Basic Course on R:
Entering and Importing Data Practical

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1 Entering and Importing Data

1.1 Use R to do the following exercises.

1.1.1 Enter the following into a data structure with the name `color`:

- purple
- yellow
- red
- brown
- green
- purple
- red
- purple

1.1.2 Display the 2nd element of `color`.

1.1.3 Enter the following into a data structure with the name `weight`:

- 23
- 21
- 18
- 26
- 25
- 22
- 26
- 19

1.1.4 What are the lengths of `color` and `weight`? Use a function to answer this.

1.1.5 Join `color` and `weight` together using `cbind()` and assign it to the object `micecbind`.

1.1.6 What is the data structure of `micecbind`? What are the dimensions? Are the weights still numbers (`num`) or were they converted to characters (`chr`)?

1.1.7 Now join `color` and `weight` together using `data.frame()` with argument `stringsAsFactors = FALSE` and assign it to the object `micedf`.

1.1.8 What is the data structure of `micedf`? What are the dimensions? Are the weights still numbers (`num`) or were they converted to characters (`chr`)?

1.1.9 Display only the 3rd row of `micedf`.

1.1.10 Display only the 2nd column ("weight") of `micedf`. Do so in two different ways.

1.1.11 Display the dimensions of `micedf`.

1.1.12 Assign the following strings to the row names of `micedf`:

- mouse1
- mouse2
- mouse3
- mouse4
- mouse5
- mouse6
- mouse7
- mouse8

Hint: try using `paste`.

1.1.13 Create a list containing three elements and assign it to `mylist`:

- `micedf`
- A data frame of `micedf` with a new column called `double` that is 2 times the second column of `micedf` (`weight`).
- The names of `micedf`.

1.1.14 Assign these names to `mylist`: `first`, `second`, `third`.

1.1.15 Display `mylist`. What does it look like?

1.1.16 Display only the second element of `mylist`. Do so in two different ways.

1.1.17 Write `micedf` to a file called "micedf1.csv".

1.1.18 Open "micedf1.csv" in Excel and describe what you see. Repeat the step above but do not include row names and call the file "micedf2.csv". How is the output different from "micedf1.csv"?

1.1.19 Now read in "micedf1.csv" and "micedf2.csv" into R in two new objects (`newmice1` and `newmice2`, respectively). Describe any differences between the two objects. What are the dimensions of each object?

1.1.20 Read in "micedf1.csv" into R (assign to object `newmice3`). Use the argument `row.names` to indicate that the first column should be row names and do not allow strings to be turned into factors. Display the object and the structure of the object and describe how it is different from `newmice1` and `micedf`. What are the dimensions of `newmice3`?

1.2 Use R to do the following exercises on the `Puromycin` data.

1.2.1 Load the `Puromycin` data using the `data()` function.

1.2.2 What is the data structure of `Puromycin`? What are the dimensions (use a function other than `str`)?

1.2.3 What are the names of `Puromycin`? Use a function other than `str`.

1.2.4 What are the levels of the `state` variable? Use a function other than `str`.

1.2.5 Display the rate for all concentrations less than 0.10 in the treated group.

1.2.6 What are the row indices for the concentrations of 0.22?

If you want to save your work: save your R session and/or source code!