

Summary Graphs of NUTR630 Intake

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Contents

Analysis	1
What Majors	1
What Topics are Students Interested In?	3
Student Experience Data	5
Online Resources	5
GradeCraft Familiarity	6
Session Information	7

```
library(readr)
filename <- 'https://docs.google.com/spreadsheets/d/e/2PACX-1vSDRxu3Ur53iZVsg5Gg9nArNiKY2-xguRzoeWl-wQ5l
data <- read_csv(filename)
```

These data can be found in /Users/davebrid/Documents/GitHub/TeachingLectures/Michigan/NUTR630/Evaluation/Pre-Semester Survey/2018 in a file named <https://docs.google.com/spreadsheets/d/e/2PACX-1vSDRxu3Ur53iZVsg5Gg9nArNiKY2-SU6dmcBTgb-cQiY/pub?gid=830256665&single=true&output=csv>. This script was most recently updated on Mon Sep 3 12:11:30 2018.

Analysis

What Majors

```
library(forcats)
#grouped with most common 4

count.majors <-
  data %>%
  mutate(`Which discipline most closely matches your undergraduate degree?` = fct_lump(as.factor(data$`Which discipline most closely matches your undergraduate degree?` =
    fct_recode(`Which discipline most closely matches your undergraduate degree?`,
      "Neuroscience" = "Psychology-related (Psychology, Neuroscience, etc.)",
      "Nutrition" = "Food Quality & Safety",
      "Nutrition" = "Nutrition & dietetics (minor in biology)",
      "Nutrition" = "Dietetics",
      "Biological Sciences" = "Biochemistry")) %>%
  group_by(`Which discipline most closely matches your undergraduate degree?`) %>%
  count() %>%
  arrange(desc(n))

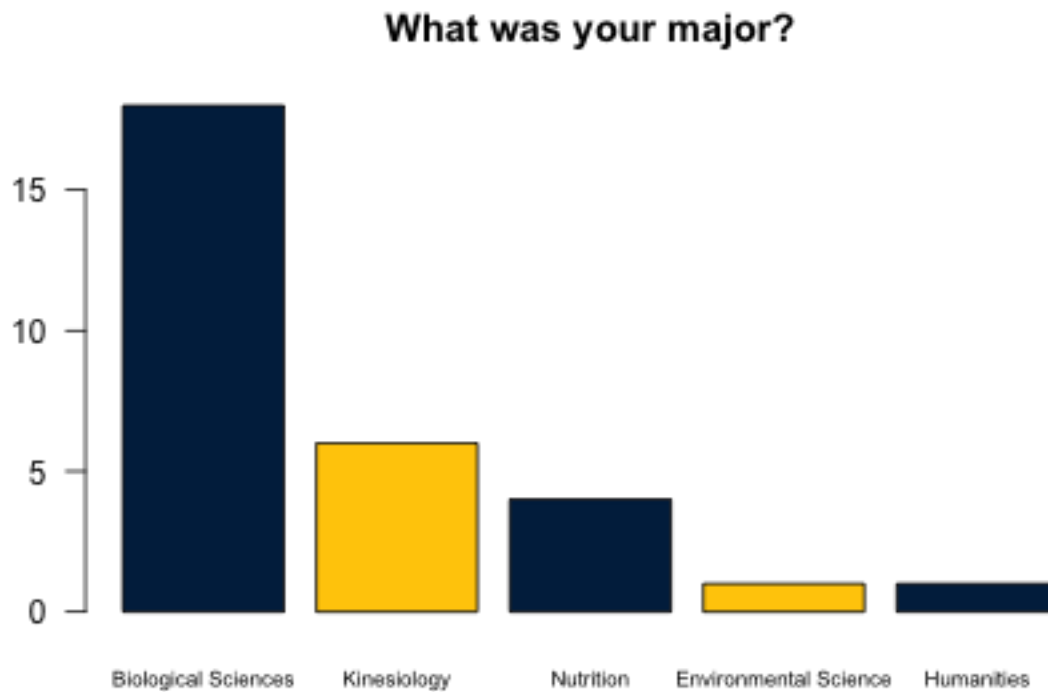
with(count.majors, barplot(n,
  las=1,
  cex.names=0.66,
```

```

main="What was your major?",
col=color.scheme,
names.arg=`Which discipline most closely matches your undergraduate degree?`)

library(ggplot2)

