Introduction to Data Linkage

ID 529: Data Management and Analytic Workflows in R

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Motivation

- **We've discussed:**
  - **Data manipulation** using `dplyr`
  - **Leveraging `tidyverse` packages** to work with specific types of data
    - Numeric, factors, text strings, dates/times, etc.

- **However, we've only considered data manipulation in the context of individual datasets**
  - We are often interested in combining data from multiple different files or sources
  - Need tools that help us work with and combine multiple datasets

Learning objectives

- **Understand the basic principles of data linkage**
  - Common methods implemented for joining datasets
  - How methods differ, and why these differences should inform your approach

- **Learn about different R functions available for data linkage**
  - `dplyr` two-table verbs

- **Learn how to implement `dplyr` two-table verbs to link datasets**
  - Mutating joins
  - Filtering joins
  - Set operations

Background

Why do we need data linkage?

- It's rare that all the data we need for an analysis are contained within a single file
- Often interested in combining data across two or more files or sources
- For example, NHANES generates a number of datasets for each survey cycle
  - Separate files for demographics, clinical exams, laboratory tests, questionnaires, etc.
  - Participant data from a given survey cycle must be linked across multiple datasets with a unique identifier
  - **This is how the `ID529data::nhanes_id529` dataset was created!**

```
# A tibble: 14 × 2
   Data.File.Name Data.File.Description
   <chr>          <chr>
 1 BPX_J          Blood Pressure
 2 BMX_J          Body Measures
 3 OHXDEN_J       Oral Health - Dentition
 4 OHXREF_J       Oral Health - Recommendation of…
 5 DXXFEM_J       Dual-Energy X-ray Absorptiometr…
 6 DXX_J          Dual-Energy X-ray Absorptiometr…
 7 DXXSPN_J       Dual-Energy X-ray Absorptiometr…
 8 LUX_J          Liver Ultrasound Transient Elas…
 9 DXXAG_J        Dual-Energy X-ray Absorptiometr…
10 BPXO_J         Blood Pressure - Oscillometric …
11 AUX_J          Audiometry
12 AUXAR_J        Audiometry - Acoustic Reflex
13 AUXTYM_J       Audiometry - Tympanometry
14 AUXWBR_J       Audiometry - Wideband Reflectan…
```

```
# A tibble: 10 × 2
   Data.File.Name Data.File.Description
   <chr>          <chr>
 1 DR1TOT_J       Dietary Interview - Total Nutri…
 2 DR2TOT_J       Dietary Interview - Total Nutri…
 3 DR1IFF_J       Dietary Interview - Individual …
 4 DR2IFF_J       Dietary Interview - Individual …
 5 DS1IDS_J       Dietary Supplement Use 24-Hour …
 6 DSQTOT_J       Dietary Supplement Use 30-Day -…
 7 DS2IDS_J       Dietary Supplement Use 24-Hour …
 8 DS1TOT_J       Dietary Supplement Use 24-Hour …
 9 DS2TOT_J       Dietary Supplement Use 24-Hour …
10 DSQIDS_J       Dietary Supplement Use 30-Day -…
```

https://id529.github.io/

How do we link datasets together in R?

- **There are many R functions that allow us to link data**
  - `base R` includes the `merge()`, `rbind()`, `cbind()` functions
  - `dplyr` has many functions (verbs) for performing two-table operations

- **We will focus on `dplyr`**
  - `dplyr` functions tend to be more consistent, and intuitive to implement
  - Can be combined into chained data manipulation sequences (`|> or %>%`)
  - Also offers additional types of joins such as semi-joins and anti-joins

`dplyr` two table verbs

Three classes of `dplyr` verbs that work with two tables at a time

- **Mutating joins**
  - **Combine variables** from multiple tables
  - Adds new columns to one table with matched rows from another table
  - **Two types:**
    - **Inner join:** `inner_join()`
    - **Outer joins:** `left_join()`, `right_join()`, `full_join()`
- **Filtering joins**
  - **Filter rows** from one table if they match a row in a second table
    - Unmatched rows are discarded if join condition is not met
  - Great tools for identifying row mismatches between tables
  - `semi_join()`, `anti_join`

https://id529.github.io/

https://dplyr.tidyverse.org/articles/two-table.html

`dplyr` two table verbs (cont.)

