

# Intro to the Tidyverse

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## 1 Introduction to the Tidyverse

The Tidyverse is a collection of R packages that can be used together for many different data science practices. They share syntax and are very versatile. For most users, the Tidyverse provides a structure of “best practices” that will allow a user to do just about anything with data.

We can load the Tidyverse as a single package in R:

```
library(tidyverse)

-- Attaching packages ----- tidyverse 1.3.2 --
v ggplot2 3.4.0      v purrr   1.0.0
v tibble  3.1.8      v dplyr   1.0.10
v tidyr   1.2.1      v stringr 1.5.0
v readr   2.1.3      v forcats 0.5.2

-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
```

The tidyverse package contains the following packages: 1.) ggplot2: the best graphing package in R

2.) dplyr: most of our data wrangling tools come from here

3.) tidyr: tools for data tidying (cleaning, reshaping)

4.) readr: tools for reading in different types of data – this is where the read\_csv() function comes from

5.) purrr: tools for working with functions and vectors (useful but likely not right away for beginners)

6.) stringr: functions to help us work with strings (like sentences, paragraphs, lists, etc)

7.) forcats: “for categories” - makes working with factors (categorical data) easier!

[Learn more about the Tidyverse](#)

This section contains some worked examples of Tidyverse best practices for data manipulation.

If you just want a quick refresher, you can take a look at the **cheat sheet** below!

**R For Data Science Cheat Sheet**  
Tidyverse for Beginners  
Learn More R for Data Science Interactively at [www.datacamp.com](http://www.datacamp.com)

**Tidyverse**  
The tidyverse is a powerful collection of R packages that are actually data tools for transforming and visualizing data. All packages of the tidyverse share an underlying philosophy and common APIs.  
The core packages are:  
• **ggplot2**, which implements the grammar of graphics. You can use it to visualize your data.  
• **dplyr** is a grammar of data manipulation. You can use it to solve the most common data manipulation challenges.  
• **tidyr** helps you to create tidy data or data where each variable is in a column, each observation is a row and each value is a cell.  
• **readr** is a fast and friendly way to read rectangular data.  
• **purrr** enhances R's functional programming (FP) toolkit by providing a complete and consistent set of tools for working with functions and vectors.  
• **tibble** is a modern re-imagining of the data frame.  
• **stringr** provides a cohesive set of functions designed to make working with strings as easy as possible  
• **forcats** provide a suite of useful tools that solve common problems with factors.  
You can install the complete tidyverse with:  
`> install.packages("tidyverse")`  
Then, load the core tidyverse and make it available in your current R session by running:  
`> library(tidyverse)`  
Note: there are many other tidyverse packages with more specialised usage. They are not loaded automatically with library(tidyverse), so you'll need to load each one with its own call to library().

**Useful Functions**  
`> tidyverse_conflicts()` Conflicts between tidyverse and other packages  
`> tidyverse_deps()` List all tidyverse dependencies  
`> tidyverse_logos()` Get tidyverse logo, using ASCII or unicode characters  
`> tidyverse_packages()` List all tidyverse packages  
`> tidyverse_update()` Update tidyverse packages

**Loading in the data**  
`> library(datasets)` Load the datasets package  
`> library(ggplot2)` Load the ggplot2 package  
`> attach(iris)` Attach iris data to the R search path

