Making Paleontology—fauna excercise 8 in R

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1 Preparation

If you're curious about learning R, this exercise could be a fun little first challenge!

While excel works, it often introduces problems that shouldn't be there: in this exercise it isn't able to plot the age in millions of years ago (`Ma`) as a date, because it doesn't have enough digits for conversion. As a workaround you can convert it to kyr in stead.

That is obviously stupid. And it's not the only frustrating excel thing you may run into. One of the nice things about using a scripting language—such as python or R—instead, is that your work becomes reproducible and you and others can use your tricks again in the future!

Here we show you how you could do this exercise in R. Please play around first and enjoy the struggle for a bit.

1.1 installation

Install R and RStudio. R is the programming language and RStudio is a friendly graphical interface (or technically Integrated Development Environment) for R.

If you don't know how, you can follow many online guides, such as this edX course. Note that for Mac users there are some additional installation steps required.

Install the required packages—extensions of R that make life even easier!—by opening RStudio and going to the bottom-left panel (the terminal) and typing, e.g.:

```
install.packages("ggplot2")
```

Or, if you want to use ggplot2, dplyr, purrr, etc., which I highly recommend, install them all at once with:

```
install.packages("tidyverse")
```

since they are part of the tidyverse, a collection of packages that makes R amazing.

1.2 load the libraries

These commands make the package functions available for use in your session:

```
library(readr)      # to read in the csv file (or use readxslx to read in excel files)
library(ggplot2)    # for plotting
library(patchwork)  # for composite plots
library(dplyr)      # for tidy data manipulation
library(tidyr)
```

```
Attaching package: ‘dplyr’

The following objects are masked from ‘package:stats’:

    filter, lag

The following objects are masked from ‘package:base’:

    intersect, setdiff, setequal, union
```

1.3 getting started

As a start, I highly recommend reading through the freely available book R for data science by Hadley Wickham. You can also try the datacamp Introduction to R online course, which helped me get started initially. One last resource to get you started is to install the package `swirl` and interactively learn the basics right from R.

```
install.packges("swirl")
library(swirl)
swirl()
```

1.4 getting help

When you have problems or questions, have a look at any error messages if present and consult the documentation of the function of interest with, `?function_name` or search for a topic with `??topic`.

e.g., enter:

```
?ggplot
```

in the terminal.

Ḩ When you have questions, search! This is not considered cheating! StackOverflow, your search engine, and sometimes even twitter `#Rlang` are your friends!

2 Practical 8

2.1 read the data

I prepared a slightly cleaner CSV sheet, which we can read into R more easily. You can download it here:

See the end of the document for a copy-pastable version.

I rename some columns here so that I can type less and we don't have spaces in the column names.

```
strat <- read_csv("biostrat_clean.csv", skip = 1) %>%
  rename(c(bio = "LOCAL BIOZONE", age = "NUMERICAL AGE in MA", loc = "LOCCODE", n_m12 =
 dry = "% DRY RODENTS", catholic = "% CATHOLIC", wet = "% WET RODENTS")) %>%
  select(-LOCCODE_1)
```

```
Parsed with column specification:
cols(
  .default = col_double(),
  ‘LOCAL BIOZONE‘ = col_character(),
  LOCCODE = col_character(),
  LOCCODE_1 = col_character()
)
See spec(...) for full column specifications.
Warning message:
Duplicated column names deduplicated: ’LOCCODE’ =
’LOCCODE_1’ [64]
```

The output tells us how it read the csv file and what types each column was identified as.

