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TIDYING DATA TUTORIAL

Contents


```
## Last updated on 2019-04-26
```

Before you start

During this tutorial, we'll use several r-packages. Make sure to install and load them, if needed.

```
library(dplyr)
library(tidyr)
library(stringr)
```

Our old friend dplyr will provide us with some functions to combined different datasets into one. We will use tidyr to transform datasets, and stringr to do some munipulations of character variables.

This tutorial consist of two major parts:

1. Merging datasets
2. Transforming datasets

Thereafter, in an additional part, we will go through a case study as an example.

Disclaimer

1. There are many datasets used in this tutorial. A loadscript has been provided to create all datasets for you. Just run the script and you are good to go.

2. This is a new tutorial and will likely contains typos and other errors. If you find one, please send to `gert.janssenswillen@uhasselt.be`. You will be repayed with eternal kindness (but not on exams.)

Let's get started!

1 Merging data

We can merge different datasets by **joining** or **binding**.

- We **join** different datasets which contain different information about the same observations. For example, we can have 1) a dataset of countries with their population and 2) a dataset of countries with their life expectancy. These we can *join* together.

```
countries_population
```

```
## # A tibble: 114 x 2
##    country                  pop
##    <fct>                  <int>
##  1 Equatorial Guinea     551201
##  2 Serbia              10150265
##  3 Iceland               301931
##  4 Sweden               9031088
##  5 Trinidad and Tobago  1056608
##  6 Austria              8199783
##  7 Kuwait               2505559
##  8 Sudan               42292929
##  9 Lesotho              2012649
## 10 Iran                69453570
## # ... with 104 more rows
```

```
countries_lifeExp
```

```
## # A tibble: 85 x 2
##    country         lifeExp
##    <fct>             <dbl>
##  1 Poland             75.6
##  2 Canada             80.7
##  3 Madagascar         59.4
##  4 Uganda             51.5
##  5 Mauritania         64.2
```

```
##  6 Hong Kong, China    82.2
##  7 Namibia             52.9
##  8 Finland             79.3
##  9 Eritrea             58.0
## 10 Costa Rica          78.8
## # ... with 75 more rows
```

- We **bind** different datasets which contain the same information on different observations. For example, we can have 1) a dataset of European countries with their population and 2) a dataset of African countries with their population. We can *bind* these two together. [1]

[1] There are actually ofther cases in which we can bind datasets together, but please don't bother about that for now. Just remind: bind different observations, join different information]

```
population_africa
```

```
## # A tibble: 52 x 2
##    country                       pop
##    <fct>                       <int>
##  1 Algeria                  33333216
##  2 Angola                   12420476
##  3 Benin                     8078314
##  4 Botswana                  1639131
##  5 Burkina Faso             14326203
##  6 Burundi                   8390505
##  7 Cameroon                 17696293
##  8 Central African Republic  4369038
##  9 Chad                     10238807
## 10 Comoros                    710960
## # ... with 42 more rows
```

```
population_europe
```

```
## # A tibble: 30 x 2
##    country                     pop
##    <fct>                     <int>
##  1 Albania                 3600523
##  2 Austria                 8199783
##  3 Belgium                10392226
##  4 Bosnia and Herzegovina  4552198
##  5 Bulgaria                7322858
##  6 Croatia                 4493312
##  7 Czech Republic         10228744
##  8 Denmark                 5468120
##  9 Finland                 5238460
## 10 France                 61083916
## # ... with 20 more rows
```

Let's see how we can join data.

1.1 Joining data

Remember, we join datasets if they contain different information on the same observations. This means that there needs to be a way to *link* the datasets. These links we call *ids* or *keys*.

If we have population and life expectancy data about countries, than the name, code or abbreviation of the country is our key to link both datasets.

Note that, when both datasets use different keys, for example one uses the name (Belgium) and the other the code (BE), we cannot join them. In such a case, we would need to recode one of the variables or find another datasets which can serve as an intermediary link (i.e. one that contains both the names and the codes. There exist many different country codes, so this is a common problem. But we are good to go in our case)

The join functions we will introduce in a second will always look for variables with the same names in both tables and uses these as the keys to link them. You can explicitly set the keys using the by argument. This is especially useful if

a) The keys have a different name in both datasets. For example country vs ctry
b) Not all common variables are actually keys.

For now, we will always let the keys be chosen by the functions. A message will tell us which keys they used.

Now, there are 4 ways to join datasets.

- inner_join
- left_join
- right_join
- full_join

Why four? Well, if we want to join two datasets, it typically happens that they don't contain information on *exactly* the same observations. Have a closer look at the population and life expectancy data. The first one contains information on 114 countries and the second one contains information on 85 countries. So they can impossibly contain information on the same set of countries. The different joins will tackles this problem differently.

1.1.1 Inner join

Inner join means: I only keep information about keys that occur in both tables. So, if I don't have the population of country A, I don't want its life expectancy.

```r
inner_join(countries_population, countries_lifeExp)
```

```
## Joining, by = "country"
```

```
## # A tibble: 67 x 3
##    country                   pop lifeExp
##    <fct>                   <int>   <dbl>
##  1 Equatorial Guinea      551201    51.6
##  2 Serbia               10150265    74.0
##  3 Iceland                301931    81.8
##  4 Trinidad and Tobago   1056608    69.8
##  5 Iran                 69453570    71.0
##  6 Namibia               2055080    52.9
##  7 United Kingdom       60776238    79.4
##  8 South Africa         43997828    49.3
##  9 Sao Tome and Principe  199579    65.5
## 10 Mongolia              2874127    66.8
## # ... with 57 more rows
```

This join gives us 67 observations, which is the subset of countries on which we have both types of information. Also note how the `inner_join` tells you which key it used.

1.1.2 *Left join*

Left join means: I keep all information in my first (left) table. So, even if I don't have the life expectancy, still give me the population. The missing part of the new observation (i.e. the life expectancy), is now NA.

```r
left_join(countries_population, countries_lifeExp)
```

```
## Joining, by = "country"
```

```
## # A tibble: 114 x 3
##    country                 pop lifeExp
##    <fct>                 <int>   <dbl>
##  1 Equatorial Guinea    551201    51.6
##  2 Serbia             10150265    74.0
##  3 Iceland              301931    81.8
##  4 Sweden              9031088    NA
##  5 Trinidad and Tobago 1056608    69.8
##  6 Austria             8199783    NA
##  7 Kuwait              2505559    NA
##  8 Sudan              42292929    NA
##  9 Lesotho             2012649    NA
## 10 Iran               69453570    71.0
## # ... with 104 more rows
```

This join gives us 114 observations, which is the number of countries for which we have information on the population. Also note how it inserts NA's for the lifeExp variable.

```
left_join(countries_population, countries_lifeExp) %>%
    summary()
```

```
## Joining, by = "country"
```

```
##         country          pop
##  Afghanistan:  1   Min.   :1.996e+05
##  Albania    :  1   1st Qu.:4.400e+06
##  Algeria    :  1   Median :1.106e+07
##  Argentina  :  1   Mean   :4.986e+07
##  Australia  :  1   3rd Qu.:3.338e+07
##  Austria    :  1   Max.   :1.319e+09
##  (Other)    :108
##     lifeExp
##  Min.   :39.61
##  1st Qu.:58.74
##  Median :71.42
##  Mean   :67.27
##  3rd Qu.:78.08
##  Max.   :82.21
##  NA's   :47
```

1.1.3 *Right join*

Right join means: the opposite of left join. I keep all information in my second (right) table.

```
right_join(countries_population, countries_lifeExp)
```

```
## Joining, by = "country"
```

```
## # A tibble: 85 x 3
##    country               pop lifeExp
##    <fct>               <int>   <dbl>
##  1 Poland                 NA    75.6
##  2 Canada           33390141    80.7
##  3 Madagascar       19167654    59.4
##  4 Uganda           29170398    51.5
##  5 Mauritania        3270065    64.2
##  6 Hong Kong, China  6980412    82.2
##  7 Namibia           2055080    52.9
##  8 Finland                NA    79.3
```

```
##  9 Eritrea           4906585    58.0
## 10 Costa Rica        4133884    78.8
## # ... with 75 more rows
```

This join gives us 85 observations, which is the number of countries for which we have information on the life expectancy.

