>
```

Mission: Average population exposed by concentration

Let’s imagine we want to see what proportion of population exposed to different nitrate concentrations. Results should look something like:

```
# A tibble: 3 × 2
  conc_cat       avg_prop
  <chr>             <dbl>
1 pop_0-3ug/L    0.593
2 pop_>10-20ug/L 0.000678
3 pop_>20ug/L    0.000129
```

Remove some columns we don’t need

```r
wide <- wide %>%
  select(!ends_with("exceedances"))
wide
```

```
# A tibble: 88 × 9
    year quarter pop_on_sampled_PWS `pop_0-3ug/L` `pop_>3-5ug/L` `pop_>5-10ug/
   <dbl> <chr>                <dbl>         <dbl>          <dbl>          <db
 1  1999 Q1                  106720         67775              0
 2  1999 Q2                   85541         55476              0              2
 3  1999 Q3                  559137        319252         231186              2
 4  1999 Q4                   26995         25969            420
 5  2000 Q1                   34793          5904              0
 6  2000 Q2                  184521        157396              0
 7  2000 Q3                   42081         20407            345
 8  2000 Q4                  407219        358828            995              4
 9  2001 Q1                   90054         49552            150
10  2001 Q2                   83521         43633           2536
# ℹ 78 more rows
# ℹ 3 more variables: `pop_>10-20ug/L` <dbl>, `pop_>20ug/L` <dbl>,
#   `pop_on_PWS_with_non-detect` <dbl>
```

Reshaping data from **wide to long**

```
long <- wide %>%
  pivot_longer(!c(year, quarter, pop_on_sampled_PWS),
               names_to = "conc_cat",
               values_to = "conc_count")
long
```

```
# A tibble: 528 × 5
    year quarter pop_on_sampled_PWS conc_cat                       conc_count
   <dbl> <chr>                <dbl> <chr>                               <dbl>
 1  1999 Q1                  106720 pop_0-3ug/L                         67775
 2  1999 Q1                  106720 pop_>3-5ug/L                            0
 3  1999 Q1                  106720 pop_>5-10ug/L                          32
 4  1999 Q1                  106720 pop_>10-20ug/L                          0
 5  1999 Q1                  106720 pop_>20ug/L                             0
 6  1999 Q1                  106720 pop_on_PWS_with_non-detect          38913
 7  1999 Q2                   85541 pop_0-3ug/L                         55476
 8  1999 Q2                   85541 pop_>3-5ug/L                            0
 9  1999 Q2                   85541 pop_>5-10ug/L                         212
10  1999 Q2                   85541 pop_>10-20ug/L                         60
# ℹ 518 more rows
```

Reshaping data from **wide to long**

Un-pivoted columns (`year`, `quarter`, `pop_on_sampled_PWS`) are still columns.

```
long
```

```
# A tibble: 528 × 5
    year quarter pop_on_sampled_PWS conc_cat                     conc_count
   <dbl> <chr>                <dbl> <chr>                             <dbl>
 1  1999 Q1                  106720 pop_0-3ug/L                       67775
 2  1999 Q1                  106720 pop_>3-5ug/L                          0
 3  1999 Q1                  106720 pop_>5-10ug/L                        32
 4  1999 Q1                  106720 pop_>10-20ug/L                        0
 5  1999 Q1                  106720 pop_>20ug/L                           0
 6  1999 Q1                  106720 pop_on_PWS_with_non-detect        38913
 7  1999 Q2                   85541 pop_0-3ug/L                       55476
 8  1999 Q2                   85541 pop_>3-5ug/L                          0
 9  1999 Q2                   85541 pop_>5-10ug/L                       212
10  1999 Q2                   85541 pop_>10-20ug/L                       60
# ℹ 518 more rows
```

Cleaning up long data

Let’s make the `conc_count` into a proportion.

```
long <- long %>%
  mutate(conc_prop = conc_count / pop_on_sampled_PWS)
long
```

```
# A tibble: 528 × 6
    year quarter pop_on_sampled_PWS conc_cat                conc_count conc_prop
   <dbl> <chr>                <dbl> <chr>                        <dbl>     <dbl>
 1  1999 Q1                  106720 pop_0-3ug/L                  67775  0.635
 2  1999 Q1                  106720 pop_>3-5ug/L                     0  0
 3  1999 Q1                  106720 pop_>5-10ug/L                   32  0.000300
 4  1999 Q1                  106720 pop_>10-20ug/L                   0  0
 5  1999 Q1                  106720 pop_>20ug/L                      0  0
 6  1999 Q1                  106720 pop_on_PWS_with_non-de…      38913  0.365
 7  1999 Q2                   85541 pop_0-3ug/L                  55476  0.649
 8  1999 Q2                   85541 pop_>3-5ug/L                     0  0
 9  1999 Q2                   85541 pop_>5-10ug/L                  212  0.00248
10  1999 Q2                   85541 pop_>10-20ug/L                  60  0.000701
# ℹ 518 more rows
```

Mission: Average population exposed by concentration

Now our data is more tidy, and we can take the averages easily!

