

Getting started in R

without tears

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Are you ready to become an
A R T I S T?



What is R?



Isotopes - RStudio

File Edit Code View Plots Session Build Debug Profile Tools Help

Go to file/function Addins

Collagen_Final.R x

```

1 library(tidyverse)
2 library(readxl)
3 library(gridExtra)
4 library(ggpubr)
5
6
7
8
9 #library(ggsignif)
10
11 ##### Set up -----
12
13 # assign input files
14 input.collagen <- c("Vagnari Collagen/Input/VagnariCN_06.xlsx")
15 input.details <- c("Vagnari Collagen/Input/Details.xlsx")
16 input.comp.human <- c("Vagnari Collagen/Input/VagnariHumans.xlsx")
17 input.comp.fauna <- c("Vagnari Collagen/Input/VagnariCompCollagen02.xlsx")
18

```

Set up
Quality indicators
Sum stats
Herb v Omni
Single axis by site
Single axis together
Histograms
Faceted by taxa
STATS
Set-up
Checking data
.. Extreme outliers
.. Normality
.... Model residuals
.... Check separately
.. Variance
.... Levene test
ANOVA
.. Kruskal Wallis

Environment History Connections Tutorial

Import Dataset

Global Environment

Values

| Variable | Value |
|------------------|--|
| input.collagen | "Vagnari Collagen/Input/VagnariCN_06.xlsx" |
| input.comp.fa... | "Vagnari Collagen/Input/VagnariCompCo..." |
| input.comp.hu... | "Vagnari Collagen/Input/VagnariHumans...." |
| input.details | "Vagnari Collagen/Input/Details.xlsx" |

Files Plots Packages Help Viewer

New Folder Delete Rename More

C:\Users\atren\Dropbox\R code\Isotopes\ Vagnari Collagen

| Name | Size | Modified |
|------------------------|---------|-----------------------|
| .. | | |
| Collagen_Final.R | 28 KB | May 9, 2023, 12:29 AM |
| rKIN.R | 17.6 KB | Feb 28, 2023, 9:41 AM |
| CollagenPlots02.R | 16.5 KB | Nov 11, 2021, 6:04 PM |
| CollagenPlots06.R | 10.5 KB | Jul 5, 2022, 4:11 PM |
| CollagenPlots.R | 9 KB | Nov 4, 2021, 1:50 PM |
| Collagen_Ttest.R | 9 KB | Jun 8, 2022, 6:39 PM |
| CollagenPlots05.R | 7.9 KB | Jun 8, 2022, 2:39 PM |
| Collagen_Ttest03.R | 5.4 KB | Jan 27, 2023, 6:22 PM |
| CollagenPlots_bySite.R | 5.4 KB | Nov 11, 2021, 7:22 PM |
| Collagen_Ttest02.R | 4.9 KB | Jul 5, 2022, 5:28 PM |
| Rhistory | 1.7 KB | Jul 5, 2022, 11:46 AM |

Console Terminal x Jobs x

C:\Users\atren\Dropbox\R code\Isotopes\

```

combine

> library(ggpubr)
Warning message:
package 'ggpubr' was built under R version 4.0.5
> # assign input files
> input.collagen <- c("Vagnari Collagen/Input/VagnariCN_06.xlsx")
> input.details <- c("Vagnari Collagen/Input/Details.xlsx")
> input.comp.human <- c("Vagnari Collagen/Input/VagnariHumans.xlsx")
> input.comp.fauna <- c("Vagnari Collagen/Input/VagnariCompCollagen02.xlsx")
>