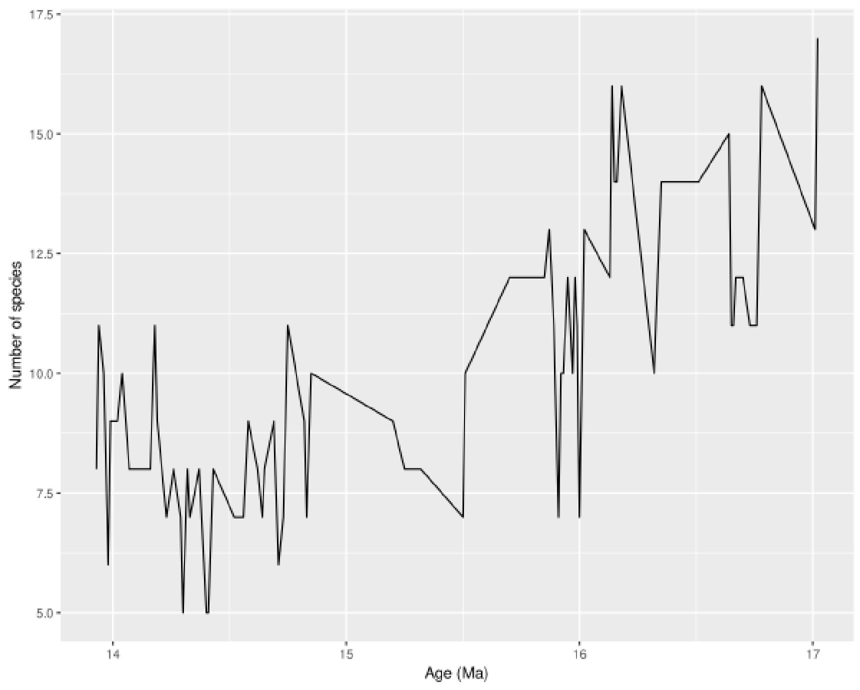
You can also read in the raw excel file directly with the package `readxl` if you want.

2.2 Graph of the species number per locality.

The first exercise is the easiest. We take our data `strat` and pipe it (`%>%`) to the `ggplot` function. You can read this as: take `strat` and then do `ggplot` with it.

Within the plot we specify so-called aesthetics with `aes`. This links columns of the data to things we can plot, in this case `x` and `y` for a simple scatter plot. Because we are dealing with a time series (albeit a discontinuos one) it is customary to plot the series with a line, which we add with `geom_line`.

```
strat %>%
  ggplot(aes(x = age, y = N)) +
  geom_line() +
  labs(x = "Age (Ma)", y = "Number of species")
```



To learn more about creating plots with `ggplot2`, I highly recommend following the online course data visualisation with ggplot2 and chapter 3 of r4ds: data visualisation.

If you don't like the gray grid behind the data, have a look at `?theme`. You can easily change the plot to a black and white classical plot with a `+ theme_classic()` at the end.

2.3 Graph of habitat preference

2.3.1 tidy the data

For this plot we need to re-arrange the data a little bit. Right now all the percentages of the rodents are in different column. For easy plotting and data processing, usually we want so-called `tidy` data. This means that each row corresponds to one observation.

In this case that would mean we'd repeat the age and location code three times, with one new variable `percentage` and another with the `habitat`.

```
strat_hab <- strat %>%
  # remove all non-essential columns and rename for easy access
  select(age, loc, dry, catholic, wet) %>%
  # convert to long-format (this is something to look up and learn!)
  pivot_longer(cols = c(dry, catholic, wet), values_to = "percentage", names_to = "habi
```

To illustrate, we switch from:

bio	age	loc	D.franconicus	D.koenigswaldi	D.larteti	Ligerimys ellipticus	Keramidom
E	13.93	LUM19	nil	nil	4	nil	nil
nil	13.94	LP4B	nil	nil	28.9	nil	nil
nil	13.96	LP4A	nil	nil	32.4	nil	nil
nil	13.97	LUM14	nil	nil	60.2	nil	nil
nil	13.98	LUM18	nil	nil	49.1	nil	nil
nil	13.99	LUM17	nil	nil	25	nil	nil

to:

