Joining data

Extended Materials

You can find the original, extended version of this chapter here.

This page describes ways to "join", "match", "link" "bind", and otherwise combine data frames.

It is uncommon that your epidemiological analysis or workflow does not involve multiple sources of data, and the linkage of multiple datasets. Perhaps you need to connect laboratory data to patient clinical outcomes, or Google mobility data to infectious disease trends, or even a dataset at one stage of analysis to a transformed version of itself.

In this page we demonstrate code to:

- Conduct *joins* of two data frames such that rows are matched based on common values in identifier columns
- Join two data frames based on *probabilistic* (likely) matches between values
- Expand a data frame by directly *binding* or ("appending") rows or columns from another data frame

Data Preparation

Load packages

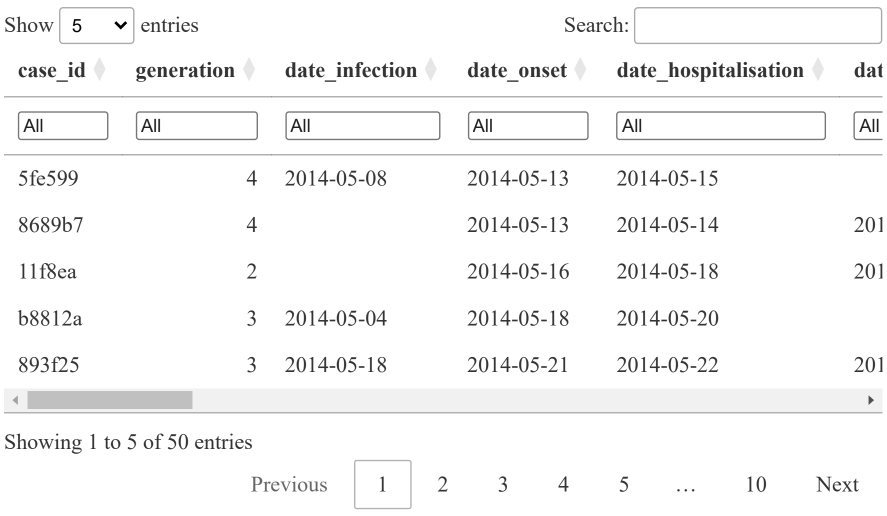
```r
pacman::p_load(
  rio,            # import and export
  here,           # locate files
  tidyverse,      # data management and visualisation
  RecordLinkage,  # probabilistic matches
  fastLink        # probabilistic matches
)
```

Import data

To begin, we import the cleaned linelist of cases from a simulated Ebola epidemic. If you want to follow along, click to download the "clean" linelist (as .rds file).

```r
# import case linelist
linelist <- import("linelist_cleaned.rds")
```

The first 50 rows of the linelist are displayed below.



Show 5 entries Search:

case_id	generation	date_infection	date_onset	date_hospitalisation	dat
All	All	All	All	All	All
5fe599	4	2014-05-08	2014-05-13	2014-05-15	
8689b7	4		2014-05-13	2014-05-14	201
11f8ea	2		2014-05-16	2014-05-18	201
b8812a	3	2014-05-04	2014-05-18	2014-05-20	
893f25	3	2014-05-18	2014-05-21	2014-05-22	201

Showing 1 to 5 of 50 entries

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Example datasets

In the joining section below, we will use the following datasets:

1) A "miniature" version of the case `linelist`, containing only the columns `case_id`, `date_onset`, and `hospital`, and only the first 10 rows

2) A separate data frame named `hosp_info`, which contains more details about each hospital

In the section on probabilistic matching, we will use two different small datasets. The code to create those datasets is given in that section.

* "Miniature" case linelist

Below is the the miniature case linelist, which contains only 10 rows and only columns `case_id`, `date_onset`, and `hospital`.

```
linelist_mini <- linelist %>%                 # start with original linelist
  select(case_id, date_onset, hospital) %>%   # select columns
  head(10)                                    # only take the first 10 rows
```

Show 10 entries Search:

case_id	date_onset	hospital
5fe599	2014-05-13	Other
8689b7	2014-05-13	Missing
11f8ea	2014-05-16	St. Mark's Maternity Hospital (SMMH)
b8812a	2014-05-18	Port Hospital
893f25	2014-05-21	Military Hospital
be99c8	2014-05-22	Port Hospital
07e3e8	2014-05-27	Missing
369449	2014-06-02	Missing
f393b4	2014-06-05	Missing
1389ca	2014-06-05	Missing