```
long %>%
  group_by(conc_cat) %>%
  summarize("avg_prop" = mean(conc_prop))
```

```
# A tibble: 6 × 2
  conc_cat                        avg_prop
  <chr>                              <dbl>
1 pop_0-3ug/L                     0.593
2 pop_>10-20ug/L                  0.000678
3 pop_>20ug/L                     0.000129
4 pop_>3-5ug/L                    0.182
5 pop_>5-10ug/L                   0.0189
6 pop_on_PWS_with_non-detect 0.206
```

Reshaping data from **wide to long**

There are many ways to **select** the columns we want. Check out https://dplyr.tidyverse.org/reference/dplyr_tidy_select.html to look at more column selection options.

pivot_wider...

Reshaping data from **long to wide**

`pivot_wider()` - spreads row data into columns (`tidyr` package)

- `names_from =` the old column whose contents will be spread into multiple new column names.
- `values_from =` the old column whose contents will fill in the values of those new columns.

```
{wide_data} <- {long_data} %>%
  pivot_wider(names_from = {Old column name: contains new column names},
              values_from = {Old column name: contains new cell values})
```

Reshaping data from **long to wide**

```
long_vacc
```

```
# A tibble: 3 × 2
  Month            Rate
  <chr>           <dbl>
1 June_vacc_rate  0.516
2 May_vacc_rate   0.514
3 April_vacc_rate 0.511
```

```
wide_vacc <- long_vacc %>% pivot_wider(names_from = "Month",
                                       values_from = "Rate")
wide_vacc
```

```
# A tibble: 1 × 3
  June_vacc_rate May_vacc_rate April_vacc_rate
           <dbl>         <dbl>           <dbl>
1          0.516         0.514           0.511
```

Reshaping nitrate exposure data

What if we wanted different columns for each quarter?

```
long
```

```
# A tibble: 528 × 6
    year quarter pop_on_sampled_PWS conc_cat                conc_count conc_prop
   <dbl> <chr>                <dbl> <chr>                        <dbl>     <dbl>
 1  1999 Q1                  106720 pop_0-3ug/L                  67775  0.635
 2  1999 Q1                  106720 pop_>3-5ug/L                     0  0
 3  1999 Q1                  106720 pop_>5-10ug/L                   32  0.000300
 4  1999 Q1                  106720 pop_>10-20ug/L                   0  0
 5  1999 Q1                  106720 pop_>20ug/L                      0  0
 6  1999 Q1                  106720 pop_on_PWS_with_non-de…      38913  0.365
 7  1999 Q2                   85541 pop_0-3ug/L                  55476  0.649
 8  1999 Q2                   85541 pop_>3-5ug/L                     0  0
 9  1999 Q2                   85541 pop_>5-10ug/L                  212  0.00248
10  1999 Q2                   85541 pop_>10-20ug/L                  60  0.000701
# ℹ 518 more rows
```

Reshaping nitrate exposure data

```
wide <- long %>%
  select(!c(pop_on_sampled_PWS, conc_count)) %>%
  pivot_wider(names_from = "quarter", values_from = "conc_prop")
wide
```

