Data Cleaning

Recap on summarization

- `summary(x)`: quantile information
- `count(x)`: what unique values do you have?
  - `distinct()`: what are the distinct values?
  - `n_distinct()` with `pull()`: how many distinct values?
- `group_by()`: changes all subsequent functions
  - combine with `summarize()` to get statistics per group
  - combine with `mutate()` to add column
- `summarize()` with `n()` gives the count (NAs included)

 Day 4 Cheatsheet

Recap on data classes

- There are two types of number class objects: integer and double
- Logic class objects only have `TRUE` or `FALSE` (without quotes)
- `class()` can be used to test the class of an object x
- `as.CLASS_NAME(x)` can be used to change the class of an object x
- Factors are a special character class that has levels - more on that soon!
- tibbles show column classes!
- two dimensional object classes include: data frames, tibbles, matrices, and lists
- Dates can be handled with the `lubridate` package
- Make sure you choose the right function for the way the date is formatted!

 Day 4 Cheatsheet

Data Cleaning

In general, data cleaning is a process of investigating your data for inaccuracies, or recoding it in a way that makes it more manageable.

 MOST IMPORTANT RULE - LOOK AT YOUR DATA!

Dealing with Missing Data

Missing data types

One of the most important aspects of data cleaning is missing values.

Types of “missing” data:

- `NA` - general missing data
- `NaN` - stands for “**N**ot **a N**umber”, happens when you do 0/0.
- `Inf` and `-Inf` - Infinity, happens when you divide a positive number (or negative number) by 0.

Finding Missing data

- `is.na` - looks for `NAN` and `NA`
- `is.nan`- looks for `NAN`
- `is.infinite` - looks for Inf or -Inf

```
test <- c(0,NA, -1)
test/0
```

```
[1]  NaN   NA -Inf
```

```
test <- test/0
is.na(test)
```

```
[1]  TRUE  TRUE FALSE
```

```
is.nan(test)
```

```
[1]  TRUE FALSE FALSE
```

```
is.infinite(test)
```

```
[1] FALSE FALSE  TRUE
```

Useful checking functions

`any()` can help you check if there are any `NA` values in a vector

```
test
```

```
[1]  NaN   NA -Inf
```

```
any(is.na(test))
```

```
[1] TRUE
```

Finding NA values with count()

Check the values for your variables, are they what you expect?

`count()` is a great option because it helps you check if rare values make sense.

Let's look at the CO heat-related ER visits dataset again.

```
er <- read_csv(file =
    "https://daseh.org/data/CO_ER_heat_visits.csv")
er |> count(visits)
```

```
# A tibble: 37 × 2
   visits     n
    <dbl> <int>
 1      0   339
 2     11     2
 3     12     5
 4     13     8
 5     14     3
 6     15     2
 7     16     3
 8     17     3
 9     18     5
10     19     7
# ℹ 27 more rows
```

naniar

Sometimes you need to look at lots of data though… the `naniar` package is a good option.

```
#install.packages("naniar")
library(naniar)
```

"Artwork by @allison_horst". https://allisonhorst.com/

naniar: `pct_complete()`

This can tell you if there are missing values in the dataset.

```
pct_complete(er)
```

```
[1] 73.65451
```

Or for a particular variable:

```
er |> select(visits) |>
  pct_complete()
```

```
[1] 60.54688
```

```
er |> select(rate) |>
  pct_complete()
```

```
[1] 60.54688
```

naniar::`miss_var_summary()`

To get the percent missing (and counts) for each variable as a table, use this function:

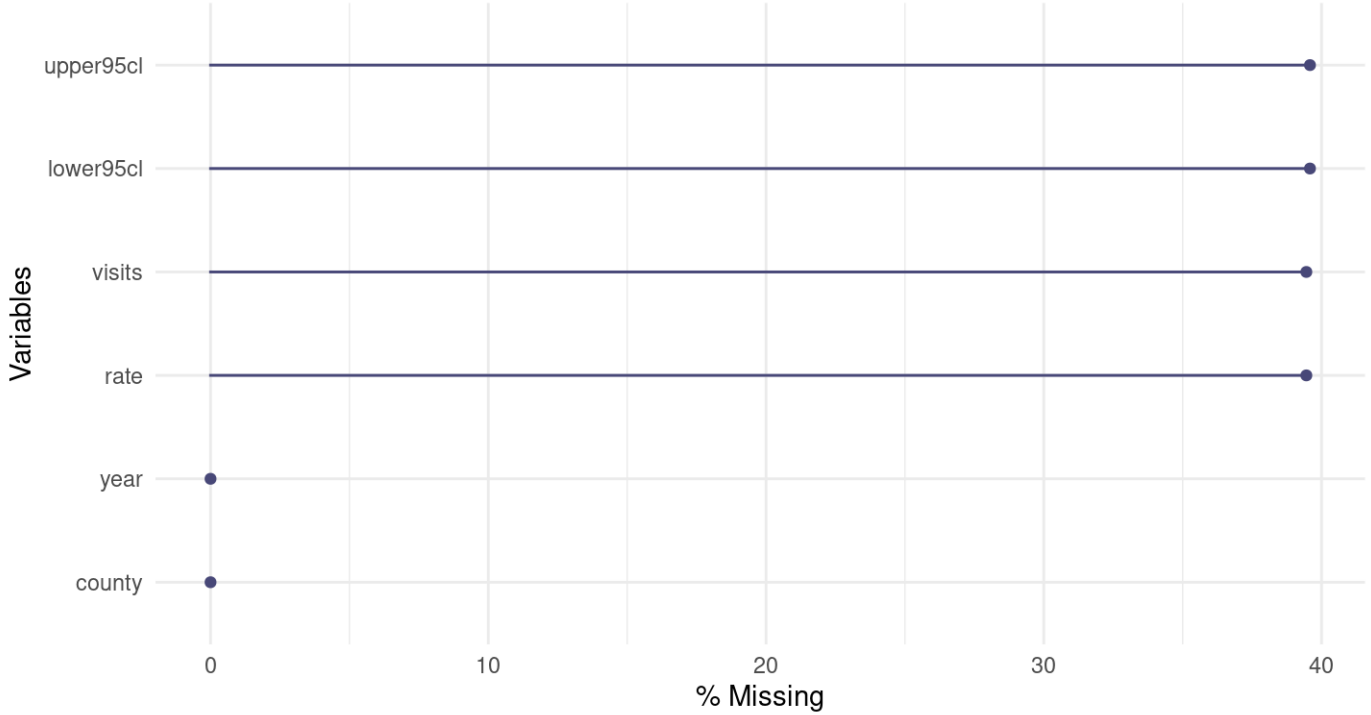
```
miss_var_summary(er)
```

```
# A tibble: 6 × 3
  variable  n_miss pct_miss
  <chr>      <int>    <num>
1 lower95cl    304     39.6
2 upper95cl    304     39.6
3 rate         303     39.5
4 visits       303     39.5
5 county         0      0
6 year           0      0
```

naniar plots

The `gg_miss_var()` function creates a nice plot about the number of missing values for each variable, (need a data frame).

```
gg_miss_var(er, show_pct = TRUE)
```



Missing Data Issues

Recall that mathematical operations with `NA` often result in `NA`s.

```
sum(c(1,2,3,NA))
```

```
[1] NA
```

```
mean(c(1,2,3,NA))
```

```
[1] NA
```

```
median(c(1,2,3,NA))
```

```
[1] NA
```

Missing Data Issues

This is also true for logical data. Recall that `TRUE` is evaluated as 1 and `FALSE` is evaluated as 0.

```
x <- c(TRUE, TRUE, TRUE, TRUE, FALSE, NA)
sum(x)
```

```
[1] NA
```

```
sum(x, na.rm = TRUE)
```

```
[1] 4
```

filter() and missing data

Be **careful** with missing data using subsetting!