Showing 1 to 10 of 10 entries Previous 1 Next

* Hospital information data frame

Below is the code to create a separate data frame with additional information about seven hospitals (the catchment population, and the level of care available). Note that the name "Military Hospital" belongs to two different hospitals - one a primary level serving 10000 residents and the other a secondary level serving 50280 residents.

```
# Make the hospital information data frame
hosp_info = data.frame(
  hosp_name     = c("central hospital", "military", "military", "port", "St. Mark's", "ign
  catchment_pop = c(1950280, 40500, 10000, 50280, 12000, 5000, 4200),
  level         = c("Tertiary", "Secondary", "Primary", "Secondary", "Secondary", "Primary
)
```

Here is this data frame:

Show 7 entries Search:

hosp_name	catchment_pop	level
central hospital	1950280	Tertiary
military	40500	Secondary
military	10000	Primary
port	50280	Secondary
St. Mark's	12000	Secondary
ignace	5000	Primary
sisters	4200	Primary

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Pre-cleaning

Traditional joins (non-probabilistic) are case-sensitive and require exact character matches between values in the two data frames. To demonstrate some of the cleaning steps you might need to do before initiating a join, we will clean and align the `linelist_mini` and `hosp_info` datasets now.

Identify differences

We need the values of the `hosp_name` column in the `hosp_info` data frame to match the values of the `hospital` column in the `linelist_mini` data frame.

Here are the values in the `linelist_mini` data frame, printed with the **base** R function `unique()`:

```
unique(linelist_mini$hospital)
```

```
[1] "Other"
[2] "Missing"
[3] "St. Mark's Maternity Hospital (SMMH)"
[4] "Port Hospital"
[5] "Military Hospital"
```

and here are the values in the `hosp_info` data frame:

```
unique(hosp_info$hosp_name)
```

```
[1] "central hospital" "military"         "port"             "St. Mark's"
[5] "ignace"           "sisters"
```

You can see that while some of the hospitals exist in both data frames, there are many differences in spelling.

Align values

We begin by cleaning the values in the `hosp_info` data frame. We can re-code values with logical criteria using **dplyr**'s `case_when()` function. For the four hospitals that exist in both data frames we change the values to align with the values in `linelist_mini`. The other hospitals we leave the values as they are (`TRUE ~ hosp_name`).

CAUTION: Typically when cleaning one should create a new column (e.g. `hosp_name_clean`), but for ease of demonstration we show modification of the old column

```
hosp_info <- hosp_info %>%
  mutate(
    hosp_name = case_when(
      # criteria                           # new value
      hosp_name == "military"            ~ "Military Hospital",
      hosp_name == "port"                ~ "Port Hospital",
      hosp_name == "St. Mark's"          ~ "St. Mark's Maternity Hospital (SMMH)",
      hosp_name == "central hospital"    ~ "Central Hospital",
      TRUE                               ~ hosp_name
      )
    )
```

The hospital names that appear in both data frames are aligned. There are two hospitals in `hosp_info` that are not present in `linelist_mini` - we will deal with these later, in the join.

```
unique(hosp_info$hosp_name)
```

```
[1] "Central Hospital"
[2] "Military Hospital"
[3] "Port Hospital"
[4] "St. Mark's Maternity Hospital (SMMH)"
[5] "ignace"
[6] "sisters"
```

Prior to a join, it is often easiest to convert a column to all lowercase or all uppercase. If you need to convert all values in a column to UPPER or lower case, use `mutate()` and wrap the column with one of these functions from **stringr**.

`str_to_upper()`
`str_to_upper()`
`str_to_title()`

dplyr joins

The **dplyr** package offers several different join functions. **dplyr** is included in the **tidyverse** package. These join functions are described below, with simple use cases.

Many thanks to https://github.com/gadenbuie for the informative gifs!

General syntax

The join commands can be run as standalone commands to join two data frames into a new object, or they can be used within a pipe chain (`%>%`) to merge one data frame into another as it is being cleaned or otherwise modified.

In the example below, the function `left_join()` is used as a standalone command to create the a new `joined_data` data frame. The inputs are data frames 1 and 2 (`df1` and `df2`). The first data frame listed is the baseline data frame, and the second one listed is joined *to* it.