**dplyr**  
**Filter**  
`filter()` allows you to select a subset of rows in a data frame.  
`> iris %>% filter(Species=="virginica")` Select iris data of species "virginica"  
`> iris %>% filter(Species=="virginica", Sepal.Length > 6)` Select iris data of species "virginica" and sepal length greater than 6.  
**Arrange**  
`arrange()` sorts the observations in a dataset in ascending or descending order based on one of its variables.  
`> iris %>% arrange(Sepal.Length)` Sort in ascending order of sepal length  
`> iris %>% arrange(desc(Sepal.Length))` Sort in descending order of sepal length  
Combine multiple dplyr verbs in a row with the pipe operator %>%:  
`> iris %>% filter(Species=="virginica") %>% arrange(desc(Sepal.Length))` Filter for species "virginica" then arrange in descending order of sepal length  
**Mutate**  
`mutate()` allows you to update or create new columns of a data frame.  
`> iris %>% mutate(Sepal.Length=Sepal.Length*10)` Change Sepal.Length to be in millimeters  
`> iris %>% mutate(SLMm=Sepal.Length*10)` Create a new column called SLMm  
Combine the verbs filter(), arrange(), and mutate():  
`> iris %>% filter(Species=="virginica") %>% mutate(SLMm=Sepal.Length*10) %>% arrange(desc(SLMm))`  
**Summarize**  
`summarize()` allows you to turn many observations into a single data point.  
`> iris %>% summarize(medianSL=median(Sepal.Length))` Summarize to find the median sepal length  
`> iris %>% filter(Species=="virginica") %>% summarize(medianSL=median(Sepal.Length))` Filter for virginica then summarize the median sepal length  
You can also summarize multiple variables at once:  
`> iris %>% filter(Species=="virginica") %>% summarize(medianSL=median(Sepal.Length), maxSL=max(Sepal.Length))`  
`group_by()` allows you to summarize within groups instead of summarizing the entire dataset:  
`> iris %>% group_by(Species) %>% summarize(medianSL=median(Sepal.Length), maxSL=max(Sepal.Length))` Find median and max sepal length of each species  
`> iris %>% filter(Sepal.Length>6) %>% group_by(Species) %>% summarize(medianPL=median(Petal.Length), maxPL=max(Petal.Length))` Find median and max petal length of each species with sepal length > 6

**ggplot2**  
**Scatter plot**  
Scatter plots allow you to compare two variables within your data. To do this with ggplot2, you use geom\_point().  
`> iris_small <- iris %>% filter(Sepal.Length > 5)`  
`> ggplot(iris_small, aes(x=Petal.Length, y=Petal.Width)) + geom_point()` Compare petal width and length  
**Additional Aesthetics**  
• **Color**  
`> ggplot(iris_small, aes(x=Petal.Length, y=Petal.Width, color=Species)) + geom_point()`  
• **Size**  
`> ggplot(iris_small, aes(x=Petal.Length, y=Petal.Width, color=Species, size=Sepal.Length)) + geom_point()`  
**Faceting**  
`> ggplot(iris_small, aes(x=Petal.Length, y=Petal.Width)) + geom_point() + facet_wrap(~Species)`  
**Line Plots**  
`> by_year <- gapminder %>% group_by(year) %>% summarize(medianGdpPerCap=median(gdpPerCap))`  
`> ggplot(by_year, aes(x=year, y=medianGdpPerCap)) + geom_line() + expand_limits(y=0)`  
**Bar Plots**  
`> by_species <- iris %>% filter(Sepal.Length>6) %>% group_by(Species) %>% summarize(medianPL=median(Petal.Length))`  
`> ggplot(by_species, aes(x=Species, y=medianPL)) + geom_col()`  
**Histograms**  
`> ggplot(iris_small, aes(x=Petal.Length)) + geom_histogram()`  
**Box Plots**  
`> ggplot(iris_small, aes(x=Species, y=Sepal.Width)) + geom_boxplot()`

**DataCamp**  
Learn R for Data Science Interactively

## 1.1 Read in some data

We can mess with a few data sets that are built into R or into R packages.

A common one is `mtcars`, which is part of base R (attributes of a bunch of cars)

```
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

Another fun one is `CO2`, which is also part of base R (CO2 uptake from different plants). Note: `co2` (no caps) is also a dataset in R. It's just the CO2 concentration at Maona Loa observatory every year (as a list).

```
head(CO2)
```

	Plant	Type	Treatment	conc	uptake
1	Qn1	Quebec	nonchilled	95	16.0
2	Qn1	Quebec	nonchilled	175	30.4
3	Qn1	Quebec	nonchilled	250	34.8
4	Qn1	Quebec	nonchilled	350	37.2
5	Qn1	Quebec	nonchilled	500	35.3
6	Qn1	Quebec	nonchilled	675	39.2

You are welcome to use these to practice with or you can choose from any of the datasets in the ‘`datasets`’ or ‘`MASS`’ packages (you have to load the package to get the datasets).

You can also load in your own data or pick something from online, as we learned how to do last time.

Let's stick with what we know for now– I will use the penguins data from the `palmerpenguins` package

### load the data