```

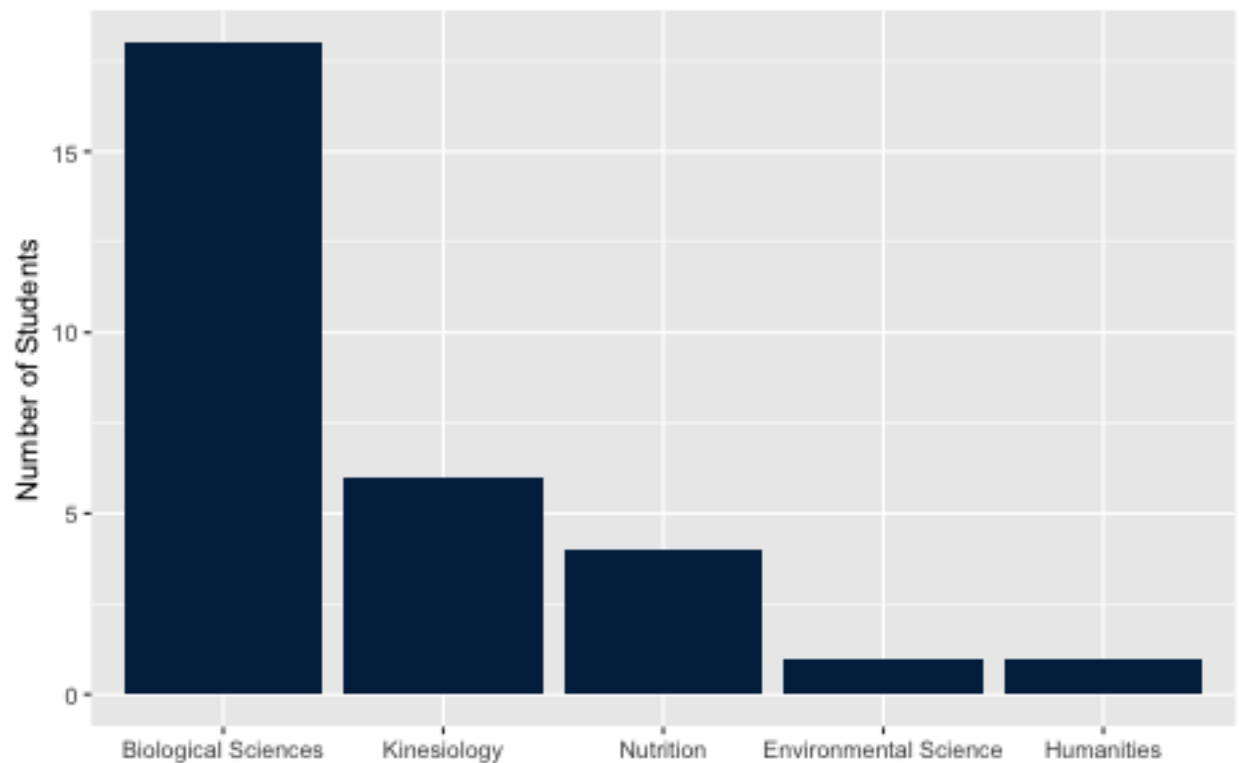


```

ggplot(count.majors,aes(y=n,x=reorder(`Which discipline most closely matches your undergraduate degree?`
  geom_bar(stat='identity',fill=color.scheme[1]) +
  labs(y="Number of Students",
    title="Which discipline most closely matches your undergraduate degree?",
    x="")

```

Which discipline most closely matches your undergraduate degree?



