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My Example Computed Manuscript Created in Rmarkdown

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Abstract A mock computed manuscript created in RStudio using {Rmarkdown}. The {Bookdown} and {Rticles} packages were used to output the text in Springer Nature's desired manuscript format.

Keywords

1 Introduction

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see http://rmarkdown.rstudio.com.

Here we'll add some references from Zotero (Perkel 2020): (Fisch et al. 2015; Argelaguet et al. 2021; Lê Cao et al. 2021).

Markdown documents can include inline equations written in \LaTeX , such as F=ma. Here is an equation on its own line:

$$a^2 + b^2 = c^2$$

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 ${\bf Table~1}~{\bf Original~subject~data}$

ID	class	wt	_	ID	class	wt	_	ID	class	wt
1	GRP_3	76	_	34	GRP_1	269	_	67	GRP_3	182
2	GRP_{-3}	295	_	35	GRP_{-3}	277	_	68	GRP_{-3}	151
3	GRP_{-3}	186	_	36	GRP_3	159	_	69	GRP_{-3}	295
4	GRP_{-3}	162	_	37	GRP_{-3}	217	_	70	GRP_{-3}	224
5	GRP_2	257	_	38	GRP_3	106	_	71	GRP_3	219
6	GRP_1	278	_	39	GRP_3	98	_	72	GRP_3	158
7	GRP_{-3}	116	_	40	GRP_{-2}	202	_	73	GRP_{-1}	224
8	GRP_3	297	_	41	GRP_3	178	_	74	GRP_3	187
9	GRP_3	75	_	42	GRP_{-1}	142	_	75	GRP_3	186
10	GRP_3	162	_	43	GRP_2	90	_	76	GRP_2	173
11	GRP_{-1}	295	_	44	GRP_{-3}	207	_	77	GRP_1	123
12	GRP_3	144		45	GRP_3	138		78	GRP_{-3}	216
13	GRP_3	235		46	GRP_3	288		79	GRP_2	152
14	GRP_{-3}	242		47	GRP_3	177		80	GRP_{-3}	157
15	GRP_3	179	_	48	GRP_{-1}	132	_	81	GRP_3	291
16	GRP_{-1}	184		49	GRP_3	204		82	GRP_{-2}	149
17	GRP_{-3}	248	_	50	GRP_{-3}	86	_	83	GRP_{-1}	246
18	GRP_{-1}	273		51	GRP_3	294		84	GRP_3	287
19	GRP_{-3}	185		52	GRP_3	137		85	GRP_{-3}	221
20	GRP_3	283	_	53	GRP_{-2}	225	_	86	GRP_3	295
21	GRP_{-1}	259	_	54	GRP_3	84	_	87	GRP_1	243
22	GRP_2	148	_	55	GRP_{-2}	123	_	88	GRP_2	138
23	GRP_{-2}	273		56	GRP_{-3}	256		89	GRP_{-1}	144
24	GRP_{-1}	295		57	GRP_{-3}	180		90	GRP_{-3}	156
25	GRP_2	285	_	58	GRP_3	281	_	91	GRP_3	109
26	GRP_3	211	_	59	GRP_{-2}	179	_	92	GRP_{-2}	138
27	GRP_{-2}	79	_	60	GRP_{-3}	288	_	93	GRP_{-1}	162
28	GRP_3	192	_	61	GRP_3	84	_	94	GRP_3	87
29	GRP_2	236	_	62	GRP_{-3}	296	_	95	GRP_2	176
30	GRP_{-1}	201	_	63	GRP_{-2}	108	_	96	GRP_3	232
31	GRP_2	224	_	64	GRP_2	197	_	97	GRP_{-1}	122
32	GRP_2	161	_	65	GRP_{-3}	297	_	98	GRP_1	249
33	GRP ₋ 1	189	_	66	GRP_3	179	_	99	GRP_3	226

2 Results

2.1 Inline computation

One 'killer feature' of computed manuscripts is the ability to compute and insert values into the text rather than requiring authors to input them manually. That circumvents the possibility that the author will enter an incorrect number, or forget to update them should new data arise.

For instance, imagine we are analyzing data from a clinical trial:

We have **99** subjects in our study (Table 1). The average weight is **196.17** (range: **75-297**). (The numbers in **bold face type** are computed values.)