```
library(palmerpenguins)
penguins
```

```

# A tibble: 344 x 8
  species island    bill_length_mm bill_depth_mm flipper_~1 body_~2 sex    year
  <fct>   <fct>          <dbl>          <dbl>        <int>    <int> <fct> <int>
1 Adelie  Torgersen        39.1           18.7          181     3750 male  2007
2 Adelie  Torgersen        39.5           17.4          186     3800 fema~ 2007
3 Adelie  Torgersen        40.3           18            195     3250 fema~ 2007
4 Adelie  Torgersen        NA             NA             NA       NA <NA> 2007
5 Adelie  Torgersen        36.7           19.3          193     3450 fema~ 2007
6 Adelie  Torgersen        39.3           20.6          190     3650 male  2007
7 Adelie  Torgersen        38.9           17.8          181     3625 fema~ 2007
8 Adelie  Torgersen        39.2           19.6          195     4675 male  2007
9 Adelie  Torgersen        34.1           18.1          193     3475 <NA> 2007
10 Adelie Torgersen        42            20.2          190     4250 <NA> 2007
# ... with 334 more rows, and abbreviated variable names 1: flipper_length_mm,
# 2: body_mass_g

```

**add the dataframe to our environment** As you learned in the Rstudio basics tutorial above, one of the four main panels of the RStudio window contains the Environment tab. In this tab, we can see data that are stored locally in our session of R. While penguins is pre-loaded in R, it is nice to make a local copy so we can modify it easily. Here's how we do that:

```
penguins<-penguins
```

Here, the name of the new dataframe we want in our environment is to the left of the arrow and the name of the object we are calling is to the right. In simpler terms, we are defining a new dataframe called penguins (or any name we want) and it is defined as just an exact copy of penguins (the object that is already defined within palmerpenguins). This is the simplest example – we will quickly move on to more complex things. You will see that when you run this the dataframe 'penguins' appears in the local environment. You can call your local file anything you want, it does not need to be an exact copy of the original name! Choose names that are meaningful to you, but keep the names short and avoid spaces and other special characters as much as possible.

## 2 Tidyverse data wrangling

### 2.1 Select or remove columns/rows

Let's look at penguins

```
head(penguins)
```

```
# A tibble: 6 x 8
  species island  bill_length_mm bill_depth_mm flipper_l~1 body_~2 sex  year
  <fct>   <fct>          <dbl>          <dbl>          <int>    <int> <fct> <int>
1 Adelie Torgersen      39.1           18.7           181     3750 male  2007
2 Adelie Torgersen      39.5           17.4           186     3800 fema~ 2007
3 Adelie Torgersen      40.3           18             195     3250 fema~ 2007
4 Adelie Torgersen      NA             NA             NA       NA <NA>  2007
5 Adelie Torgersen      36.7           19.3           193     3450 fema~ 2007
6 Adelie Torgersen      39.3           20.6           190     3650 male  2007
# ... with abbreviated variable names 1: flipper_length_mm, 2: body_mass_g
```

Now let's say we only really care about species and bill length. We can select those columns to keep and remove the rest of the columns because they are just clutter at this point. There are two ways we can do this: 1.) Select the columns we want to keep 2.) Select the columns we want to remove

Here are two ways to do that:

**Base R example** For those with some coding experience you may like this method as this syntax is common in other coding languages

**Step 1.)** Count the column numbers. Column 1 is the left most column. Remember we can use `ncol()` to count the total number of columns (useful when we have a huge number of columns)

```
ncol(penguins) # we have 8 columns
```

```
[1] 8
```

Species is column 1 and bill length is column 3. Those are the only columns we want!

**Step 2.)** Select columns we want to keep using bracket syntax. Here we will use this basic syntax: `df[rows, columns]` We can input the rows and/or columns we want inside our brackets. If we want more than 1 row or column we will need to use a `'c()'` for concatenate (combine). To select just species and bill length we would do the following:

```
head(penguins[,c(1,3)]) #Selecting NO specific rows and 2 columns (numbers 1 and 3)
```