The third argument `by =` is where you specify the columns in each data frame that will be used to aligns the rows in the two data frames. If the names of these columns are different, provide them within a `c()` vector as shown below, where the rows are matched on the basis of common values between the column `ID` in `df1` and the column `identifier` in `df2`.

```
# Join based on common values between column "ID" (first data frame) and column "identifie
joined_data <- left_join(df1, df2, by = c("ID" = "identifier"))
```

If the `by` columns in both data frames have the exact same name, you can just provide this one name, within quotes.

```
# Joint based on common values in column "ID" in both data frames
joined_data <- left_join(df1, df2, by = "ID")
```

If you are joining the data frames based on common values across multiple fields, list these fields within the `c()` vector. This example joins rows if the values in three columns in each dataset align exactly.

```
# join based on same first name, last name, and age
joined_data <- left_join(df1, df2, by = c("name" = "firstname", "surname" = "lastname", "A
```

The join commands can also be run within a pipe chain. This will modify the data frame being piped.

In the example below, `df1` is is passed through the pipes, `df2` is joined to it, and `df` is thus modified and re-defined.

```
df1 <- df1 %>%
  filter(date_onset < as.Date("2020-03-05")) %>% # miscellaneous cleaning
  left_join(df2, by = c("ID" = "identifier"))    # join df2 to df1
```

⚠ Warning

Joins are case-specific! Therefore it is useful to convert all values to lowercase or uppercase prior to joining.

Left and right joins

A left or right join is commonly used to add information to a data frame - new information is added only to rows that already existed in the baseline data frame. These are common joins in epidemiological work as they are used to add information from one dataset into another.

In using these joins, the written order of the data frames in the command is important*.

- In a *left join*, the *first* data frame written is the baseline
- In a *right join*, the *second* data frame written is the baseline

All rows of the baseline data frame are kept. Information in the other (secondary) data frame is joined to the baseline data frame *only if there is a match via the identifier column(s).* In addition:

- Rows in the secondary data frame that do not match are dropped.
- If there are many baseline rows that match to one row in the secondary data frame (many-to-one), the secondary information is added to *each matching baseline row.*
- If a baseline row matches to multiple rows in the secondary data frame (one-to-many), all combinations are given, meaning *new rows may be added to your returned data frame!*

Example

Below is the output of a `left_join()` of `hosp_info` (secondary data frame, view here) *into* `linelist_mini` (baseline data frame, view here). The original `linelist_mini` has `nrow(linelist_mini)` rows. The modified `linelist_mini` is displayed. Note the following:

- Two new columns, `catchment_pop` and `level` have been added on the left side of `linelist_mini`
- All original rows of the baseline data frame `linelist_mini` are kept

- Any original rows of `linelist_mini` for “Military Hospital” are duplicated because it matched to *two* rows in the secondary data frame, so both combinations are returned

- The join identifier column of the secondary dataset (`hosp_name`) has disappeared because it is redundant with the identifier column in the primary dataset (`hospital`)

- When a baseline row did not match to any secondary row (e.g. when `hospital` is “Other” or “Missing”), `NA` (blank) fills in the columns from the secondary data frame

- Rows in the secondary data frame with no match to the baseline data frame (“sisters” and “ignace” hospitals) were dropped

```
linelist_mini %>%
  left_join(hosp_info, by = c("hospital" = "hosp_name"))
```

```
Warning in left_join(., hosp_info, by = c(hospital = "hosp_name")): Detected an unexpected ma
i Row 5 of `x` matches multiple rows in `y`.
i Row 4 of `y` matches multiple rows in `x`.
i If a many-to-many relationship is expected, set `relationship =
  "many-to-many"` to silence this warning.
```

Show 11 entries Search:

case_id	date_onset	hospital	catchment_pop	level
5fe599	2014-05-13	Other		
8689b7	2014-05-13	Missing		
11f8ea	2014-05-16	St. Mark's Maternity Hospital (SMMH)	12000	Secondary
b8812a	2014-05-18	Port Hospital	50280	Secondary
893f25	2014-05-21	Military Hospital	40500	Secondary
893f25	2014-05-21	Military Hospital	10000	Primary
be99c8	2014-05-22	Port Hospital	50280	Secondary
07e3e8	2014-05-27	Missing		
369449	2014-06-02	Missing		
f393b4	2014-06-05	Missing		
1389ca	2014-06-05	Missing		

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* “Should I use a right join, or a left join?”

To answer the above question, ask yourself “which data frame should retain all of its rows?” - use this one as the baseline. A *left join* keep all the rows in the first data frame written in the command, whereas a *right join* keeps all the rows in the second data frame.