```
# A tibble: 132 × 6
    year conc_cat                          Q1       Q2       Q3      Q4
   <dbl> <chr>                          <dbl>    <dbl>    <dbl>   <dbl>
 1  1999 pop_0-3ug/L                 0.635    0.649    0.571    0.962
 2  1999 pop_>3-5ug/L                0        0        0.413    0.0156
 3  1999 pop_>5-10ug/L               0.000300 0.00248  0.000379 0
 4  1999 pop_>10-20ug/L              0        0.000701 0        0
 5  1999 pop_>20ug/L                 0        0        0        0
 6  1999 pop_on_PWS_with_non-detect 0.365    0.348    0.0152   0.0224
 7  2000 pop_0-3ug/L                 0.170    0.853    0.485    0.881
 8  2000 pop_>3-5ug/L                0        0        0.00820  0.00244
 9  2000 pop_>5-10ug/L               0.00264  0.000173 0        0.00101
10  2000 pop_>10-20ug/L              0        0        0        0
# ℹ 122 more rows
```

Summary

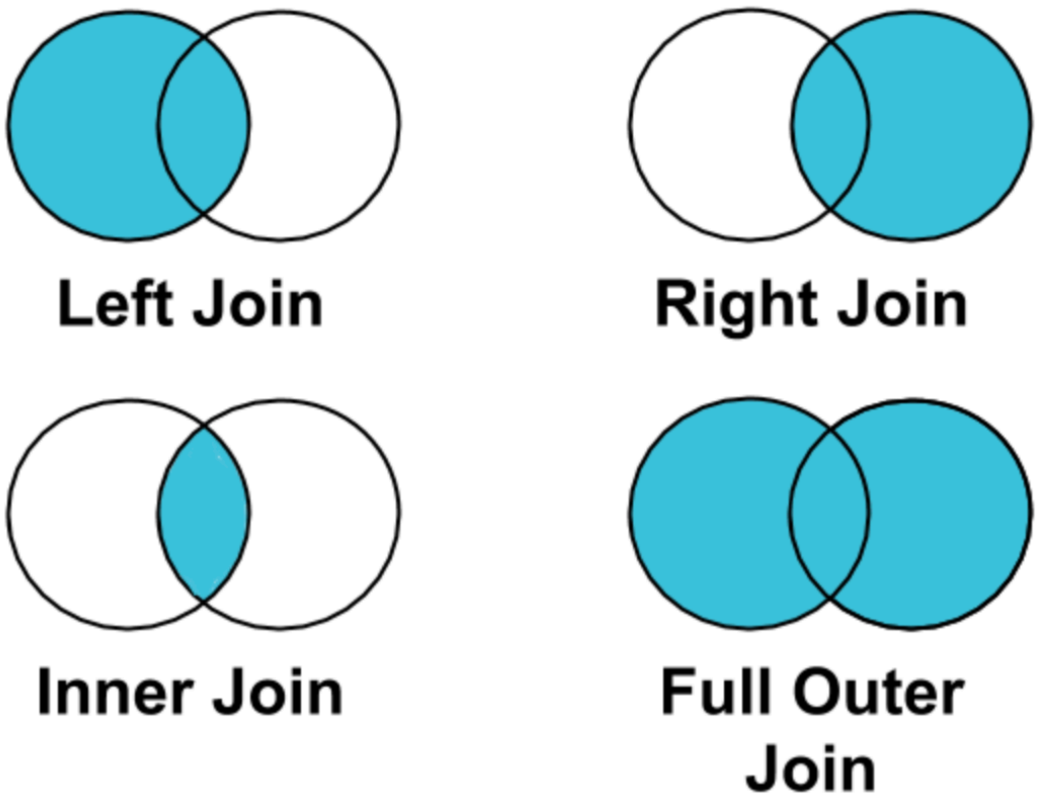
- `tidyr` package helps us convert between wide and long data
- `pivot_longer()` goes from wide -> long
  - Specify columns you want to pivot
  - Specify `names_to =` and `values_to =` for custom naming
- `pivot_wider()` goes from long -> wide
  - Specify `names_from =` and `values_from =`

Lab Part 1

- Class Website
- Lab

Joining

"Combining datasets"



Joining in `dplyr`

- Merging/joining data sets together - usually on key variables, usually “id”
- `?join` - see different types of joining for `dplyr`
- `inner_join(x, y)` - only rows that match for `x` and `y` are kept
- `full_join(x, y)` - all rows of `x` and `y` are kept
- `left_join(x, y)` - all rows of `x` are kept even if not merged with `y`
- `right_join(x, y)` - all rows of `y` are kept even if not merged with `x`
- `anti_join(x, y)` - all rows from `x` not in `y` keeping just columns from `x`.

Merging: Simple Data

```
data_As <- read_csv(
  file = "https://daseh.org/data/data_As_1.csv")
data_cold <- read_csv(
  file = "https://daseh.org/data/data_cold_1.csv")
```

