R markdown - intro and some basics

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Getting started:

R markdown can nicely combine writing and executing R script and making extensive notes.

1. Examples of text formatting:

Header 1

Header 2

Header 3

Header 4

Header 5 Header 6

- 6 level headers, serve as internal ouline links (toc)
- italics
- bold
- code
- another bullet point
 - second level bullet point
- links

2. Code Chunks:

here() starts at /Users/kristakraskura/Github_repositories/biol601_spring2024_dealing_w_data

```
# using library "here"
here::i_am("w2/w2_intro_RMarkdown.Rmd") # define "where is the current file in reference to the project
```

here() starts at /Users/kristakraskura/Github_repositories/biol601_spring2024_dealing_w_data

```
data <- read.csv(here("w1", "dfexample.csv")) # read in data, inside 'here()' we write the path to our
# to see the parent folder:
# here()</pre>
```

Some useful settings for the code chunks:

- include = FALSE prevents code and results from appearing in the finished file. R Markdown still runs the code in the chunk, and the results can be used by other chunks.
- echo = FALSE prevents code, but not the results from appearing in the finished file.
- results = 'hide' or FALSE prevents the results to be shown. Useful when
- message = FALSE prevents messages that are generated by code from appearing in the finished file.
- warning = FALSE prevents warnings that are generated by code from appearing in the finished.
- fig.width = the width of the printed figure, in inches
- fig.height = the height of the printed figure, in inches

(click tab in the section to see all the options)

3. Images (not figures):

• Use knitr::include_graphics()



4. Tables:

kable in knitr works well for html, pdf, and word document outputs.

	transect	dist from	substrate	snail	snail	snail	snail
X	position	transect	type	size	weight	aggressiveness	color
1	1.00	0.42	C	11.78	0.36	1	yellow
2	1.66	-0.40	A	11.80	0.36	1	yellow
3	2.31	-1.53	A	13.70	0.74	1	yellow
4	2.97	0.26	В	13.77	0.75	1	pink
5	3.62	0.11	$^{\mathrm{C}}$	13.08	0.62	1	blue
6	4.28	-0.54	A	14.48	0.90	1	yellow
7	4.93	0.16	$^{\mathrm{C}}$	17.13	1.43	1	pink
8	5.59	-0.40	В	14.91	0.98	1	yellow
9	6.24	-0.21	A	18.02	1.60	2	pink
10	6.90	-1.68	$^{\mathrm{C}}$	17.32	1.46	2	blue
11	7.55	-1.76	A	21.88	2.38	2	blue
12	8.21	-2.16	A	20.32	2.06	2	yellow
13	8.86	2.10	В	24.01	2.80	3	blue
14	9.52	0.00	A	23.59	2.72	3	orange
15	10.17	0.37	В	21.78	2.36	2	pink
16	10.83	0.54	A	20.01	2.00	2	blue
17	11.48	-1.14	\mathbf{C}	22.90	2.58	3	yellow
18	12.14	-0.24	$^{\mathrm{C}}$	24.82	2.96	3	yellow
19	12.79	-0.35	$^{\mathrm{C}}$	27.82	3.56	4	yellow
20	13.45	-1.46	A	25.48	3.10	3	yellow
21	14.10	-1.46	\mathbf{C}	26.53	3.31	4	pink
22	14.76	-1.24	В	31.53	4.31	5	pink
23	15.41	1.17	$^{\mathrm{C}}$	24.11	2.82	3	orange
24	16.07	-0.49	\mathbf{C}	26.22	3.24	3	yellow
25	16.72	0.90	В	29.90	3.98	4	blue
26	17.38	0.26	A	29.43	3.89	4	yellow
27	18.03	-0.93	A	28.87	3.77	4	pink
28	18.69	1.08	A	30.81	4.16	5	pink
29	19.34	1.04	В	31.69	4.34	5	blue
30	20.00	-0.96	\mathbf{C}	30.05	4.01	5	yellow

5. Figures made using imbedded script:

```
# plot code from week 1:
    ggplot(data = data, aes(x = transect.position, y = snail.size)) +
        geom_point(aes(col = substrate.type)) +
        theme(panel.background = element_blank(),
            axis.line = element_line(color = "black"),
            text = element_text(size = 20)) +
        scale_x_continuous(name = "Transect position (m)", breaks = seq(-10, 20, by =2)) +
        scale_y_continuous(name = "Snail size (mm)", breaks = seq(-10, 40, by = 5))
```

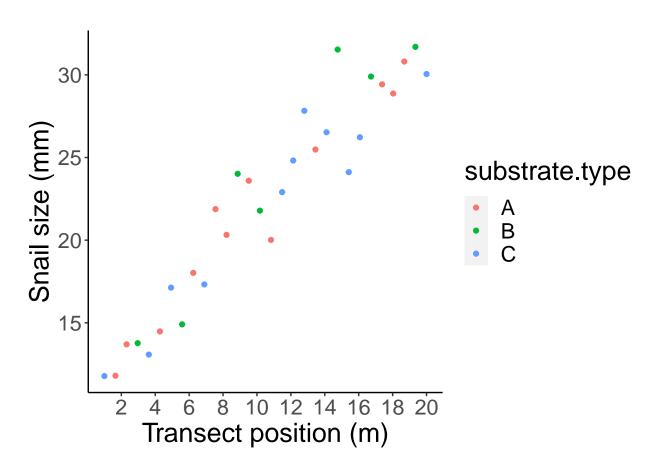


Figure 1: Figure 1. Snail body sizes along the transect position

Rendering and customization of the file

- pick a theme, or stick with a default
- render to PDF or html (some themes will not work to PDF)
- html (most common)
- table of contents
- execute the code in R markdown and show out put in R markdown is the default. To change that go to 'settings' (next to the knit) and select 'chunk output in Console'

Resources:

- \bullet Rmarkdown cheatsheet, pdf
- Rmarkdown cheatsheet, web
- themes R markdown book