Set operations

- Combine observations from two datasets, but treats observations as set elements
  - i.e., treat rows in each table as individual items in a set
    - Both tables need to contain the same columns
    - Find rows in both tables (**intersection**)
    - Find rows in either table, but not both (**union**)
    - Find rows in one table, but not other (**difference**)
- `intersect()`, `union()`, `setdiff()`

Example dataset

Overview

- NHANES dataset available on the ID529 GitHub
- The dataset includes individual-level:
  - Demographic and clinical characteristics
  - Socioeconomic parameters
  - Blood measures of PFAS/PFOA
  - Dietary intake parameters
- **For our examples, we will split these data into smaller datasets that each contain different variables, identifiers, and number of observations.**
  - **clinical:** `id1`, `age`, `race_eth`, `sbp`, `ht`, `wt`
  - **pfas:** `id1`, `pfos`, `pfoa`, `pfna`, `pfhs`, `pfde`

```r
# Create demog/clincal characteristics table (id1)
clinical <- nhanes %>%
  rename(race_eth = race_ethnicity,
         sbp = mean_BP,
         ht = height,
         wt = weight) %>%
  select(id1, age, race_eth, sbp:ht)

# Create pfas data table (id1)
pfas <- nhanes %>%
  select(id1, PFOS:PFDE) %>%
  rename_with(~ str_to_lower(.)) %>%
  filter(rowSums(is.na(.)) < 5)
```

https://id529.github.io/

https://github.com/ID529/ID529data

Example dataset

```
# Demographic and clinical characteristics
clinical
```

```
# A tibble: 2,339 × 6
   id1     age race_eth             sbp    wt    ht
   <chr> <int> <fct>              <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispanic White  105.  47.1  152.
 2 73571    76 Non-Hispanic White  126  102.   172.
 3 73574    33 <NA>                121.  56.8  158
 4 73576    16 Non-Hispanic Black  109.  67.3  170.
 5 73577    32 Hispanic            119.  79.7  166.
 6 73578    18 Hispanic            123. 109.   175.
 7 73584    13 Non-Hispanic White  109.  53.1  145.
 8 73587    14 <NA>                112  110.   169.
 9 73597    50 Non-Hispanic Black  NaN  104.   180.
10 73598    20 Hispanic            112   86.7  165
# ℹ 2,329 more rows
```

```
# PFAS data filtered for obs with data
pfas
```

```
# A tibble: 2,168 × 6
   id1    pfos  pfoa  pfna  pfhs  pfde
   <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
 1 73568   2.2  3      0.5   3     0.2
 2 73571  10.2  4.77   1.3   2     0.3
 3 73574  NA    NA      0.7   0.2   0.1
 4 73576   4.7  2.37   0.6   7.6   0.2
 5 73577   3    1.47   0.4   1.2   0.1
 6 73584   7    2.37   0.8   0.8   0.2
 7 73587  35.5  6.17   3.3   6.3   1.7
 8 73598   4.7  1.8    0.5   1.6   0.2
 9 73599   4.5  1.87   1.7   0.8   0.2
10 73600   6.3  1.67   0.5   1.6   0.2
# ℹ 2,158 more rows
```

`dplyr` mutating joins

dplyr::left_join()

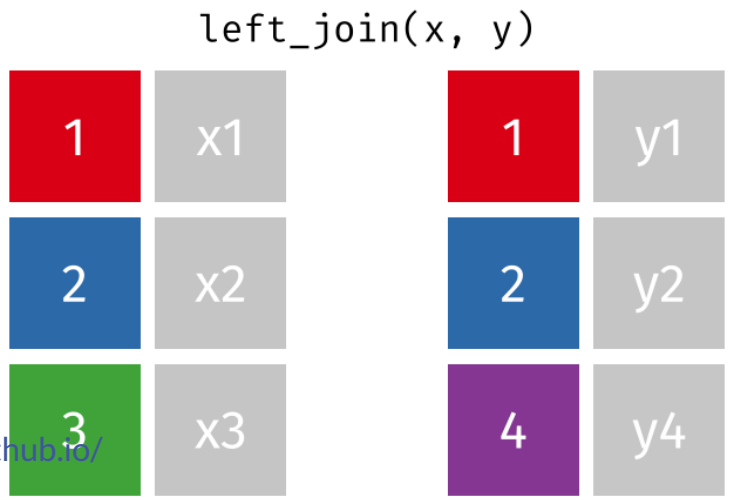
Main arguments

```
left_join(
  x, # dataset 1 (i.e., the dataset on the left side)
  y, # dataset 2 (i.e., the dataset on the right side)
  by = NULL,
  suffix = c(".x", ".y"),
  keep = FALSE
)
```