The two commands below achieve the same output - 10 rows of `hosp_info` joined *into* a `linelist_mini` baseline, but they use different joins. The result is that the column order will differ based on whether `hosp_info` arrives from the right (in the left join) or arrives from the left (in the right join). The order of the rows may also shift accordingly. But both of these consequences can be subsequently addressed, using `select()` to re-order columns or `arrange()` to sort rows.

```
# The two commands below achieve the same data, but with differently ordered rows and colu
left_join(linelist_mini, hosp_info, by = c("hospital" = "hosp_name"))
right_join(hosp_info, linelist_mini, by = c("hosp_name" = "hospital"))
```

Here is the result of `hosp_info` into `linelist_mini` via a left join (new columns incoming from the right)

```
Warning in left_join(linelist_mini, hosp_info, by = c(hospital = "hosp_name")): Detected an u
i Row 5 of `x` matches multiple rows in `y`.
i Row 4 of `y` matches multiple rows in `x`.
i If a many-to-many relationship is expected, set `relationship =
  "many-to-many"` to silence this warning.
```

Show 11 entries Search:

case_id	date_onset	hospital	catchment_pop	level
5fe599	2014-05-13	Other		
8689b7	2014-05-13	Missing		
11f8ea	2014-05-16	St. Mark's Maternity Hospital (SMMH)	12000	Secondary
b8812a	2014-05-18	Port Hospital	50280	Secondary
893f25	2014-05-21	Military Hospital	40500	Secondary
893f25	2014-05-21	Military Hospital	10000	Primary
be99c8	2014-05-22	Port Hospital	50280	Secondary
07e3e8	2014-05-27	Missing		
369449	2014-06-02	Missing		
f393b4	2014-06-05	Missing		
1389ca	2014-06-05	Missing		

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Here is the result of `hosp_info` into `linelist_mini` via a right join (new columns incoming from the left)

```
Warning in right_join(hosp_info, linelist_mini, by = c(hosp_name = "hospital")): Detected an
i Row 4 of `x` matches multiple rows in `y`.
i Row 5 of `y` matches multiple rows in `x`.
i If a many-to-many relationship is expected, set `relationship =
  "many-to-many"` to silence this warning.
```

Show 11 entries Search:

hosp_name	catchment_pop	level	case_id	date_onset
Military Hospital	40500	Secondary	893f25	2014-05-21
Military Hospital	10000	Primary	893f25	2014-05-21
Port Hospital	50280	Secondary	b8812a	2014-05-18
Port Hospital	50280	Secondary	be99c8	2014-05-22
St. Mark's Maternity Hospital (SMMH)	12000	Secondary	11f8ea	2014-05-16
Other			5fe599	2014-05-13
Missing			8689b7	2014-05-13
Missing			07e3e8	2014-05-27
Missing			369449	2014-06-02
Missing			f393b4	2014-06-05
Missing			1389ca	2014-06-05

Showing 1 to 11 of 11 entries Previous 1 Next

Also consider whether your use-case is within a pipe chain (`%>%`). If the dataset in the pipes is the baseline, you will likely use a left join to add data to it.

Full join

A full join is the most *inclusive* of the joins - it returns all rows from both data frames.

If there are any rows present in one and not the other (where no match was found), the data frame will include them and become longer. `NA` missing values are used to fill-in any gaps created. As you join, watch the number of columns and rows carefully to troubleshoot case-sensitivity and exact character matches.

The "baseline" data frame is the one written first in the command. Adjustment of this will not impact which records are returned by the join, but it can impact the resulting column order, row order, and which identifier columns are retained.

Example

Below is the output of a `full_join()` of `hosp_info` (originally `nrow(hosp_info)`, view here) *into* `linelist_mini` (originally `nrow(linelist_mini)`, view here). Note the following:

- All baseline rows are kept (`linelist_mini`)
- Rows in the secondary that do not match to the baseline are kept ("ignace" and "sisters"), with values in the corresponding baseline columns `case_id` and `onset` filled in with missing values
- Likewise, rows in the baseline data frame that do not match to the secondary ("Other" and "Missing") are kept, with secondary columns `catchment_pop` and `level` filled-in with missing values
- In the case of one-to-many or many-to-one matches (e.g. rows for "Military Hospital"), all possible combinations are returned (lengthening the final data frame)
- Only the identifier column from the baseline is kept (`hospital`)

```r
linelist_mini %>%
  full_join(hosp_info, by = c("hospital" = "hosp_name"))
```

```
Warning in full_join(., hosp_info, by = c(hospital = "hosp_name")): Detected an unexpected ma
i Row 5 of `x` matches multiple rows in `y`.
i Row 4 of `y` matches multiple rows in `x`.
i If a many-to-many relationship is expected, set `relationship =
  "many-to-many"` to silence this warning.
```