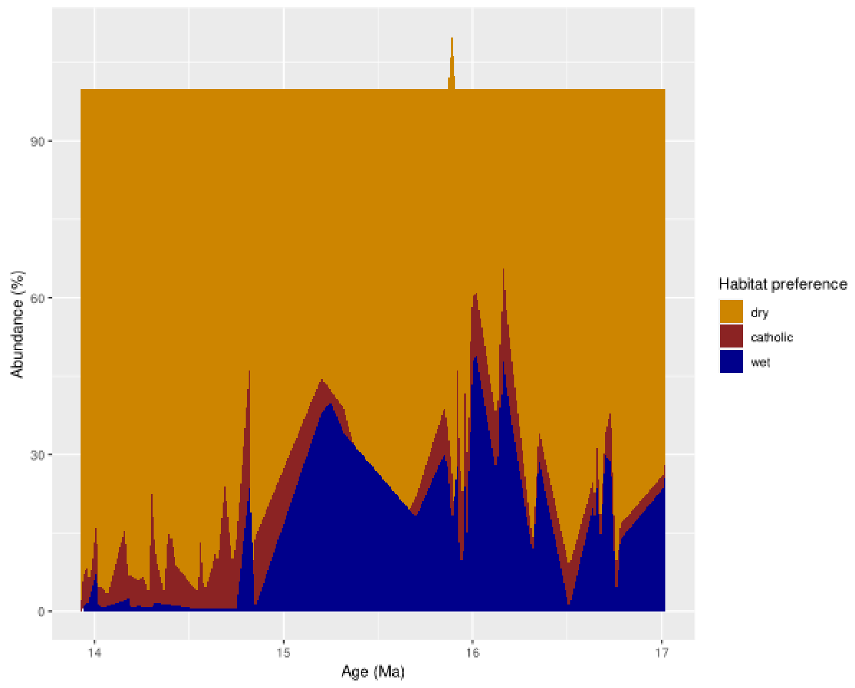
age	loc	habitat	percentage
13.93	LUM19	dry	97.9
13.93	LUM19	catholic	2.1
13.93	LUM19	wet	nil
13.94	LP4B	dry	93.2
13.94	LP4B	catholic	6
13.94	LP4B	wet	0.8

read up on creating tidy data in r4ds chapter 12.

2.3.2 create the plot

With the tidy data, creating an area chart is very easy:

```
strat_hab %>%
  ggplot(aes(x = age, y = percentage, fill = factor(habitat, levels = c("dry", "catholi
  # this plots each line as a polygon
  geom_area() +
  scale_fill_manual(values = c("dry" = "orange3", "catholic" = "brown4", "wet" = "blue4
  labs(x = "Age (Ma)", y = "Abundance (%)", fill = "Habitat preference")
```



Here we adjust the colours manually. Note that generally it's not nice to use manual colour scales because it's hard to estimate what colourblind people are able to see well. In this case, with only 3 values and where specific colours can make intuitive sense, I set it manually. I like to use `viridis::scale_fill_viridis` often!

Oh, and what does `::` mean you ask? It means: look in package `viridis` for the function `scale_fill_viridis`.

2.3.3 what's up at 16 Ma?

Notice the weird outlier near 16 Ma, where the total is larger than 100%!

Let's figure out which sample it is.

```
strat_hab %>%
  group_by(age, loc) %>%
  summarize(total = sum(percentage)) %>%
  # filter those rows where the percentage is not 100
  filter(total > 100 | total < 100)
```

age	loc	total
15.87	COL-D	99.8
15.89	COL-C	110

You will always have some noise in your data. With R, it's quite easy to drill down into where it is and what causes it. Unfortunately, it won't stop you from making mistakes in the first place .

2.4 Graph of Diversity and Equity

2.4.1 compute diversity and equity

Read the handout about how we calculate diversity and equity.

1. by column We `mutate_at` here to do calculations for many columns. However, this is an instance in which having this as tidy data would make some more complex examples easier!

   First we'll do the calculations in the way the dataframe is already set up.

   ```
   strat_div <- strat %>%
     # first square all the species abundances
     mutate_at(vars(D.franconicus:Keramidomys), ~ . ^ 2) %>%
     # this overwrites the columns! use a named list if you want new columns in
     # stead. then calculate diversity and evennes
     mutate(diversity = 1 / (rowSums(select(., D.franconicus:Keramidomys), na.rm = TR
    evenness = diversity / N)
   ```

   You don't have to understand all the steps here, since this is not the approach I would recommend.

2. tidy In stead, I would recommend to tidy your data as follows:

   ```
   tidystrat <- strat %>%
     # remove the columns we are not interested in
     select(-c(dry, catholic, wet, n_m12)) %>%
     # convert the species abundances to tidy format
     pivot_longer(D.franconicus:Keramidomys, names_to = "species", values_to = "abunc

   ev <- tidystrat %>%
     # and for each age and locality, original row
     group_by(age, loc) %>%
     # calculate the diversity (be very careful where you place parentheses!)
     # notice that now we don't have to calculate the squares first.
   ```

```
  summarize(diversity = 1 / sum(abundance ^ 2, na.rm = TRUE),
    # calculate the number of species
    n_manual = sum(abundance > 0, na.rm = TRUE),
    # and for comparison get the ones from the original sheet
    n_from_sheet = mean(N, na.rm = TRUE)) %>%
  # calculate evenness
  mutate(evenness = diversity / n_manual)
```

While this is a little bit more code, I think it is more legible and it will make the next steps easier.