- x = Data frame 1 (left table)
- y = Data frame 2 (right table)
- by = Column names(s) of variables to match rows by (key)
- suffix = Character string appended to column names that appear in both x and y
- keep= If TRUE, preserve the join keys from both x and y

Description

- Adds columns from y (right table) to x (left table)
- All rows from x are preserved in the join
  - i.e., keeps all rows from x regardless of whether there's a match in y
- Of the joins, used most frequently
  - Allow you to add new variables from other tables



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

dplyr::left_join() example

```
# Print clinical dataset
clinical
```

```
# A tibble: 2,339 × 6
   id1     age race_eth             sbp    wt    ht
   <chr> <int> <fct>              <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispanic White  105.  47.1  152.
 2 73571    76 Non-Hispanic White  126  102.   172.
 3 73574    33 <NA>                121.  56.8  158
 4 73576    16 Non-Hispanic Black  109.  67.3  170.
 5 73577    32 Hispanic            119.  79.7  166.
 6 73578    18 Hispanic            123. 109.   175.
 7 73584    13 Non-Hispanic White  109.  53.1  145.
 8 73587    14 <NA>                112  110.   169.
 9 73597    50 Non-Hispanic Black  NaN  104.   180.
10 73598    20 Hispanic            112   86.7  165
# ℹ 2,329 more rows
```

```
# Print PFAS dataset
pfas
```

```
# A tibble: 2,168 × 6
   id1    pfos  pfoa  pfna  pfhs  pfde
   <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
 1 73568   2.2  3      0.5   3     0.2
 2 73571  10.2  4.77   1.3   2     0.3
 3 73574  NA   NA      0.7   0.2   0.1
 4 73576   4.7  2.37   0.6   7.6   0.2
 5 73577   3    1.47   0.4   1.2   0.1
 6 73584   7    2.37   0.8   0.8   0.2
 7 73587  35.5  6.17   3.3   6.3   1.7
 8 73598   4.7  1.8    0.5   1.6   0.2
 9 73599   4.5  1.87   1.7   0.8   0.2
10 73600   6.3  1.67   0.5   1.6   0.2
# ℹ 2,158 more rows
```

```
# Perform a left join
left_join(x = clinical, y = pfas, by = "id1")
```

```
# A tibble: 2,339 × 11
   id1     age race_eth       sbp    wt    ht  pfos
   <chr> <int> <fct>        <dbl> <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispan…  105.  47.1  152.   2.2
 2 73571    76 Non-Hispan…  126  102.   172.  10.2
 3 73574    33 <NA>         121.  56.8  158   NA
 4 73576    16 Non-Hispan…  109.  67.3  170.   4.7
 5 73577    32 Hispanic     119.  79.7  166.   3
 6 73578    18 Hispanic     123. 109.   175.  NA
 7 73584    13 Non-Hispan…  109.  53.1  145.   7
 8 73587    14 <NA>         112  110.   169.  35.5
 9 73597    50 Non-Hispan…  NaN  104.   180.  NA
10 73598    20 Hispanic     112   86.7  165    4.7
# ℹ 2,329 more rows
# ℹ 4 more variables: pfoa <dbl>, pfna <dbl>,
#   pfhs <dbl>, pfde <dbl>
```

dplyr::right_join()

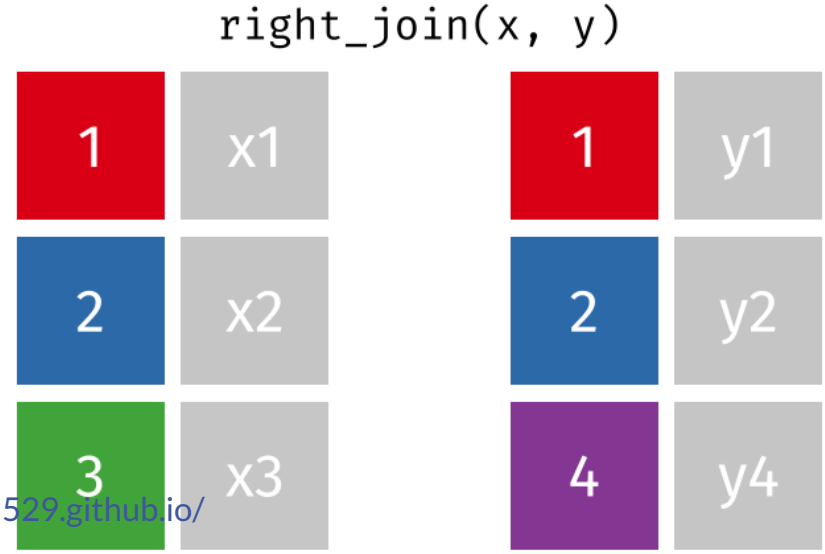
Main arguments

```
right_join(
  x,
  y,
  by = NULL,
  suffix = c(".x", ".y"),
  keep = FALSE
)
```