```
data_As
```

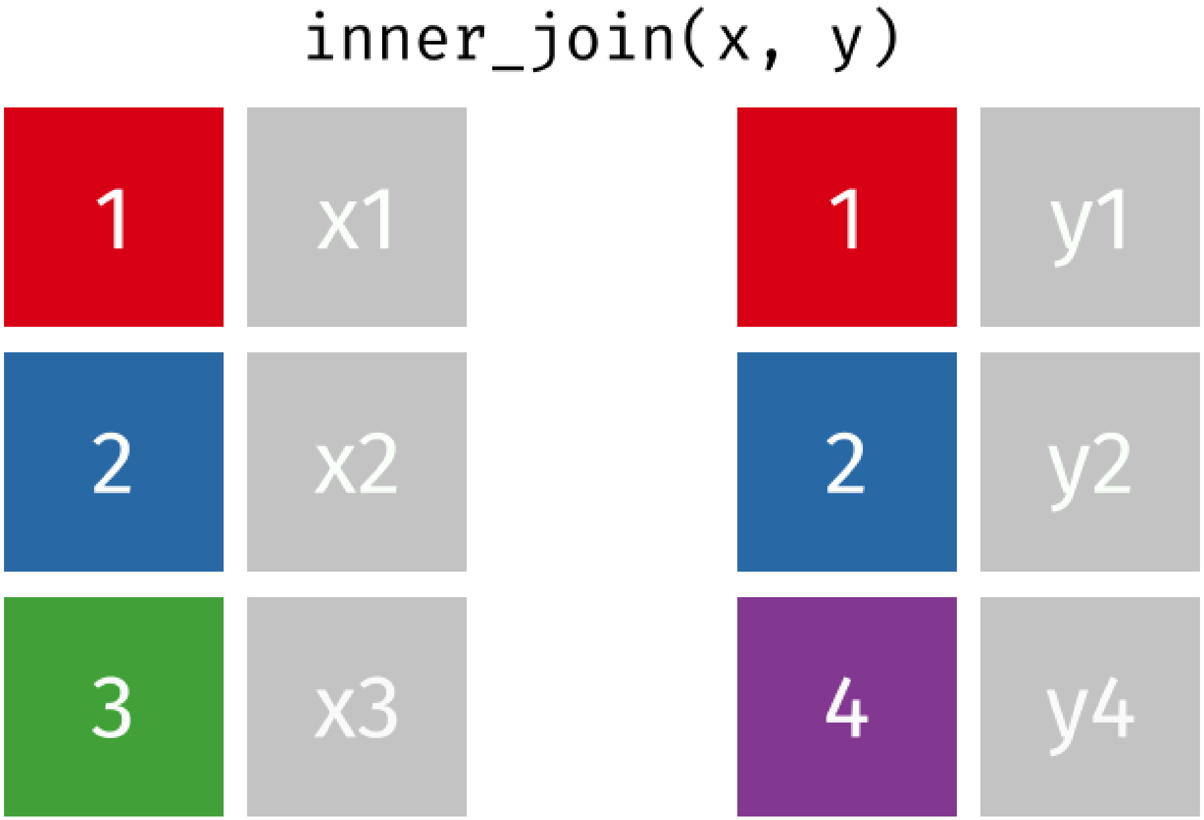
```
# A tibble: 2 × 3
  State   June_vacc_rate May_vacc_rate
  <chr>            <dbl>         <dbl>
1 Alabama          0.516         0.514
2 Alaska           0.627         0.626
```

```
data_cold
```

```
# A tibble: 2 × 2
  State  April_vacc_rate
  <chr>            <dbl>
1 Maine            0.795
2 Alaska           0.623
```

Inner Join

https://github.com/gadenbuie/tidyexplain/blob/main/images/inner-join.gif



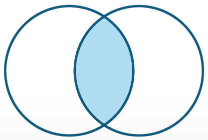
Inner Join

```
ij <- inner_join(data_As, data_cold)
```

```
Joining with `by = join_by(State)`
```

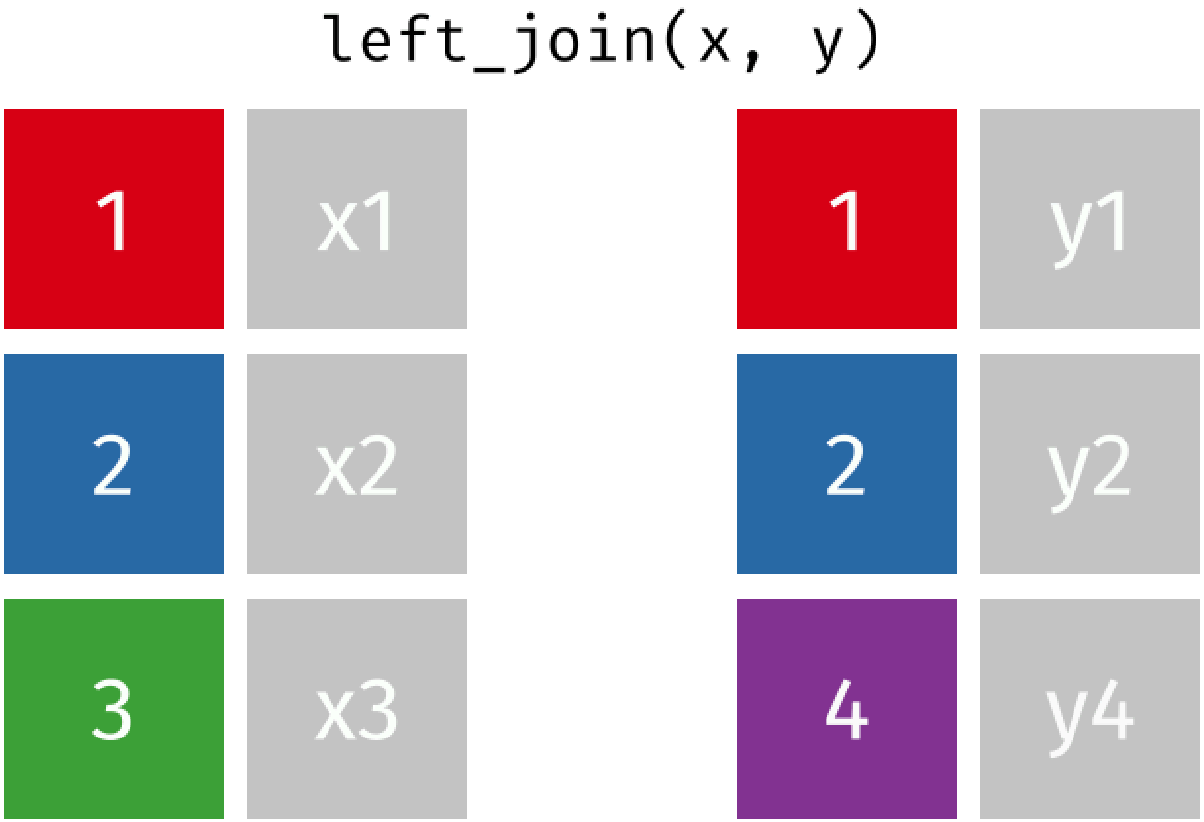
```
ij
```

