BDP2-448 Lovasz

Benjamin Chan (chanb@ohsu.edu)

2019-07-20

# Import data

getwd()

## [1] "C:/Users/Ben/Google Drive/Work/BDP2-448-Lovasz"

f <- "data/raw/Becky-Bedding Exposure Study Data for Stats.2.xlsx"

Import data file *data/raw/Becky-Bedding Exposure Study Data for Stats.2.xlsx*

df <- f %>% read\_excel()

## readxl works best with a newer version of the tibble package.  
## You currently have tibble v1.4.2.  
## Falling back to column name repair from tibble <= v1.4.2.  
## Message displays once per session.

oldnames <- names(df)  
newnames <- c("id",  
 "sex",  
 "time",  
 "bedding",  
 "order",  
 "room",  
 "foodIntakeNormalized",  
 "orts",  
 "foodIntakeRaw",  
 "cumulativeFoodIntakeNormalized")  
names(df) <- newnames  
data.frame(oldnames, newnames) %>% kable()

|  |  |
| --- | --- |
| oldnames | newnames |
| Mouse ID | id |
| Sex | sex |
| Time (hr) | time |
| Bedding | bedding |
| Order | order |
| Housing Room | room |
| Normalized food intake (mg food/g BW) | foodIntakeNormalized |
| Orts (g) | orts |
| Raw food intake (g) | foodIntakeRaw |
| Normalized cumulative food intake (mg food/g BW) | cumulativeFoodIntakeNormalized |

Remove outlier

df %>%  
 dplyr::select(id, sex, time, bedding, foodIntakeNormalized) %>%  
 filter(id == 42 & bedding == "B") %>%  
 kable()

## Warning: package 'bindrcpp' was built under R version 3.5.2

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| id | sex | time | bedding | foodIntakeNormalized |
| 42 | M | 2 | B | 21.24892 |
| 42 | M | 4 | B | 137.03382 |
| 42 | M | 12 | B | -63.03972 |
| 42 | M | 24 | B | 23.99276 |
| 42 | M | 36 | B | 128.67490 |
| 42 | M | 48 | B | 10.18150 |

df <-  
 df %>%  
 filter(!(id == 42 & bedding == "B"))

Plot data.

G <-  
 df %>%  
 ggplot() +  
 aes(x = time, y = foodIntakeNormalized, color = bedding) +  
 geom\_line(aes(group = id), alpha = 1/4) +  
 geom\_boxplot(aes(group = time)) +  
 facet\_grid(sex ~ bedding) +  
 scale\_color\_brewer(palette = "Set1") +  
 scale\_x\_continuous("Time\n(hours)", breaks = c(2, 4, 12, 24, 36, 48)) +  
 scale\_y\_continuous("Food intake, normalized\n(mg food/g body weight)") +  
 theme\_bw() +  
 theme(legend.position = "none",  
 panel.grid.major.x = element\_blank(),  
 panel.grid.minor.x = element\_blank())  
ggsave("figures/lineplot.png", dpi = 300)

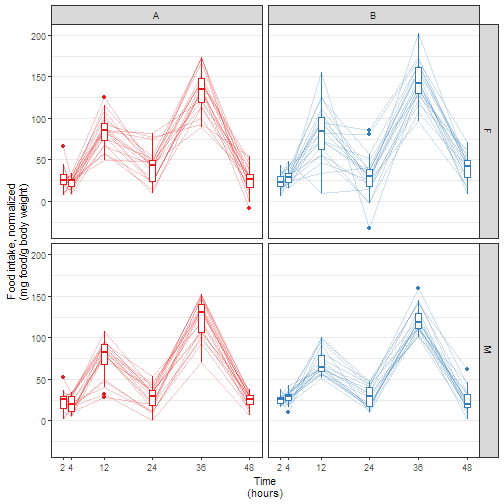
## Saving 7 x 7 in image

ggsave("figures/lineplot.svg", dpi = 300)

## Saving 7 x 7 in image

## Warning: package 'gdtools' was built under R version 3.5.2

G



plot of chunk lineplot

# New analysis

Prior analysis is archived in commit f3ce92.