- x = Data frame 1 (left table)
- y = Data frame 2 (right table)
- by = Column names(s) of variables to match rows by (key)
- suffix = Character string appended to column names that appear in both x and y
- keep= If TRUE, preserve the join keys from both x and y

Description

- Adds columns from x (left table) to y (right table)
- All rows from y are preserved in the join
  - i.e., keeps all rows from y regardless of whether there's a match in x



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

dplyr::right_join() example

```
# Print clincal dataset
clinical
```

```
# A tibble: 2,339 × 6
   id1     age race_eth              sbp    wt    ht
   <chr> <int> <fct>               <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispanic White  105.  47.1  152.
 2 73571    76 Non-Hispanic White  126  102.   172.
 3 73574    33 <NA>                121.  56.8  158
 4 73576    16 Non-Hispanic Black  109.  67.3  170.
 5 73577    32 Hispanic            119.  79.7  166.
 6 73578    18 Hispanic            123. 109.   175.
 7 73584    13 Non-Hispanic White  109.  53.1  145.
 8 73587    14 <NA>                112  110.   169.
 9 73597    50 Non-Hispanic Black  NaN  104.   180.
10 73598    20 Hispanic            112   86.7  165
# ℹ 2,329 more rows
```

```
# Print PFAS dataset
pfas
```

```
# A tibble: 2,168 × 6
   id1    pfos  pfoa  pfna  pfhs  pfde
   <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
 1 73568   2.2  3      0.5   3     0.2
 2 73571  10.2  4.77   1.3   2     0.3
 3 73574  NA   NA      0.7   0.2   0.1
 4 73576   4.7  2.37   0.6   7.6   0.2
 5 73577   3    1.47   0.4   1.2   0.1
 6 73584   7    2.37   0.8   0.8   0.2
 7 73587  35.5  6.17   3.3   6.3   1.7
 8 73598   4.7  1.8    0.5   1.6   0.2
 9 73599   4.5  1.87   1.7   0.8   0.2
10 73600   6.3  1.67   0.5   1.6   0.2
# ℹ 2,158 more rows
```

```
right_join(x = clinical, y = pfas, by = "id1")
```

```
# A tibble: 2,168 × 11
   id1     age race_eth       sbp    wt    ht  pfos
   <chr> <int> <fct>        <dbl> <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispan…  105.  47.1  152.   2.2
 2 73571    76 Non-Hispan…  126  102.   172.  10.2
 3 73574    33 <NA>         121.  56.8  158   NA
 4 73576    16 Non-Hispan…  109.  67.3  170.   4.7
 5 73577    32 Hispanic     119.  79.7  166.   3
 6 73584    13 Non-Hispan…  109.  53.1  145.   7
 7 73587    14 <NA>         112  110.   169.  35.5
 8 73598    20 Hispanic     112   86.7  165    4.7
 9 73599    13 Non-Hispan…  118   44.9  159.   4.5
10 73600    37 Non-Hispan…  149. 126.   185.   6.3
# ℹ 2,158 more rows
# ℹ 4 more variables: pfoa <dbl>, pfna <dbl>,
#   pfhs <dbl>, pfde <dbl>
```

dplyr::inner_join()

