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My Example Computed Manuscript

Created in Rmarkdown

Jeffrey M. Perkel ·

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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:

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

2 Results

2.1 Inline computation

The 'killer feature' of computed manuscripts is their ability to compute and insert values and figures into the text rather than requiring authors to input

Jeffrey M. Perkel
Springer Nature, 1 New York Plaza, New York, NY
E-mail: `jeffrey.perkel@nature.com`

them manually. That circumvents the possibility that the author will enter an incorrect number, or forget to update a figure or value should new data arise.

Imagine we are analyzing data from a clinical trial. We have grouped subjects in three bins and measured the concentration of some metabolite. (These data are simulated.)

Rather than analyzing those data and then copying the results into our manuscript, we can use the programming language `R` to do that in the manuscript itself. Simply enclose the code inside backticks, with the letter `r`. For instance, to calculate the circumference and area of a circle with radius $r = 10$, you could write "A = `` `r pi * r^2` `` " and "C = `` `r 2 * pi * r` ``. Those evaluate to"A = **314.159** and C = **62.832**".

Returning to our dataset, we have **99** (simulated) subjects in our study. The average metabolite concentration is **185.36** (range: **78**-**298**). We have **32** subjects in Group 1, **43** subjects in Group 2, and **24** in Group 3. (The numbers in **bold face type** throughout this document are computed values.)

Now suppose we get another tranche of data. There are **60** subjects in this new dataset. Their average concentration is **185.13** (range: **77**-**299**).

Combining the two datasets, we have a total of **159** subjects (Table 1). The revised average metabolite concentration is **185.28** (range: **77**-**299**). We now have **55** subjects in Group 1, **60** subjects in Group 2, and **44** in Group 3.

2.2 Data tables

2.3 Plotting the data

We can also create and include figures during manuscript creation. Here we plot boxplots of our clinical trial data. The data are shown in Figure 1. Note that this figure number (as well as the table number above) is automatically generated.

3 Code

The following code was used to load, merge, and plot the (simulated) clinical trial data:

```
# load libraries
library(tidyverse)
library(ggbeeswarm)
library(bookdown)
```

```
# read in some initial data
df1 <- read_csv('data/example-data-1.csv')
```

Table 1 Final subject data

ID	Class	Conc	—	ID	Class	Conc	—	ID	Class	Conc
ID_1	Group 2	153	—	ID_54	Group 2	280	—	ID_107	Group 3	170
ID_2	Group 1	224	—	ID_55	Group 2	175	—	ID_108	Group 3	78
ID_3	Group 2	127	—	ID_56	Group 2	223	—	ID_109	Group 1	129
ID_4	Group 2	194	—	ID_57	Group 3	295	—	ID_110	Group 1	137
ID_5	Group 1	251	—	ID_58	Group 1	275	—	ID_111	Group 3	217
ID_6	Group 1	81	—	ID_59	Group 2	120	—	ID_112	Group 1	227
ID_7	Group 2	100	—	ID_60	Group 1	78	—	ID_113	Group 3	81
ID_8	Group 1	270	—	ID_61	Group 3	78	—	ID_114	Group 2	248
ID_9	Group 2	100	—	ID_62	Group 3	140	—	ID_115	Group 1	211
ID_10	Group 1	161	—	ID_63	Group 3	294	—	ID_116	Group 1	113
ID_11	Group 3	158	—	ID_64	Group 3	295	—	ID_117	Group 1	216
ID_12	Group 3	118	—	ID_65	Group 3	285	—	ID_118	Group 3	91
ID_13	Group 2	143	—	ID_66	Group 2	129	—	ID_119	Group 3	258
ID_14	Group 2	258	—	ID_67	Group 3	148	—	ID_120	Group 2	85
ID_15	Group 3	224	—	ID_68	Group 1	281	—	ID_121	Group 3	181
ID_16	Group 3	254	—	ID_69	Group 3	295	—	ID_122	Group 3	216
ID_17	Group 3	190	—	ID_70	Group 2	111	—	ID_123	Group 1	222
ID_18	Group 2	148	—	ID_71	Group 2	132	—	ID_124	Group 3	252
ID_19	Group 1	89	—	ID_72	Group 2	261	—	ID_125	Group 1	166
ID_20	Group 2	89	—	ID_73	Group 1	122	—	ID_126	Group 2	204
ID_21	Group 3	253	—	ID_74	Group 2	124	—	ID_127	Group 2	243
ID_22	Group 3	231	—	ID_75	Group 1	234	—	ID_128	Group 3	198
ID_23	Group 1	112	—	ID_76	Group 2	184	—	ID_129	Group 1	119
ID_24	Group 2	277	—	ID_77	Group 3	272	—	ID_130	Group 1	198
ID_25	Group 2	197	—	ID_78	Group 1	242	—	ID_131	Group 3	151
ID_26	Group 2	208	—	ID_79	Group 2	277	—	ID_132	Group 3	115
ID_27	Group 2	193	—	ID_80	Group 3	236	—	ID_133	Group 3	237
ID_28	Group 3	141	—	ID_81	Group 1	101	—	ID_134	Group 2	178
ID_29	Group 1	206	—	ID_82	Group 3	218	—	ID_135	Group 1	275
ID_30	Group 2	168	—	ID_83	Group 2	130	—	ID_136	Group 2	178
ID_31	Group 2	298	—	ID_84	Group 1	128	—	ID_137	Group 3	267
ID_32	Group 1	144	—	ID_85	Group 3	252	—	ID_138	Group 1	95
ID_33	Group 2	241	—	ID_86	Group 1	198	—	ID_139	Group 1	108
ID_34	Group 2	221	—	ID_87	Group 1	169	—	ID_140	Group 2	77
ID_35	Group 1	112	—	ID_88	Group 2	185	—	ID_141	Group 1	299
ID_36	Group 3	246	—	ID_89	Group 1	216	—	ID_142	Group 3	222
ID_37	Group 2	190	—	ID_90	Group 2	185	—	ID_143	Group 1	85
ID_38	Group 1	177	—	ID_91	Group 2	97	—	ID_144	Group 1	273
ID_39	Group 1	148	—	ID_92	Group 2	165	—	ID_145	Group 3	115
ID_40	Group 2	290	—	ID_93	Group 3	89	—	ID_146	Group 1	290
ID_41	Group 2	151	—	ID_94	Group 2	221	—	ID_147	Group 2	269
ID_42	Group 2	159	—	ID_95	Group 1	162	—	ID_148	Group 2	97
ID_43	Group 2	113	—	ID_96	Group 1	131	—	ID_149	Group 1	229
ID_44	Group 1	249	—	ID_97	Group 1	93	—	ID_150	Group 3	176
ID_45	Group 1	124	—	ID_98	Group 2	240	—	ID_151	Group 2	164
ID_46	Group 3	87	—	ID_99	Group 2	86	—	ID_152	Group 3	172
ID_47	Group 1	166	—	ID_100	Group 2	219	—	ID_153	Group 1	222
ID_48	Group 1	196	—	ID_101	Group 2	243	—	ID_154	Group 1	285
ID_49	Group 1	112	—	ID_102	Group 2	213	—	ID_155	Group 2	153
ID_50	Group 1	289	—	ID_103	Group 1	177	—	ID_156	Group 3	132
ID_51	Group 2	161	—	ID_104	Group 3	197	—	ID_157	Group 2	156
ID_52	Group 3	270	—	ID_105	Group 2	198	—	ID_158	Group 1	260
ID_53	Group 2	237	—	ID_106	Group 1	120	—	ID_159	Group 2	201

