BDP2-448 Lovasz

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getwd()

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

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

Import data file *../data/raw/Becky-Bedding Exposure Study Data for Stats.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## readxl works best with a newer version of the tibble package.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, group = id, color = bedding) +  
 geom\_line(alpha = 1/4) +  
 facet\_wrap(~ 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.minor = element\_blank())  
ggsave("../figures/lineplot.png", width = 7, height = 4, dpi = 300)  
ggsave("../figures/lineplot.svg", width = 7, height = 4, dpi = 300)

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

t <- 36

Reshape data to mouse-level analytic data set. Data point at t = 36 is used to evaluate difference between A and B bedding types.

Outcome variable is diff.

* Positive values indicate the mouse ate more at t = 36 with bedding type A
* Negative values indicate the mouse ate more at t = 36 with bedding type B

dfA <-  
 df %>%  
 filter(time == t) %>%  
 filter(bedding == "A") %>%  
 select(id, foodIntakeNormalized) %>%  
 rename(A = foodIntakeNormalized)

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

dfB <-  
 df %>%  
 filter(time == t) %>%  
 filter(bedding == "B") %>%  
 select(id, foodIntakeNormalized) %>%  
 rename(B = foodIntakeNormalized)  
dfDiff <-  
 merge(dfA, dfB, by = "id") %>%  
 mutate(diff = A - B)  
covariates <-  
 df %>%  
 filter(order == 1) %>%  
 select(id, sex, order, bedding, room) %>%  
 unique() %>%  
 mutate(isBeddingAFirst = order == 1 & bedding == "A")  
dfDiff <-  
 merge(dfDiff, covariates, by = "id") %>%  
 select(-c(order, bedding))

Exploratory comparisons.

dfDiff %>%  
 group\_by(sex) %>%  
 summarize(n = n(), mean = mean(diff), sd = sd(diff)) %>%  
 kable(digits = 1)

|  |  |  |  |
| --- | --- | --- | --- |
| sex | n | mean | sd |
| F | 20 | -9.0 | 41.3 |
| M | 20 | -27.3 | 67.7 |

dfDiff %>%  
 group\_by(room) %>%  
 summarize(n = n(), mean = mean(diff), sd = sd(diff)) %>%  
 kable(digits = 1)

|  |  |  |  |
| --- | --- | --- | --- |
| room | n | mean | sd |
| 0543 | 15 | 2.0 | 29 |
| 0545C | 25 | -30.3 | 65 |

dfDiff %>%  
 group\_by(isBeddingAFirst) %>%  
 summarize(n = n(), mean = mean(diff), sd = sd(diff)) %>%  
 kable(digits = 1)

|  |  |  |  |
| --- | --- | --- | --- |
| isBeddingAFirst | n | mean | sd |
| FALSE | 20 | -57.5 | 53.4 |
| TRUE | 20 | 21.2 | 18.7 |

Models.

lm(diff ~ 1, data = dfDiff) %>% tidy() %>% kable(digits = 3)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| term | estimate | std.error | statistic | p.value |
| (Intercept) | -18.179 | 8.872 | -2.049 | 0.047 |

There appears to be a significant difference in the amount of food intake at t = 36. Food intake is higher with bedding type B.

lm(diff ~ sex, data = dfDiff) %>% tidy() %>% kable(digits = 3)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| term | estimate | std.error | statistic | p.value |
| (Intercept) | -9.044 | 12.537 | -0.721 | 0.475 |
| sexM | -18.270 | 17.730 | -1.030 | 0.309 |

lm(diff ~ room, data = dfDiff) %>% tidy() %>% kable(digits = 3)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| term | estimate | std.error | statistic | p.value |
| (Intercept) | 1.960 | 14.084 | 0.139 | 0.890 |
| room0545C | -32.222 | 17.814 | -1.809 | 0.078 |

However, the difference is no longer apparent when adjusting for sex or room.

lm(diff ~ isBeddingAFirst, data = dfDiff) %>% tidy() %>% kable(digits = 3)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| term | estimate | std.error | statistic | p.value |
| (Intercept) | -57.535 | 8.947 | -6.431 | 0 |
| isBeddingAFirstTRUE | 78.712 | 12.653 | 6.221 | 0 |

The difference appears to depend on which bedding type the mouse experiences first. Mice that experience bedding type A first have higher food intakes at t = 36 with bedding type A. Mice that experience bedding type B first have higher food intakes at t = 36 with bedding type B.