Now suppose we get another tranche of data:

 ${\bf Table~2}~{\rm New~subject~data}$

ID	class	wt	_	ID	class	wt	_	ID	class	wt
1	GRP_{-3}	292	_	21	GRP_{-3}	251	_	41	GRP_3	100
2	GRP_3	167		22	GRP_2	149	_	42	GRP_{-1}	76
3	GRP_2	115	_	23	GRP_2	269	_	43	GRP_{-3}	208
4	GRP_{-3}	199	_	24	GRP_{-3}	207	_	44	GRP_3	128
5	GRP_3	238	_	25	GRP_3	197	_	45	GRP_2	123
6	$GRP_{-}1$	202		26	GRP_2	116	_	46	GRP_3	159
7	GRP_{-3}	103	_	27	GRP_{-2}	78	_	47	GRP_{-2}	228
8	GRP_3	232	_	28	GRP_{-1}	82	_	48	GRP_{-1}	78
9	GRP_{-1}	103	_	29	GRP_{-3}	219	_	49	GRP_{-3}	189
10	GRP_3	169		30	GRP_3	235	_	50	GRP_2	265
11	GRP_3	291	_	31	GRP_3	280	_	51	GRP_3	93
12	GRP_3	226		32	GRP_{-1}	208	_	52	GRP_3	78
13	GRP_1	97	_	33	GRP_2	119	_	53	GRP_3	196
14	GRP_3	173		34	GRP_{-3}	240	_	54	GRP_3	278
15	GRP_2	99		35	GRP_3	225	_	55	GRP_3	226
16	GRP_3	186	_	36	GRP_{-3}	297	_	56	GRP_{-3}	214
17	GRP_3	183		37	GRP_{-1}	162	_	57	GRP_3	261
18	GRP_3	132	_	38	GRP_3	237	_	58	GRP_3	272
19	GRP_2	278	_	39	GRP_{-3}	226	_	59	GRP_{-1}	298
20	GRP_3	112	_	40	GRP ₋ 3	168	_	60	GRP_3	109

There are 60 subjects in this new dataset (Table 2). Their average weight is 185.68 (range: 76-298).

Combining the two datasets, we have a total of **159** subjects. The revised average weight is **192.21** (range: **75-298**).

2.2 The Fibonacci sequence

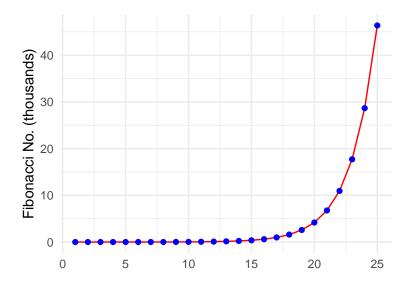
As Rmarkdown documents can do anything R can do, we can also create and include figures. For instance, we can calculate the first **25** numbers in the Fibonacci sequence. The data are shown in Figure 1. Note that this figure number (as well as the table numbers above) are automatically generated.

3 Methods

The following code was used in section 2.1 to create the original clinical trial data:

```
# create a mock dataset
n_subjs <- 99
subjID <- 1:n_subjs
# generate 99 random #s between 0 and 10</pre>
```

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 ${\bf Fig.~1}~$ The first 26 numbers of the Fibonacci sequence

```
tmp <- floor(runif(n_subjs, min = 0, max = 10))</pre>
# assign those numbers to any of 3 subject groups
fn <- function(x) {</pre>
  if (x > 7) 'GRP_1'
  else if (x > 5) 'GRP_2'
  else 'GRP_3'
subj_class <- sapply(tmp, fn)</pre>
\# pick random weights between 75 and 300
wts <- floor(runif(n_subjs, min = 75, max = 300))
# combine the data into a table
df <- data.frame(ID = subjID, class = subj_class, wt = wts)</pre>
# display the table, splitting the 99 rows into 3 cols wide
tmp <- cbind(df[1:33,], rep('|', 33),</pre>
             df[34:66,], rep('|', 33),
             df[67:99,])
names(tmp) <- c('ID', 'class', 'wt', '|', 'ID', 'class', 'wt',
                 '|', 'ID', 'class', 'wt')
knitr::kable(tmp, format = 'latex', booktabs = TRUE,
             caption = "Original subject data")
```

The following code was used in section 2.2 to calculate and plot the Fibonacci sequence:

```
# calculate the first `n` Fibonacci numbers
fibonacci <- function(n) {</pre>
  stopifnot(n > 2)
  ar < -rep(0, n)
  ar[1] <- f1 <- 0
  ar[2] < -f2 < -1
  for (i in 3:n) {
    f3 <- f1 + f2
    ar[i] <- f3
    f1 <- f2
    f2 <- f3
  }
  return (ar)
}
ncalc <- 25
f <- fibonacci(ncalc)</pre>
df <- data.frame(1:ncalc, f)</pre>
names(df) <- c("x", "y")
div <- 1000
p <- ggplot(df) +</pre>
  geom_line(aes(x, y/div), color = "red") +
  geom_point(aes(x, y/div), color = "blue") +
  scale_y\_continuous(limits = c(0, max(df$y)/div)) +
  xlab("") +
  ylab("Fibonacci No. (thousands)") +
  theme_minimal()
p
```

References

- Argelaguet, Ricard, Anna S. E. Cuomo, Oliver Stegle, and John C. Marioni. 2021. "Computational Principles and Challenges in Single-Cell Data Integration." *Nature Biotechnology*, May, 1–14. https://doi.org/10.1038/s41587-021-00895-7.
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