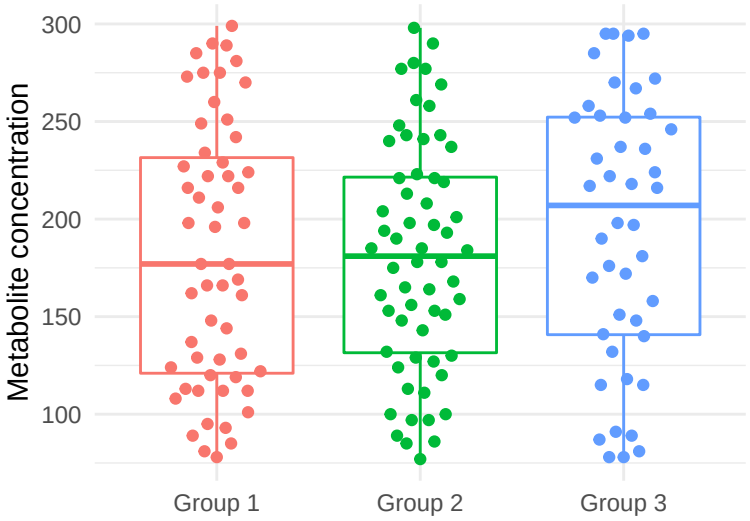

Fig. 1 Metabolite concentration of clinical trial subjects

```
# read new dataset
df2 <- read_csv('data/example-data-2.csv')
```

```
# merge datasets
final_data <- rbind(df1, df2)
```

```
# plot the data
final_data %>%
  ggplot(aes(x = class, y = conc, color = class)) +
  geom_boxplot() +
  ggbeeswarm::geom_quasirandom(width = 0.25) +
  xlab("") +
  ylab("Metabolite concentration") +
  theme_minimal() +
  theme(legend.position = "none")
```

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.

Fisch, K. M., T. Meissner, L. Gioia, J.-C. Ducom, T. M. Carland, S. Loguercio, and A. I. Su. 2015. "Omics Pipe: A Community-Based Framework for

Reproducible Multi-Omics Data Analysis." *Bioinformatics* 31 (11): 1724–28. https://doi.org/10.1093/bioinformatics/btv061.

Lê Cao, Kim-Anh, Al J. Abadi, Emily F. Davis-Marcisak, Lauren Hsu, Arshi Arora, Alexis Coullomb, Atul Deshpande, et al. 2021. "Community-Wide Hackathons to Identify Central Themes in Single-Cell Multi-Omics." *Genome Biology* 22 (1): 220. https://doi.org/10.1186/s13059-021-02433-9.

Perkel, Jeffrey M. 2020. "Streamline Your Writing and Collaborations with These Reference Managers." *Nature* 585 (7823): 149–50. https://doi.org/10.1038/d41586-020-02491-2.