Inspect `tidystrat` to see what it looks like!

```
head(tidystrat)
```

bio	age	loc	N	species	abundance
E	13.93	LUM19	8	D.franconicus	nil
E	13.93	LUM19	8	D.koenigswaldi	nil
E	13.93	LUM19	8	D.larteti	4
E	13.93	LUM19	8	D.hispanicus	nil
E	13.93	LUM19	8	D.moralesi	nil
E	13.93	LUM19	8	D.jordensi	nil

Note that again the `N of SPECIES` in the original sheet is slightly different from our calculated one:

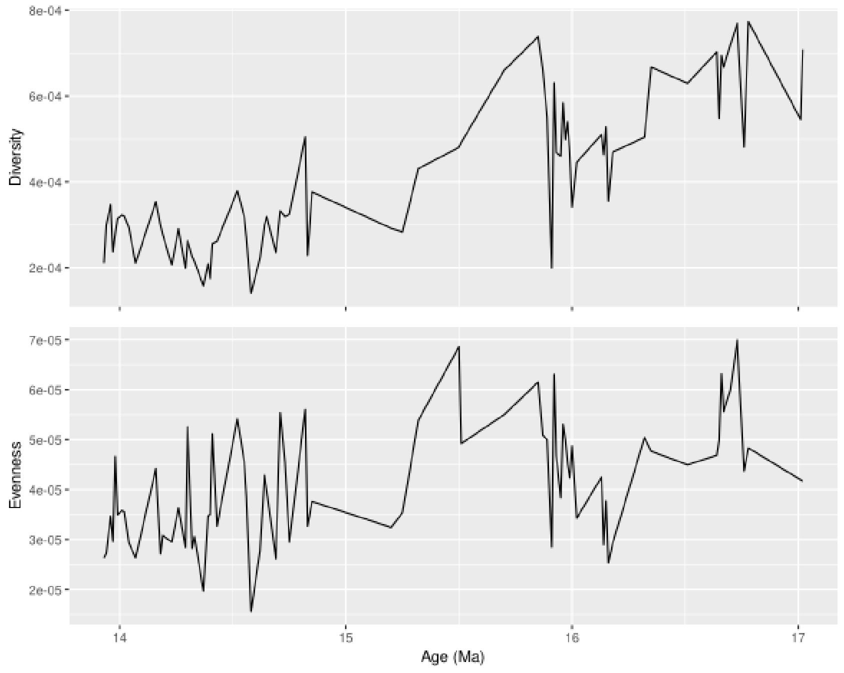
```
ev %>%
  filter(n_manual != n_from_sheet)
```

age	loc	diversity	n_manual	n_from_sheet	evenness
13.96	LP4A	0.000346865721341954	8	10	4.33582151677443e-05
15.87	COL-D	0.000661489409554553	12	13	5.51241174628794e-05

