Title Goes Here

Myfirstname Mylastname1,✉, and Yourfirstname Yourlastname2

08 December, 2021

Text of abstract

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2 University of Another Place

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Keywords: keyword 1; keyword 2; keyword 3

Highlights: These are the highlights.

##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':  
##   
## filter, lag

## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union

# 1 Introduction

This is a replication of figure 1a from1 (Fig. ??).

# 2 Background

# 3 Methods

# 4 Results

#> # A tibble: 6 × 21  
#> Order Family Genus Species Genus.Species McNab.Name Mass.g BMR.W `BMR.kJ/h`  
#> <chr> <chr> <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl>  
#> 1 Monot… Tachyg… Tachy… aculea… Tachyglossus… <NA> 2140 1.56 5.63  
#> 2 Monot… Tachyg… Zaglo… bartoni Zaglossus ba… <NA> 10300 6.78 24.4   
#> 3 Monot… Ornith… Ornit… anatin… Ornithorhync… <NA> 1300 2.61 9.4   
#> 4 Didel… Didelp… Calur… derbia… Caluromys de… <NA> 357 1.14 4.09  
#> 5 Didel… Didelp… Graci… microt… Gracilinanus… Marmosa m… 13 0.106 0.38  
#> 6 Didel… Didelp… Thyla… elegans Thylamys ele… <NA> 40 0.239 0.86  
#> # … with 12 more variables: Temperature.C <dbl>, Notes...11 <chr>,  
#> # Reference <chr>, Food <chr>, Climate <chr>, Habitat <chr>, Substrate <chr>,  
#> # Torpor <chr>, Islands <chr>, Mountains <chr>, Tree.Name <chr>,  
#> # Notes...21 <chr>

#>   
#> Call:  
#> lm(formula = log10(BMR.W) ~ log10(Mass.g), data = sub\_data)  
#>   
#> Coefficients:  
#> (Intercept) log10(Mass.g)   
#> -1.7084 0.7179  
#>   
#> Call:  
#> lm(formula = log10(BMR.W) ~ (log10(Mass.g)^2) + log10(Mass.g),   
#> data = sub\_data)  
#>   
#> Coefficients:  
#> (Intercept) log10(Mass.g)   
#> -1.7084 0.7179

Figure ?? shows how we can have a caption and cross-reference for a plot

# 5 Discussion

# 6 Conclusion

# 7 Acknowledgements

# 8 References

1. Kolokotrones, T., Van Savage, Deeds, E. J. & Fontana, W. Curvature in metabolic scaling. *Nature* **464**, 753–756 (2010).

### 8.0.1 Colophon

This report was generated on 2021-12-08 11:05:15 using the following computational environment and dependencies:

#> ─ Session info 👃🏻 🤶🏾 🖕🏿 ─────────────────────────────────────────────────  
#> hash: nose: light skin tone, Mrs. Claus: medium-dark skin tone, middle finger: dark skin tone  
#>   
#> setting value  
#> version R version 4.1.2 (2021-11-01)  
#> os macOS Big Sur 10.16  
#> system x86\_64, darwin17.0  
#> ui X11  
#> language (EN)  
#> collate en\_US.UTF-8  
#> ctype en\_US.UTF-8  
#> tz America/Los\_Angeles  
#> date 2021-12-08  
#> pandoc 2.14.0.3 @ /Applications/RStudio.app/Contents/MacOS/pandoc/ (via rmarkdown)  
#>   
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#> backports 1.4.0 2021-11-23 [1] CRAN (R 4.1.0)  
#> bookdown 0.24 2021-09-02 [1] CRAN (R 4.1.0)  
#> broom 0.7.10 2021-10-31 [1] CRAN (R 4.1.0)  
#> cachem 1.0.6 2021-08-19 [1] CRAN (R 4.1.0)  
#> callr 3.7.0 2021-04-20 [1] CRAN (R 4.1.0)  
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#> colorspace 2.0-2 2021-06-24 [1] CRAN (R 4.1.0)  
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#> desc 1.4.0 2021-09-28 [1] CRAN (R 4.1.0)  
#> devtools 2.4.2 2021-06-07 [1] CRAN (R 4.1.0)  
#> digest 0.6.28 2021-09-23 [1] CRAN (R 4.1.0)  
#> dplyr \* 1.0.7 2021-06-18 [1] CRAN (R 4.1.0)  
#> ellipsis 0.3.2 2021-04-29 [1] CRAN (R 4.1.0)  
#> evaluate 0.14 2019-05-28 [1] CRAN (R 4.1.0)  
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#> gtable 0.3.0 2019-03-25 [1] CRAN (R 4.1.0)  
#> haven 2.4.3 2021-08-04 [1] CRAN (R 4.1.0)  
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#> magrittr 2.0.1 2020-11-17 [1] CRAN (R 4.1.0)  
#> memoise 2.0.1 2021-11-26 [1] CRAN (R 4.1.0)  
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#> scales 1.1.1 2020-05-11 [1] CRAN (R 4.1.0)  
#> sessioninfo 1.2.1 2021-11-02 [1] CRAN (R 4.1.0)  
#> stringi 1.7.6 2021-11-29 [1] CRAN (R 4.1.0)  
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#> tibble \* 3.1.6 2021-11-07 [1] CRAN (R 4.1.0)  
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#>   
#> [1] /Library/Frameworks/R.framework/Versions/4.1/Resources/library  
#>   
#> ──────────────────────────────────────────────────────────────────────────────

The current Git commit details are:

#> Local: main /Users/ronghao/Desktop/Stanford/BIOS207 Software/Kolokotrones  
#> Remote: main @ origin (https://github.com/Ronghao94/Kolokotrones.git)  
#> Head: [79a7170] 2021-12-08: Update NAMESPACE to include subset\_data()