BDP2-448 Lovasz

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# 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## readxl works best with a newer version of the tibble package.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 |

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)

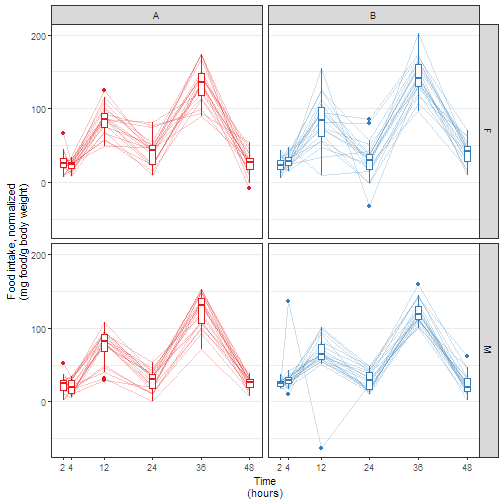
## Saving 7 x 7 in image

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)

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

M %>%   
 tidy() %>%  
 filter(effect == "fixed") %>%  
 kable(digits = 3)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| effect | group | term | estimate | std.error | df | statistic | p.value |
| fixed | fixed | (Intercept) | 11.018 | 2.123 | 429 | 5.191 | 0.000 |
| fixed | fixed | beddingB | 0.427 | 2.074 | 429 | 0.206 | 0.837 |
| fixed | fixed | time4 | -0.778 | 2.183 | 429 | -0.357 | 0.722 |
| fixed | fixed | time12 | 66.280 | 3.364 | 429 | 19.704 | 0.000 |
| fixed | fixed | time24 | 12.518 | 2.690 | 429 | 4.653 | 0.000 |
| fixed | fixed | time36 | 118.356 | 3.356 | 429 | 35.265 | 0.000 |
| fixed | fixed | time48 | 3.367 | 2.938 | 429 | 1.146 | 0.252 |
| fixed | fixed | beddingB:time4 | 3.590 | 3.256 | 429 | 1.103 | 0.271 |
| fixed | fixed | beddingB:time12 | -0.494 | 3.649 | 429 | -0.135 | 0.892 |
| fixed | fixed | beddingB:time24 | -6.888 | 2.552 | 429 | -2.699 | 0.007 |
| fixed | fixed | beddingB:time36 | 1.774 | 3.874 | 429 | 0.458 | 0.647 |
| fixed | fixed | beddingB:time48 | 5.941 | 4.294 | 429 | 1.383 | 0.167 |