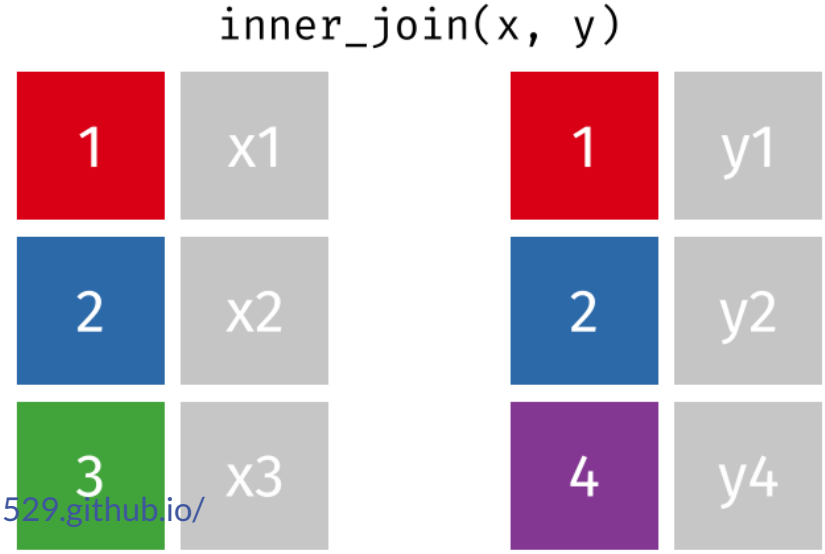
Main arguments

```
inner_join(
  x,
  y,
  by = NULL,
  copy = FALSE,
  suffix = c(".x", ".y"),
  ...,
  keep = FALSE
)
```

- x = Data frame x
- y = Data frame y
- by= Column name(s) to join x and y by
- suffix= Suffix to append to duplicate vars
- keep= Keep the join key from both x and y

Description

- Returns rows that match in **both** x and y
  - Unmatched rows are dropped
- Most restrictive of the mutating joins



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

dplyr::inner_join() example

```
# Print clinical dataset
clinical
```

```
# A tibble: 2,339 × 6
   id1     age race_eth              sbp    wt    ht
   <chr> <int> <fct>               <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispanic White  105.  47.1  152.
 2 73571    76 Non-Hispanic White  126  102.   172.
 3 73574    33 <NA>                121.  56.8  158
 4 73576    16 Non-Hispanic Black  109.  67.3  170.
 5 73577    32 Hispanic            119.  79.7  166.
 6 73578    18 Hispanic            123. 109.   175.
 7 73584    13 Non-Hispanic White  109.  53.1  145.
 8 73587    14 <NA>                112  110.   169.
 9 73597    50 Non-Hispanic Black  NaN  104.   180.
10 73598    20 Hispanic            112   86.7  165
# ℹ 2,329 more rows
```

```
# Print PFAS dataset
pfas
```

```
# A tibble: 2,168 × 6
   id1    pfos  pfoa  pfna  pfhs  pfde
   <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
 1 73568   2.2  3      0.5   3     0.2
 2 73571  10.2  4.77   1.3   2     0.3
 3 73574  NA   NA      0.7   0.2   0.1
 4 73576   4.7  2.37   0.6   7.6   0.2
 5 73577   3    1.47   0.4   1.2   0.1
 6 73584   7    2.37   0.8   0.8   0.2
 7 73587  35.5  6.17   3.3   6.3   1.7
 8 73598   4.7  1.8    0.5   1.6   0.2
 9 73599   4.5  1.87   1.7   0.8   0.2
10 73600   6.3  1.67   0.5   1.6   0.2
# ℹ 2,158 more rows
```

```
# Perform an inner join
inner_join(x = clinical, y = pfas, by = "id1")
```

```
# A tibble: 2,168 × 11
   id1     age race_eth       sbp    wt    ht  pfos
   <chr> <int> <fct>        <dbl> <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispan…  105.  47.1  152.   2.2
 2 73571    76 Non-Hispan…  126  102.   172.  10.2
 3 73574    33 <NA>         121.  56.8  158   NA
 4 73576    16 Non-Hispan…  109.  67.3  170.   4.7
 5 73577    32 Hispanic     119.  79.7  166.   3
 6 73584    13 Non-Hispan…  109.  53.1  145.   7
 7 73587    14 <NA>         112  110.   169.  35.5
 8 73598    20 Hispanic     112   86.7  165    4.7
 9 73599    13 Non-Hispan…  118   44.9  159.   4.5
10 73600    37 Non-Hispan…  149. 126.   185.   6.3
# ℹ 2,158 more rows
# ℹ 4 more variables: pfoa <dbl>, pfna <dbl>,
#   pfhs <dbl>, pfde <dbl>
```

dplyr::full_join()