```
# A tibble: 6 x 2
  species bill_length_mm
  <fct>      <dbl>
1 Adelie      39.1
2 Adelie      39.5
3 Adelie      40.3
4 Adelie       NA
5 Adelie      36.7
6 Adelie      39.3
```

**IMPORTANT** When we do this kind of manipulation it is super helpful to NAME the output. In the above example I didn't do that. If I don't name the output I cannot easily call it later. If I do name it, I can use it later and see it in my 'Environment' tab. So, I should do this:

```
pens<-penguins[,c(1,3)]
head(pens)
```

```
# A tibble: 6 x 2
  species bill_length_mm
  <fct>      <dbl>
1 Adelie      39.1
2 Adelie      39.5
3 Adelie      40.3
4 Adelie       NA
5 Adelie      36.7
6 Adelie      39.3
```

Now, here's how you do the same selection step by removing the columns you **DO NOT** want.

```
pens2<-penguins[,-c(2,4:8)] #NOTE that ':' is just shorthand for all columns between 4 and
head(pens2)
```

```
# A tibble: 6 x 2
  species bill_length_mm
  <fct>      <dbl>
1 Adelie      39.1
2 Adelie      39.5
3 Adelie      40.3
4 Adelie       NA
```

```
5 Adelie          36.7
6 Adelie          39.3
```

---

### Tidyverse example (select())

Perhaps that example above was a little confusing? This is why we like Tidyverse! We can do the same thing using the `select()` function in Tidyverse and it is easier!

I still want just species and bill length. Here's how I select them:

```
head(select(penguins, species, bill_length_mm))
```

```
# A tibble: 6 x 2
  species bill_length_mm
  <fct>      <dbl>
1 Adelie      39.1
2 Adelie      39.5
3 Adelie      40.3
4 Adelie      NA
5 Adelie      36.7
6 Adelie      39.3
```

EASY. Don't forget to **name the output** for use later :)

Like this:

```
shortpen<-select(penguins, species, bill_length_mm)
head(shortpen)
```

```
# A tibble: 6 x 2
  species bill_length_mm
  <fct>      <dbl>
1 Adelie      39.1
2 Adelie      39.5
3 Adelie      40.3
4 Adelie      NA
5 Adelie      36.7
6 Adelie      39.3
```

---

## 2.2 Subsetting and filtering data

Sometimes we only want to look at data from a subset of the data frame

For example, maybe we only want to examine data from chinstrap penguins in the penguins data. OR perhaps we only care about 4 cylinder cars in mtcars. We can filter out the data we don't want easily using Tidyverse (filter) or base R (subset)

### Tidyverse example - Using filter()

Let's go ahead and filter the penguins data to only include chinstraps and the mtcars data to only include 4 cylinder cars

The syntax for filter is: filter(df, column ==><== number or factor)

```
#filter penguins to only contain chinstrap
chins<-filter(penguins, species=='Chinstrap')
head(chins)
```

```
# A tibble: 6 x 8
  species island bill_length_mm bill_depth_mm flipper_le~1 body_~2 sex year
  <fct>    <fct>      <dbl>         <dbl>         <int>    <int> <fct> <int>
1 Chinstrap Dream      46.5           17.9           192     3500 fema~ 2007
2 Chinstrap Dream      50             19.5           196     3900 male  2007
3 Chinstrap Dream     51.3           19.2           193     3650 male  2007
4 Chinstrap Dream     45.4           18.7           188     3525 fema~ 2007
5 Chinstrap Dream     52.7           19.8           197     3725 male  2007
6 Chinstrap Dream     45.2           17.8           198     3950 fema~ 2007
# ... with abbreviated variable names 1: flipper_length_mm, 2: body_mass_g
```

```
#confirm that we only have chinstraps
chins$species
```

```
[1] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[8] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[15] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[22] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[29] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[36] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[43] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[50] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
```



```
[57] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
[64] Chinstrap Chinstrap Chinstrap Chinstrap Chinstrap
Levels: Adelie Chinstrap Gentoo
```

Now for mtcars...