What Topics are Students Interested In?

```
library(sjPlot)

student.interest.data <-
  data %>%
  select(starts_with('Please answer these questions about your interests')) %>%
  rename("Biochemistry - Interest" = "Please answer these questions about your interests [Macronutrient]",
         "Biochemistry - Important" = "Please answer these questions about your interests [Macronutrient]",
         "Digestion - Interest" = "Please answer these questions about your interests [Comprehensive understanding]",
         "Digestion - Important" = "Please answer these questions about your interests [Comprehensive understanding]")
  mutate(`Biochemistry - Interest` = fct_recode(`Biochemistry - Interest`,
                                                '1'="Strongly Agree",
                                                '2'="Agree",
                                                '3'="Neutral",
                                                '4'="Disagree",
                                                '5'="Strongly Disagree")) %>%
  mutate(`Biochemistry - Important` = fct_recode(`Biochemistry - Important`,
                                                '1'="Strongly Agree",
                                                '2'="Agree",
                                                '3'="Neutral",
                                                '4'="Disagree",
                                                '5'="Strongly Disagree")) %>%
  mutate(`Digestion - Interest` = fct_recode(`Digestion - Interest`,
```

```

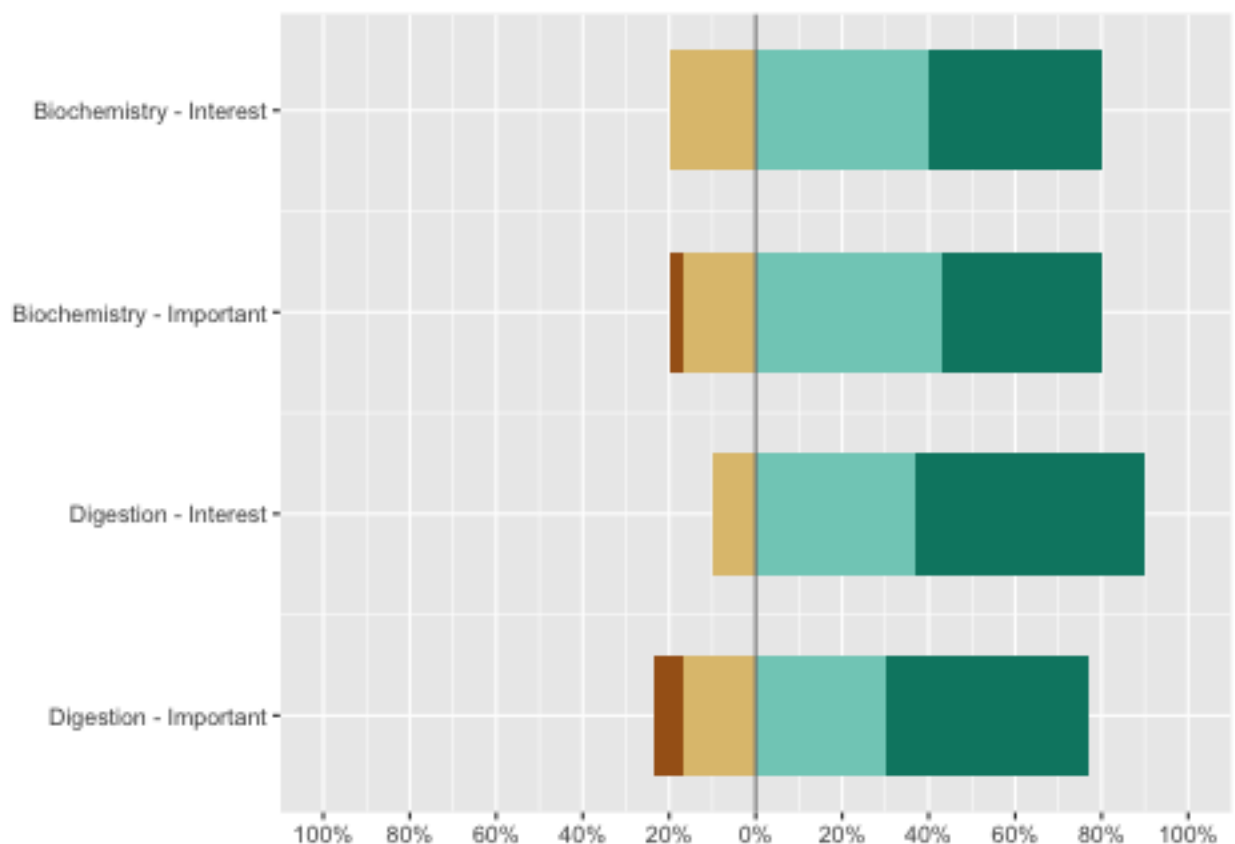
      '1'="Strongly Agree",
      '2'="Agree",
      '3'="Neutral",
      '4'="Disagree",
      '5'="Strongly Disagree")) %>%

mutate(`Digestion - Important`= fct_recode(`Digestion - Important`,
      '1'="Strongly Agree",
      '2'="Agree",
      '3'="Neutral",
      '4'="Disagree",
      '5'="Strongly Disagree")) %>%

mutate(`Biochemistry - Interest`=as.numeric(as.character(`Biochemistry - Interest`))) %>%
mutate(`Biochemistry - Important`=as.numeric(as.character(`Biochemistry - Important`))) %>%
mutate(`Digestion - Interest`=as.numeric(as.character(`Digestion - Interest`))) %>%
mutate(`Digestion - Important`=as.numeric(as.character(`Digestion - Important`)))

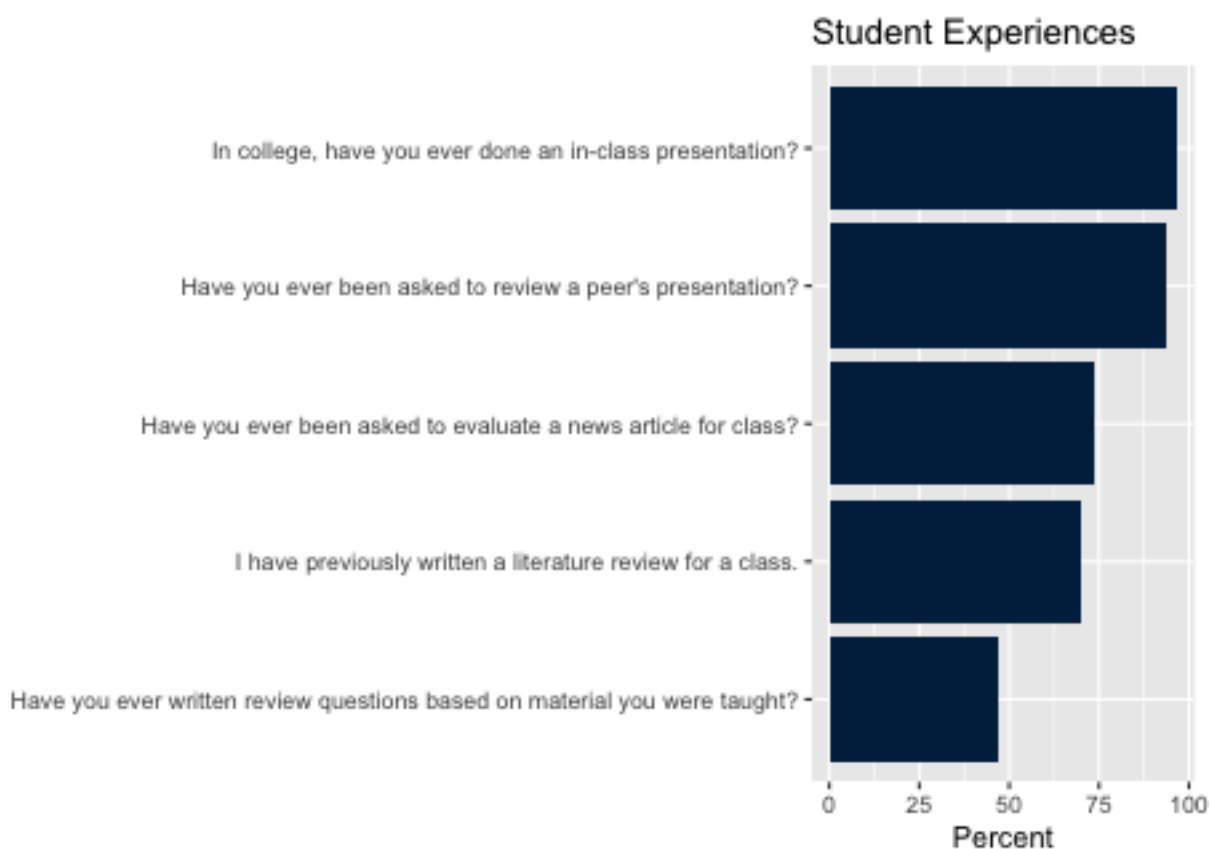
plot_likert(student.interest.data,
  sort.frq=NULL,
  values='hide',
  reverse.colors=TRUE,
  show.legend=FALSE,
  show.n=FALSE)