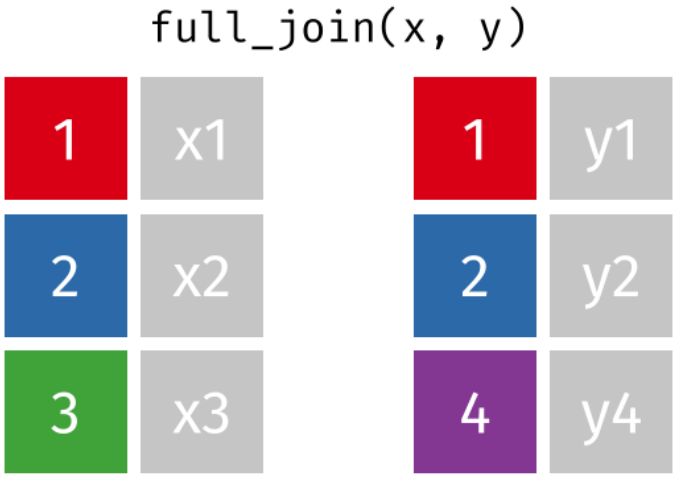
Main arguments

```
full_join(
  x,
  y,
  by = NULL,
  suffix = c(".x", ".y"),
  keep = FALSE
)
```

- x = Data frame x
- y = Data frame y
- by= Column name(s) to join x and y by
- suffix= Suffix to append to duplicate vars
- keep= Keep the join key from both x and y

Description

- Returns all rows in x or y
- Least restrictive
  - No observations are removed



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

dplyr::full_join() example

```
# Print clinical datast
clinical
```

```
# A tibble: 2,339 × 6
   id1     age race_eth              sbp    wt    ht
   <chr> <int> <fct>               <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispanic White  105.  47.1  152.
 2 73571    76 Non-Hispanic White  126  102.   172.
 3 73574    33 <NA>                121.  56.8  158
 4 73576    16 Non-Hispanic Black  109.  67.3  170.
 5 73577    32 Hispanic            119.  79.7  166.
 6 73578    18 Hispanic            123. 109.   175.
 7 73584    13 Non-Hispanic White  109.  53.1  145.
 8 73587    14 <NA>                112  110.   169.
 9 73597    50 Non-Hispanic Black  NaN  104.   180.
10 73598    20 Hispanic            112   86.7  165
# ℹ 2,329 more rows
```

```
# Print PFAS dataset
pfas
```

```
# A tibble: 2,168 × 6
   id1    pfos  pfoa  pfna  pfhs  pfde
   <chr> <dbl> <dbl> <dbl> <dbl> <dbl>
 1 73568   2.2  3      0.5   3     0.2
 2 73571  10.2  4.77   1.3   2     0.3
 3 73574  NA   NA      0.7   0.2   0.1
 4 73576   4.7  2.37   0.6   7.6   0.2
 5 73577   3    1.47   0.4   1.2   0.1
 6 73584   7    2.37   0.8   0.8   0.2
 7 73587  35.5  6.17   3.3   6.3   1.7
 8 73598   4.7  1.8    0.5   1.6   0.2
 9 73599   4.5  1.87   1.7   0.8   0.2
10 73600   6.3  1.67   0.5   1.6   0.2
# ℹ 2,158 more rows
```

```
# Perform full join
full_join(x = clinical, y = pfas, by = "id1")
```

```
# A tibble: 2,339 × 11
   id1     age race_eth       sbp    wt    ht  pfos
   <chr> <int> <fct>        <dbl> <dbl> <dbl> <dbl>
 1 73568    26 Non-Hispan…  105.  47.1  152.   2.2
 2 73571    76 Non-Hispan…  126  102.   172.  10.2
 3 73574    33 <NA>         121.  56.8  158   NA
 4 73576    16 Non-Hispan…  109.  67.3  170.   4.7
 5 73577    32 Hispanic     119.  79.7  166.   3
 6 73578    18 Hispanic     123. 109.   175.  NA
 7 73584    13 Non-Hispan…  109.  53.1  145.   7
 8 73587    14 <NA>         112  110.   169.  35.5
 9 73597    50 Non-Hispan…  NaN  104.   180.  NA
10 73598    20 Hispanic     112   86.7  165    4.7
# ℹ 2,329 more rows
# ℹ 4 more variables: pfoa <dbl>, pfna <dbl>,
#   pfhs <dbl>, pfde <dbl>
```

https://id529.github.io/

`dplyr` filtering joins

dplyr::semi_join()