`filter()` removes missing values by default. Because R can't tell for sure if an `NA` value meets the condition. To keep them need to add `is.na()` conditional.

Think about if this is OK or not - it depends on your data!

filter() and missing data

What if NA values represent values that are so low it is undetectable?

Filter will drop them from the data.

```
er |> filter(visits > 0)
```

```
# A tibble: 126 × 6
   county  rate lower95cl upper95cl visits  year
   <chr>  <dbl>     <dbl>     <dbl>  <dbl> <dbl>
 1 Adams   6.73     NA         9.24     29  2011
 2 Adams   4.84      2.85     NA        23  2012
 3 Adams   6.84      4.36      9.31     31  2013
 4 Adams   3.08      1.71      4.85     15  2014
 5 Adams   3.36      1.89      5.23     16  2015
 6 Adams   8.85      6.12     11.6      42  2016
 7 Adams   6.63      4.29      8.98     32  2017
 8 Adams   7.11      4.77      9.44     37  2018
 9 Adams   6.76      4.53      8.99     36  2019
10 Adams   4.76      2.82      6.70     24  2020
# ℹ 116 more rows
```

filter() and missing data

`is.na()` can help us keep them.

```
er |> filter(visits > 0 | is.na(visits))
```

```
# A tibble: 429 × 6
   county  rate lower95cl upper95cl visits  year
   <chr>  <dbl>     <dbl>     <dbl>  <dbl> <dbl>
 1 Adams   6.73     NA         9.24     29  2011
 2 Adams   4.84      2.85     NA        23  2012
 3 Adams   6.84      4.36      9.31     31  2013
 4 Adams   3.08      1.71      4.85     15  2014
 5 Adams   3.36      1.89      5.23     16  2015
 6 Adams   8.85      6.12     11.6      42  2016
 7 Adams   6.63      4.29      8.98     32  2017
 8 Adams   7.11      4.77      9.44     37  2018
 9 Adams   6.76      4.53      8.99     36  2019
10 Adams   4.76      2.82      6.70     24  2020
# ℹ 419 more rows
```

To remove **rows** with **NA** values for a **variable** use **drop_na( )**

A function from the `tidyr` package. (Need a data frame to start!)

Disclaimer: Don't do this unless you have thought about if dropping `NA` values makes sense based on knowing what these values mean in your data. **Also consider if you need those rows for values for other variables.**

```
dim(er)
```

```
[1] 768   6
```

```
er_drop <- er |> drop_na(lower95cl)
dim(er_drop)
```

```
[1] 464   6
```

Let's take a look

Can still have NAs for other columns

```
er_drop
```

```
# A tibble: 464 × 6
   county  rate lower95cl upper95cl visits  year
   <chr>  <dbl>     <dbl>     <dbl>  <dbl> <dbl>
 1 Adams   4.84      2.85     NA         23  2012
 2 Adams   6.84      4.36      9.31      31  2013
 3 Adams   3.08      1.71      4.85      15  2014
 4 Adams   3.36      1.89      5.23      16  2015
 5 Adams   8.85      6.12     11.6       42  2016
 6 Adams   6.63      4.29      8.98      32  2017
 7 Adams   7.11      4.77      9.44      37  2018
 8 Adams   6.76      4.53      8.99      36  2019
 9 Adams   4.76      2.82      6.70      24  2020
10 Adams   6.93      4.61      9.25      35  2021
# ℹ 454 more rows
```

To remove rows with NA values for a data frame use drop_na( )

This function of the `tidyr` package drops rows with **any** missing data in **any** column when used on a df.

```
er_drop <- er |> drop_na()
er_drop
```

```
# A tibble: 463 × 6
   county  rate lower95cl upper95cl visits  year
   <chr>  <dbl>     <dbl>     <dbl>  <dbl> <dbl>
 1 Adams   6.84      4.36      9.31     31  2013
 2 Adams   3.08      1.71      4.85     15  2014
 3 Adams   3.36      1.89      5.23     16  2015
 4 Adams   8.85      6.12     11.6      42  2016
 5 Adams   6.63      4.29      8.98     32  2017
 6 Adams   7.11      4.77      9.44     37  2018
 7 Adams   6.76      4.53      8.99     36  2019
 8 Adams   4.76      2.82      6.70     24  2020
 9 Adams   6.93      4.61      9.25     35  2021
10 Adams   8.23      5.81     10.6      45  2022
# ℹ 453 more rows
```

Drop **columns** with any missing values

Use the `miss_var_which()` function from `naniar`

```
miss_var_which(er)# which columns have missing values
```

```
[1] "rate"      "lower95cl" "upper95cl" "visits"
```

Drop **columns** with any missing values

`miss_var_which` and function from `naniar` (need a data frame)

```
er_drop <- er |> select(!miss_var_which(er))
er_drop
```

```
# A tibble: 768 × 2
   county  year
   <chr>  <dbl>
 1 Adams   2011
 2 Adams   2012
 3 Adams   2013
 4 Adams   2014
 5 Adams   2015
 6 Adams   2016
 7 Adams   2017
 8 Adams   2018
 9 Adams   2019
10 Adams   2020
# ℹ 758 more rows
```

Change a value to be `NA`

Let's say we think that all 0 values should be `NA`.

Maybe we think the person who entered the CO heat-related ER visits data made a mistake in how they coded missing data.

```
er |> count(visits)
```

```
# A tibble: 37 × 2
   visits     n
    <dbl> <int>
 1      0   339
 2     11     2
 3     12     5
 4     13     8
 5     14     3
 6     15     2
 7     16     3
 8     17     3
 9     18     5
10     19     7
# ℹ 27 more rows
```

Change a value to be `NA`

The `na_if()` function of `dplyr` can be helpful for changing all 0 values to `NA`.

```
er_nozero <- er |>
  mutate(visits = na_if(visits, 0))

er_nozero |> count(visits)
```

```
# A tibble: 36 × 2
   visits     n
    <dbl> <int>
 1     11     2
 2     12     5
 3     13     8
 4     14     3
 5     15     2
 6     16     3
 7     17     3
 8     18     5
 9     19     7
10     20     2
# ℹ 26 more rows
```

Change `NA` to be a value

The `replace_na()` function (part of the `tidyr` package), can do the opposite of `na_if()`. (note that you must use numeric values as replacement - we will show how to replace with character strings soon)

```
er |>
  mutate(visits = replace_na(visits, 0)) |>
  count(visits)
```

```
# A tibble: 36 × 2
   visits     n
    <dbl> <int>
 1      0   642
 2     11     2
 3     12     5
 4     13     8
 5     14     3
 6     15     2
 7     16     3
 8     17     3
 9     18     5
10     19     7
# ℹ 26 more rows
```

Think about NA

THINK ABOUT YOUR DATA FIRST!