```
# A tibble: 1 × 4
  State  June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>           <dbl>         <dbl>           <dbl>
1 Alaska          0.627         0.626           0.623
```



Left Join

https://raw.githubusercontent.com/gadenbuie/tidyexplain/main/images/left-join.gif



Left Join

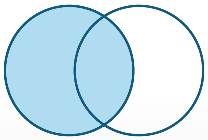
“Everything to the left of the comma”

```
lj <- left_join(data_As, data_cold)
```

```
Joining with `by = join_by(State)`
```

```
lj
```

```
# A tibble: 2 × 4
  State   June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>            <dbl>         <dbl>           <dbl>
1 Alabama          0.516         0.514          NA    
2 Alaska           0.627         0.626           0.623
```

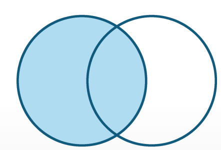


Install `tidylog` package to log outputs

```
# install.packages("tidylog")
library(tidylog)
left_join(data_As, data_cold)
```

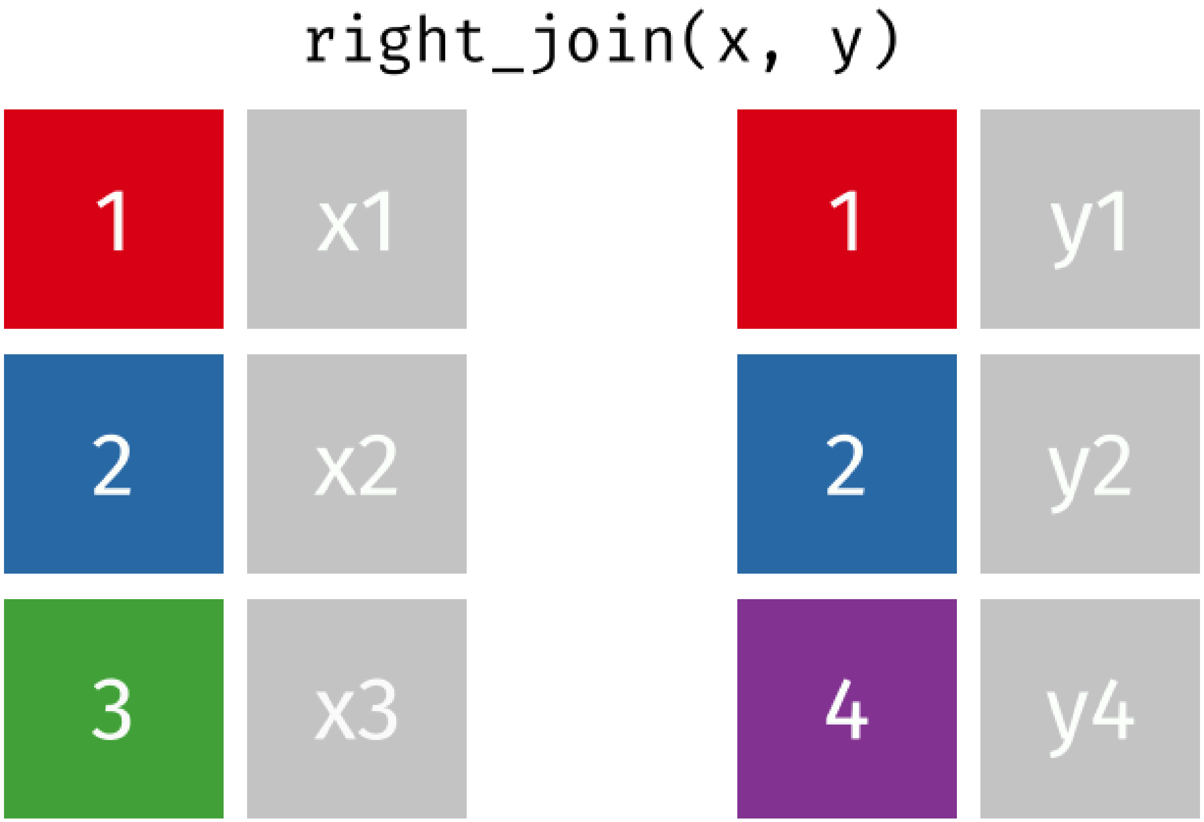
```
Joining with `by = join_by(State)`
left_join: added one column (April_vacc_rate)
> rows only in data_As 1
> rows only in data_cold (1)
> matched rows 1
> ===
> rows total 2