On Thu, May 2, 2019 at 12:44 PM Becky Lovasz [lovasz@ohsu.edu](mailto:lovasz@ohsu.edu) wrote:

Hi Ben,

My project was put on the back burner for a while, and I'm picking it back up again. I discussed the results below with my research advisor. Can you please compare normalized food intake for Bedding A vs. Bedding B, regardless of bedding exposure order, at each time point separately? We'd like to see males only, females only, and all mice combined. Thanks for your help!

random <- formula(~ 1 | id)  
cs <-  
 corSymm(form = random, fixed = FALSE) %>%  
 Initialize(data = df)  
ctrl <- lmeControl(opt = "optim",  
 maxIter = 500, msMaxIter = 500,  
 tolerance = 1e-6, niterEM = 25, msMaxEval = 200, msTol = 1e-7)  
testContrast <- function (nlmeObj, contrast) {  
 require(multcomp)  
 g <- glht(nlmeObj, linfct = c(contrast)) %>% summary()  
 x <- g[["test"]][["coefficients"]]  
 dir <- ifelse(x > 0, "higher", "lower")  
 s <- g[["test"]][["sigma"]]  
 p <- g[["test"]][["pvalues"]][[1]]  
 result <- data.frame(contrast = contrast,  
 coefficient = x,  
 sigma = s,  
 pvalue = p,  
 effsize = abs(x),  
 direction = dir,  
 stringsAsFactors = FALSE)  
 rownames(result) <- NULL  
 result  
}

## All mice combined

Use nlme::lme(). Specify a general correlation structure with corSymm(). Use this output.

fixed <- formula(foodIntakeNormalized ~  
 bedding +  
 time +  
 bedding \* time)  
M <-  
 df %>%  
 mutate(time = factor(time)) %>%  
 lme(fixed, data = ., random = random, correlation = cs, control = ctrl)  
M %>%   
 tidy() %>%  
 filter(effect == "fixed") %>%  
 kable(digits = 3)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| effect | group | term | estimate | std.error | df | statistic | p.value |
| fixed | fixed | (Intercept) | 12.009 | 1.999 | 423 | 6.008 | 0.000 |
| fixed | fixed | beddingB | -0.069 | 2.114 | 423 | -0.033 | 0.974 |
| fixed | fixed | time4 | -3.229 | 1.906 | 423 | -1.695 | 0.091 |
| fixed | fixed | time12 | 67.429 | 3.333 | 423 | 20.234 | 0.000 |
| fixed | fixed | time24 | 11.936 | 2.637 | 423 | 4.526 | 0.000 |
| fixed | fixed | time36 | 118.441 | 3.172 | 423 | 37.338 | 0.000 |
| fixed | fixed | time48 | 3.342 | 2.974 | 423 | 1.124 | 0.262 |
| fixed | fixed | beddingB:time4 | 5.972 | 2.674 | 423 | 2.233 | 0.026 |
| fixed | fixed | beddingB:time12 | -1.335 | 3.340 | 423 | -0.400 | 0.690 |
| fixed | fixed | beddingB:time24 | -6.099 | 2.483 | 423 | -2.456 | 0.014 |
| fixed | fixed | beddingB:time36 | 1.803 | 3.864 | 423 | 0.467 | 0.641 |
| fixed | fixed | beddingB:time48 | 5.783 | 4.362 | 423 | 1.326 | 0.186 |

testBeddingEffect <-   
 bind\_rows(testContrast(M, "beddingB = 0"),  
 testContrast(M, "beddingB + beddingB:time4 = 0"),  
 testContrast(M, "beddingB + beddingB:time12 = 0"),  
 testContrast(M, "beddingB + beddingB:time24 = 0"),  
 testContrast(M, "beddingB + beddingB:time36 = 0"),  
 testContrast(M, "beddingB + beddingB:time48 = 0"))  
testBeddingEffect %>% kable(digits = 3)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| contrast | coefficient | sigma | pvalue | effsize | direction |
| beddingB = 0 | -0.069 | 2.114 | 0.974 | 0.069 | lower |
| beddingB + beddingB:time4 = 0 | 5.903 | 1.770 | 0.001 | 5.903 | higher |
| beddingB + beddingB:time12 = 0 | -1.404 | 2.924 | 0.631 | 1.404 | lower |
| beddingB + beddingB:time24 = 0 | -6.168 | 2.520 | 0.014 | 6.168 | lower |
| beddingB + beddingB:time36 = 0 | 1.734 | 3.475 | 0.618 | 1.734 | higher |
| beddingB + beddingB:time48 = 0 | 5.714 | 3.067 | 0.062 | 5.714 | higher |

test1 <- testBeddingEffect

## By sex

Use nlme::lme(). Specify a general correlation structure with corSymm(). Use this output.