```
#filter mtcars to only contain 4 cylinder cars
cars4cyl<-filter(mtcars, cyl == "4")
head(cars4cyl)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Fiat 128	32.4	4	78.7	66	4.08	2.200	19.47	1	1	4	1
Honda Civic	30.4	4	75.7	52	4.93	1.615	18.52	1	1	4	2
Toyota Corolla	33.9	4	71.1	65	4.22	1.835	19.90	1	1	4	1

```
#confirm it worked
str(cars4cyl) #str shows us the observations and variables in each column
```

```
'data.frame':  11 obs. of  11 variables:
 $ mpg : num  22.8 24.4 22.8 32.4 30.4 33.9 21.5 27.3 26 30.4 ...
 $ cyl : num  4 4 4 4 4 4 4 4 4 4 ...
 $ disp: num  108 146.7 140.8 78.7 75.7 ...
 $ hp  : num  93 62 95 66 52 65 97 66 91 113 ...
 $ drat: num  3.85 3.69 3.92 4.08 4.93 4.22 3.7 4.08 4.43 3.77 ...
 $ wt  : num  2.32 3.19 3.15 2.2 1.61 ...
 $ qsec: num  18.6 20 22.9 19.5 18.5 ...
 $ vs  : num  1 1 1 1 1 1 1 1 0 1 ...
 $ am  : num  1 0 0 1 1 1 0 1 1 1 ...
 $ gear: num  4 4 4 4 4 4 3 4 5 5 ...
 $ carb: num  1 2 2 1 2 1 1 1 2 2 ...
```

```
cars4cyl$cyl #shows us only the observations in the cyl column!
```

```
[1] 4 4 4 4 4 4 4 4 4 4 4
```

**Base R example (subset)** In this case, the subset() function that is in base R works almost exactly like the filter() function. You can essentially use them interchangeably.

```
#subset mtcars to include only 4 cylinder cars
cars4cyl2.0<-subset(mtcars, cyl=='4')
cars4cyl2.0
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Fiat 128	32.4	4	78.7	66	4.08	2.200	19.47	1	1	4	1
Honda Civic	30.4	4	75.7	52	4.93	1.615	18.52	1	1	4	2
Toyota Corolla	33.9	4	71.1	65	4.22	1.835	19.90	1	1	4	1
Toyota Corona	21.5	4	120.1	97	3.70	2.465	20.01	1	0	3	1
Fiat X1-9	27.3	4	79.0	66	4.08	1.935	18.90	1	1	4	1
Porsche 914-2	26.0	4	120.3	91	4.43	2.140	16.70	0	1	5	2
Lotus Europa	30.4	4	95.1	113	3.77	1.513	16.90	1	1	5	2
Volvo 142E	21.4	4	121.0	109	4.11	2.780	18.60	1	1	4	2

---

## 2.3 Add new columns or change existing ones

**Adding a new column** Sometimes we may want to do some math on a column (or a series of columns). Maybe we want to calculate a ratio, volume, or area. Maybe we just want to scale a variable by taking the log or changing it from cm to mm. We can do all of this with the `mutate()` function in Tidyverse!

```
#convert bill length to cm (and make a new column)
head(penguins)
```

```
# A tibble: 6 x 8
  species island  bill_length_mm bill_depth_mm flipper_l~1 body_~2 sex  year
  <fct>   <fct>          <dbl>          <dbl>          <int>   <int> <fct> <int>
1 Adelie Torgersen      39.1           18.7           181     3750 male  2007
2 Adelie Torgersen      39.5           17.4           186     3800 fema~ 2007
3 Adelie Torgersen      40.3           18            195     3250 fema~ 2007
4 Adelie Torgersen      NA             NA             NA       NA <NA>  2007
5 Adelie Torgersen      36.7           19.3           193     3450 fema~ 2007
6 Adelie Torgersen      39.3           20.6           190     3650 male  2007
# ... with abbreviated variable names 1: flipper_length_mm, 2: body_mass_g
```

```
mutpen<-(mutate(penguins, bill_length_cm=bill_length_mm/10))
head(mutpen)
```