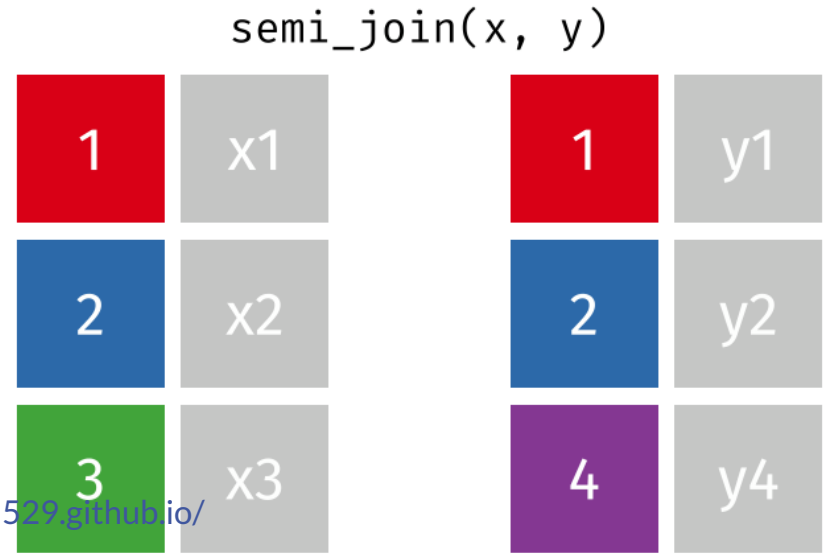
Main arguments

```
semi_join(x,
          y,
          by = NULL,
)
```

- x = Data frame 1 (left)
- y = Data frame 2 (right)
- by = Column names(s) of variables to match rows by (key)

Description

- Keeps all observations in x that have a match in y
- Useful for filtering x by the presence of a match in y



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

dplyr::anti_join()

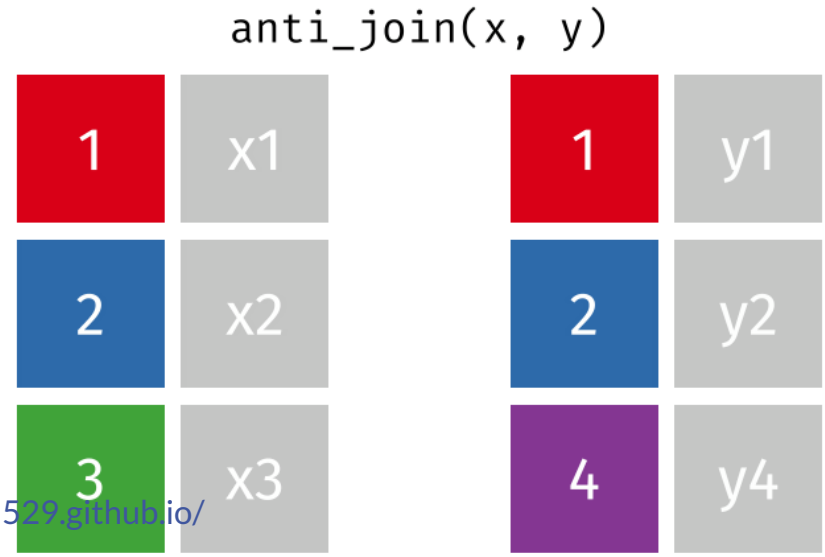
Main arguments

```
anti_join(x,
          y
          by = NULL
)
```

- x = Data frame 1 (left)
- y = Data frame 2 (right)
- by = Column names(s) of variables to match rows by (key)

Description

- Returns rows from x where there is no match in y
- Useful when you want to filter the first table by the absence of a match in the second table
  - That is, identify observations in x that don't appear in y



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

`dplyr` set operations

dplyr::union()