- Sometimes removing NA values leads to distorted math - be careful!
- Think about what your NA means for your data (are you sure ?).
  - Is an NA for values so low they could not be reported?
  - Or is it if it was too low and also if there was a different issue (like no one reported)?

Think about NA

If it is something more like a zero then you might want it included in your data like a zero instead of an NA.

Example: - survey reports NA if student has never tried cigarettes - survey reports 0 if student has tried cigarettes but did not smoke that week

 You might want to keep the NA values so that you know the original sample size.

Word of caution

- Calculating percentages will give you a different result depending on your choice to include NA values.!

This is because the denominator changes.

Word of caution - Percentages with NA

```
count(er, visits) |> mutate(percent = (n/(sum(n)) *100))
```

```
# A tibble: 37 × 3
   visits     n percent
    <dbl> <int>   <dbl>
 1      0   339  44.1
 2     11     2   0.260
 3     12     5   0.651
 4     13     8   1.04
 5     14     3   0.391
 6     15     2   0.260
 7     16     3   0.391
 8     17     3   0.391
 9     18     5   0.651
10     19     7   0.911
# ℹ 27 more rows
```

Word of caution - Percentages with `NA`

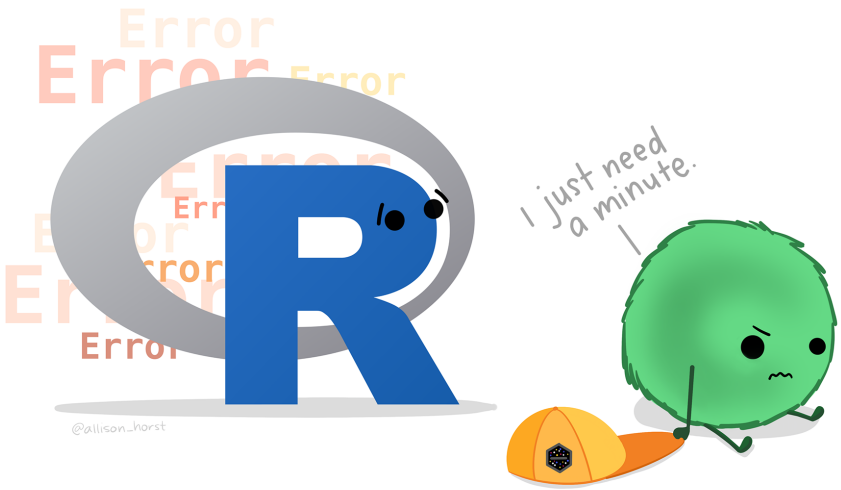
```
er |> drop_na(visits) |>
  count(visits) |> mutate(percent = (n/(sum(n)) *100))
```

```
# A tibble: 36 × 3
   visits     n percent
    <dbl> <int>   <dbl>
 1      0   339  72.9
 2     11     2   0.430
 3     12     5   1.08
 4     13     8   1.72
 5     14     3   0.645
 6     15     2   0.430
 7     16     3   0.645
 8     17     3   0.645
 9     18     5   1.08
10     19     7   1.51
# ℹ 26 more rows
```

Should you be dividing by the total count with `NA` values included?
It depends on your data and what `NA` might mean.
Pay attention to your data and your `NA` values!

Don’t forget about the common issues

- Extra or Missing commas
- Extra or Missing parentheses
- Case sensitivity
- Spelling



GUT CHECK: What function can be used to remove NA values from a full dataframe or for an individual column?

A. `drop_nulls()`

B. `drop_na()`

C. `rem_na()`

GUT CHECK: How can you keep NA values when using `filter`?

A. include `| is.na()`

B. include `& is.na()`

Summary

- `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 - can't confirm or deny if condition is met (need `| is.na()` to keep them)
- `drop_na()` can help you remove `NA` values from a variable or an entire data frame
- `NA` values can change your calculation results
- think about what `NA` values represent - don't drop them if you shouldn't
- `na_if()` will make `NA` values for a particular value
- `replace_na()` will replace `NA values with a particular value

Lab Part 1

- Class Website
- Lab. Day 5 Cheatsheet

Recoding Variables

Example of Recoding

Let's upload some practice data about microplastics. Maybe we measured the level of microplastics in someone who eats a fish versus someone who is a vegetarian.

https://www.medicalnewstoday.com/articles/what-do-we-know-about-microplastics-in-food#Common-microplastics-in-food
https://www.sciencedirect.com/science/article/pii/S0045653523028072
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5708064/

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

```
Rows: 12 Columns: 4
── Column specification ────────────────────────────────────────────────────────
Delimiter: ","
chr (2): Foods, microplastic
dbl (2): blood_level_start_nM, blood_level_change_nM

ℹ Use `spec()` to retrieve the full column specification for this data.
ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message
```

microplastics data

```
plastics
```

```
# A tibble: 12 × 4
   Foods microplastic blood_level_start_nM blood_level_change_nM
   <chr> <chr>                        <dbl>                  <dbl>
 1 A     Dioxin                           1                    2.5
 2 B     Dioxin                           7                    2.5
 3 B     Other                            2                    0.5
 4 A     Bisphenol A                      3                   -0.5
 5 B     BPA                              5                    0.5
 6 B     dioxin                           8                    0.5
 7 A     bpa                              6                    2.5
 8 B     Other                            5                    3.5
 9 B     dioxin                           2                    0.5
10 A     bpa                              1                    1.5
11 B     BPA                              7                    1.5
12 B     Other                            3                    2.5
```

Oh dear…

This needs lots of recoding.

```
plastics |>
  count(microplastic)
```

```
# A tibble: 6 × 2
  microplastic     n
  <chr>        <int>
1 BPA              2
2 Bisphenol A      1
3 Dioxin           2
4 Other            3
5 bpa              2
6 dioxin           2
```

`dplyr` can help!

Using Excel to find all of the different ways `microplastic` has been coded, could be hectic! In `dplyr` you can use the `case_when` function.

Or you can use `case_when()`

The `case_when()` function of `dplyr` can help us to do this as well.

It is more flexible and powerful.

(need `mutate` here too!)

Or you can use **case_when( )**

Need quotes for conditions and new values!

```
plastics |>
  mutate(microplastic_recoded = case_when(
                                microplastic == "Bisphenol A" ~ "BPA",
                                microplastic == "bpa" ~ "BPA",
                                microplastic == "dioxin" ~"Dioxin"))  |>
  count(microplastic, microplastic_recoded)

# A tibble: 6 × 3
  microplastic microplastic_recoded     n
  <chr>        <chr>                <int>
1 BPA          <NA>                     2
2 Bisphenol A  BPA                      1
3 Dioxin       <NA>                     2
4 Other        <NA>                     3
5 bpa          BPA                      2
6 dioxin       Dioxin                   2
```

What happened?

We seem to have `NA` values!