This suggests that a crossover design might not be the most optimal study design for this research question.

An alternative analysis is to assume a model that ignores the cross-sectional study design. Instead, the model includes order as a fixed effect and an interaction between bedding and order. The model also includes a random intercept effect for mouse.

dfRanEff <-  
 df %>%  
 filter(time == t) %>%  
 select(id, foodIntakeNormalized, order, bedding, sex, room) %>%  
 mutate(order = factor(order))  
dfRanEff %>%  
 group\_by(bedding, order) %>%  
 summarize(n = n(), mean = mean(foodIntakeNormalized), sd = sd(foodIntakeNormalized)) %>%  
 kable(digits = 1)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| bedding | order | n | mean | sd |
| A | 1 | 20 | 143.9 | 18.3 |
| A | 2 | 20 | 85.7 | 53.1 |
| B | 1 | 20 | 143.2 | 23.6 |
| B | 2 | 20 | 122.7 | 18.8 |

lmer(foodIntakeNormalized ~ bedding + order + bedding \* order + (1 | id),   
 data = dfRanEff) %>%   
 tidy(conf.int = TRUE) %>%   
 kable(digits = 3)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| effect | group | term | estimate | std.error | statistic | conf.low | conf.high |
| fixed | NA | (Intercept) | 143.880 | 7.129 | 20.183 | 129.908 | 157.852 |
| fixed | NA | beddingB | -0.659 | 10.082 | -0.065 | -20.419 | 19.100 |
| fixed | NA | order2 | -58.194 | 10.082 | -5.772 | -77.953 | -38.435 |
| fixed | NA | beddingB:order2 | 37.676 | 15.699 | 2.400 | 6.907 | 68.445 |
| ran\_pars | id | sd\_\_(Intercept) | 14.694| NA| NA| NA| NA| |ran\_pars |Residual |sd\_\_Observation | 28.293| NA| NA| NA| NA| |

R session information.

## [1] "Run time: 2019-02-04 19:20:52"

## 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 broom.mixed\_0.2.3  
## [4] lme4\_1.1-19 Matrix\_1.2-14 svglite\_1.2.1   
## [7] broom\_0.5.1 readxl\_1.2.0 forcats\_0.3.0   
## [10] stringr\_1.3.1 dplyr\_0.7.8 purrr\_0.2.5   
## [13] readr\_1.3.1 tidyr\_0.8.2 tibble\_1.4.2   
## [16] ggplot2\_3.1.0 tidyverse\_1.2.1 magrittr\_1.5   
## [19] checkpoint\_0.4.5 rmarkdown\_1.11 knitr\_1.20   
##   
## loaded via a namespace (and not attached):  
## [1] TMB\_1.7.15 tidyselect\_0.2.5 reshape2\_1.4.3   
## [4] glmmTMB\_0.2.2.0 splines\_3.5.1 haven\_2.0.0   
## [7] lattice\_0.20-35 colorspace\_1.3-2 generics\_0.0.2   
## [10] htmltools\_0.3.6 rlang\_0.3.0.1 nloptr\_1.2.1   
## [13] pillar\_1.3.1 glue\_1.3.0 withr\_2.1.2   
## [16] RColorBrewer\_1.1-2 modelr\_0.1.2 bindr\_0.1.1   
## [19] plyr\_1.8.4 munsell\_0.5.0 gtable\_0.2.0   
## [22] cellranger\_1.1.0 rvest\_0.3.2 coda\_0.19-2   
## [25] evaluate\_0.12 labeling\_0.3 highr\_0.7   
## [28] Rcpp\_0.12.19 scales\_1.0.0 backports\_1.1.3   
## [31] jsonlite\_1.6 hms\_0.4.2 digest\_0.6.18   
## [34] stringi\_1.2.4 grid\_3.5.1 cli\_1.0.1   
## [37] tools\_3.5.1 lazyeval\_0.2.1 crayon\_1.3.4   
## [40] pkgconfig\_2.0.2 MASS\_7.3-50 xml2\_1.2.0   
## [43] lubridate\_1.7.4 minqa\_1.2.4 assertthat\_0.2.0   
## [46] httr\_1.4.0 rstudioapi\_0.8 R6\_2.3.0   
## [49] nlme\_3.1-137 compiler\_3.5.1