Report-hormone-analysis

tmuylder

11/4/2020

Analysis of file hormone.csv

This script analyzes the dataset of the hormone experiment performed on 01/01/2020. It contains the statistical analysis and plotting of figure 2D of the paper.

Here is a reference to a paper (Munafo et al., 2017).

1. Import libraries

If not already installed, install the packages by uncommenting following line)

```
library(ggplot2)
```

2. Data analysis

2.1 Import samples

Import dataset with proper name handling & rename third column.

```
hormone <- read.csv2("data/20201102-hormone.csv")
names(hormone)[3] <- "Concentration"
hormone
```

```
summary(hormone)
```

```
##     Patient      Drug  Concentration
##  Min.   : 1.00   A:6   Min.   : 8.40
##  1st Qu.: 3.75   B:6   1st Qu.:17.75
##  Median : 6.50         Median :37.30
##  Mean   : 6.50         Mean   :35.23
##  3rd Qu.: 9.25         3rd Qu.:49.15
##  Max.   :12.00         Max.   :60.30
```

2.2 Create figures

Create plot effect of drug A and B on concentration of substance X measured in blood of patients.

```
ggplot(hormone, aes(Drug,Concentration)) +
  stat_summary(fun=mean, geom="bar") +
  stat_summary(fun.data=mean_cl_normal, geom="errorbar", width=0.25) + geom_point() +
  coord_flip()
```

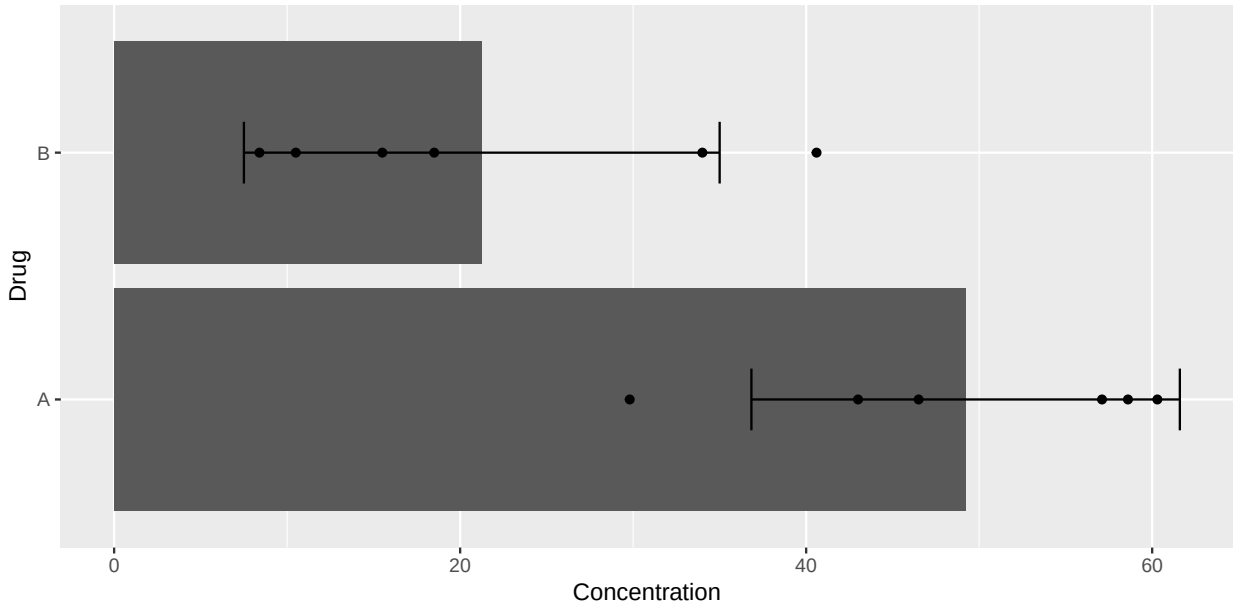

Figure 1: Result of drug on hormone concentration

3. Discussion

There is a clear influence of the choice of drugs on the concentration of hormones present in patients blood.

4. Conclusion

5. Final notes

This report was created with built with 3.6.2. The following packages were used for the analysis

```
sessionInfo()
```

```
## R version 3.6.2 (2019-12-12)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 18362)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.1252
## [2] LC_CTYPE=English_United States.1252
## [3] LC_MONETARY=English_United States.1252
```

```
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] ggplot2_3.3.2
##
## loaded via a namespace (and not attached):
##  [1] highr_0.8           RColorBrewer_1.1-2  pillar_1.4.6
##  [4] compiler_3.6.2      base64enc_0.1-3     tools_3.6.2
##  [7] rpart_4.1-15        digest_0.6.26       checkmate_2.0.0
## [10] htmlTable_2.1.0     evaluate_0.14       lifecycle_0.2.0
## [13] tibble_3.0.4        gtable_0.3.0        lattice_0.20-38
## [16] png_0.1-7           pkgconfig_2.0.3     rlang_0.4.8
## [19] Matrix_1.2-18       rstudioapi_0.11     yaml_2.2.1
## [22] xfun_0.18           gridExtra_2.3       cluster_2.1.0
## [25] withr_2.3.0         dplyr_1.0.2         stringr_1.4.0
## [28] knitr_1.30          htmlwidgets_1.5.2   generics_0.0.2
## [31] vctrs_0.3.4         nnet_7.3-12         grid_3.6.2
## [34] tidyselect_1.1.0    data.table_1.13.0   glue_1.4.2
## [37] R6_2.4.1            jpeg_0.1-8.1        survival_3.1-8
## [40] foreign_0.8-72      rmarkdown_2.5       latticeExtra_0.6-29
## [43] Formula_1.2-4       farver_2.0.3        purrr_0.3.4
## [46] magrittr_1.5        backports_1.1.10    scales_1.1.1
## [49] Hmisc_4.4-1         ellipsis_0.3.1      htmltools_0.5.0
## [52] splines_3.6.2       colorspace_1.4-1    labeling_0.3
## [55] stringi_1.4.6       munsell_0.5.0       crayon_1.3.4
```

6. References

Some final note

Munafo, M. R., Nosek, B. A., Bishop, D. V. M., Button, K. S., Chambers, C. D., Percie Du Sert, N., Simonsohn, U., Wagenmakers, E. J., Ware, J. J., & Ioannidis, J. P. A. (2017). A manifesto for reproducible science. *Nature Human Behaviour*, *1*(1), 1–9. https://doi.org/10.1038/s41562-016-0021