We didn't specify what happens to values that were already `Other` or `Dioxin` or `BPA`.

```
plastics |>
  mutate(microplastic_recoded = case_when(
                                microplastic == "Bisphenol A" ~ "BPA",
                                microplastic == "bpa" ~ "BPA",
                                microplastic == "dioxin" ~"Dioxin"))  |>
  count(microplastic, microplastic_recoded)
```

`case_when()` drops unspecified values

Note that automatically values not reassigned explicitly by `case_when()` will be `NA` unless otherwise specified.

```
# General Format - this is not code!
{data_input} |>
  mutate({variable_to_fix} = case_when({Variable_fixing}
              /some condition/ ~ {value_for_con},
                      .default = {value_for_not_meeting_condition}) # need this t
```

{value_for_not_meeting_condition} could be something new or it can be the original values of the column

case_when with .default = original variable name

```
plastics |>
  mutate(microplastic_recoded = case_when(
                                microplastic == "Bisphenol A" ~ "BPA",
                                microplastic == "bpa" ~ "BPA",
                                microplastic =="dioxin" ~"Dioxin",
                                .default = microplastic)) |>
  count(microplastic_recoded)

# A tibble: 3 × 2
  microplastic_recoded     n
  <chr>                <int>
1 BPA                      5
2 Dioxin                   4
3 Other                    3
```

Typically it is good practice to include the .default statement

You never know if you might be missing something - and if a value already was an NA it will stay that way.

```
plastics |>
  mutate(microplastic_recoded = case_when(
                                microplastic == "Bisphenol A" ~ "BPA",
                                microplastic == "bpa" ~ "BPA",
                                microplastic == "dioxin" ~"Dioxin",
                                .default = microplastic)) |>
  count(microplastic, microplastic_recoded)
```

case_when() can also overwrite/update a variable

You need to specify what we want in the first part of `mutate`.

```
plastics |>
  mutate(microplastic = case_when(
                              microplastic == "Bisphenol A" ~ "BPA",
                              microplastic == "bpa" ~ "BPA",
                              microplastic == "dioxin" ~"Dioxin",
                              .default = microplastic)) |>
  count(microplastic)

# A tibble: 3 × 2
  microplastic     n
  <chr>        <int>
1 BPA              5
2 Dioxin           4
3 Other            3
```

More complicated case_when()

`case_when` can do complicated statements and can match many patterns at a time.

```
plastics |>
  mutate(microplastic_recoded = case_when(
    microplastic %in% c("dioxin", "Dioxin") ~ "Dioxin",
    microplastic %in% c("BPA", "bpa", "Bisphenol A") ~ "BPA",
                     .default = microplastic)) |>

  count(microplastic, microplastic_recoded)
```

```
# A tibble: 6 × 3
  microplastic microplastic_recoded     n
  <chr>        <chr>                <int>
1 BPA          BPA                      2
2 Bisphenol A  BPA                      1
3 Dioxin       Dioxin                   2
4 Other        Other                    3
5 bpa          BPA                      2
6 dioxin       Dioxin                   2
```

Another reason for **case_when( )**

`case_when` can do very sophisticated comparisons!

Here we create a new variable called `Effect`.

```
plastics <- plastics |>
      mutate(Effect = case_when(
                      blood_level_change_nM > 0 ~ "Increase",
                      blood_level_change_nM == 0 ~ "Same",
                      blood_level_change_nM < 0 ~ "Decrease"))

head(plastics)
```

```
# A tibble: 6 × 5
  Foods microplastic blood_level_start_nM blood_level_change_nM Effect
  <chr> <chr>                       <dbl>                  <dbl> <chr>
1 A     Dioxin                          1                    2.5 Increase
2 B     Dioxin                          7                    2.5 Increase
3 B     Other                           2                    0.5 Increase
4 A     Bisphenol A                     3                   -0.5 Decrease
5 B     BPA                             5                    0.5 Increase
6 B     dioxin                          8                    0.5 Increase
```

Now it is easier to see what is happening

```
plastics |>
  count(Foods, Effect)

# A tibble: 3 × 3
  Foods Effect       n
  <chr> <chr>    <int>
1 A     Decrease     1
2 A     Increase     3
3 B     Increase     8
```

Note that if you change data classes this might impact .default

```
plastics <- plastics |>
      mutate(Effect = case_when(
                        blood_level_change_nM > 0 ~ "Increase",
                        blood_level_change_nM == 0 ~ "Same",
                        blood_level_change_nM < 0 ~ "Decrease",
                        .default = blood_level_change_nM))
# this will give an error!

plastics <- plastics |>
      mutate(Effect = case_when(
                        blood_level_change_nM > 0 ~ "Increase",
                        blood_level_change_nM == 0 ~ "Same",
                        blood_level_change_nM < 0 ~ "Decrease",
                        .default = as.character(blood_level_change_nM)))
# this works!
```

multiple conditions with **case_when** recoding

```
plastics |>
      mutate(Amt_change = case_when(
                        blood_level_change_nM > 0 & blood_level_change_nM < 2 ~ "Sma
                        blood_level_change_nM >= 2 ~ "Large",
                        blood_level_change_nM < 0 & blood_level_change_nM > -2 ~ "Sm
                        blood_level_change_nM <= -2 ~ "Large",
                        blood_level_change_nM == 0 ~ "none")) |>
  head()
```

```
# A tibble: 6 × 6
  Foods microplastic blood_level_start_nM blood_level_change_nM Effect
  <chr> <chr>                       <dbl>                  <dbl> <chr>
1 A     Dioxin                          1                    2.5 Increase
2 B     Dioxin                          7                    2.5 Increase
3 B     Other                           2                    0.5 Increase
4 A     Bisphenol A                     3                   -0.5 Decrease
5 B     BPA                             5                    0.5 Increase
6 B     dioxin                          8                    0.5 Increase
# ℹ 1 more variable: Amt_change <chr>
```

GUT CHECK: we need to use what function with **`case_when()`** to modify or create a new variable?

A. `modify()`

B. `select()`

C. `mutate()`

GUT CHECK: If we want all unspecified values to remain the same with `case_when()`, how should we complete the `.default` statement?

A. = the name of the variable we are modifying or using as source

B. = “same”

Working with strings

Strings in R

- R can do much more than find exact matches for a whole string!

The `stringr` package

The `stringr` package:

- Modifying or finding **part** or all of a character string
- We will not cover `grep` or `gsub` - base R functions
  - are used on forums for answers
- Almost all functions start with `str_*`

`stringr`

`str_detect`, and `str_replace` search for matches to argument pattern within each element of a **character vector** (not data frame or tibble!).

- `str_detect` - returns `TRUE` if `pattern` is found
- `str_replace` - replaces `pattern` with `replacement`

`str_detect()`

The `string` argument specifies what to check
The `pattern` argument specifies what to check for (case sensitive)

```
Effect <- pull(plastics) |> head(n = 6)
Effect
```

```
[1] "Increase" "Increase" "Increase" "Decrease" "Increase" "Increase"
```

```
str_detect(string = Effect, pattern = "d")
```

```
[1] FALSE FALSE FALSE FALSE FALSE FALSE
```

```
str_detect(string = Effect, pattern = "D")
```

```
[1] FALSE FALSE FALSE  TRUE FALSE FALSE
```

`str_replace()`

The `string` argument specifies what to check
The `pattern` argument specifies what to check for
The `replacement` argument specifies what to replace the pattern with

```
str_replace(string = Effect, pattern = "D", replacement = "d")
```

```
[1] "Increase" "Increase" "Increase" "decrease" "Increase" "Increase"
```