```



Student Experience Data

```
student.exp.data <-  
  data %>%  
    select(`I have previously written a literature review for a class.`,  
           `In college, have you ever done an in-class presentation?`, `Have you ever been asked to review a peer's  
  
countYes = function(v){length(v[v=="Yes"])}  
student.exp.data.summary <- sapply(student.exp.data, countYes)  
student.exp.data.summary <- as_tibble(student.exp.data.summary)  
student.exp.data.summary$Question <- rownames(student.exp.data.summary)  
  
ggplot(student.exp.data.summary, aes(x=reorder(Question, value), y=value/dim(student.exp.data)[1]*100)) +  
  geom_bar(stat='identity', fill=color.scheme[1]) + coord_flip() +  
  labs(x="", y="Percent", title="Student Experiences")
```

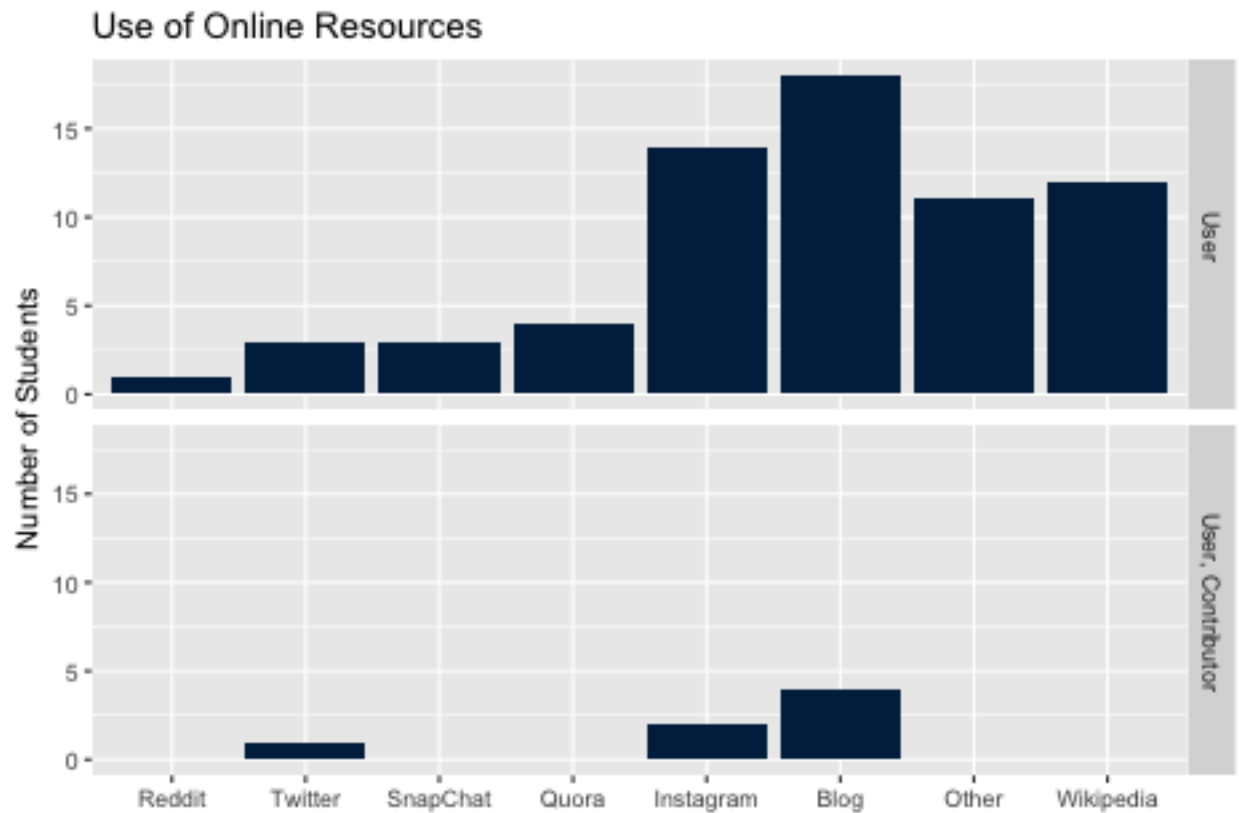


Online Resources

```
online.data <-  
  data %>%  
    select(starts_with("Which of the following online resources do you use for learning about nutrition?  
colnames(online.data) <- gsub(".*\\[|\\]", "", colnames(online.data))  
  
online.data.summary <-
```

```
gather(online.data, key="Tool", value="Use") %>%
group_by(Tool) %>%
count(Use) %>%
na.omit