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 | 0.427 | 2.074 | 0.837 | 0.427 | higher |
| beddingB + beddingB:time4 = 0 | 4.017 | 2.455 | 0.102 | 4.017 | higher |
| beddingB + beddingB:time12 = 0 | -0.067 | 3.318 | 0.984 | 0.067 | lower |
| beddingB + beddingB:time24 = 0 | -6.461 | 2.570 | 0.012 | 6.461 | lower |
| beddingB + beddingB:time36 = 0 | 2.201 | 3.426 | 0.521 | 2.201 | higher |
| beddingB + beddingB:time48 = 0 | 6.367 | 3.046 | 0.037 | 6.367 | 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) | 13.760 | 2.966 | 418 | 4.640 | 0.000 |
| fixed | fixed | beddingB | -4.249 | 2.739 | 418 | -1.552 | 0.122 |
| fixed | fixed | time4 | -1.033 | 3.123 | 418 | -0.331 | 0.741 |
| fixed | fixed | time12 | 68.281 | 4.688 | 418 | 14.564 | 0.000 |
| fixed | fixed | time24 | 17.025 | 3.692 | 418 | 4.611 | 0.000 |
| fixed | fixed | time36 | 123.016 | 4.507 | 418 | 27.296 | 0.000 |
| fixed | fixed | time48 | 0.022 | 3.882 | 418 | 0.006 | 0.996 |
| fixed | fixed | sexM | -4.488 | 4.194 | 38 | -1.070 | 0.291 |
| fixed | fixed | beddingB:time4 | 4.852 | 4.618 | 418 | 1.051 | 0.294 |
| fixed | fixed | beddingB:time12 | 5.986 | 4.989 | 418 | 1.200 | 0.231 |
| fixed | fixed | beddingB:time24 | -8.713 | 3.585 | 418 | -2.430 | 0.016 |
| fixed | fixed | beddingB:time36 | 6.814 | 5.489 | 418 | 1.241 | 0.215 |
| fixed | fixed | beddingB:time48 | 19.092 | 5.376 | 418 | 3.551 | 0.000 |
| fixed | fixed | beddingB:sexM | 9.708 | 3.873 | 418 | 2.507 | 0.013 |
| fixed | fixed | time4:sexM | 0.060 | 4.417 | 418 | 0.014 | 0.989 |
| fixed | fixed | time12:sexM | -5.604 | 6.631 | 418 | -0.845 | 0.399 |
| fixed | fixed | time24:sexM | -11.136 | 5.222 | 418 | -2.132 | 0.034 |
| fixed | fixed | time36:sexM | -12.754 | 6.374 | 418 | -2.001 | 0.046 |
| fixed | fixed | time48:sexM | 5.882 | 5.490 | 418 | 1.071 | 0.285 |
| fixed | fixed | beddingB:time4:sexM | -2.514 | 6.531 | 418 | -0.385 | 0.701 |
| fixed | fixed | beddingB:time12:sexM | -13.611 | 7.056 | 418 | -1.929 | 0.054 |
| fixed | fixed | beddingB:time24:sexM | 4.052 | 5.070 | 418 | 0.799 | 0.425 |
| fixed | fixed | beddingB:time36:sexM | -10.179 | 7.763 | 418 | -1.311 | 0.191 |
| fixed | fixed | beddingB:time48:sexM | -27.071 | 7.603 | 418 | -3.560 | 0.000 |

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 | -4.249 | 2.739 | 0.121 | 4.249 | lower |
| beddingB + beddingB:time4 = 0 | 0.603 | 3.425 | 0.860 | 0.603 | higher |
| beddingB + beddingB:time12 = 0 | 1.737 | 4.712 | 0.712 | 1.737 | higher |
| beddingB + beddingB:time24 = 0 | -12.962 | 3.365 | 0.000 | 12.962 | lower |
| beddingB + beddingB:time36 = 0 | 2.565 | 4.985 | 0.607 | 2.565 | higher |
| beddingB + beddingB:time48 = 0 | 14.843 | 3.993 | 0.000 | 14.843 | higher |
| beddingB + beddingB:sexM = 0 | 5.459 | 2.739 | 0.046 | 5.459 | higher |
| beddingB + beddingB:sexM + beddingB:time4:sexM = 0 | 2.946 | 5.749 | 0.608 | 2.946 | higher |
| beddingB + beddingB:sexM + beddingB:time12:sexM = 0 | -8.152 | 6.862 | 0.235 | 8.152 | lower |
| beddingB + beddingB:sexM + beddingB:time24:sexM = 0 | 9.511 | 4.917 | 0.053 | 9.511 | higher |
| beddingB + beddingB:sexM + beddingB:time36:sexM = 0 | -4.719 | 7.415 | 0.525 | 4.719 | lower |
| beddingB + beddingB:sexM + beddingB:time48:sexM = 0 | -21.612 | 6.697 | 0.001 | 21.612 | 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 6.46 mg/g lower with bedding type B compared to A (p-value: 0.012). At 48 hours, food intake is 6.37 mg/g higher with bedding type B compared to A (p-value: 0.037).

Among female mice, there is a difference in food intake by bedding type at 24 and 48 hours. At 24 hours, food intake is 13 mg/g lower with bedding type B compared to A (p-value: 0.00012). At 48 hours, food intake is 14.8 mg/g higher with bedding type B compared to A (p-value: 0.0002).

Among male mice, there is a difference in food intake by bedding type at 2 and 48 hours. At 2 hours, food intake is 5.46 mg/g higher with bedding type B compared to A (p-value: 0.046). At 48 hours, food intake is 21.6 mg/g lower with bedding type B compared to A (p-value: 0.0013).

# R session information

For debugging purposes.

## [1] "Run time: 2019-05-23 20:56:39"

## 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] bindrcpp\_0.2.2 gdtools\_0.1.7 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