`st_replace()` only replaces the first instance of the pattern in each value

`str_replace_all()` can be used to replace all instances within each value

```
str_replace(string = Effect, pattern = "e", replacement = "E")
```

```
[1] "IncrEase" "IncrEase" "IncrEase" "DEcrease" "IncrEase" "IncrEase"
```

```
str_replace_all(string = Effect, pattern = "e", replacement = "E")
```

```
[1] "IncrEasE" "IncrEasE" "IncrEasE" "DEcrEasE" "IncrEasE" "IncrEasE"
```

Subsetting part of a string

`str_sub()` allows you to subset part of a string
The `string` argument specifies what strings to work with
The `start` argument specifies position of where to start
The `end` argument specifies position of where to end

```
str_sub(string = Effect, start = 1, end = 3)
```

```
[1] "Inc" "Inc" "Inc" "Dec" "Inc" "Inc"
```

`filter` and `stringr` functions

```
head(plastics, n = 4)
```

```
# A tibble: 4 × 5
  Foods microplastic blood_level_start_nM blood_level_change_nM Effect
  <chr> <chr>                        <dbl>                  <dbl> <chr>
1 A     Dioxin                           1                    2.5 Increase
2 B     Dioxin                           7                    2.5 Increase
3 B     Other                            2                    0.5 Increase
4 A     Bisphenol A                      3                   -0.5 Decrease
```

```
plastics |>
  filter(str_detect(string = microplastic,
                    pattern = "B"))
```

```
# A tibble: 3 × 5
  Foods microplastic blood_level_start_nM blood_level_change_nM Effect
  <chr> <chr>                        <dbl>                  <dbl> <chr>
1 A     Bisphenol A                      3                   -0.5 Decrease
2 B     BPA                              5                    0.5 Increase
3 B     BPA                              7                    1.5 Increase
```

OK back to our original problem

```
count(plastics, microplastic)

# A tibble: 6 × 2
  microplastic     n
  <chr>        <int>
1 BPA              2
2 Bisphenol A      1
3 Dioxin           2
4 Other            3
5 bpa              2
6 dioxin           2
```

`case_when()` made an improvement

But we still might miss a strange value - like a misspelling

```
plastics |>
  mutate(microplastic_recoded = case_when(
    microplastic %in% c("Dioxin", "dioxin") ~ "Dioxin",
    microplastic %in% c("BPA", "bpa", "Bisphenol A") ~ "BPA",
    .default = microplastic))
```

`case_when()` improved with `stringr`

`^` indicates the beginning of a character string `$` indicates the end

```
plastics |>
  mutate(microplastic_recoded = case_when(
    str_detect(string = microplastic, pattern = "^b|^B") ~ "BPA",
    str_detect(string = microplastic, pattern = "^d|^D") ~ "Dioxin",
    .default =  microplastic)) |>
  count(microplastic, microplastic_recoded)
```

```
# A tibble: 6 × 3
  microplastic microplastic_recoded     n
  <chr>        <chr>                <int>
1 BPA          BPA                      2
2 Bisphenol A  BPA                      1
3 Dioxin       Dioxin                   2
4 Other        Other                    3
5 bpa          BPA                      2
6 dioxin       Dioxin                   2
```

This is a more robust solution! It will catch typos as long as the first letter is correct.

That's better!

GUT CHECK: What `stringr` function helps us find a string pattern?

A. `str_replace()`

B. `str_find()`

C. `str_detect()`

Separating and uniting data

Uniting columns

The `unite()` function can help combine columns
The `col` argument specifies new column name
The `sep` argument specifies what separator to use when combining -default is "_"
The `remove` argument specifies if you want to drop the old columns

```
plastics_comb <- plastics |>
  unite(Foods, Effect, col = "change", remove = TRUE)

plastics_comb

# A tibble: 12 × 4
   change     microplastic blood_level_start_nM blood_level_change_nM
   <chr>      <chr>                       <dbl>                  <dbl>
 1 A_Increase Dioxin                          1                    2.5
 2 B_Increase Dioxin                          7                    2.5
 3 B_Increase Other                           2                    0.5
 4 A_Decrease Bisphenol A                     3                   -0.5
 5 B_Increase BPA                             5                    0.5
 6 B_Increase dioxin                          8                    0.5
 7 A_Increase bpa                             6                    2.5
 8 B_Increase Other                           5                    3.5
 9 B_Increase dioxin                          2                    0.5
10 A_Increase bpa                             1                    1.5
11 B_Increase BPA                             7                    1.5
12 B_Increase Other                           3                    2.5
```

Separating columns based on a separator

The `separate()` function from `tidyr` can split a column into multiple columns.
The `col` argument specifies what column to work with
The `into` argument specifies names of new columns
The `sep` argument specifies what to separate by

```
plastics_comb <- plastics_comb |>
  separate(col = change, into = c("Foods", "Change"), sep = "_" )
plastics_comb
```

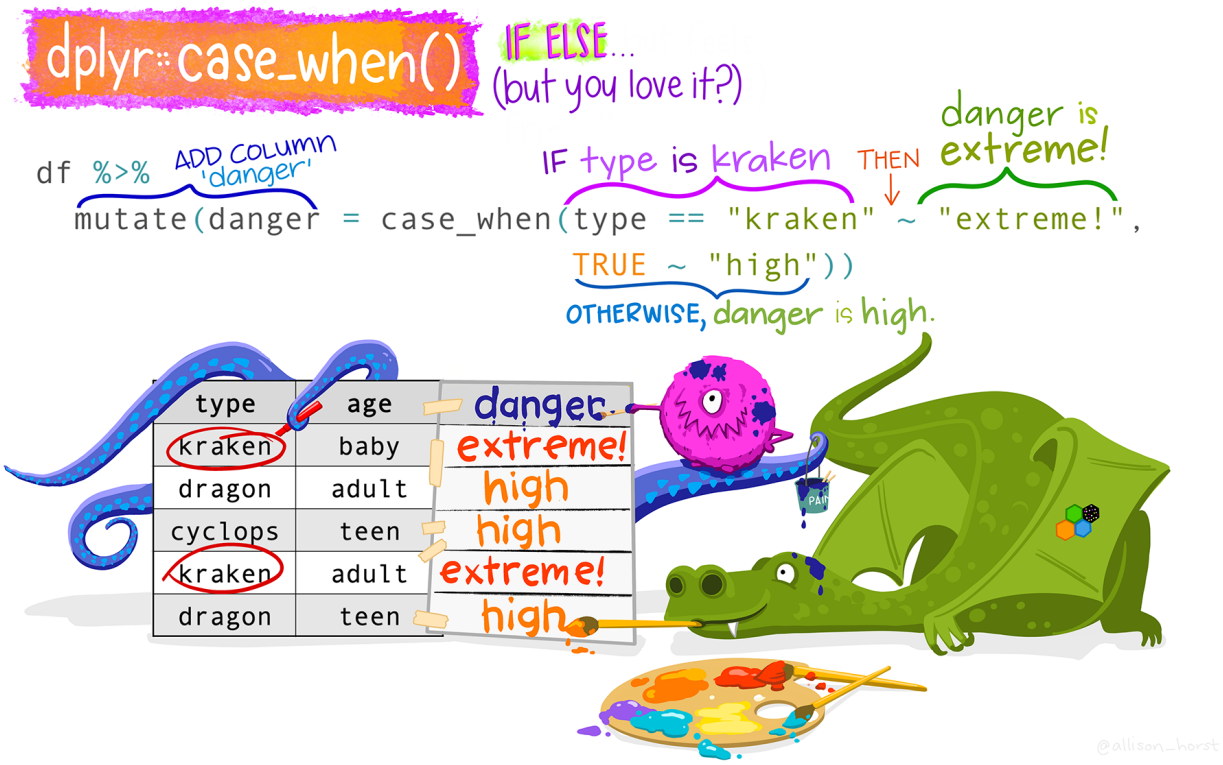
```
# A tibble: 12 × 5
   Foods Change   microplastic blood_level_start_nM blood_level_change_nM
   <chr> <chr>    <chr>                       <dbl>                  <dbl>
 1 A     Increase Dioxin                          1                    2.5
 2 B     Increase Dioxin                          7                    2.5
 3 B     Increase Other                           2                    0.5
 4 A     Decrease Bisphenol A                     3                   -0.5
 5 B     Increase BPA                             5                    0.5
 6 B     Increase dioxin                          8                    0.5
 7 A     Increase bpa                             6                    2.5
 8 B     Increase Other                           5                    3.5
 9 B     Increase dioxin                          2                    0.5
10 A     Increase bpa                             1                    1.5
11 B     Increase BPA                             7                    1.5
12 B     Increase Other                           3                    2.5
```