1.1.4 *Full join*

Full join means: I want to keep all information I have. So also populations for countries without life expectancy and vice versa remain in the dataset. All missing information is filled in as NA.

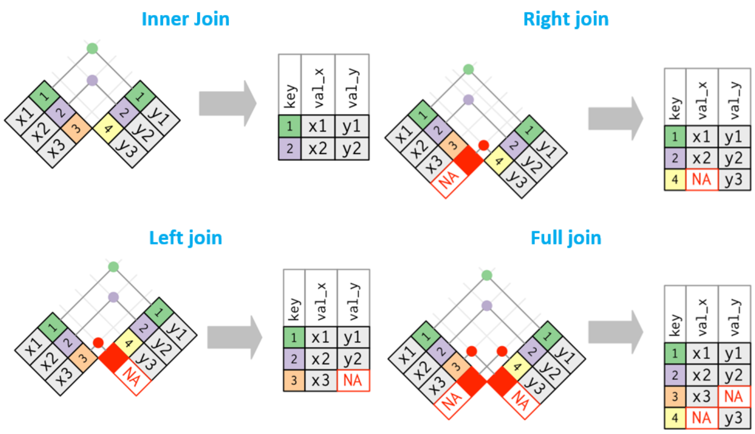
```
full_join(countries_population, countries_lifeExp)
```

```
## Joining, by = "country"
```

```
## # A tibble: 132 x 3
##    country                 pop lifeExp
##    <fct>                 <int>   <dbl>
##  1 Equatorial Guinea    551201    51.6
##  2 Serbia             10150265    74.0
##  3 Iceland              301931    81.8
##  4 Sweden              9031088    NA
##  5 Trinidad and Tobago  1056608    69.8
##  6 Austria             8199783    NA
##  7 Kuwait              2505559    NA
##  8 Sudan              42292929    NA
##  9 Lesotho             2012649    NA
## 10 Iran               69453570    71.0
## # ... with 122 more rows
```

This join gives us 132 observations, which is the total number of countries for which we have at least one piece of information.

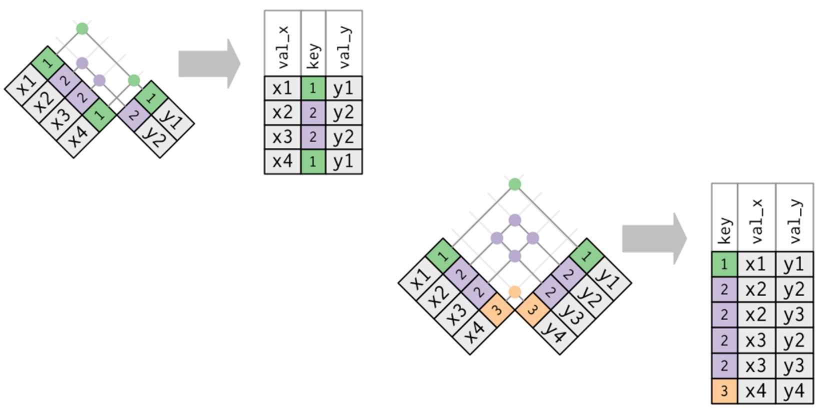
A schematical overview of the four types can be seen below. The coloured numbers represent the keys (countries in our example) while the x and y values represent the values (population and life expectancy in our example). Of course, there can be as many values as there are, it doesn't just have to be one. We will see other examples soon enough.



1.1.5 *Duplicates*

Sometimes one or both datasets contain duplicate keys: for example, we have information of the population in each country for more than a single year, so for each country we have more than one observation. In such cases, each observation will be joined multiple times, as in the figure below.[2]

[2] Of course, if we have both population data about multiple years and life expectancy data about multiple years, we should just include the *year* as a key variable. We don't want them to mix up. In that case, each observation is defined by both country and year.



1.2 *An example*

The package nycflights13 contains different datasets about flights from NYC in 2013.

```
library(nycflights13)
```

One of the datasets is called flights

```
flights %>% glimpse
```

```
## Observations: 336,776
```

```
## Variables: 19
## $ year           <int> 2013, 2013, 2013,...
## $ month          <int> 1, 1, 1, 1, 1, 1,...
## $ day            <int> 1, 1, 1, 1, 1, 1,...
## $ dep_time       <int> 517, 533, 542, 54...
## $ sched_dep_time <int> 515, 529, 540, 54...
## $ dep_delay      <dbl> 2, 4, 2, -1, -6, ...
## $ arr_time       <int> 830, 850, 923, 10...
## $ sched_arr_time <int> 819, 830, 850, 10...
## $ arr_delay      <dbl> 11, 20, 33, -18, ...
## $ carrier        <chr> "UA", "UA", "AA",...
## $ flight         <int> 1545, 1714, 1141,...
## $ tailnum        <chr> "N14228", "N24211...
## $ origin         <chr> "EWR", "LGA", "JF...
## $ dest           <chr> "IAH", "IAH", "MI...
## $ air_time       <dbl> 227, 227, 160, 18...
## $ distance       <dbl> 1400, 1416, 1089,...
## $ hour           <dbl> 5, 5, 5, 5, 6, 5,...
## $ minute         <dbl> 15, 29, 40, 45, 0...
## $ time_hour      <dttm> 2013-01-01 05:00...
```

Another one is airlines; with more information on the arilines, evidently.

```
airlines %>% glimpse
```

```
## Observations: 16
## Variables: 2
## $ carrier <chr> "9E", "AA", "AS", "B6", ...
## $ name    <chr> "Endeavor Air Inc.", "Am...
```

You can see they have the carrier variable in common, which contains a code for each airline. We can add the name of the airline to the flights

```
flights %>% inner_join(airlines)
```

```
## Joining, by = "carrier"
```

```
## # A tibble: 336,776 x 20
##     year month   day dep_time sched_dep_time
##    <int> <int> <int>    <int>          <int>
##  1  2013     1     1      517            515
##  2  2013     1     1      533            529
##  3  2013     1     1      542            540
##  4  2013     1     1      544            545
```

```
##  5  2013     1     1      554            600
##  6  2013     1     1      554            558
##  7  2013     1     1      555            600
##  8  2013     1     1      557            600
##  9  2013     1     1      557            600
## 10  2013     1     1      558            600
## # ... with 336,766 more rows, and 15 more
## #   variables: dep_delay <dbl>,
## #   arr_time <int>, sched_arr_time <int>,
## #   arr_delay <dbl>, carrier <chr>,
## #   flight <int>, tailnum <chr>,
## #   origin <chr>, dest <chr>,
## #   air_time <dbl>, distance <dbl>,
## #   hour <dbl>, minute <dbl>,
## #   time_hour <dttm>, name <chr>
```

Note that we did an inner join and our number of flights didn't decrease. This means that every carrier in flights is also available in airlines. In other words, for all carriers we have seen flights of, we know the name of the airline.