# A tibble: 2 × 4
  State   June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>            <dbl>         <dbl>           <dbl>
1 Alabama          0.516         0.514          NA    
2 Alaska           0.627         0.626           0.623
```



Right Join

https://raw.githubusercontent.com/gadenbuie/tidyexplain/main/images/right-join.gif



Right Join

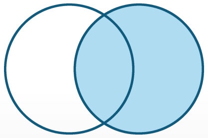
“Everything to the right of the comma”

```
rj <- right_join(data_As, data_cold)
```

```
Joining with `by = join_by(State)`
right_join: added one column (April_vacc_rate)
> rows only in data_As (1)
> rows only in data_cold 1
> matched rows 1
> ===
> rows total 2
```

```
rj
```

```
# A tibble: 2 × 4
  State  June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>           <dbl>         <dbl>           <dbl>
1 Alaska          0.627         0.626           0.623
2 Maine          NA            NA               0.795
```



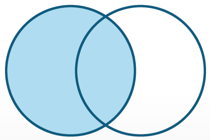
Left Join: Switching arguments

```
lj2 <- left_join(data_cold, data_As)
```

```
Joining with `by = join_by(State)`
left_join: added 2 columns (June_vacc_rate, May_vacc_rate)
> rows only in data_cold 1
> rows only in data_As (1)
> matched rows 1
> ===
> rows total 2
```

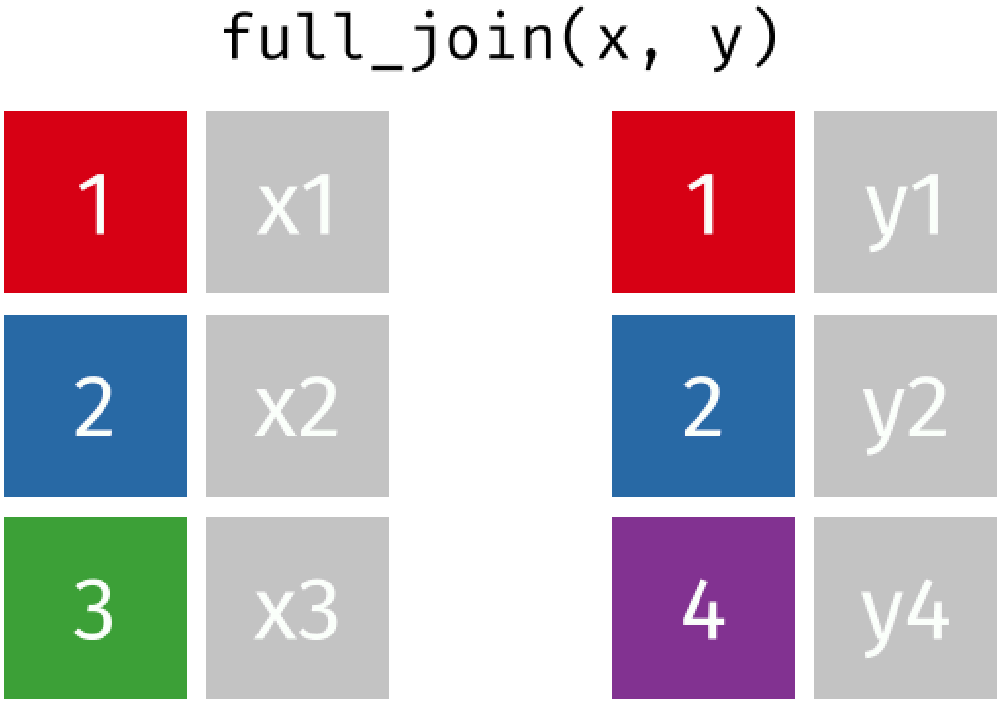
```
lj2
```