Summary

- `case_when()` requires `mutate()` when working with dataframes/tibbles
- `case_when()` can recode **entire values** based on **conditions** (need quotes for conditions and new values)
    - remember `case_when()` needs `.default = varaible` to keep values that aren't specified by conditions, otherwise will be `NA`

Note: you might see the `recode()` function, it only does some of what `case_when()` can do, so we skipped it, but it is in the extra slides at the end.

Summary continued



"Artwork by @allison_horst". https://allisonhorst.com/

Summary Continued

- `stringr` package has great functions for looking for specific **parts of values** especially `filter()` and `str_detect()` combined
- `stringr` also has other useful string functions like `str_detect()` (finding patterns in a column or vector), `str_subset()` (parsing text), `str_replace()` (replacing the first instance in values), `str_replace_all()` (replacing all instances in each value) and **more**!
- `separate()` can split columns into additional columns
- `unite()` can combine columns
- `:` can indicate when you want to start and end with columns next to one another

Lab Part 2

- Class Website
- Lab. • Day 5 Cheatsheet • Posit's `stringr` Cheatsheet

Image by Gerd Altmann from Pixabay

Extra Slides

`n_complete_row()` evaluating how many columns are complete for each row

```
head(plastics_comb)
```

```
# A tibble: 6 × 5
  Foods Change   microplastic blood_level_start_nM blood_level_change_nM
  <chr> <chr>    <chr>                        <dbl>                  <dbl>
1 A     Increase Dioxin                           1                    2.5
2 B     Increase Dioxin                           7                    2.5
3 B     Increase Other                            2                    0.5
4 A     Decrease Bisphenol A                      3                   -0.5
5 B     Increase BPA                              5                    0.5
6 B     Increase dioxin                           8                    0.5
```

```
head(plastics_comb) |> n_complete_row()
```

```
[1] 5 5 5 5 5 5
```

`recode()` function

This is similar to `case_when()` but it can't do as much.

(need `mutate` for data frames/tibbles!)

```
# General Format - this is not code!
{data_input} |>
  mutate({variable_to_fix_or_new} = recode({Variable_fixing}, {old_value} = {new
                                           {another_old_value} = {new_value}))
```

recode() function

Need quotes for new values! Tolerates quotes for old values.

```
plastics |>
  mutate(microplastic_recoded = recode(microplastic,
                         "Bisphenol A" =  "BPA",
                                 "bpa" = "BPA",
                              "dioxin" = "Dioxin") |>
  count(microplastic, microplastic_recoded)
```

recode()

```
plastics |>
  mutate(microplastic_recoded = recode(microplastic,
                         "Bisphenol A" =  "BPA",
                                 "bpa" = "BPA",
                              "dioxin" = "Dioxin")) |>
  count(microplastic, microplastic_recoded)

# A tibble: 6 × 3
  microplastic microplastic_recoded     n
  <chr>        <chr>                <int>
1 BPA          BPA                      2
2 Bisphenol A  BPA                      1
3 Dioxin       Dioxin                   2
4 Other        Other                    3
5 bpa          BPA                      2
6 dioxin       Dioxin                   2
```

Can update or overwrite variables with recode too!

Just use the same variable name to change the variable within mutate.

```
plastics |>
  mutate(microplastic = recode(microplastic,
                       "Bisphenol A" =  "BPA",
                               "bpa" = "BPA",
                           "dioxin" = "Dioxin")) |>
  count(microplastic)

# A tibble: 3 × 2
  microplastic     n
  <chr>        <int>
1 BPA              5
2 Dioxin           4
3 Other            3
```

More complicated case_when

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

Rows: 8035 Columns: 67
── Column specification ────────────────────────────────────────────────────────
Delimiter: ","
chr  (3): CaliforniaCounty, ApproxLocation, CES4.0PercRange
dbl (64): CensusTract, ZIP, Longitude, Latitude, CES4.0Score, CES4.0Percenti...

ℹ Use `spec()` to retrieve the full column specification for this data.
ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message

set.seed(123)
ces |> mutate(new_col_case_when =
                case_when(Longitude < -121 & Latitude > 37.8 ~ "Distract A",
                          .default = "District B")) |>
                select(Longitude, Latitude, new_col_case_when) |>
                slice_sample(n = 6)

# A tibble: 6 × 3
  Longitude Latitude new_col_case_when
      <dbl>    <dbl> <chr>
1     -118.     34.1 District B
2     -118.     34.2 District B
3     -118.     34.1 District B
4     -122.     37.9 Distract A
5     -118.     33.7 District B
6     -118.     33.9 District B
```

Don't need **case_when( )** if just calculating new variables

```
ces |> mutate(num_col_mutate = Longitude * Latitude) |> pull(num_col_mutate)
```