Show 15 entries Search:

case_id	date_onset	hospital	catchment_pop	level
5fe599	2014-05-13	Other		
8689b7	2014-05-13	Missing		
11f8ea	2014-05-16	St. Mark's Maternity Hospital (SMMH)	12000	Secondary
b8812a	2014-05-18	Port Hospital	50280	Secondary
893f25	2014-05-21	Military Hospital	40500	Secondary
893f25	2014-05-21	Military Hospital	10000	Primary
be99c8	2014-05-22	Port Hospital	50280	Secondary
07e3e8	2014-05-27	Missing		
369449	2014-06-02	Missing		
f393b4	2014-06-05	Missing		
1389ca	2014-06-05	Missing		
		Central Hospital	1950280	Tertiary
		ignace	5000	Primary
		sisters	4200	Primary

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Inner join

An inner join is the most *restrictive* of the joins - it returns only rows with matches across both data frames.
This means that the number of rows in the baseline data frame may actually *reduce*. Adjustment of which data frame is the "baseline" (written first in the function) will not impact which rows are returned, but it will impact the column order, row order, and which identifier columns are retained.

Example

Below is the output of an `inner_join()` of `linelist_mini` (baseline) with `hosp_info` (secondary). Note the following:

- Baseline rows with no match to the secondary data are removed (rows where `hospital` is "Missing" or "Other")

- Likewise, rows from the secondary data frame that had no match in the baseline are removed (rows where `hosp_name` is "sisters" or "ignace")

- Only the identifier column from the baseline is kept (`hospital`)

```
linelist_mini %>%
  inner_join(hosp_info, by = c("hospital" = "hosp_name"))
```

```
Warning in inner_join(., hosp_info, by = c(hospital = "hosp_name")): Detected an unexpected r
i Row 5 of `x` matches multiple rows in `y`.
i Row 4 of `y` matches multiple rows in `x`.
i If a many-to-many relationship is expected, set `relationship =
  "many-to-many"` to silence this warning.
```

Show 12 entries Search:

case_id	date_onset	hospital	catchment_pop	level
11f8ea	2014-05-16	St. Mark's Maternity Hospital (SMMH)	12000	Secondary
b8812a	2014-05-18	Port Hospital	50280	Secondary
893f25	2014-05-21	Military Hospital	40500	Secondary
893f25	2014-05-21	Military Hospital	10000	Primary
be99c8	2014-05-22	Port Hospital	50280	Secondary

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Semi join

A semi join is a "filtering join" which uses another dataset *not to add rows or columns, but to perform filtering.*

A **semi-join keeps all observations in the baseline data frame that have a match in the secondary data frame** (but does not add new columns nor duplicate any rows for multiple matches). Read more about these "filtering" joins here.

As an example, the below code returns rows from the `hosp_info` data frame that have matches in `linelist_mini` based on hospital name.

```
hosp_info %>%
  semi_join(linelist_mini, by = c("hosp_name" = "hospital"))
```

```
                           hosp_name catchment_pop     level
1                  Military Hospital         40500 Secondary
2                  Military Hospital         10000   Primary
3                      Port Hospital         50280 Secondary
4 St. Mark's Maternity Hospital (SMMH)         12000 Secondary
```

Anti join

The anti join is another "filtering join" that returns rows in the baseline data frame that *do not* have a match in the secondary data frame.

Read more about filtering joins here.

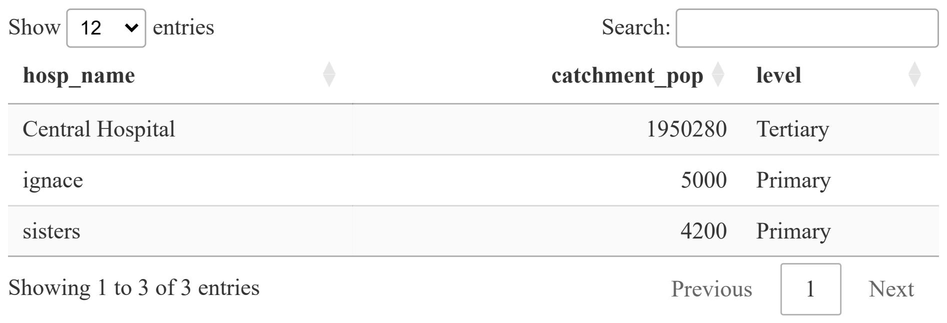
Common scenarios for an anti-join include identifying records not present in another data frame, troubleshooting spelling in a join (reviewing records that *should have* matched), and examining records that were excluded after another join.