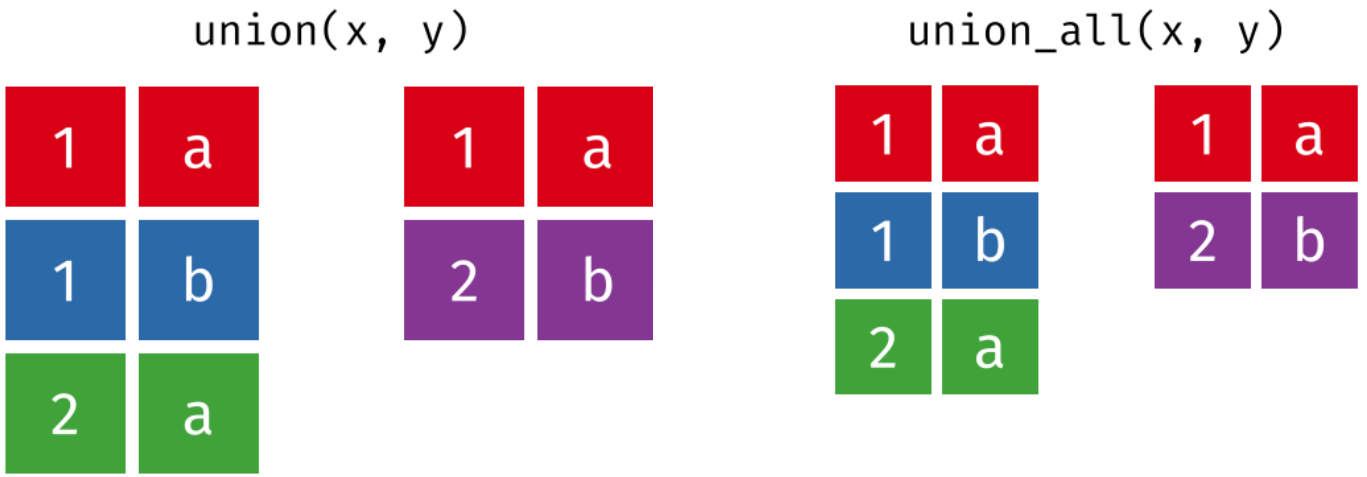
Main arguments

```
union(x, y)
union_all(x, y)
```

- x = Data frame 1 (left)
- y = Data frame 2 (right)

Description

- union()
  - Return unique observations in x and y
- union_all()
  - Return unique and duplicate observations in x and y



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

dplyr::setdiff()

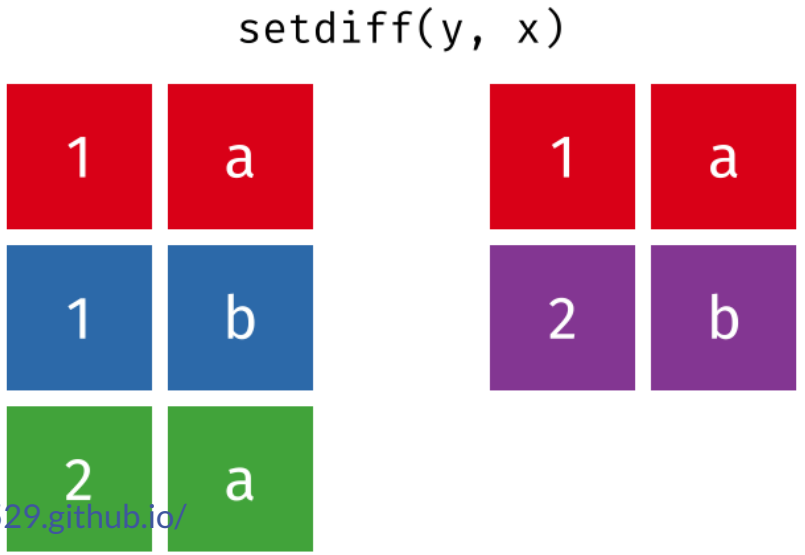
Main arguments

```
setdiff(x, y, ...)
```

- x = Data frame 1 (left)
- y = Data frame 2 (right)

Description

- Returns the rows that are in the first table but not in the second
  - That is, return observations in x, but not in y



https://id529.github.io/

Gif Source: https://github.com/gadenbuie/tidyexplain

Key takeaways

- **Joining together two or more datasets is a routine component of data analysis workflows**
  - Different types of joins are useful in different situations
  - It's important to be aware of how and when to use each (left, right, inner, etc.)
    - All have distinct implications for how the underlying data are manipulated
- Like all data manipulation tasks, joining data can get complicated!
- **Common challenges include:**
  - Inconsistencies in unique identifiers
  - Duplicate records and missing values
  - Non-unique identifiers (require matching data frames on two or more variables)
  - Joining datasets can be complex and requires a good understanding of the data structure
- **`dplyr` includes a number of two-table functions (verbs)**
  - Like other `dplyr` verbs, two-table verbs are:
    - Intuitive to use
    - Can be incorporated into a sequence of data cleaning operations using the pipe operator

Resources

- **`dplyr` Two-table verbs vignette:** https://dplyr.tidyverse.org/articles/two-table.html
- **R for Data Science - Relational Data:** https://r4ds.had.co.nz/relational-data.html
- **The Epidemiologist R Handbook:** https://epirhandbook.com/en/new_pages/joining_matching.html

Activity

- **Clone the repository here:** https://github.com/dmarengi/joining_data

- **ID 529 dataset details:** https://github.com/ID529/ID529data