For a more advanced example, let's look at weather.

```
weather %>% glimpse
```

```
## Observations: 26,115
## Variables: 15
## $ origin     <chr> "EWR", "EWR", "EWR", ...
## $ year       <dbl> 2013, 2013, 2013, 201...
## $ month      <dbl> 1, 1, 1, 1, 1, 1, 1, ...
## $ day        <int> 1, 1, 1, 1, 1, 1, 1, ...
## $ hour       <int> 1, 2, 3, 4, 5, 6, 7, ...
## $ temp       <dbl> 39.02, 39.02, 39.02, ...
## $ dewp       <dbl> 26.06, 26.96, 28.04, ...
## $ humid      <dbl> 59.37, 61.63, 64.43, ...
## $ wind_dir   <dbl> 270, 250, 240, 250, 2...
## $ wind_speed <dbl> 10.35702, 8.05546, 11...
## $ wind_gust  <dbl> NA, NA, NA, NA, NA, N...
## $ precip     <dbl> 0, 0, 0, 0, 0, 0, 0, ...
## $ pressure   <dbl> 1012.0, 1012.3, 1012....
## $ visib      <dbl> 10, 10, 10, 10, 10, 1...
## $ time_hour  <dttm> 2013-01-01 01:00:00,...
```

It contains information on place and time: the same we also have for flights, and it contains several variables about the weather (wind, temperature, precipitation, etc.)

Let's join the flights data with the weather.

```
flights <- flights %>% inner_join(airlines) %>%
    inner_join(weather)
```

```
## Joining, by = "carrier"
```

```
## Joining, by = c("year", "month", "day", "origin", "hour", "time_hour")
```

```
flights %>% glimpse
```

```
## Observations: 335,220
## Variables: 29
## $ year           <dbl> 2013, 2013, 2013,...
## $ month          <dbl> 1, 1, 1, 1, 1, 1,...
## $ day            <int> 1, 1, 1, 1, 1, 1,...
## $ dep_time       <int> 517, 533, 542, 54...
## $ sched_dep_time <int> 515, 529, 540, 54...
## $ dep_delay      <dbl> 2, 4, 2, -1, -6, ...
## $ arr_time       <int> 830, 850, 923, 10...
## $ sched_arr_time <int> 819, 830, 850, 10...
## $ arr_delay      <dbl> 11, 20, 33, -18, ...
## $ carrier        <chr> "UA", "UA", "AA",...
## $ flight         <int> 1545, 1714, 1141,...
## $ tailnum        <chr> "N14228", "N24211...
## $ origin         <chr> "EWR", "LGA", "JF...
## $ dest           <chr> "IAH", "IAH", "MI...
## $ air_time       <dbl> 227, 227, 160, 18...
## $ distance       <dbl> 1400, 1416, 1089,...
## $ hour           <dbl> 5, 5, 5, 5, 6, 5,...
## $ minute         <dbl> 15, 29, 40, 45, 0...
## $ time_hour      <dttm> 2013-01-01 05:00...
## $ name           <chr> "United Air Lines...
## $ temp           <dbl> 39.02, 39.92, 39....
## $ dewp           <dbl> 28.04, 24.98, 26....
## $ humid          <dbl> 64.43, 54.81, 61....
## $ wind_dir       <dbl> 260, 250, 260, 26...
## $ wind_speed     <dbl> 12.65858, 14.9601...
## $ wind_gust      <dbl> NA, 21.86482, NA,...
## $ precip         <dbl> 0, 0, 0, 0, 0, 0,...
## $ pressure       <dbl> 1011.9, 1011.4, 1...
## $ visib          <dbl> 10, 10, 10, 10, 1...
```

Note that the second join used variables year, month, origin, hour and time_hour to join the weather of the correct place and time to each flight.

1.3 *Binding data*

The data we joined above were always different pieces of information which we somehow linked (same country, same, time, same place, same airline, etc.) Sometimes we have dataset on separate objects which are not linked, but contain the same information. Recall the datasets on African and European countries.

```
population_africa
```

```
## # A tibble: 52 x 2
##    country                       pop
##    <fct>                       <int>
##  1 Algeria                  33333216
##  2 Angola                   12420476
##  3 Benin                     8078314
##  4 Botswana                  1639131
##  5 Burkina Faso             14326203
##  6 Burundi                   8390505
##  7 Cameroon                 17696293
##  8 Central African Republic  4369038
##  9 Chad                     10238807
## 10 Comoros                    710960
## # ... with 42 more rows
```

```
population_europe
```

```
## # A tibble: 30 x 2
##    country                     pop
##    <fct>                     <int>
##  1 Albania                 3600523
##  2 Austria                 8199783
##  3 Belgium                10392226
##  4 Bosnia and Herzegovina  4552198
##  5 Bulgaria                7322858
##  6 Croatia                 4493312
##  7 Czech Republic         10228744
##  8 Denmark                 5468120
##  9 Finland                 5238460
## 10 France                 61083916
## # ... with 20 more rows
```

These observation are not linked (there is no link between an African country and a European one), but they contain the same pieces of information (i.e. population).

We can **bind** these **rows** together.

```
bind_rows(population_africa, population_europe)
```

```
## # A tibble: 82 x 2
##    country                       pop
##    <fct>                       <int>
##  1 Algeria                  33333216
##  2 Angola                   12420476
##  3 Benin                     8078314
##  4 Botswana                  1639131
##  5 Burkina Faso             14326203
##  6 Burundi                   8390505
##  7 Cameroon                 17696293
##  8 Central African Republic  4369038
##  9 Chad                     10238807
## 10 Comoros                    710960
## # ... with 72 more rows
```

Note that we had 52 African countries and 30 European countries. Together, this makes for 82 countries.

For bind rows, it is not necesarry to have exactly the same information. Suppose that we have life expectancy for African countries, but not for European. Consider the dataset `information_africa`.

```
information_africa
```

```
## # A tibble: 52 x 3
##    country                       pop lifeExp
##    <fct>                       <int>   <dbl>
##  1 Algeria                  33333216    72.3
##  2 Angola                   12420476    42.7
##  3 Benin                     8078314    56.7
##  4 Botswana                  1639131    50.7
##  5 Burkina Faso             14326203    52.3
##  6 Burundi                   8390505    49.6
##  7 Cameroon                 17696293    50.4
##  8 Central African Republic  4369038    44.7
##  9 Chad                     10238807    50.7
## 10 Comoros                    710960    65.2
## # ... with 42 more rows
```

And we bind these two datasets.

```
bind_rows(information_africa, population_europe) %>%
    summary
```

```
##     country        pop
```

```
## Albania: 1   Min.   :   199579
## Algeria: 1   1st Qu.:  4174074
## Angola : 1   Median :  9951961
## Austria: 1   Mean   : 18483393
## Belgium: 1   3rd Qu.: 19755656
## Benin  : 1   Max.   :135031164
## (Other):76
##    lifeExp
## Min.   :39.61
## 1st Qu.:47.83
## Median :52.93
## Mean   :54.81
## 3rd Qu.:59.44
## Max.   :76.44
## NA's   :30
```

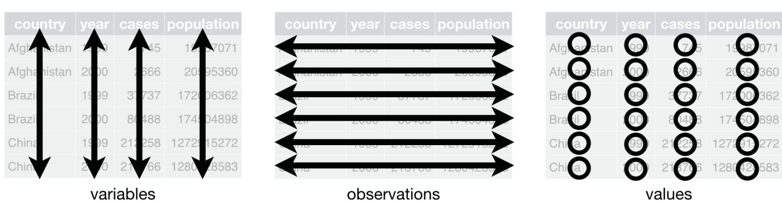
What we could have expected did indeed happen: the 30 European countries received an NA for life expectancy. However, be wary: if both datasets have different information, maybe bind_rows is not what you are looking for, and maybe you need a join? Be sure that you understand how your datasets related to one another and how you should combine them. [3]

[3] That said, one more remark on merging data. If there is a bind_rows, there must surely be a bind_cols for binding columns? Yes, there is. However, we will not use this function (hurray!). bind_cols can do as it says: binding columns together just like bind_rows binds rows together. However, binding columns together means that we have 2 sets of information about the same observations? That sounds a lot like it needs a join, doesn't it? Indeed! The main difference between bind_rows and joins is that joins will combine rows that have the same key. However, bind_rows will combine rows by position, i.e. the first row of dataset A will be combined with first row of dataset B. It won't be looking at any keys. So if dataset A and B are in a different order, you have messed up your data. So, just forget about bind_cols. Bind_rows and joins should be able to get you where you want to be.

