FACTOR RELEVELLING EXAMPLE

A Practical Foray into Lengthy Subtitle Management, Iris Dataset Tampering,

and the Unceasing Pursuit of Stakeholder-Friendly Data Presentation.

From Markdown Mastery to Factor Finagling:

This work entitled

Factor relevelling example

A Practical Foray into Lengthy Subtitle Management, Iris Dataset Tampering,

and the Unceasing Pursuit of Stakeholder-Friendly Data Presentation.

From Markdown Mastery to Factor Finagling:

was compiled by

Márton Kiss MD

This document has been meticulously compiled by the author, who assures the application of the finest methodologies and the most comprehensive professional knowledge available at the time of writing. The author guarantees that every effort has been made to ensure the accuracy and reliability of the information contained within, reflecting a rigorous approach to research, analysis, and attention to detail.

<div style="text-align:center">

Márton Kiss MD, Applied Biostatistician today()

</div>

Chapter 1 Summary

This is a lightweight document for me to kink out the particulars of producing serious-looking but verstile documents. Rendering for 10 minutes would be unpalatable for this document, however I wanted it to serve some useful purpose besides flaunting my template.

Chapter 2 Relevelling & *Forcats*

Factors sometimes get on my nerve. Their levels' order keep changing, you want to switch between human readable (stakeholder readable) and easy-to-type names, etc.

Take a look at the *'iris'* dataset. Species is clearly a factor.

```
unique(iris$Species)
```

[1] setosa versicolor virginica Levels: setosa versicolor virginica

Lets rename some species. The below code is a bit bloated but intuitive IMHO.

```
library(dplyr)

iris_recode <- iris %>%
  mutate(Species_hr =
           forcats::fct_recode( Species,
                                 smelly =
         as.character(unique(iris$Species)[1]),
                                 fluffy =
         as.character(unique(iris$Species)[2])
                                 #Didn't recode 'virginica' asan example
                                 ))
```

And to test the results, lets see what a printout would say. Can I reference said table? Lets try (**??**):

```
set.seed(12345)

iris_recode %>%
  .[sort(sample(nrow(.),10)),] %>%
    knitr::kable(label = "atable",
                 # NEEDS both label and caption for referencing
                 caption = "Example cases from the recoded table")
```

Example cases from the recoded table

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species	Species_hr
2	4.9	3.0	1.4	0.2	setosa	smelly
38	4.9	3.6	1.4	0.1	setosa	smelly
51	7.0	3.2	4.7	1.4	versicolor	fluffy
58	4.9	2.4	3.3	1.0	versicolor	fluffy
75	6.4	2.9	4.3	1.3	versicolor	fluffy
86	6.0	3.4	4.5	1.6	versicolor	fluffy
93	5.8	2.6	4.0	1.2	versicolor	fluffy
96	5.7	3.0	4.2	1.2	versicolor	fluffy
142	6.9	3.1	5.1	2.3	virginica	virginica
146	6.7	3.0	5.2	2.3	virginica	virginica

3 Notes

Information regarding the compilation of this document:

```
knitr::opts_chunk$set(comment = NA)
sessionInfo() %>% report::report() %>% cat()
```

Analyses were conducted using the R Statistical language (version 4.3.0; R Core
Team, 2023) on Windows 10 x64 (build 19045), using the packages rmarkdown
(version 2.22; Allaire J et al., 2023), lme4 (version 1.1.33; Bates D et al., 2015),
Matrix (version 1.5.4.1; Bates D et al., 2023), effects (version 4.2.2; Fox J,
Weisberg S, 2019), carData (version 3.0.5; Fox J et al., 2022), lubridate (version
1.9.2; Grolemund G, Wickham H, 2011), DHARMa (version 0.4.6; Hartig F, 2022),
huxtable (version 5.5.2; Hugh-Jones D, 2022), labelled (version 2.11.0; Larmarange
J, 2023), emmeans (version 1.8.6; Lenth R, 2023), nlme (version 3.1.162; Pinheiro J
et al., 2023), gtsummary (version 1.7.1; Sjoberg D et al., 2021), ggplot2 (version
3.4.2; Wickham H, 2016), readxl (version 1.4.2; Wickham H, Bryan J, 2023),
roxygen2 (version 7.2.3; Wickham H et al., 2022), dplyr (version 1.1.2; Wickham H

et al., 2023), knitr (version 1.43; Xie Y, 2023), pagedown (version 0.20; Xie Y et al., 2022) and kableExtra (version 1.3.4; Zhu H, 2021).

3.1 References

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This document was compiled at:

```
Sys.time()
```

```
[1] "2023-06-14 09:52:11 CEST"
```

```
save.image(file = here::here("inst","states","cookbook_out.Rdata"))
```

4 Appendix

This is how put all your code into an appendix.

```
knitr::opts_chunk$set(echo = TRUE,
                      fig.align = 'center',
                      warning = FALSE,
                      message = FALSE)

unique(iris$Species)

library(dplyr)

iris_recode <- iris %>%
  mutate(Species_hr =
           forcats::fct_recode( Species,
                                smelly =
         as.character(unique(iris$Species)[1]),
                                fluffy =
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                                #Didn't recode 'virginica' asan example
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set.seed(12345)

iris_recode %>%
  .[sort(sample(nrow(.),10)),] %>%
    knitr::kable(label = "atable",
                 # NEEDS both label and caption for referencing
                 caption = "Example cases from the recoded table")

knitr::opts_chunk$set(comment = NA)
sessionInfo() %>% report::report() %>% cat()

Sys.time()
save.image(file = here::here("inst","states","cookbook_out.Rdata"))

# This throws a warning everytime so lets forget about it
#| tidy=TRUE
```