2.4.2 create the plots

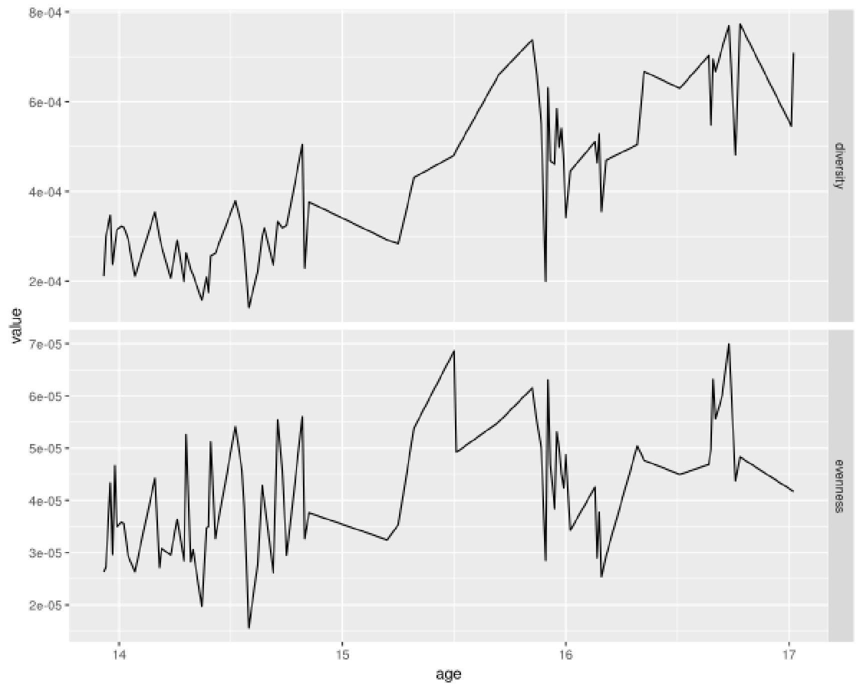
First we create the plot based on `strat_div`, the original data with the new columns for diversity and evenness. We create two separate plots and then add them together as subplots using the package `patchwork`. This is perfect when you have to make many adjustments to your subfigures.

```
p_div <- strat_div %>%
  ggplot(aes(x = age, y = diversity)) +
  geom_line() +
  labs(y = "Diversity")
p_eq <- strat_div %>%
  ggplot(aes(x = age, y = evenness)) +
  geom_line() +
  labs(y = "Evenness")
# we use patchwork to put the two pluts together
(p_div & theme(axis.title.x = element_blank(), axis.text.x = element_blank())) / p_eq +
```



And to show that the tidy way results in the same plot, we tidy the data even further and then using `facets`.

```
ev %>%
  select(age, loc, diversity, evenness) %>%
  pivot_longer(diversity:evenness, names_to = "measure", values_to = "value") %>%
  ggplot(aes(x = age, y = value)) +
  geom_line() +
  facet_grid(rows = vars(measure), scales = "free_y")
```



3 conclusion

This was a quick look into some of the features of `R` for data analysis and plotting. I hope this will have peaked your interest and will get you to use excel only as a way of entering data ;-).

4 sessionInfo

This just shows you which version of R and which packages I have installed in case there are future updates.

```
sessionInfo()

R version 3.6.3 (2020-02-29)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Arch Linux

Matrix products: default
BLAS:   /usr/lib/libopenblasp-r0.3.8.so
```

```
LAPACK: /usr/lib/liblapack.so.3.9.0

locale:
 [1] LC_CTYPE=en_US.UTF-8       LC_NUMERIC=C
 [3] LC_TIME=en_US.UTF-8        LC_COLLATE=en_US.UTF-8
 [5] LC_MONETARY=en_US.UTF-8    LC_MESSAGES=en_US.UTF-8
 [7] LC_PAPER=en_US.UTF-8       LC_NAME=C
 [9] LC_ADDRESS=C               LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] patchwork_1.0.0 tidyr_1.0.2     dplyr_0.8.5     ggplot2_3.3.0
[5] readr_1.3.1     devtools_2.2.2  usethis_1.5.1

loaded via a namespace (and not attached):
 [1] Rcpp_1.0.3        compiler_3.6.3    pillar_1.4.3      prettyunits_1.1.1
 [5] remotes_2.1.1     tools_3.6.3       testthat_2.3.2    digest_0.6.25
 [9] pkgbuild_1.0.6    pkgload_1.0.2     memoise_1.1.0     tibble_2.1.3
[13] lifecycle_0.2.0   gtable_0.3.0      pkgconfig_2.0.3   rlang_0.4.5
[17] cli_2.0.2         withr_2.1.2       desc_1.2.0        fs_1.3.2
[21] vctrs_0.2.3       hms_0.5.3         tidyselect_1.0.0  rprojroot_1.3-2
[25] grid_3.6.3        glue_1.3.1        R6_2.4.1          processx_3.4.2
[29] fansi_0.4.1       sessioninfo_1.1.1 farver_2.0.3      purrr_0.3.3
[33] callr_3.4.2       magrittr_1.5      backports_1.1.5   scales_1.1.0
[37] ps_1.3.2          ellipsis_0.3.0    assertthat_0.2.1  colorspace_1.4-1
[41] labeling_0.3      utf8_1.1.4        munsell_0.5.0     crayon_1.3.4
```