fixed <- formula(foodIntakeNormalized ~  
 bedding +  
 time +  
 sex +  
 bedding \* time +  
 bedding \* sex +  
 sex \* time +  
 bedding \* time \* sex)  
M <-  
 df %>%  
 mutate(time = factor(time)) %>%  
 lme(fixed, data = ., random = random, correlation = cs, control = ctrl)  
M %>%   
 tidy() %>%  
 filter(effect == "fixed") %>%  
 kable(digits = 3)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| effect | group | term | estimate | std.error | df | statistic | p.value |
| fixed | fixed | (Intercept) | 14.728 | 2.767 | 412 | 5.322 | 0.000 |
| fixed | fixed | beddingB | -4.916 | 2.778 | 412 | -1.770 | 0.078 |
| fixed | fixed | time4 | -4.227 | 2.704 | 412 | -1.563 | 0.119 |
| fixed | fixed | time12 | 70.537 | 4.636 | 412 | 15.215 | 0.000 |
| fixed | fixed | time24 | 16.446 | 3.627 | 412 | 4.535 | 0.000 |
| fixed | fixed | time36 | 122.335 | 4.270 | 412 | 28.652 | 0.000 |
| fixed | fixed | time48 | -0.057 | 3.932 | 412 | -0.015 | 0.988 |
| fixed | fixed | sexM | -4.611 | 3.935 | 38 | -1.172 | 0.249 |
| fixed | fixed | beddingB:time4 | 9.344 | 3.725 | 412 | 2.509 | 0.012 |
| fixed | fixed | beddingB:time12 | 2.898 | 4.605 | 412 | 0.629 | 0.530 |
| fixed | fixed | beddingB:time24 | -7.123 | 3.500 | 412 | -2.035 | 0.043 |
| fixed | fixed | beddingB:time36 | 7.871 | 5.446 | 412 | 1.445 | 0.149 |
| fixed | fixed | beddingB:time48 | 19.282 | 5.462 | 412 | 3.530 | 0.000 |
| fixed | fixed | beddingB:sexM | 9.694 | 3.967 | 412 | 2.444 | 0.015 |
| fixed | fixed | time4:sexM | 2.112 | 3.826 | 412 | 0.552 | 0.581 |
| fixed | fixed | time12:sexM | -7.571 | 6.577 | 412 | -1.151 | 0.250 |
| fixed | fixed | time24:sexM | -10.346 | 5.139 | 412 | -2.013 | 0.045 |
| fixed | fixed | time36:sexM | -10.412 | 6.049 | 412 | -1.721 | 0.086 |
| fixed | fixed | time48:sexM | 5.765 | 5.563 | 412 | 1.036 | 0.301 |
| fixed | fixed | beddingB:time4:sexM | -6.733 | 5.304 | 412 | -1.269 | 0.205 |
| fixed | fixed | beddingB:time12:sexM | -8.596 | 6.568 | 412 | -1.309 | 0.191 |
| fixed | fixed | beddingB:time24:sexM | 2.122 | 5.001 | 412 | 0.424 | 0.672 |
| fixed | fixed | beddingB:time36:sexM | -12.094 | 7.739 | 412 | -1.563 | 0.119 |
| fixed | fixed | beddingB:time48:sexM | -26.667 | 7.789 | 412 | -3.424 | 0.001 |

testBeddingEffect <-   
 bind\_rows(testContrast(M, "beddingB = 0"),  
 testContrast(M, "beddingB + beddingB:time4 = 0"),  
 testContrast(M, "beddingB + beddingB:time12 = 0"),  
 testContrast(M, "beddingB + beddingB:time24 = 0"),  
 testContrast(M, "beddingB + beddingB:time36 = 0"),  
 testContrast(M, "beddingB + beddingB:time48 = 0"),  
 testContrast(M, "beddingB + beddingB:sexM = 0"),  
 testContrast(M, "beddingB + beddingB:sexM + beddingB:time4:sexM = 0"),  
 testContrast(M, "beddingB + beddingB:sexM + beddingB:time12:sexM = 0"),  
 testContrast(M, "beddingB + beddingB:sexM + beddingB:time24:sexM = 0"),  
 testContrast(M, "beddingB + beddingB:sexM + beddingB:time36:sexM = 0"),  
 testContrast(M, "beddingB + beddingB:sexM + beddingB:time48:sexM = 0"))  
testBeddingEffect %>% kable(digits = 3)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| contrast | coefficient | sigma | pvalue | effsize | direction |
| beddingB = 0 | -4.916 | 2.778 | 0.077 | 4.916 | lower |
| beddingB + beddingB:time4 = 0 | 4.429 | 2.508 | 0.077 | 4.429 | higher |
| beddingB + beddingB:time12 = 0 | -2.018 | 4.148 | 0.627 | 2.018 | lower |
| beddingB + beddingB:time24 = 0 | -12.038 | 3.341 | 0.000 | 12.038 | lower |
| beddingB + beddingB:time36 = 0 | 2.955 | 5.053 | 0.559 | 2.955 | higher |
| beddingB + beddingB:time48 = 0 | 14.366 | 4.025 | 0.000 | 14.366 | higher |
| beddingB + beddingB:sexM = 0 | 4.778 | 2.832 | 0.092 | 4.778 | higher |
| beddingB + beddingB:sexM + beddingB:time4:sexM = 0 | -1.955 | 4.514 | 0.665 | 1.955 | lower |
| beddingB + beddingB:sexM + beddingB:time12:sexM = 0 | -3.818 | 6.247 | 0.541 | 3.818 | lower |
| beddingB + beddingB:sexM + beddingB:time24:sexM = 0 | 6.900 | 4.885 | 0.158 | 6.900 | higher |
| beddingB + beddingB:sexM + beddingB:time36:sexM = 0 | -7.316 | 7.466 | 0.327 | 7.316 | lower |
| beddingB + beddingB:sexM + beddingB:time48:sexM = 0 | -21.889 | 6.821 | 0.001 | 21.889 | lower |