```
  [1] -4628.628 -4626.923 -4626.181 -4627.226 -4627.539 -4626.747 -4626.999
  [8] -4627.869 -4627.019 -4625.697 -4625.301 -4625.090 -4623.895 -4624.469
 [15] -4625.011 -4624.364 -4625.312 -4624.039 -4623.577 -4623.748 -4623.065
 [22] -4622.705 -4623.340 -4622.929 -4622.560 -4621.886 -4622.292 -4620.986
 [29] -4622.073 -4623.599 -4623.264 -4622.834 -4622.748 -4622.293 -4622.547
 [36] -4623.105 -4624.034 -4624.719 -4624.272 -4624.876 -4626.124 -4625.382
 [43] -4623.124 -4623.478 -4621.235 -4621.058 -4620.332 -4620.480 -4621.368
 [50] -4621.776 -4621.443 -4621.355 -4621.027 -4620.606 -4620.087 -4620.586
 [57] -4620.667 -4620.065 -4619.671 -4619.019 -4619.601 -4619.386 -4617.044
 [64] -4618.494 -4617.961 -4618.796 -4619.591 -4618.345 -4618.680 -4619.270
 [71] -4619.649 -4618.712 -4617.975 -4617.781 -4617.642 -4617.198 -4617.174
 [78] -4614.951 -4615.876 -4615.344 -4616.535 -4616.034 -4616.425 -4617.171
 [85] -4619.375 -4615.766 -4615.195 -4614.288 -4613.738 -4613.512 -4614.361
 [92] -4614.937 -4614.010 -4613.137 -4610.191 -4610.268 -4609.656 -4610.560
 [99] -4611.650 -4612.492 -4612.416 -4612.547 -4612.646 -4612.075 -4609.889
[106] -4611.035 -4610.860 -4611.366 -4610.500 -4623.748 -4634.191 -4634.396
[113] -4634.714 -4634.751 -4633.355 -4633.094 -4633.820 -4633.931 -4633.377
[120] -4632.642 -4632.643 -4631.540 -4631.832 -4631.933 -4632.268 -4630.211
[127] -4631.774 -4631.392 -4631.163 -4630.990 -4630.892 -4630.246 -4629.335
[134] -4629.593 -4630.078 -4630.249 -4630.470 -4630.591 -4629.353 -4629.166
[141] -4628.991 -4628.580 -4629.126 -4628.569 -4627.522 -4628.107 -4628.018
[148] -4628.139 -4628.419 -4627.845 -4627.639 -4627.768 -4626.305 -4622.760
[155] -4623.706 -4616.068 -4619.294 -4619.348 -4619.609 -4618.471 -4618.285
[162] -4617.670 -4616.879 -4615.446 -4614.954 -4612.562 -4614.192 -4615.984
[169] -4616.531 -4617.827 -4620.699 -4603.301 -4611.086 -4604.367 -4605.354
[176] -4605.684 -4604.115 -4603.565 -4603.244 -4601.757 -4602.313 -4601.495
[183] -4600.486 -4600.793 -4609.306 -4609.328 -4609.417 -4607.750 -4607.706
[190] -4608.804 -4608.021 -4608.092 -4606.686 -4606.445 -4604.696 -4605.782
```

case_when( ) if you want NA values

```
ces |> mutate(num_new =  case_when(
  Longitude < -121 & Latitude > 37.8 ~  Longitude * Latitude),
  .default = NA) |>
  pull(num_new)
```

```
  [1] -4628.628 -4626.923 -4626.181 -4627.226 -4627.539 -4626.747 -4626.999
  [8] -4627.869 -4627.019 -4625.697 -4625.301 -4625.090 -4623.895 -4624.469
 [15] -4625.011 -4624.364 -4625.312 -4624.039 -4623.577 -4623.748 -4623.065
 [22] -4622.705 -4623.340 -4622.929 -4622.560 -4621.886 -4622.292        NA
 [29] -4622.073 -4623.599 -4623.264 -4622.834 -4622.748 -4622.293 -4622.547
 [36] -4623.105 -4624.034 -4624.719 -4624.272 -4624.876 -4626.124 -4625.382
 [43] -4623.124 -4623.478 -4621.235 -4621.058 -4620.332 -4620.480 -4621.368
 [50] -4621.776 -4621.443 -4621.355        NA        NA        NA        NA
 [57] -4620.667        NA        NA        NA        NA        NA        NA
 [64]        NA        NA        NA        NA        NA        NA        NA
 [71] -4619.649        NA        NA        NA        NA        NA        NA
 [78]        NA        NA        NA        NA        NA        NA        NA
 [85] -4619.375        NA        NA        NA        NA        NA        NA
 [92]        NA        NA        NA        NA        NA        NA        NA
 [99]        NA        NA        NA        NA        NA        NA        NA
[106]        NA        NA        NA        NA -4623.748 -4634.191 -4634.396
[113] -4634.714 -4634.751 -4633.355 -4633.094 -4633.820 -4633.931 -4633.377
[120] -4632.642 -4632.643 -4631.540 -4631.832 -4631.933 -4632.268 -4630.211
[127] -4631.774 -4631.392 -4631.163 -4630.990 -4630.892 -4630.246 -4629.335
[134] -4629.593 -4630.078 -4630.249 -4630.470 -4630.591 -4629.353 -4629.166
[141] -4628.991 -4628.580 -4629.126 -4628.569 -4627.522 -4628.107 -4628.018
[148] -4628.139 -4628.419 -4627.845 -4627.639 -4627.768 -4626.305 -4622.760
[155] -4623.706        NA        NA        NA        NA        NA        NA
[162]        NA        NA        NA        NA        NA        NA        NA
[169]        NA        NA        NA        NA        NA        NA        NA
```

String Splitting

- `str_split(string, pattern)` - splits strings up - returns list!

```
library(stringr)
x <- c("I really like writing R code")
df <- tibble(x = c("I really", "like writing", "R code programs"))
y <- unlist(str_split(x, " "))
y
```

```
[1] "I"       "really"  "like"    "writing" "R"       "code"
```

```
length(y)
```

```
[1] 6
```

A bit on Regular Expressions

- http://www.regular-expressions.info/reference.html
- They can use to match a large number of strings in one statement
- `.` matches any single character
- `*` means repeat as many (even if 0) more times the last character
- `?` makes the last thing optional
- `^` matches start of vector `^a` - starts with “a”
- `$` matches end of vector `b$` - ends with “b”

Let's look at modifiers for `stringr`

```
?modifiers
```

- `fixed` - match everything exactly
- `ignore_case` is an option to not have to use `tolower`

Using a fixed expression

One example case is when you want to split on a period "**.**". In regular expressions **.** means **ANY** character, so we need to specify that we want R to interpret "." as simply a period.

```
str_split("I.like.strings", ".")

[[1]]
 [1] "" "" "" "" "" "" "" "" "" "" "" "" "" "" "" ""

str_split("I.like.strings", fixed("."))

[[1]]
[1] "I"       "like"    "strings"

str_split("I.like.strings", "\\.")

[[1]]
[1] "I"       "like"    "strings"
```

Pasting strings with **paste** and **paste0**

Paste can be very useful for joining vectors together:

```
paste("Visit", 1:5, sep = "_")
```

```
[1] "Visit_1" "Visit_2" "Visit_3" "Visit_4" "Visit_5"
```

```
paste("Visit", 1:5, sep = "_", collapse = "_")
```

```
[1] "Visit_1_Visit_2_Visit_3_Visit_4_Visit_5"
```

```
# and paste0 can be even simpler see ?paste0
paste0("Visit",1:5) # no space!
```

```
[1] "Visit1" "Visit2" "Visit3" "Visit4" "Visit5"
```

Comparison of `stringr` to base R - not covered

Splitting Strings

Substringing

`stringr`

- `str_split(string, pattern)` - splits strings up - returns list!

Splitting String:

In `stringr`, `str_split` splits a vector on a string into a `list`

```
library(stringr)
x <- c("I really", "like writing", "R code programs")
y <- str_split(x, pattern =  " ") # returns a list
y
```

```
[[1]]
[1] "I"      "really"

[[2]]
[1] "like"    "writing"

[[3]]
[1] "R"        "code"     "programs"
```

'Find' functions: stringr compared to base R

Base R does not use these functions. Here is a "translator" of the `stringr` function to base R functions

- `str_detect` - similar to `grepl` (return logical)
- `grep(value = FALSE)` is similar to `which(str_detect())`
- `str_subset` - similar to `grep(value = TRUE)` - return value of matched
- `str_replace` - similar to `sub` - replace one time
- `str_replace_all` - similar to `gsub` - replace many times

Important Comparisons

Base R:

- Argument order is `(pattern, x)`
- Uses option `(fixed = TRUE)`

`stringr`

- Argument order is `(string, pattern)` aka `(x, pattern)`
- Uses function `fixed(pattern)`

some data to work with