```

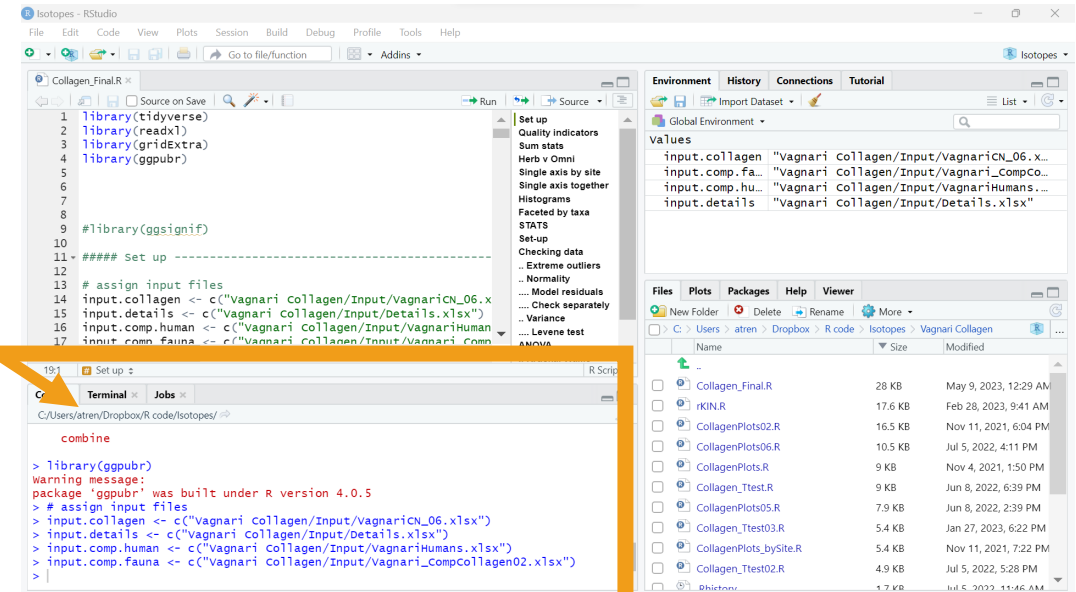
Strong, fast, powerful.....and not very clever.



Strong, fast, powerful.....and not very clever.

Working directory = where R Studio looks for your file

- What is your working directory?
Type `getwd()` in your console and press enter
- The working directory can be set be
`Session > Set Working Directory`



File types



Workshops.Rproj



1_GettingStarted.R

- Projects = home for associated files.
Automatically sets wd for all sub-folders
- Scripts = code in a text document

R language and packages



- Object oriented language
 - We create objects (nouns) and we will apply functions (verbs) to them
 - Vocabulary and functions a mix of 'base R' and packages (needing installation/loading)

```
CollData <- read_xlsx("CollagenResults.xlsx", .name_repair = "universal")
```

Object Function() Arguments

Options to specify what you want the function read_xlsx() to do. Must be divided by comma!

= or 'put into'

Remember, strong but not very clever!

R objects

data.frame basically a table: a collection of columns (vectors), all of the same length, and all with column names

vectors collection of values of the same kind (like a list but not)

- Character (text)
- Number
- Factor - categorical, ordered unique entries (levels)

value item in a vector

Interacting with and applying functions to common objects

str(CollData)

Function() Object – dataframe we just created through import

- Mostly manipulating dataframes (tables) and vectors
- Using R language and **Tidyverse**
- **Tidyverse** =
 - Collection of R packages designed for data science. Efficient to learn because they share an underlying design philosophy, grammar, and data structures
 - Can do same thing in base R, but Tidyverse more intuitive



Key syntax

`<-` ‘put into’ or ‘equals’ `ExampleObject <- c(“donkey”)`

`%>%` A tidyverse pipe.....think like ‘then’ or ‘then do this’

`Slvalues.A <- CollData %>% # make new object Slvalues.A, get CollData, then
select(ASIL, dI3C, dI5N) # select columns`

`# We can do the same thing in base R, but it is less intuitive`

`Slvalues.B <- CollData[,c("ASIL", "dI3C", "dI5N")]`

Let's get cooking

Make a new project in your R Analysis folder:

- File > New Project > New Directory > New Project
- Name the directory **May2023Workshop**
- Find this folder on your laptop and move all workshop files into it
- Make 'Input' and 'Output' folders in your project; put the excel example files in 'Input'
- Open the session I script file



TASK I

- Make a new dataframe called 'Slvalues' that contains column for ASIL, Date, precent C, precent N, dI3C, dI5N
- Use a tidyverse pipe (%>%) like in example one



We can add and manipulate columns using base R or tidyverse

Here we're adding a new column with the atomic C:N ratio

Equation using values from per.C
and per.N columns from Svalues df

Base R

Svalues\$C.N <- Svalues\$per.C/Svalues\$per.N*14/12

\$ = column from df
Put into C.N column
in Svalues df

Tidyverse

Svalues <- Svalues.C %>%

Start with Svalues df, then...