test2 <- testBeddingEffect

# Interpretation

Using a model that does not distinguish male and female mice, there is a slight difference in food intake by bedding type at 24 and 48 hours. At 24 hours, food intake is 6.17 mg/g lower with bedding type B compared to A (p-value: 0.014). At 48 hours, food intake is 5.71 mg/g higher with bedding type B compared to A (p-value: 0.062).

Among female mice, there is a difference in food intake by bedding type at 24 and 48 hours. At 24 hours, food intake is 12 mg/g lower with bedding type B compared to A (p-value: 0.00031). At 48 hours, food intake is 14.4 mg/g higher with bedding type B compared to A (p-value: 0.00036).

Among male mice, there is a difference in food intake by bedding type at 2 and 48 hours. At 2 hours, food intake is 4.78 mg/g higher with bedding type B compared to A (p-value: 0.092). At 48 hours, food intake is 21.9 mg/g lower with bedding type B compared to A (p-value: 0.0013).

# R session information

For debugging purposes.

## [1] "Run time: 2019-07-20 11:56:04"

## R version 3.5.1 (2018-07-02)  
## Platform: x86\_64-w64-mingw32/x64 (64-bit)  
## Running under: Windows 10 x64 (build 17134)  
##   
## Matrix products: default  
##   
## attached base packages:  
## [1] stats graphics grDevices utils datasets methods base   
##   
## other attached packages:  
## [1] gdtools\_0.1.7 bindrcpp\_0.2.2 multcomp\_1.4-8   
## [4] TH.data\_1.0-9 MASS\_7.3-50 survival\_2.43-3   
## [7] mvtnorm\_1.0-8 broom.mixed\_0.2.3 nlme\_3.1-137   
## [10] lme4\_1.1-19 Matrix\_1.2-14 svglite\_1.2.1   
## [13] broom\_0.5.1 readxl\_1.2.0 forcats\_0.3.0   
## [16] stringr\_1.3.1 dplyr\_0.7.8 purrr\_0.2.5   
## [19] readr\_1.3.1 tidyr\_0.8.2 tibble\_1.4.2   
## [22] ggplot2\_3.1.0 tidyverse\_1.2.1 magrittr\_1.5   
## [25] checkpoint\_0.4.5 rmarkdown\_1.11 knitr\_1.21   
##   
## loaded via a namespace (and not attached):  
## [1] Rcpp\_0.12.19 lubridate\_1.7.4 lattice\_0.20-35   
## [4] zoo\_1.8-4 assertthat\_0.2.0 digest\_0.6.18   
## [7] R6\_2.3.0 cellranger\_1.1.0 plyr\_1.8.4   
## [10] backports\_1.1.3 evaluate\_0.12 coda\_0.19-2   
## [13] highr\_0.7 httr\_1.4.0 pillar\_1.3.1   
## [16] rlang\_0.3.0.1 lazyeval\_0.2.1 rstudioapi\_0.8   
## [19] minqa\_1.2.4 nloptr\_1.2.1 labeling\_0.3   
## [22] splines\_3.5.1 TMB\_1.7.15 munsell\_0.5.0   
## [25] compiler\_3.5.1 modelr\_0.1.2 xfun\_0.4   
## [28] pkgconfig\_2.0.2 htmltools\_0.3.6 tidyselect\_0.2.5   
## [31] glmmTMB\_0.2.2.0 codetools\_0.2-15 crayon\_1.3.4   
## [34] withr\_2.1.2 grid\_3.5.1 jsonlite\_1.6   
## [37] gtable\_0.2.0 scales\_1.0.0 cli\_1.0.1   
## [40] stringi\_1.2.4 reshape2\_1.4.3 xml2\_1.2.0   
## [43] generics\_0.0.2 sandwich\_2.5-0 RColorBrewer\_1.1-2  
## [46] tools\_3.5.1 glue\_1.3.0 hms\_0.4.2   
## [49] colorspace\_1.3-2 rvest\_0.3.2 bindr\_0.1.1   
## [52] haven\_2.0.0