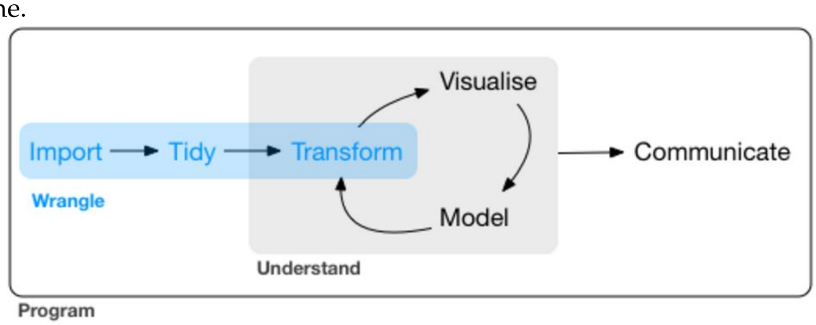
2
Transforming data

Next to merging data, we will also be learn how to transform data. The difference? For merging we need two datasets, for transforming, we will only use a single one.

The main goal of transforming our data is to make sure it is *tidy*. This means: every row is an observation, and every column is a variable.



Now, tidying is primarily important in the initial fase of your project, as shown in the figure below. However, it can also be useful during analyses. For some graph, it might happen that you need to transform your data - change what your observations are. This makes data transformation both essential and difficult. It is very important to understand what the current shape of your data is, and in which shape you need it to be for your analysis. This requires practice and time.



We will discuss four different transformations [1].

There are 2 easy transformations:

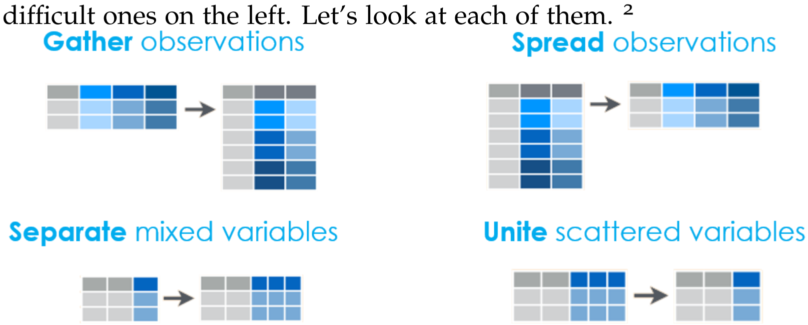
[1] Note that we used the term *transformation* for different things. We have used it before to transform *variables* (recode factors, rescale numerics, etc). At this moment we use it to transform *data*, which means that we are talking about multiple variable or complete datasets. The word choice is not to confuse you, we are actually doing the same thing, but at different levels.

1. Combine variables
2. Split variables

and 2 difficult ones

3. Spread a dataset
4. Gather a dataset

Below we show the schematically - the easy ones on the right, and the difficult ones on the left. Let's look at each of them. [2]



[2] Note that all the join and transformation functions discussed here are included on the cheatsheet of Data Manipulation. Make sure you can use it during exercises and exams!

2.1 *Unite variables*

We use the function `unite` when we have several variables that we want to combine into a single one. The syntax for unite is as follows. Suppose we have information about students, with a first_name and last_name, and we want a single "name" variable.

```
students
```

```
## # A tibble: 10 x 2
##    first_name last_name
##    <chr>      <chr>
##  1 Joa        Khamani
##  2 Aakarsh    Marlisha
##  3 Jeffory    Tymire
##  4 Elaysia    Nikeisha
##  5 Delaine    Takashi
##  6 Bud        Ilani
##  7 Kim        Sheridan
##  8 Imanuel    Dollie
##  9 Rashaad    Monico
## 10 Catherine  Ashli
```

```
students %>% unite(col = name, first_name, last_name)
```

```
## # A tibble: 10 x 1
##    name
```

```
##    <chr>
##  1 Joa_Khamani
##  2 Aakarsh_Marlisha
##  3 Jeffory_Tymire
##  4 Elaysia_Nikeisha
##  5 Delaine_Takashi
##  6 Bud_Ilani
##  7 Kim_Sheridan
##  8 Imanuel_Dollie
##  9 Rashaad_Monico
## 10 Catherine_Ashli
```

We first specify the name for the new column (which here is just name), then we list all columns we want to unite. Note that be default, unite will put a _ between the colums. We can change this with the argument sep.

```
students %>% unite(col = name, first_name, last_name,
    sep = " ")
```

```
## # A tibble: 10 x 1
##    name
##    <chr>
##  1 Joa Khamani
##  2 Aakarsh Marlisha
##  3 Jeffory Tymire
##  4 Elaysia Nikeisha
##  5 Delaine Takashi
##  6 Bud Ilani
##  7 Kim Sheridan
##  8 Imanuel Dollie
##  9 Rashaad Monico
## 10 Catherine Ashli
```

Sometimes we also prefer to keep the original variables. We can ask not te remove them as follows.

```
students %>% unite(col = name, first_name, last_name,
    sep = " ", remove = F)
```

```
## # A tibble: 10 x 3
##    name             first_name last_name
##    <chr>            <chr>      <chr>
##  1 Joa Khamani      Joa        Khamani
##  2 Aakarsh Marlisha Aakarsh    Marlisha
##  3 Jeffory Tymire   Jeffory    Tymire
```

```
## 4 Elaysia Nikeisha Elaysia    Nikeisha
## 5 Delaine Takashi  Delaine    Takashi
## 6 Bud Ilani        Bud        Ilani
## 7 Kim Sheridan     Kim        Sheridan
## 8 Imanuel Dollie   Imanuel    Dollie
## 9 Rashaad Monico   Rashaad    Monico
## 10 Catherine Ashli Catherine  Ashli
```

2.2 *Separate variables*

Separate works the other way around: it separates a single variable into multiple ones. Suppose we have a list of students (students2) with their full names, and we want to separate them. [3]

[3] Note how you spell separate. An e, followed by an a, another a, and another e. Can you remember that? Congratulations, you have just avoided a series of very common mistakes!

```
students_2
```

```
## # A tibble: 10 x 1
##    name
##    <chr>
##  1 Alex Maybelline
##  2 Felicitas Langston
##  3 Torrin Ireland
##  4 Saadiya Dalessandro
##  5 Balal Mckaila
##  6 Grazia Sianna
##  7 Faust Rachel
##  8 Kathie Jerelyn
##  9 Donnamae Maurin
## 10 Burrell Mckenzie
```

We can use separate in a similar way. First tell which column you want separated. Then tell them into which columns you want to put the pieces.[4]

[4] Note that the col argument in unite is the new column, the col argument in separate is the existing column! Also note that the new columns created by separate should be given as a character vector, not as a list of unquoted names like we did in unite.

```
students_2 %>% separate(col = name, into = c("first_name",
    "last_name"))
```

```
## # A tibble: 10 x 2
##    first_name last_name
##    <chr>      <chr>
##  1 Alex       Maybelline
##  2 Felicitas  Langston
##  3 Torrin     Ireland
##  4 Saadiya    Dalessandro
##  5 Balal      Mckaila
##  6 Grazia     Sianna
```

```
##   7 Faust      Rachel
##   8 Kathie     Jerelyn
##   9 Donnamae   Maurin
## 10 Burrell    Mckenzie
```

Default, separate will split the columns on any character which is not alphanumerical: anything except numbers and letters. So, he correctly used spaces, which with we are perfectly happy. If you want to changes this, you can again set the sep argument. For example, when there is a combined surname like Janssen-Swilden (let's say such a ridiculous name actually exists), it would be split on the - sign. We don't want that, so we should tell separate to split only on spaces, i.e. sep = " ".