As with `right_join()` and `left_join()`, the *baseline* data frame (listed first) is important. The returned rows are from the baseline data frame only. Notice in the gif below that row in the secondary data frame (purple row 4) is not returned even though it does not match with the baseline.

* Simple `anti_join()` example

For a simple example, let's find the `hosp_info` hospitals that do not have any cases present in `linelist_mini`. We list `hosp_info` first, as the baseline data frame. The hospitals which are not present in `linelist_mini` are returned.

```r
hosp_info %>%
  anti_join(linelist_mini, by = c("hosp_name" = "hospital"))
```



Show 12 entries Search:

hosp_name	catchment_pop	level
Central Hospital	1950280	Tertiary
ignace	5000	Primary
sisters	4200	Primary

Showing 1 to 3 of 3 entries

* Complex `anti_join()` example

For another example, let us say we ran an `inner_join()` between `linelist_mini` and `hosp_info`. This returns only a subset of the original `linelist_mini` records, as some are not present in `hosp_info`.

```
linelist_mini %>%
  inner_join(hosp_info, by = c("hospital" = "hosp_name"))
```

```
Warning in inner_join(., hosp_info, by = c(hospital = "hosp_name")): Detected an unexpected 
i Row 5 of `x` matches multiple rows in `y`.
i Row 4 of `y` matches multiple rows in `x`.
i If a many-to-many relationship is expected, set `relationship =
  "many-to-many"` to silence this warning.
```

Show 8 entries Search:

case_id	date_onset	hospital	catchment_pop	level
11f8ea	2014-05-16	St. Mark's Maternity Hospital (SMMH)	12000	Secondary
b8812a	2014-05-18	Port Hospital	50280	Secondary
893f25	2014-05-21	Military Hospital	40500	Secondary
893f25	2014-05-21	Military Hospital	10000	Primary
be99c8	2014-05-22	Port Hospital	50280	Secondary

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To review the `linelist_mini` records that were excluded during the inner join, we can run an anti-join with the same settings (`linelist_mini` as the baseline).

```r
linelist_mini %>%
  anti_join(hosp_info, by = c("hospital" = "hosp_name"))
```

Show 8 entries Search:

case_id	date_onset	hospital
5fe599	2014-05-13	Other
8689b7	2014-05-13	Missing
07e3e8	2014-05-27	Missing
369449	2014-06-02	Missing
f393b4	2014-06-05	Missing
1389ca	2014-06-05	Missing

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To see the `hosp_info` records that were excluded in the inner join, we could also run an anti-join with `hosp_info` as the baseline data frame.

Binding and aligning

Another method of combining two data frames is "binding" them together. You can also think of this as "appending" or "adding" rows or columns.

This section will also discuss how to "align" the order of rows of one data frame to the order in another data frame. This topic is discussed below in the section on Binding columns.

Bind rows

To bind rows of one data frame to the bottom of another data frame, use `bind_rows()` from **dplyr**. It is very inclusive, so any column present in either data frame will be included in the output. A few notes:

- Unlike the **base** R version `row.bind()`, **dplyr**'s `bind_rows()` does not require that the order of columns be the same in both data frames. As long as the column names are spelled identically, it will align them correctly.

- You can optionally specify the argument `.id =`. Provide a character column name. This will produce a new column that serves to identify which data frame each row originally came from.

- You can use `bind_rows()` on a `list` of similarly-structured data frames to combine them into one data frame.

One common example of row binding is to bind a "total" row onto a descriptive table made with **dplyr**'s `summarise()` function. Below we create a table of case counts and median CT values by hospital with a total row.