```
# A tibble: 2 × 4
  State  April_vacc_rate June_vacc_rate May_vacc_rate
  <chr>            <dbl>          <dbl>         <dbl>
1 Maine            0.795         NA            NA
2 Alaska           0.623          0.627         0.626
```



Full Join

https://raw.githubusercontent.com/gadenbuie/tidyexplain/main/images/full-join.gif



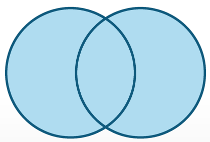
Full Join

```
fj <- full_join(data_As, data_cold)
```

```
Joining with `by = join_by(State)`
full_join: added one column (April_vacc_rate)
> rows only in data_As 1
> rows only in data_cold 1
> matched rows 1
> ===
> rows total 3
```

```
fj
```

```
# A tibble: 3 × 4
  State   June_vacc_rate May_vacc_rate April_vacc_rate
  <chr>            <dbl>         <dbl>           <dbl>
1 Alabama          0.516         0.514          NA    
2 Alaska           0.627         0.626           0.623
3 Maine           NA            NA               0.795
```



Watch out for "`includes duplicates`"

```
data_As <- read_csv(
  file = "https://daseh.org/data/data_As_2.csv")
data_cold <- read_csv(
  file = "https://daseh.org/data/data_cold_2.csv")
```

```
data_As
```

```
# A tibble: 2 × 2
  State   state_bird
  <chr>   <chr>
1 Alabama wild turkey
2 Alaska  willow ptarmigan
```

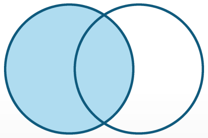
```
data_cold
```

```
# A tibble: 3 × 3
  State  vacc_rate month
  <chr>      <dbl> <chr>
1 Maine      0.795 April
2 Alaska     0.623 April
3 Alaska     0.626 May
```

Watch out for “`includes duplicates`”

```
lj <- left_join(data_As, data_cold)
```

```
Joining with `by = join_by(State)`
left_join: added 2 columns (vacc_rate, month)
> rows only in data_As 1
> rows only in data_cold (1)
> matched rows 2 (includes duplicates)
> ===
> rows total 3
```



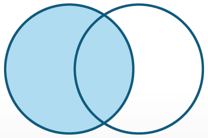
Watch out for “**`includes duplicates`**”

Data including the joining column (“State”) has been duplicated.

```
lj
```

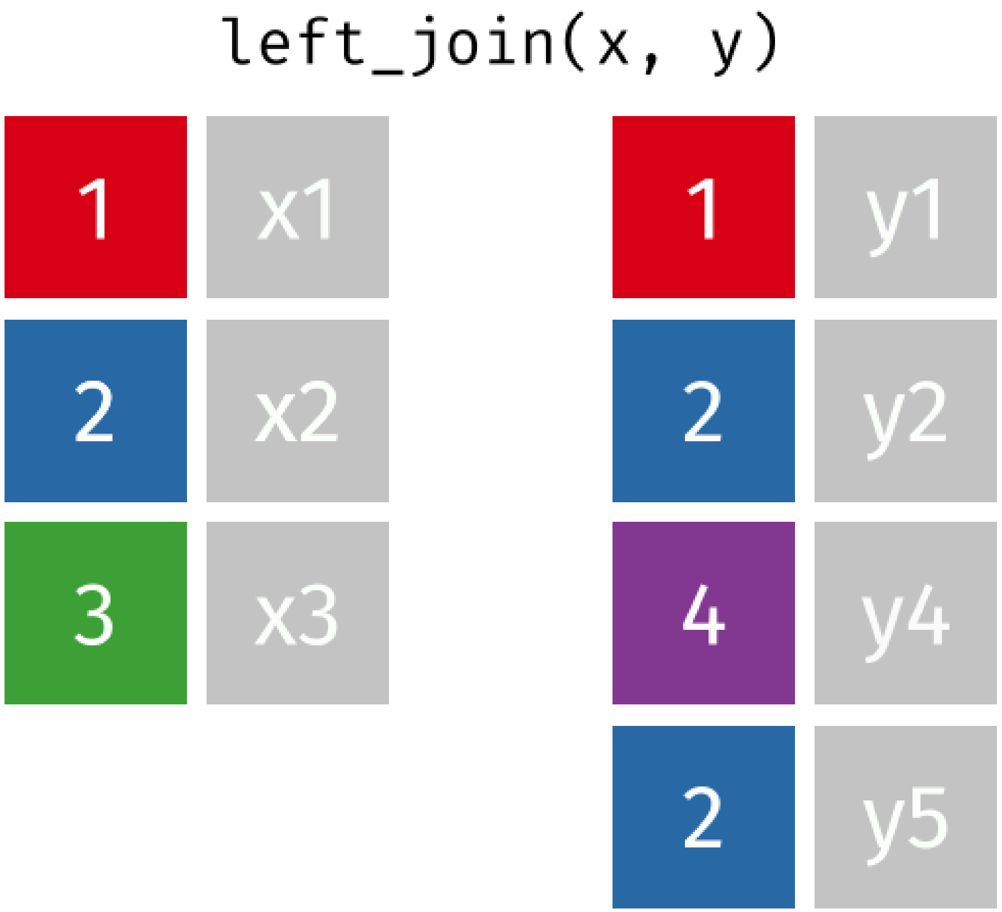
```
# A tibble: 3 × 4
  State   state_bird        vacc_rate month
  <chr>   <chr>                 <dbl> <chr>
1 Alabama wild turkey          NA     <NA>
2 Alaska  willow ptarmigan      0.623 April
3 Alaska  willow ptarmigan      0.626 May
```

Note that “Alaska willow ptarmigan” appears twice.



Watch out for “`includes duplicates`”

https://github.com/gadenbuie/tidyexplain/blob/main/images/left-join-extra.gif



Stop `tidylog`

`unloadNamespace()` does the opposite of `library()`.

