

Lesson 2: Base R vs Tidy R - Homework Answers

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Answers to Questions:

1. Let's explore Tidyverse!

a. Think of Tidyverse as a family of packages. Which packages are loaded with {tidyverse}? What do each of these packages do? Check out: <https://tidyverse.tidyverse.org/>

```
# You can find out by looking at the packages that are loaded when you use  
library(tidyverse)  
  
# Or, here is a screenshot from the https://tidyverse.tidyverse.org/#usage website:  
webshot::webshot("https://tidyverse.tidyverse.org/", "tidyverse_usage.png",  
  cliprect = c(500, 5, 600, 505))
```

Usage

`library(tidyverse)` will load the core tidyverse packages:

- `ggplot2`, for data visualisation.
- `dplyr`, for data manipulation.
- `tidyr`, for data tidying.
- `readr`, for data import.
- `purrr`, for functional programming.
- `tibble`, for tibbles, a modern re-imagining of data frames.
- `stringr`, for strings.
- `forcats`, for factors.

You also get a condensed summary of conflicts with other packages you have loaded

```
library(tidyverse)
#> — Attaching packages —————
#> ✓ ggplot2 3.2.1      ✓ purrr   0.3.3
#> ✓ tibble  2.1.3      ✓ dplyr   0.8.3
```

b. Which package is `pivot_wider` from?

```
?pivot_wider
# {tidyr}
```

c. Which package is `rename` from?

```
?rename
# {dplyr}
```

d. Can you use `{tidyverse}` without `{base}` R?

```
# Nope! {Tidyverse} is built on {Base} R.
```

2. Let's play with some data!

You can view the dataset `CO2` in more detail using `View(CO2)` and learn about it using `?CO2`. `CO2` comes from the `{datasets}` package which should already be automatically loaded in your R.

Some info about the `CO2` dataset: “The `CO2` data frame has 84 rows and 5 columns of data from an experiment on the cold tolerance of the grass species *Echinochloa crus-galli*.”

```
# Note: This function or data set name (in this case, data set)
# may occur in other packages so here I am using the "::" to say I
# specifically want the data 'CO2' from {datasets}.
CO2<-data.frame(datasets::CO2)
(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
```

a. `rename()` the “conc” column to “Concentration mL/L” and “Treatment” column to “condition”. The new name for the conc column is not a great name (dare I say ‘tidy’ name?) so we’ll fix that in the next question. Assign your object here as a new object (name up to you!).

```
CO2_a<-dplyr::rename(CO2,
  "Concentration mL/L" = "conc")
(head(CO2_a))
```

```
##   Plant   Type Treatment Concentration mL/L 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
```

b. Use the `{janitor}` function `clean_names` on the new CO2 data you just created in 2a. What does it do? How did `{janitor}` change our “Concentration mL/L” column?

Again, assign your object here as a new object (name up to you!).

```
CO2_b<-janitor::clean_names(CO2_a)
(head(CO2_b))
```

```
##   plant   type treatment concentration_m_l_l 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
```

```
# clean_names changed the "conc" column from "Concncentration mL/L" to "concncentration_m_l_l"
```

c. Use `pivot_wider` make columns of uptake (values_from) for each plant (names_from) in your new data set from question 2b.

This is not a 'tidy' way of looking at data, but is good practice! Assign your object here as a new object (name up to you!).

```
C02_c<-tidyr::pivot_wider(data = C02_b, names_from = plant, values_from = uptake)
(head(C02_c))
```

```
## # A tibble: 6 x 15
##   type treatment concncentration_m_l_l Qn1 Qn2 Qn3 Qc1 Qc2 Qc3 Mn1 Mn2 Mn3 Mc1
##   <fct> <fct>          <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Queb~ nonchill~      95 16   13.6 16.2   NA   NA   NA   NA   NA   NA   NA
## 2 Queb~ nonchill~     175 30.4 27.3 32.4   NA   NA   NA   NA   NA   NA   NA
## 3 Queb~ nonchill~     250 34.8 37.1 40.3   NA   NA   NA   NA   NA   NA   NA
## 4 Queb~ nonchill~     350 37.2 41.8 42.1   NA   NA   NA   NA   NA   NA   NA
## 5 Queb~ nonchill~     500 35.3 40.6 42.9   NA   NA   NA   NA   NA   NA   NA
## 6 Queb~ nonchill~     675 39.2 41.4 43.9   NA   NA   NA   NA   NA   NA   NA
## # ... with 2 more variables: Mc2 <dbl>, Mc3 <dbl>
```

d. Use `pivot_longer` to undo what you did in 2c using the data that you created in 2c.

To see how to get the old names back, check out the `names_to` and `values_to` variable in `?pivot_longer`. This will likely incur some new rows with NAs, so you'll need to remove that here with `values_drop_na`. You can check if you actually got it back to original form by seeing if the dimensions of the data.frame are the same as the original dataset. As stated earlier, `dim(datasets::C02)` was 84 rows and 5 columns.

```
C02_d<-tidyr::pivot_longer(data = C02_c,
  cols = c(Qn1:Mc3), #Alternatively: cols = c(4:15),
  names_to = "plant",
  values_to = "uptake",
  values_drop_na = TRUE)

(head(C02_d))
```

```
## # A tibble: 6 x 5
##   type treatment concncentration_m_l_l plant uptake
##   <fct> <fct>          <dbl> <chr>   <dbl>
## 1 Quebec nonchilled      95 Qn1     16
## 2 Quebec nonchilled      95 Qn2    13.6
## 3 Quebec nonchilled      95 Qn3    16.2
## 4 Quebec nonchilled     175 Qn1    30.4
## 5 Quebec nonchilled     175 Qn2    27.3
## 6 Quebec nonchilled     175 Qn3    32.4
```

```
dim(C02_d)
```

```
## [1] 84 5
```