mutate(C.N2 = (per.C/per.N)*(14/12))

create a new column using
mutate() function

TASK 2

- Import [Vaiglova_2023_collagen.xlsx](#) into a new df called **NeoGreece**
- Hint: copy/paste and edit the code from line 20 above



Changing column values: very verbose mutate()

```
NeoGreece2 <- NeoGreece2 %>%      # NeoGreece2 then...  
  mutate(TaxonGroup = Taxon ) %>% # make new column (new name = old name)  
  mutate(TaxonGroup = replace(TaxonGroup, TaxonGroup == "sheep", "sheep/goat"))
```

and replace()

in the TaxonGroup column, where TaxonGroup has == "sheep", with "sheep/goat"

Change / mutate() the TaxonGroup column

Changing column values: very verbose mutate()

```
NeoGreece2 <- NeoGreece2 %>%  
  mutate(TaxonGroup = Taxon ) %>%  
  mutate(TaxonGroup = replace(TaxonGroup, TaxonGroup == "sheep", "sheep/goat"))
```

The same is possible in base R:

```
NeoGreece2$TaxonGroup <- NeoGreece2$Taxon ←
```

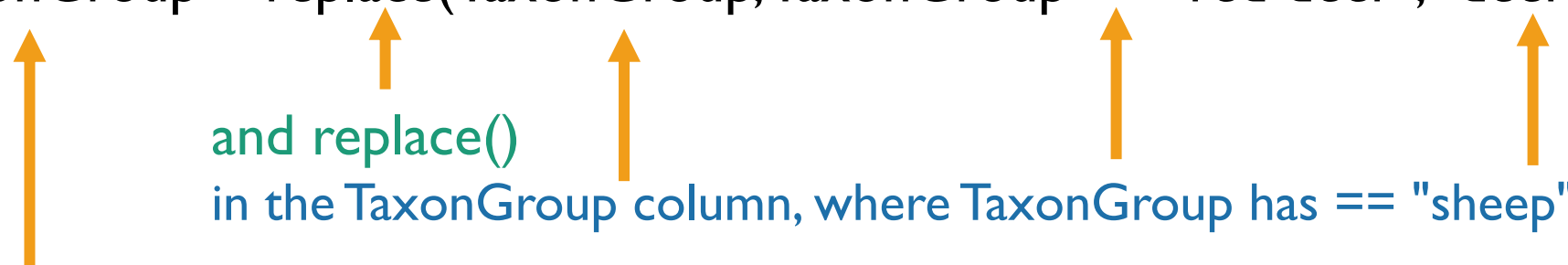
Make new TaxonGroup column and
put Taxon column into it

```
NeoGreece2$TaxonGroup[NeoGreece2$TaxonGroup == 'sheep'] <- 'sheep/goat'
```

In TaxonGroup column, where TaxonGroup column is “sheep” put in with “sheep/goat”

Changing column values: very verbose mutate()

```
NeoGreece2 <- NeoGreece2 %>%      # NeoGreece2 then...
  mutate(TaxonGroup = Taxon ) %>% # make new column (new name = old name)
  mutate(TaxonGroup = replace(TaxonGroup, TaxonGroup == "sheep", "sheep/goat"),
  TaxonGroup = replace(TaxonGroup, TaxonGroup == "goat", "sheep/goat"),
  TaxonGroup = replace(TaxonGroup, TaxonGroup == "roe deer", "deer"),
  TaxonGroup = replace(TaxonGroup, TaxonGroup == "red deer", "deer"))
```



and replace()
in the TaxonGroup column, where TaxonGroup has == "sheep", with "sheep/goat"

Change / mutate() the TaxonGroup column

Coding without tears

- Embrace the errors
 - Missing , or () – R Studio can help with this
 - Misspelling or capitalization problem
 - “Greece” and “greece” are different to R!
 - Not loading the needed packages
 - Working directory problems – use projects, don’t move your files
 - Numbers as text – use `str()` to check the class of your data
 - Text needs `==`
 - Make abundant use of `#` to leave yourself notes on what you are doing and why!