Separate will create exactly as many columns as the number of names you provide in into. If he finds more or less pieces than that number for any observation, he will warn you about this. If there are less, NA will appear, if there are more, the last ones will be discarded. Also, you can use remove = F to keep the original variables.

Now let's get ready for those difficult ones!

2.3 *Spread data*

We can use spread to take a pair of variables - a *key* and a *value* - and spread them over different columns: one for each *key* with the corresponding *value* in it.

If at this moment you hear it thundering in Keulen, it might be time for you to revise earlier tutorials. Because we have actually already seen spread before (Did we?) (Yes we did.)

The following example might refresh things a bit.

```
library(ggplot2)
diamonds %>% count(color, clarity)
```

```
## # A tibble: 56 x 3
##    color clarity     n
```

```
##     <ord> <ord>   <int>
##   1 D     I1         42
##   2 D     SI2      1370
##   3 D     SI1      2083
##   4 D     VS2      1697
##   5 D     VS1       705
##   6 D     VVS2      553
##   7 D     VVS1      252
##   8 D     IF         73
##   9 E     I1        102
##  10 E     SI2      1713
## # ... with 46 more rows
```

```
diamonds %>% count(color, clarity) %>% spread(clarity,
    n)
```

```
## # A tibble: 7 x 9
##   color    I1   SI2   SI1   VS2   VS1  VVS2
##   <ord> <int> <int> <int> <int> <int> <int>
## 1 D        42  1370  2083  1697   705   553
## 2 E       102  1713  2426  2470  1281   991
## 3 F       143  1609  2131  2201  1364   975
## 4 G       150  1548  1976  2347  2148  1443
## 5 H       162  1563  2275  1643  1169   608
## 6 I        92   912  1424  1169   962   365
## 7 J        50   479   750   731   542   131
## # ... with 2 more variables: VVS1 <int>,
## #   IF <int>
```

When we *spread* data, we go from a *long* dataset to a *wide* dataset. Just look back at the example and the schematic figure. Make sure to remember this.

2.4 Gather data

If we already knew spread, gather is a piece of cake. It does the opposite of spread. How straightforward! So, with gather we go from a *wide* dataset to a *long* dataset, by *gathering* several observations into a single one.

Just look at this figure.

Let's look at an example.

The dataset below shows the population for every country on earth after each 5 year interval, starting in 1952, ending in 2007.

```
yearly_population
```

```
## # A tibble: 142 x 14
##    country continent '1952' '1957' '1962'
##    <fct>   <fct>      <int>  <int>  <int>
##  1 Afghan~ Asia      8.43e6 9.24e6 1.03e7
##  2 Albania Europe    1.28e6 1.48e6 1.73e6
##  3 Algeria Africa    9.28e6 1.03e7 1.10e7
##  4 Angola  Africa    4.23e6 4.56e6 4.83e6
##  5 Argent~ Americas  1.79e7 1.96e7 2.13e7
##  6 Austra~ Oceania   8.69e6 9.71e6 1.08e7
##  7 Austria Europe    6.93e6 6.97e6 7.13e6
##  8 Bahrain Asia      1.20e5 1.39e5 1.72e5
##  9 Bangla~ Asia      4.69e7 5.14e7 5.68e7
## 10 Belgium Europe    8.73e6 8.99e6 9.22e6
## # ... with 132 more rows, and 9 more
## #   variables: '1967' <int>, '1972' <int>,
## #   '1977' <int>, '1982' <int>,
## #   '1987' <int>, '1992' <int>,
## #   '1997' <int>, '2002' <int>, '2007' <int>
```

Pretty well-arranged table, isn't it? Let's make a line plot of the evolution. We would need time (years) on the x-asis and population on the y-axis. But. . . ? Well, f*ck me! Those variables don't exist?! How can I make my line plot?

Let's *gather* the data into those to variables.

- The key argument is the **new** variable in which we want old variable **names** to go. In our case, we want all the years as a *time* variable, so we can use them, instead of being scatterd over 12 variables.
- The value argument is the **new** variable in which the **values** of the old variables go. Thus, these would be the population numbers.

- After that, we specify all the columns we want to gather. In our case all years. So, we can just say that we don't want to gather country and continent instead.[5]

  Let's see what happens.

```
yearly_population %>% gather(key = time, value = population,
    -country, -continent)
```

```
## # A tibble: 1,704 x 4
##    country     continent time  population
##    <fct>       <fct>     <chr>      <int>
##  1 Afghanistan Asia      1952     8425333
##  2 Albania     Europe    1952     1282697
##  3 Algeria     Africa    1952     9279525
##  4 Angola      Africa    1952     4232095
##  5 Argentina   Americas  1952    17876956
##  6 Australia   Oceania   1952     8691212
##  7 Austria     Europe    1952     6927772
##  8 Bahrain     Asia      1952      120447
##  9 Bangladesh  Asia      1952    46886859
## 10 Belgium     Europe    1952     8730405
## # ... with 1,694 more rows
```

Well, exactly the opposite of spread, isn't it? A bunch of old variables (1952, 1957, 1962, etc.) are *gathered* into a single new variable time. While the contents of those old variables are placed next to them in the population variable.

Note how we went from a dataset with 13 colums and 142 rows (= WIDE) to a dataset with only 3 columns but 1704 rows (= LONG).

So, let's wrap this up.

- For gather, key and value are *new* columnames. You can choose them as you like (just like I chose time and population)
- For spread, key and value are *existing* columns. The ones you want to spread out.
- With gather, you provide a list of *existing* columns which you want to gather/combine. You can also say which you don't want using -. In fact, you can use all the select-tricks here. If you don't tell it anything except for key and value, all columns will be gathered.
- With gather, only key and value are necessary arguemnts.

Easy, isn't it?

Unfortunately, no. It isn't.