```
unloadNamespace("tidylog")
```

Using the `by` argument

By default joins use the intersection of column names. If `by` is specified, it uses that.

```r
full_join(data_As, data_cold, by = "State")
```

```
# A tibble: 4 × 4
  State   state_bird       vacc_rate month
  <chr>   <chr>                <dbl> <chr>
1 Alabama wild turkey         NA     <NA>
2 Alaska  willow ptarmigan     0.623 April
3 Alaska  willow ptarmigan     0.626 May
4 Maine   <NA>                 0.795 April
```

Using the **by** argument

You can join based on multiple columns by using something like `by = c(col1, col2)`.

If the datasets have two different names for the same data, use:

```
full_join(x, y, by = c("a" = "b"))
```

`anti_join` : what's missing

Entries in `data_As` but not in `data_cold`

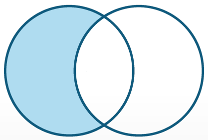
```
anti_join(data_As, data_cold, by = "State")
```

```
# A tibble: 1 × 2
  State   state_bird
  <chr>   <chr>
1 Alabama wild turkey
```

Entries in `data_cold` but not in `data_As`

```
anti_join(data_cold, data_As, by = "State") # order switched
```

```
# A tibble: 1 × 3
  State vacc_rate month
  <chr>     <dbl> <chr>
1 Maine     0.795 April
```



Summary

- Merging/joining data sets together - assumes all column names that overlap
  - use the `by = c("a" = "b")` if they differ
- `inner_join(x, y)` - only rows that match for `x` and `y` are kept
- `full_join(x, y)` - all rows of `x` and `y` are kept
- `left_join(x, y)` - all rows of `x` are kept even if not merged with `y`
- `right_join(x, y)` - all rows of `y` are kept even if not merged with `x`
- Use the `tidylog` package for a detailed summary
- `antijoin(x, y)` shows what is only in `x` (missing from `y`)

Lab Part 2

- Class Website
- Lab

Image by Gerd Altmann from Pixabay

Additional Slides

Getting the set difference with `setdiff`

We might want to determine what indexes ARE in the first dataset that AREN'T in the second.

For this to work, the datasets need the same columns.

We'll just select the index using `select()`.

```
A_states <- data_As %>% select(State)
cold_states <- data_cold %>% select(State)
```

Getting the set difference with **`setdiff`**

States in `A_states` but not in `cold_states`

```
dplyr::setdiff(A_states, cold_states)
```

```
# A tibble: 1 × 1
  State
  <chr>
1 Alabama
```

States in `cold_states` but not in `A_states`

```
dplyr::setdiff(cold_states, A_states)
```

```
# A tibble: 1 × 1
  State
  <chr>
1 Maine
```

Getting the set difference with `setdiff`

Why did we use `dplyr::setdiff`?

There is a base R function, also called `setdiff` that requires vectors.

In other words, we use `dplyr::` to be specific about the package we want to use.

More set operations can be found here:
https://dplyr.tidyverse.org/reference/setops.html

Fast manipulation using `collapse` package

https://sebkrantz.github.io/collapse/

Might be helpful if your data is very large. However, `dplyr` and `tidyr` functions are great for most applications.