```
# A tibble: 6 x 9
  species island    bill_length_mm bill_de~1 flipp~2 body_~3 sex    year bill_~4
  <fct>  <fct>          <dbl>      <dbl>  <int>  <int> <fct> <int>  <dbl>
1 Adelie Torgersen      39.1       18.7   181    3750 male   2007    3.91
2 Adelie Torgersen      39.5       17.4   186    3800 fema~ 2007    3.95
3 Adelie Torgersen      40.3        18    195    3250 fema~ 2007    4.03
4 Adelie Torgersen      NA         NA      NA      NA <NA>   2007    NA
5 Adelie Torgersen      36.7       19.3   193    3450 fema~ 2007    3.67
6 Adelie Torgersen      39.3       20.6   190    3650 male   2007    3.93
# ... with abbreviated variable names 1: bill_depth_mm, 2: flipper_length_mm,
# 3: body_mass_g, 4: bill_length_cm
```

**Change existing column** The code above makes a new column in which bill length in cm is added as a new column to the data frame. We could have also just done the math in the original column if we wanted. That would look like this:

```
head(penguins)
```

```
# A tibble: 6 x 8
  species island    bill_length_mm bill_depth_mm flipper_l~1 body_~2 sex    year
  <fct>  <fct>          <dbl>      <dbl>  <int>  <int> <fct> <int>
1 Adelie Torgersen      39.1       18.7   181    3750 male   2007
2 Adelie Torgersen      39.5       17.4   186    3800 fema~ 2007
3 Adelie Torgersen      40.3        18    195    3250 fema~ 2007
4 Adelie Torgersen      NA         NA      NA      NA <NA>   2007
5 Adelie Torgersen      36.7       19.3   193    3450 fema~ 2007
6 Adelie Torgersen      39.3       20.6   190    3650 male   2007
# ... with abbreviated variable names 1: flipper_length_mm, 2: body_mass_g
```

```
mutpen<-(mutate(penguins, bill_length_mm=bill_length_mm/10))
head(mutpen)
```

```
# A tibble: 6 x 8
  species island    bill_length_mm bill_depth_mm flipper_l~1 body_~2 sex    year
  <fct>  <fct>          <dbl>      <dbl>  <int>  <int> <fct> <int>
1 Adelie Torgersen      3.91       18.7   181    3750 male   2007
```

```

2 Adelie Torgersen      3.95      17.4      186      3800 fema~ 2007
3 Adelie Torgersen      4.03       18      195      3250 fema~ 2007
4 Adelie Torgersen      NA        NA        NA        NA <NA> 2007
5 Adelie Torgersen      3.67      19.3      193      3450 fema~ 2007
6 Adelie Torgersen      3.93      20.6      190      3650 male  2007
# ... with abbreviated variable names 1: flipper_length_mm, 2: body_mass_g

```

**NOTE** This is misleading because now the values in `bill_length_mm` are in cm. Thus, it was better to just make a new column in this case. But you don't have to make a new column every time if you would prefer not to. Just be careful.

**Column math in Base R** Column manipulation is easy enough in base R as well. We can do the same thing we did above without Tidyverse like this:

```

penguins$bill_length_cm = penguins$bill_length_mm /10
head(penguins)

```

```

# A tibble: 6 x 9
  species island  bill_length_mm bill_de~1 flipp~2 body_~3 sex  year bill_~4
  <fct>  <fct>          <dbl>      <dbl>   <int>   <int> <fct> <int>  <dbl>
1 Adelie Torgersen      39.1      18.7    181    3750 male  2007   3.91
2 Adelie Torgersen      39.5      17.4    186    3800 fema~ 2007   3.95
3 Adelie Torgersen      40.3       18    195    3250 fema~ 2007   4.03
4 Adelie Torgersen      NA        NA        NA        NA <NA> 2007   NA
5 Adelie Torgersen      36.7      19.3    193    3450 fema~ 2007   3.67
6 Adelie Torgersen      39.3      20.6    190    3650 male  2007   3.93
# ... with abbreviated variable names 1: bill_depth_mm, 2: flipper_length_mm,
# 3: body_mass_g, 4: bill_length_cm

```

## 2.4 Pivot data (wide to long / long to wide)

‘Pivoting’ data means changing the format of the data. Tidyverse and ggplot in particular tend to like data in ‘long’ format. **Long format** means few columns and many rows. **Wide format** is the opposite- many columns and fewer rows.

Wide format is usually how the human brain organizes data. For example, a spreadsheet in which every species is in its own column is wide format. You might take this sheet to the field and record present/absence or count of each species at each site or something. This is great but it might be easier for us to calculate averages or do group based analysis in R if we have a column called ‘species’ in which every single species observation is a row. This leads to A LOT of repeated categorical variables (site, date, etc), which is fine.

**Example of Long Format** The built in dataset ‘fish\_encounters’ is a simple example of long format data. Penguins, iris, and others are also in long format but are more complex