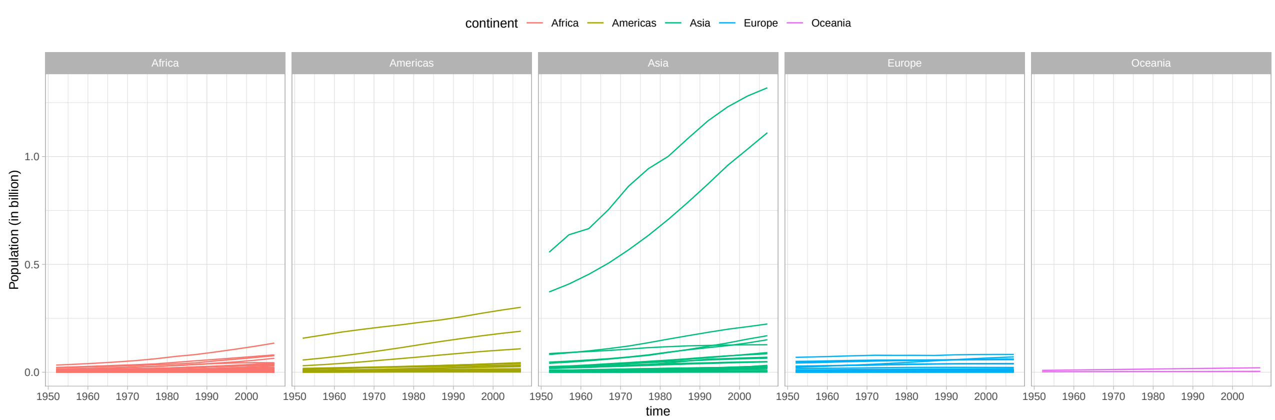
Spread and gather are probably the least intuitive functions you will learn in this course. Try to read this section several times, and

[5] Actually, there is a more important reason we want to use -country and -continent instead of listing all years, apart from being lazy. Remember that all object and variable names in R need to start with a letter, not a number? Well, the year columns clearly don't. Selecting them would need a special technique. Just saying 1952:2007 would unfortunately not work. But, luckily, that's a story for another time.

look very good at the examples. Try to see what's happening. Things can get very complicated with spread and gather, as they change the structure of your data entirely. Combining them with joins only increases the difficulty. So, don't go easy on this. Spend some time in trying to understand the functions, and learn how to use the cheatsheet. The functions are not easy at all, but you will need them sooner than you think. Let's see them at work in other example.
We will use some real-life data of the World Hearlth Organisations WHO!

Oh, I almost forgot! We would make a line plot of the population data. Well, you see, once we have gather, it gets easy. We can almost directly go to ggplot.

```
yearly_population %>% gather(key = time, value = population,
    -country, -continent) %>% mutate(time = as.numeric(time)) %>%
    ggplot(aes(time, population/(10^9), group = country,
        color = continent)) + geom_line() + facet_grid(. ~
    continent) + theme_light() + labs(y = "Population (in billion)") +
    theme(legend.position = "top")
```



Can you tell which countries are the two soaring lines in Asia? (Please tell me you can.)

So, let's study some health!

3
[Case study]: WHO

We gathered (pun intended) data about the number of (new) Tuberculosis cases broken down by

- year
- country
- age (7 groups)
- gender
- type of TB
  - new/old -> (all new in our case)
  - diagnosis method
    - rel: relapse
    - sp: smear positive
    - sn: smear negative
    - ep: extrapulmonary

  (No need to know the different diagnosis methods.)
  The data looks as follows.

```
who %>% glimpse()
```

```
## Observations: 7,240
## Variables: 60
## $ country      <chr> "Afghanistan", "Afg...
## $ iso2         <chr> "AF", "AF", "AF", "...
## $ iso3         <chr> "AFG", "AFG", "AFG"...
## $ year         <int> 1980, 1981, 1982, 1...
## $ new_sp_m014  <int> NA, NA, NA, NA, NA,...
## $ new_sp_m1524 <int> NA, NA, NA, NA, NA,...
## $ new_sp_m2534 <int> NA, NA, NA, NA, NA,...
## $ new_sp_m3544 <int> NA, NA, NA, NA, NA,...
## $ new_sp_m4554 <int> NA, NA, NA, NA, NA,...
## $ new_sp_m5564 <int> NA, NA, NA, NA, NA,...
## $ new_sp_m65   <int> NA, NA, NA, NA, NA,...
```

```
## $ new_sp_f014  <int> NA, NA, NA, NA, NA,...
## $ new_sp_f1524 <int> NA, NA, NA, NA, NA,...
## $ new_sp_f2534 <int> NA, NA, NA, NA, NA,...
## $ new_sp_f3544 <int> NA, NA, NA, NA, NA,...
## $ new_sp_f4554 <int> NA, NA, NA, NA, NA,...
## $ new_sp_f5564 <int> NA, NA, NA, NA, NA,...
## $ new_sp_f65   <int> NA, NA, NA, NA, NA,...
## $ new_sn_m014  <int> NA, NA, NA, NA, NA,...
## $ new_sn_m1524 <int> NA, NA, NA, NA, NA,...
## $ new_sn_m2534 <int> NA, NA, NA, NA, NA,...
## $ new_sn_m3544 <int> NA, NA, NA, NA, NA,...
## $ new_sn_m4554 <int> NA, NA, NA, NA, NA,...
## $ new_sn_m5564 <int> NA, NA, NA, NA, NA,...
## $ new_sn_m65   <int> NA, NA, NA, NA, NA,...
## $ new_sn_f014  <int> NA, NA, NA, NA, NA,...
## $ new_sn_f1524 <int> NA, NA, NA, NA, NA,...
## $ new_sn_f2534 <int> NA, NA, NA, NA, NA,...
## $ new_sn_f3544 <int> NA, NA, NA, NA, NA,...
## $ new_sn_f4554 <int> NA, NA, NA, NA, NA,...
## $ new_sn_f5564 <int> NA, NA, NA, NA, NA,...
## $ new_sn_f65   <int> NA, NA, NA, NA, NA,...
## $ new_ep_m014  <int> NA, NA, NA, NA, NA,...
## $ new_ep_m1524 <int> NA, NA, NA, NA, NA,...
## $ new_ep_m2534 <int> NA, NA, NA, NA, NA,...
## $ new_ep_m3544 <int> NA, NA, NA, NA, NA,...
## $ new_ep_m4554 <int> NA, NA, NA, NA, NA,...
## $ new_ep_m5564 <int> NA, NA, NA, NA, NA,...
## $ new_ep_m65   <int> NA, NA, NA, NA, NA,...
## $ new_ep_f014  <int> NA, NA, NA, NA, NA,...
## $ new_ep_f1524 <int> NA, NA, NA, NA, NA,...
## $ new_ep_f2534 <int> NA, NA, NA, NA, NA,...
## $ new_ep_f3544 <int> NA, NA, NA, NA, NA,...
## $ new_ep_f4554 <int> NA, NA, NA, NA, NA,...
## $ new_ep_f5564 <int> NA, NA, NA, NA, NA,...
## $ new_ep_f65   <int> NA, NA, NA, NA, NA,...
## $ newrel_m014  <int> NA, NA, NA, NA, NA,...
## $ newrel_m1524 <int> NA, NA, NA, NA, NA,...
## $ newrel_m2534 <int> NA, NA, NA, NA, NA,...
## $ newrel_m3544 <int> NA, NA, NA, NA, NA,...
## $ newrel_m4554 <int> NA, NA, NA, NA, NA,...
## $ newrel_m5564 <int> NA, NA, NA, NA, NA,...
## $ newrel_m65   <int> NA, NA, NA, NA, NA,...
## $ newrel_f014  <int> NA, NA, NA, NA, NA,...
## $ newrel_f1524 <int> NA, NA, NA, NA, NA,...
```

```
## $ newrel_f2534 <int> NA, NA, NA, NA, NA,...
## $ newrel_f3544 <int> NA, NA, NA, NA, NA,...
## $ newrel_f4554 <int> NA, NA, NA, NA, NA,...
## $ newrel_f5564 <int> NA, NA, NA, NA, NA,...
## $ newrel_f65   <int> NA, NA, NA, NA, NA,...
```

To be honest: quite a mess. We don't really need 60 variables for the data we just described, do we? What's going on?