The function `summarise()` is used on data grouped by hospital to return a summary data frame by hospital. But the function `summarise()` does not automatically produce a "totals" row, so we create it by summarising the data *again*, but with the data not grouped by hospital. This produces a second data frame of just one row. We can then bind these data frames together to achieve the final table.

```
# Create core table
###################
hosp_summary <- linelist %>%
  group_by(hospital) %>%                        # Group data by hospital
  summarise(                                          # Create new summary columns of indicators
    cases = n(),                                        # Number of rows per hospital-outcome gr
    ct_value_med = median(ct_blood, na.rm=T))           # median CT value per group
```

Here is the `hosp_summary` data frame:

Show 10 entries Search:

hospital	cases	ct_value_med
Central Hospital	454	22
Military Hospital	896	21
Missing	1469	21
Other	885	22
Port Hospital	1762	22
St. Mark's Maternity Hospital (SMMH)	422	22

Showing 1 to 6 of 6 entries Previous 1 Next

Create a data frame with the "total" statistics (*not grouped by hospital*). This will return just one row.

```
# create totals
###############
totals <- linelist %>%
  summarise(
    cases = n(),                               # Number of rows for whole dataset
    ct_value_med = median(ct_blood, na.rm=T))  # Median CT for whole dataset
```

And below is that `totals` data frame. Note how there are only two columns. These columns are also in `hosp_summary`, but there is one column in `hosp_summary` that is not in `totals` (`hospital`).

Show 10 entries Search:

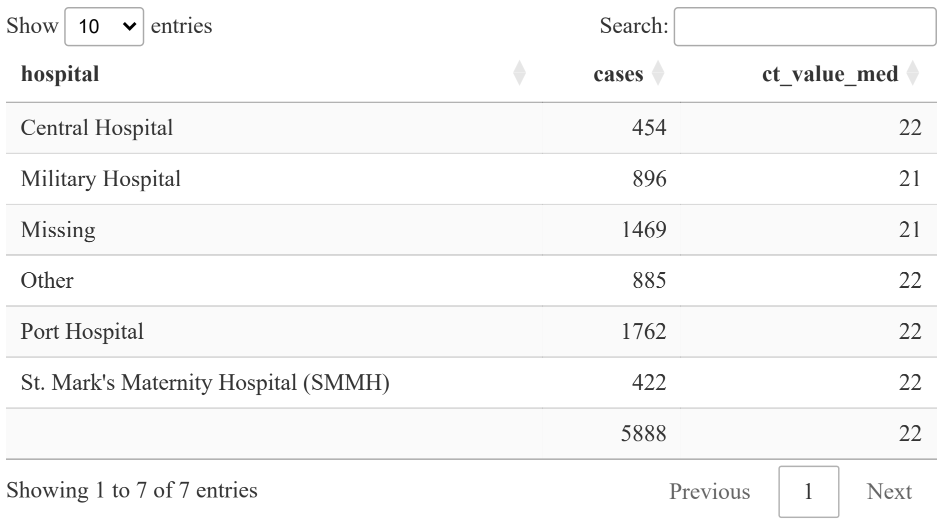
cases	ct_value_med
5888	22

Showing 1 to 1 of 1 entries Previous 1 Next

Now we can bind the rows together with `bind_rows()`.

```r
# Bind data frames together
combined <- bind_rows(hosp_summary, totals)
```

Now we can view the result. See how in the final row, an empty `NA` value fills in for the column `hospital` that was not in `hosp_summary`. You could "fill-in" this cell with "Total" using `replace_na()`.



hospital	cases	ct_value_med
Central Hospital	454	22
Military Hospital	896	21
Missing	1469	21
Other	885	22
Port Hospital	1762	22
St. Mark's Maternity Hospital (SMMH)	422	22
	5888	22

Showing 1 to 7 of 7 entries

Bind columns

There is a similar **dplyr** function `bind_cols()` which you can use to combine two data frames sideways. Note that rows are matched to each other *by position* (not like a *join* above) - for example the 12th row in each data frame will be aligned.

For an example, we bind several summary tables together. In order to do this, we also demonstrate how to re-arrange the order of rows in one data frame to match the order in another data frame, with `match()`.

Here we define `case_info` as a summary data frame of linelist cases, by hospital, with the number of cases and the number of deaths.

```
# Case information
case_info <- linelist %>%
  group_by(hospital) %>%
  summarise(
    cases = n(),
    deaths = sum(outcome == "Death", na.rm=T)
  )
```