```
Sal <- read_csv(file =
    "https://daseh.org/data/Baltimore_City_Employee_Salaries_FY2015.csv")
```

Showing difference in `str_extract`

`str_extract` extracts just the matched string

```
ss <- str_extract(Sal$Name, "Rawling")
```

```
Warning: Unknown or uninitialised column: `Name`.
```

```
head(ss)
```

```
character(0)
```

```
ss[ !is.na(ss)]
```

```
character(0)
```

Showing difference in `str_extract` and `str_extract_all`

`str_extract_all` extracts all the matched strings

```
head(str_extract(Sal$AgencyID, "\\d"))
```

```
[1] "0" "2" "6" "9" "4" "9"
```

```
head(str_extract_all(Sal$AgencyID, "\\d"), 2)
```

```
[[1]]
[1] "0" "3" "0" "3" "1"

[[2]]
[1] "2" "9" "0" "4" "5"
```

Using Regular Expressions

- Look for any name that starts with:
  - Payne at the beginning,
  - Leonard and then an S
  - Spence then capital C

```
head(grep("^Payne.*", x = Sal$name, value = TRUE), 3)
```

```
[1] "Payne El,Boaz L"          "Payne El,Jackie"
[3] "Payne Johnson,Nickole A"
```

```
head(grep("Leonard.?S", x = Sal$name, value = TRUE))
```

```
[1] "Payne,Leonard S"      "Szumlanski,Leonard S"
```

```
head(grep("Spence.*C.*", x = Sal$name, value = TRUE))
```

```
[1] "Spencer,Charles A"  "Spencer,Clarence W" "Spencer,Michael C"
```

Using Regular Expressions: `stringr`

```
head(str_subset( Sal$name, "^Payne.*"), 3)
```

```
[1] "Payne El,Boaz L"          "Payne El,Jackie"
[3] "Payne Johnson,Nickole A"
```

```
head(str_subset( Sal$name, "Leonard.?S"))
```

```
[1] "Payne,Leonard S"      "Szumlanski,Leonard S"
```

```
head(str_subset( Sal$name, "Spence.*C.*"))
```

```
[1] "Spencer,Charles A"  "Spencer,Clarence W" "Spencer,Michael C"
```

Replace

Let's say we wanted to sort the data set by Annual Salary:

```
class(Sal$AnnualSalary)
```

```
[1] "character"
```

```
sort(c("1", "2", "10")) #  not sort correctly (order simply ranks the data)
```

```
[1] "1"  "10" "2"
```

```
order(c("1", "2", "10"))
```

```
[1] 1 3 2
```

Replace

So we must change the annual pay into a numeric:

```
head(Sal$AnnualSalary, 4)
```

```
[1] "$55314.00" "$74000.00" "$64500.00" "$46309.00"
```

```
head(as.numeric(Sal$AnnualSalary), 4)
```

```
Warning in head(as.numeric(Sal$AnnualSalary), 4): NAs introduced by coercion
```

```
[1] NA NA NA NA
```

R didn't like the `$` so it thought turned them all to `NA`.

`sub()` and `gsub()` can do the replacing part in base R.

Replacing and subbing

Now we can replace the `$` with nothing (used `fixed=TRUE` because `$` means ending):

```
Sal$AnnualSalary <- as.numeric(gsub(pattern = "$", replacement="",
                                    Sal$AnnualSalary, fixed=TRUE))
Sal <- Sal[order(Sal$AnnualSalary, decreasing=TRUE), ]
Sal[1:5, c("name", "AnnualSalary", "JobTitle")]
```

```
# A tibble: 5 × 3
  name            AnnualSalary JobTitle
  <chr>                  <dbl> <chr>
1 Mosby,Marilyn J       238772 STATE'S ATTORNEY
2 Batts,Anthony W       211785 Police Commissioner
3 Wen,Leana             200000 Executive Director III
4 Raymond,Henry J       192500 Executive Director III
5 Swift,Michael         187200 CONTRACT SERV SPEC II
```

Replacing and subbing: `stringr`

We can do the same thing (with 2 piping operations!) in dplyr

```
dplyr_sal <- Sal
dplyr_sal <- dplyr_sal |>
  mutate(AnnualSalary = str_replace(AnnualSalary, fixed("$"), "")) |>
  mutate(AnnualSalary = as.numeric(AnnualSalary)) |>
  arrange(desc(AnnualSalary))
check_Sal <- Sal
rownames(check_Sal) <- NULL
all.equal(check_Sal, dplyr_sal)
```

```
[1] TRUE
```

Creating Two-way Tables

A two-way table. If you pass in 2 vectors, `table` creates a 2-dimensional table.

```
tab <- table(c(0, 1, 2, 3, 2, 3, 3, 2,2, 3),
             c(0, 1, 2, 3, 2, 3, 3, 4, 4, 3),
              useNA = "always")
tab
```

```
      0 1 2 3 4 <NA>
  0   1 0 0 0 0    0
  1   0 1 0 0 0    0
  2   0 0 2 0 2    0
  3   0 0 0 4 0    0
  <NA> 0 0 0 0 0    0
```

Creating Two-way Tables

```
tab_df <- tibble(x = c(0, 1, 2, 3, 2, 3, 3, 2,2, 3),
                 y = c(0, 1, 2, 3, 2, 3, 3, 4, 4, 3))
tab_df |> count(x, y)
```

```
# A tibble: 5 × 3
      x     y     n
  <dbl> <dbl> <int>
1     0     0     1
2     1     1     1
3     2     2     2
4     2     4     2
5     3     3     4
```

Creating Two-way Tables

```
tab_df |>
  count(x, y) |>
  group_by(x) |> mutate(pct_x = n / sum(n))

# A tibble: 5 × 4
# Groups:   x [4]
      x     y     n pct_x
  <dbl> <dbl> <int> <dbl>
1     0     0     1   1
2     1     1     1   1
3     2     2     2   0.5
4     2     4     2   0.5
5     3     3     4   1
```

Creating Two-way Tables

```
library(scales)
tab_df |>
  count(x, y) |>
  group_by(x) |> mutate(pct_x = percent(n / sum(n)))

# A tibble: 5 × 4
# Groups:   x [4]
      x     y     n pct_x
  <dbl> <dbl> <int> <chr>
1     0     0     1 100%
2     1     1     1 100%
3     2     2     2 50%
4     2     4     2 50%
5     3     3     4 100%
```

Removing columns with threshold of percent missing values

```
is.na(df) |> head(n = 3)
```

```
         x
[1,] FALSE
[2,] FALSE
[3,] FALSE
```

```
colMeans(is.na(df))#TRUE and FALSE treated like 0 and 1
```

```
x
0
```

```
which(colMeans(is.na(df)) < 0.2) #the location of the columns <.2
```

```
x
1
```

```
df |> select(which(colMeans(is.na(df)) < 0.2))# remove if over 20% missing
```

```
# A tibble: 3 × 1
  x
  <chr>
1 I really
2 like writing
3 R code programs
```