It seems that for each country and each year, the data contains one row. Let's verify.

```
who %>% count(country, year)
```

```
## # A tibble: 7,240 x 3
##    country      year     n
##    <chr>       <int> <int>
##  1 Afghanistan  1980     1
##  2 Afghanistan  1981     1
##  3 Afghanistan  1982     1
##  4 Afghanistan  1983     1
##  5 Afghanistan  1984     1
##  6 Afghanistan  1985     1
##  7 Afghanistan  1986     1
##  8 Afghanistan  1987     1
##  9 Afghanistan  1988     1
## 10 Afghanistan  1989     1
## # ... with 7,230 more rows
```

We see mostly ones. Let's check for sure.

```
who %>% count(country, year) %>% filter(n > 1)
```

```
## # A tibble: 0 x 3
## # ... with 3 variables: country <chr>,
## #   year <int>, n <int>
```

Ok. So, each year, each country, one row. We have 7240 rows because we have

```
who %>% count(year) %>% nrow
```

```
## [1] 34
```

34 years, and

```
who %>% count(country) %>% nrow()
```

```
## [1] 219
```

219 countries.

Thus we expect this many rows:

```
219 * 34
```

```
## [1] 7446
```

It seems we are missing 206 rows. I.e. there are countries for which we don't have all years, or vice versa. It is not really important here, but these are the kind of things a good data analyst checks.

Let's go back to our problem.

Of the 60 variables, the first 3 all depict country (Remember that I told you that there are different ways to abbreviate a country), and the 4th contains the year. So, there remain 56 variables.

Well, we have information on 7 age groups, 2 genders, and 4 diagnosis methods. 7 times 2 times 4 equals 56. Aha! All the different cases are putted in a different variable. That's not really easy to work with.

Why not, I heard you think?

Let's try to solve the following questions.

- How many women older, 25 or older in Belgium were diagnosed with TB in 2000? How many of those had a relaps?
- What is the total number of TB cases in Belgium in each year?
- Can you graphically show the evolution of the number of cases for different genders and age groups?

No, you can't. At least, not without a lot of work, or without tidying our data. So, let's start.

It is often helpful to think about the format we would like our data to be in, without getting lost in transformation. Ideally, we would like to have the following variables:

- country
- year
- is_new
- diagnosis
- gender
- age
- cases (the number of TB cases)

First of all, let's go to a dataset in a long format, by gathering all the different types of diagnosis and cases into a long list. We will not gather the first 4 columns. The old columns will be a variable "type", and the numbers will be called "cases".

```
who %>% gather(key = type, value = cases, -country:-year)
```

```
## # A tibble: 405,440 x 6
##    country   iso2  iso3   year type     cases
##    <chr>     <chr> <chr> <int> <chr>    <int>
##  1 Afghanis~ AF    AFG    1980 new_sp_~    NA
##  2 Afghanis~ AF    AFG    1981 new_sp_~    NA
##  3 Afghanis~ AF    AFG    1982 new_sp_~    NA
##  4 Afghanis~ AF    AFG    1983 new_sp_~    NA
##  5 Afghanis~ AF    AFG    1984 new_sp_~    NA
##  6 Afghanis~ AF    AFG    1985 new_sp_~    NA
##  7 Afghanis~ AF    AFG    1986 new_sp_~    NA
##  8 Afghanis~ AF    AFG    1987 new_sp_~    NA
##  9 Afghanis~ AF    AFG    1988 new_sp_~    NA
## 10 Afghanis~ AF    AFG    1989 new_sp_~    NA
## # ... with 405,430 more rows
```

See what happened? Take a good look.

Had you figured out that we first needed to gather the data? If yes, congratulations, you start to get what data transformation is and which transformations you need where. If no, don't worry. Remember that I told you this is a hard skill. Furthermore, there are probably different ways to do this.

We can get rid of iso2 and iso3. Note that they might be useful for joining the data with other data about countries, but we have no plans to do so. Just, let's get them out of our way.

```
who %>% gather(key = type, value = cases, -country:-year) %>%
    select(-iso2, -iso3)
```

```
## # A tibble: 405,440 x 4
##    country      year type        cases
##    <chr>       <int> <chr>       <int>
##  1 Afghanistan  1980 new_sp_m014    NA
##  2 Afghanistan  1981 new_sp_m014    NA
##  3 Afghanistan  1982 new_sp_m014    NA
##  4 Afghanistan  1983 new_sp_m014    NA
##  5 Afghanistan  1984 new_sp_m014    NA
##  6 Afghanistan  1985 new_sp_m014    NA
##  7 Afghanistan  1986 new_sp_m014    NA
##  8 Afghanistan  1987 new_sp_m014    NA
##  9 Afghanistan  1988 new_sp_m014    NA
## 10 Afghanistan  1989 new_sp_m014    NA
## # ... with 405,430 more rows
```

Now, there is a lot of information in the type variable. Actually, there are more variables in this single variable. let's separate them. (See how that thought process goes?)

First, let's look at the different levels by doing a quick count.

```
who %>% gather(key = type, value = cases, -country:-year) %>%
    select(-iso2, -iso3) %>% count(type) %>% print(n = Inf)  # I want to see all of them
```

```
## # A tibble: 56 x 2
##    type            n
##    <chr>       <int>
##  1 new_ep_f014   7240
##  2 new_ep_f1524  7240
##  3 new_ep_f2534  7240
##  4 new_ep_f3544  7240
##  5 new_ep_f4554  7240
##  6 new_ep_f5564  7240
##  7 new_ep_f65    7240
##  8 new_ep_m014   7240
##  9 new_ep_m1524  7240
## 10 new_ep_m2534  7240
## 11 new_ep_m3544  7240
## 12 new_ep_m4554  7240
## 13 new_ep_m5564  7240
## 14 new_ep_m65    7240
## 15 new_sn_f014   7240
## 16 new_sn_f1524  7240
## 17 new_sn_f2534  7240
## 18 new_sn_f3544  7240
## 19 new_sn_f4554  7240
## 20 new_sn_f5564  7240
## 21 new_sn_f65    7240
## 22 new_sn_m014   7240
## 23 new_sn_m1524  7240
## 24 new_sn_m2534  7240
## 25 new_sn_m3544  7240
## 26 new_sn_m4554  7240
## 27 new_sn_m5564  7240
## 28 new_sn_m65    7240
## 29 new_sp_f014   7240
## 30 new_sp_f1524  7240
## 31 new_sp_f2534  7240
## 32 new_sp_f3544  7240
## 33 new_sp_f4554  7240
## 34 new_sp_f5564  7240
## 35 new_sp_f65    7240
## 36 new_sp_m014   7240
## 37 new_sp_m1524  7240
```

```
## 38 new_sp_m2534  7240
## 39 new_sp_m3544  7240
## 40 new_sp_m4554  7240
## 41 new_sp_m5564  7240
## 42 new_sp_m65    7240
## 43 newrel_f014   7240
## 44 newrel_f1524  7240
## 45 newrel_f2534  7240
## 46 newrel_f3544  7240
## 47 newrel_f4554  7240
## 48 newrel_f5564  7240
## 49 newrel_f65    7240
## 50 newrel_m014   7240
## 51 newrel_m1524  7240
## 52 newrel_m2534  7240
## 53 newrel_m3544  7240
## 54 newrel_m4554  7240
## 55 newrel_m5564  7240
## 56 newrel_m65    7240
```

Oh crap. The first 42 levels are nicely separated by 2 underscores. But the last are not. It's all "newrel" instead of "new_rel". Separate will not be able to split that...