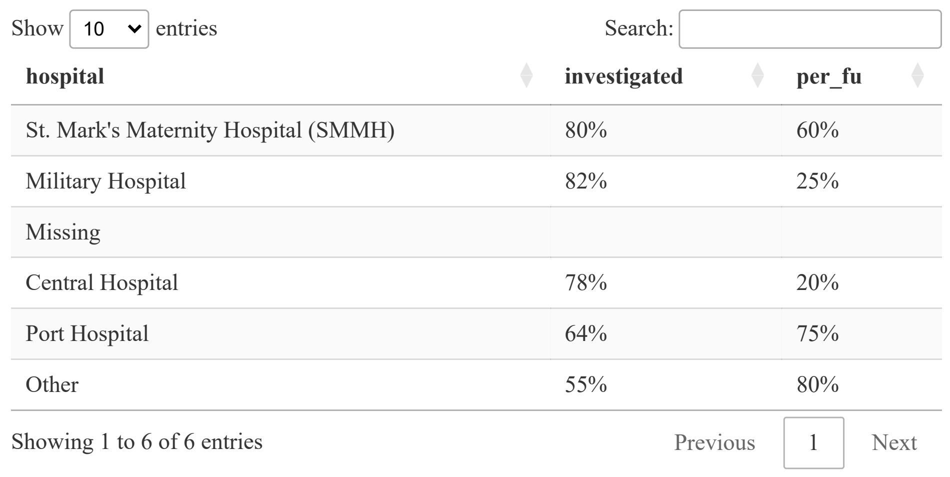
Show 10 entries   Search:

hospital	cases	deaths
Central Hospital	454	193
Military Hospital	896	399
Missing	1469	611
Other	885	395
Port Hospital	1762	785
St. Mark's Maternity Hospital (SMMH)	422	199

Showing 1 to 6 of 6 entries   Previous 1 Next

And let's say that here is a different data frame `contact_fu` containing information on the percent of exposed contacts investigated and "followed-up", again by hospital.

```
contact_fu <- data.frame(
  hospital = c("St. Mark's Maternity Hospital (SMMH)", "Military Hospital", "Missing", "Ce
  investigated = c("80%", "82%", NA, "78%", "64%", "55%"),
  per_fu = c("60%", "25%", NA, "20%", "75%", "80%")
)
```



Show 10 entries Search:

hospital	investigated	per_fu
St. Mark's Maternity Hospital (SMMH)	80%	60%
Military Hospital	82%	25%
Missing		
Central Hospital	78%	20%
Port Hospital	64%	75%
Other	55%	80%

Showing 1 to 6 of 6 entries

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Next

Note that the hospitals are the same, but are in different orders in each data frame. The easiest solution would be to use a `left_join()` on the `hospital` column, but you could also use `bind_cols()` with one extra step.

* Use `match()` to align ordering

Because the row orders are different, a simple `bind_cols()` command would result in a mismatch of data. To fix this we can use `match()` from **base** R to align the rows of a data frame in the same order as in another. We assume for this approach that there are no duplicate values in either data frame.

When we use `match()`, the syntax is `match(TARGET ORDER VECTOR, DATA FRAME COLUMN TO CHANGE)`, where the first argument is the desired order (either a stand-alone vector, or in this case a column in a data frame), and the second argument is the data frame column in the data frame that will be re-ordered. The output of `match()` is a vector of numbers representing the correct position ordering. You can read more with `?match`.

```
match(case_info$hospital, contact_fu$hospital)
```

```
[1] 4 2 3 6 5 1
```

You can use this numeric vector to re-order the data frame - place it within subset brackets `[ ]` *before the comma.* The command below creates a new data frame, defined as the old one in which the rows are ordered in the numeric vector above.

```
contact_fu_aligned <- contact_fu[match(case_info$hospital, contact_fu$hospital),]
```

Show 10 entries

Search:

hospital	investigated	per_fu
Central Hospital	78%	20%
Military Hospital	82%	25%
Missing		
Other	55%	80%
Port Hospital	64%	75%
St. Mark's Maternity Hospital (SMMH)	80%	60%

Showing 1 to 6 of 6 entries

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Now we can bind the data frame columns together, with the correct row order. Note that some columns are duplicated and will require cleaning with `rename()`. Read more aboout `bind_rows()` here.

```r
bind_cols(case_info, contact_fu)
```

```
New names:
* `hospital` -> `hospital...1`
* `hospital` -> `hospital...4`
```

```
# A tibble: 6 x 6
  hospital...1                     cases deaths hospital...4 investigated per_fu
  <chr>                            <int>  <int> <chr>        <chr>        <chr>
1 Central Hospital                   454    193 St. Mark's ~ 80%          60%
2 Military Hospital                  896    399 Military Ho~ 82%          25%
3 Missing                           1469    611 Missing      <NA>         <NA>
4 Other                              885    395 Central Hos~ 78%          20%
5 Port Hospital                     1762    785 Port Hospit~ 64%          75%
6 St. Mark's Maternity Hospital (~   422    199 Other        55%          80%
```

A **base** R alternative to `bind_cols` is `cbind()`, which performs the same operation.