```
head(fish_encounters) # here we see 3 columns that track each fish (column 1) across MANY

# A tibble: 6 x 3
  fish station seen
  <fct> <fct> <int>
1 4842 Release     1
2 4842 I80_1        1
3 4842 Lisbon      1
4 4842 Rstr         1
5 4842 Base_TD      1
6 4842 BCE          1
```

**Converting from long to wide using pivot\_wider (Tidyverse)** Although we know that long format is preferred for working in Tidyverse and doing graphing and data analysis in R, we sometimes do want data to be in wide format. There are certain functions and operations that may require wide format. This is also the format that we are most likely to use in the field. So, let’s convert fish\_encounters back to what it likely was when the data were recorded in the field..

```
#penguins long to wide using pivot_wider

widefish<-fish_encounters %>%
  pivot_wider(names_from= station, values_from = seen)

head(widefish)

# A tibble: 6 x 12
  fish Release I80_1 Lisbon Rstr Base_TD BCE BCW BCE2 BCW2 MAE MAW
  <fct> <int> <int> <int> <int> <int> <int> <int> <int> <int> <int> <int>
1 4842     1     1     1     1     1     1     1     1     1     1     1
2 4843     1     1     1     1     1     1     1     1     1     1     1
3 4844     1     1     1     1     1     1     1     1     1     1     1
4 4845     1     1     1     1     1     NA     NA     NA     NA     NA     NA
5 4847     1     1     1     NA     NA     NA     NA     NA     NA     NA     NA
6 4848     1     1     1     1     NA     NA     NA     NA     NA     NA     NA
```

The resulting data frame above is a wide version of the original in which each station now has its own column. This is likely how we would record the data in the field!

**Example of Wide Format Data** Let's just use widefish for this since we just made it into wide format :)

```
head(widefish)
```

```
# A tibble: 6 x 12
  fish Release I80_1 Lisbon Rstr Base_TD BCE BCW BCE2 BCW2 MAE MAW
  <fct> <int> <int> <int> <int> <int> <int> <int> <int> <int> <int> <int>
1 4842     1     1     1     1     1     1     1     1     1     1     1
2 4843     1     1     1     1     1     1     1     1     1     1     1
3 4844     1     1     1     1     1     1     1     1     1     1     1
4 4845     1     1     1     1     1     NA     NA     NA     NA     NA     NA
5 4847     1     1     1     NA     NA     NA     NA     NA     NA     NA     NA
6 4848     1     1     1     1     NA     NA     NA     NA     NA     NA     NA
```

**Converting from Wide to Long using pivot\_longer (Tidyverse)**

```
longfish<- widefish %>%
  pivot_longer(!fish, names_to = 'station', values_to = 'seen')
```

```
head(longfish)
```

```
# A tibble: 6 x 3
  fish station seen
  <fct> <chr> <int>
1 4842 Release     1
2 4842 I80_1         1
3 4842 Lisbon      1
4 4842 Rstr         1
5 4842 Base_TD     1
6 4842 BCE         1
```

And now we are back to our original data frame! The 'fish' means simply that we do not wish to pivot the fish column. It remains unchanged. A '!' before something in code usually means to exclude or remove. We've used names\_to and values\_to to give names to our new columns. pivot\_longer will look for factors and put those in the names\_to column and it will look for values (numeric) to put in the values\_to column.

**NOTES** There are MANY other ways to modify pivot\_wider() and pivot\_longer(). I encourage you to look in the help tab, the tidyR/ Tidyverse documentation online, and for other examples on google and stack overflow.

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