So, let's pull together a neat trick. We are going to replace all the little "newrel" part with "new_rel". How? Using the stringr package for string manipulation. It has a useful function `str_replace`. Here we go.

```
who %>% gather(key = type, value = cases, -country:-year) %>%
    select(-iso2, -iso3) %>% mutate(type = str_replace(type,
    "newrel", "new_rel")) %>% count(type) %>%
    print(n = Inf)
```

```
## # A tibble: 56 x 2
##    type             n
##    <chr>        <int>
##  1 new_ep_f014   7240
##  2 new_ep_f1524  7240
##  3 new_ep_f2534  7240
##  4 new_ep_f3544  7240
##  5 new_ep_f4554  7240
##  6 new_ep_f5564  7240
##  7 new_ep_f65    7240
##  8 new_ep_m014   7240
##  9 new_ep_m1524  7240
```

```
## 10 new_ep_m2534   7240
## 11 new_ep_m3544   7240
## 12 new_ep_m4554   7240
## 13 new_ep_m5564   7240
## 14 new_ep_m65     7240
## 15 new_rel_f014   7240
## 16 new_rel_f1524  7240
## 17 new_rel_f2534  7240
## 18 new_rel_f3544  7240
## 19 new_rel_f4554  7240
## 20 new_rel_f5564  7240
## 21 new_rel_f65    7240
## 22 new_rel_m014   7240
## 23 new_rel_m1524  7240
## 24 new_rel_m2534  7240
## 25 new_rel_m3544  7240
## 26 new_rel_m4554  7240
## 27 new_rel_m5564  7240
## 28 new_rel_m65    7240
## 29 new_sn_f014    7240
## 30 new_sn_f1524   7240
## 31 new_sn_f2534   7240
## 32 new_sn_f3544   7240
## 33 new_sn_f4554   7240
## 34 new_sn_f5564   7240
## 35 new_sn_f65     7240
## 36 new_sn_m014    7240
## 37 new_sn_m1524   7240
## 38 new_sn_m2534   7240
## 39 new_sn_m3544   7240
## 40 new_sn_m4554   7240
## 41 new_sn_m5564   7240
## 42 new_sn_m65     7240
## 43 new_sp_f014    7240
## 44 new_sp_f1524   7240
## 45 new_sp_f2534   7240
## 46 new_sp_f3544   7240
## 47 new_sp_f4554   7240
## 48 new_sp_f5564   7240
## 49 new_sp_f65     7240
## 50 new_sp_m014    7240
## 51 new_sp_m1524   7240
## 52 new_sp_m2534   7240
## 53 new_sp_m3544   7240
```

```
## 54 new_sp_m4554   7240
## 55 new_sp_m5564   7240
## 56 new_sp_m65     7240
```

That's better, isn't it? By the way, do you see how we at each point build on what we did before? This way we can easily change mistakes if we make some. Only when our data is correctly transformed, we save it, and put the code in our loadscript.

But now, we can separate the data. The first part will become the is_new variable, the second part the diagnosis variable, and the last part... well, it contaisn both the gender (f/m) and the age category. Let's just call it age_gender, and tackle that problem later.

```
who %>% gather(key = type, value = cases, -country:-year) %>%
    select(-iso2, -iso3) %>% mutate(type = str_replace(type,
    "newrel", "new_rel")) %>% separate(type, into = c("is_new",
    "diagnosis", "age_gender"))
```

```
## # A tibble: 405,440 x 6
##    country  year is_new diagnosis age_gender
##    <chr>   <int> <chr>  <chr>     <chr>
##  1 Afghan~  1980 new    sp        m014
##  2 Afghan~  1981 new    sp        m014
##  3 Afghan~  1982 new    sp        m014
##  4 Afghan~  1983 new    sp        m014
##  5 Afghan~  1984 new    sp        m014
##  6 Afghan~  1985 new    sp        m014
##  7 Afghan~  1986 new    sp        m014
##  8 Afghan~  1987 new    sp        m014
##  9 Afghan~  1988 new    sp        m014
## 10 Afghan~  1989 new    sp        m014
## # ... with 405,430 more rows, and 1 more
## #   variable: cases <int>
```

Cool, that worked! We didn't even need to tell separate how to split. He decided this automagically. What a smart boy!

Now, let's split age_gender. But on what? There is no character to split on. However, separate is so smart, we can tell him to split after the *first* character - 'cause that one is the gender, the remainder is the age. We could actually do this for any character. We just need to set sep = n, where n is our number. In this case 1. Let's try!

```
who %>% gather(key = type, value = cases, -country:-year) %>%
    select(-iso2, -iso3) %>% mutate(type = str_replace(type,
    "newrel", "new_rel")) %>% separate(type, into = c("is_new",
    "diagnosis", "age_gender")) %>% separate(age_gender,
    into = c("age", "gender"), sep = 1)
```

```
## # A tibble: 405,440 x 7
##    country  year is_new diagnosis age
##    <chr>   <int> <chr>  <chr>     <chr>
##  1 Afghan~  1980 new    sp        m
##  2 Afghan~  1981 new    sp        m
##  3 Afghan~  1982 new    sp        m
##  4 Afghan~  1983 new    sp        m
##  5 Afghan~  1984 new    sp        m
##  6 Afghan~  1985 new    sp        m
##  7 Afghan~  1986 new    sp        m
##  8 Afghan~  1987 new    sp        m
##  9 Afghan~  1988 new    sp        m
## 10 Afghan~  1989 new    sp        m
## # ... with 405,430 more rows, and 2 more
## #   variables: gender <chr>, cases <int>
```

I don't know about you, but I think this is exactly how we wanted the data to be! Let's save it now.

```
tidy_who <- who %>% gather(key = type, value = cases,
    -country:-year) %>% select(-iso2, -iso3) %>%
    mutate(type = str_replace(type, "newrel",
        "new_rel")) %>% separate(type, into = c("is_new",
    "diagnosis", "age_gender")) %>% separate(age_gender,
    into = c("gender", "age"), sep = 1)
```

And just for fun, let us solve the questions we had earlier.

- How many women older, 25 or older in Belgium were diagnosed with TB in 2000? How many of those had a relaps?

```
tidy_who %>% filter(gender == "f", !(age %in%
    c("014", "1524")), country == "Belgium", year ==
    2000) %>% group_by(diagnosis) %>% summarize(n_cases = sum(cases,
    na.rm = T))
```

```
## # A tibble: 4 x 2
##   diagnosis n_cases
##   <chr>       <int>
## 1 ep              0
## 2 rel             0
## 3 sn              0
## 4 sp             78
```

According to this data, there were 78 cases, and none of them were relapses.

- What is the total number of TB cases in Belgium in each year?

```
tidy_who %>% filter(country == "Belgium") %>%
    group_by(year) %>% summarize(n_cases = sum(cases,
    na.rm = T))
```

```
## # A tibble: 34 x 2
##     year n_cases
##    <int>   <int>
##  1  1980       0
##  2  1981       0
##  3  1982       0
##  4  1983       0
##  5  1984       0
##  6  1985       0
##  7  1986       0
##  8  1987       0
##  9  1988       0
## 10  1989       0
## # ... with 24 more rows
```

(It seems there were no cases of TB in Belgium before 1995. Or we are just missing data? That's the thing na.rm can do. You must be careful.)

- Can you graphically show the evolution of the number of cases for different genders and age groups?

```
tidy_who %>% group_by(year, age, gender) %>% summarize(n_cases = sum(cases,
    na.rm = T)) %>% ggplot(aes(year, n_cases)) +
    geom_line(color = "pink4", lwd = 1) + facet_grid(gender ~
    age) + theme_light()
```