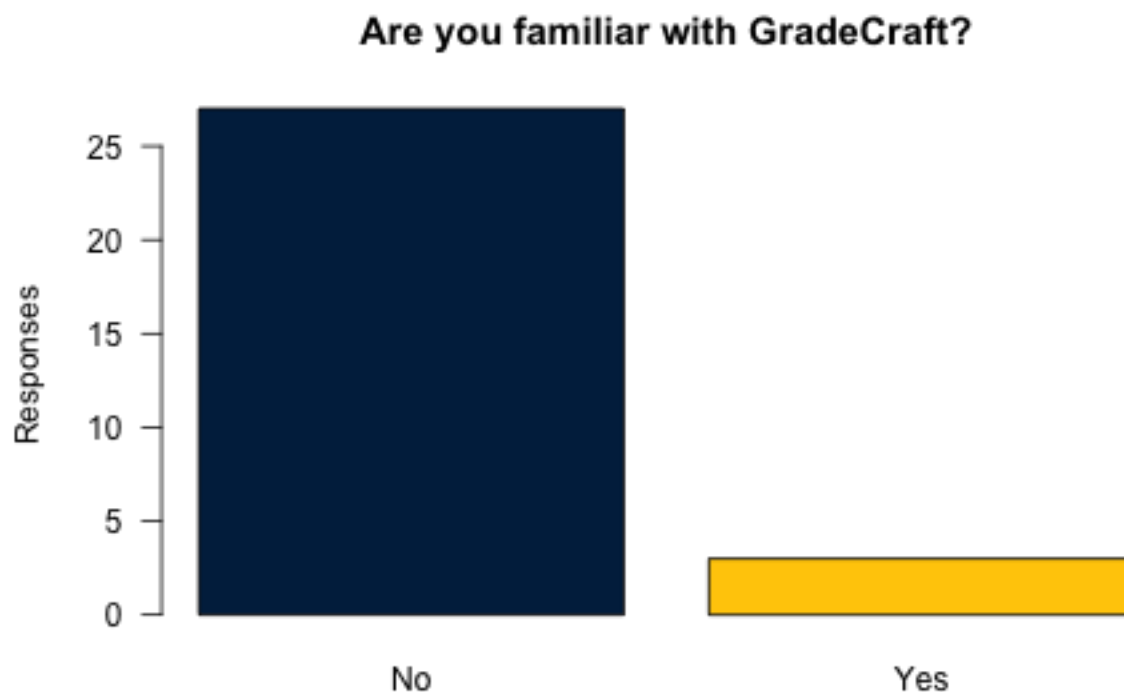
ggplot(online.data.summary, aes(y=n, x=reorder(Tool, n))) +
geom_bar(stat='identity', fill=color.scheme[1]) +
facet_grid(Use~.) +
labs(y="Number of Students", x="", title="Use of Online Resources")
```



GradeCraft Familiarity

```
gradecraft <-
data %>%
group_by(`Are you familiar with GradeCraft?`) %>%
count()

with(gradecraft, barplot(n,
las=1,
ylab="Responses",
main="Are you familiar with GradeCraft?",
col=color.scheme,
names.arg=`Are you familiar with GradeCraft?`))
```



Only 3 out of 30 students were familiar with GradeCraft.

Session Information

```
sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS High Sierra 10.13.6
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] sjPlot_2.6.0    ggplot2_3.0.0  bindrcpp_0.2.2 forcats_0.3.0
## [5] readr_1.1.1     dplyr_0.7.6    tidyr_0.8.1    knitr_1.20
##
```

```
## loaded via a namespace (and not attached):
## [1] splines_3.5.0      carData_3.0-1      modelr_0.1.2
## [4] assertthat_0.2.0   stats4_3.5.0       coin_1.2-2
## [7] yaml_2.2.0         pillar_1.3.0       backports_1.1.2
## [10] lattice_0.20-35    glue_1.3.0         digest_0.6.16
## [13] RColorBrewer_1.1-2 glmmTMB_0.2.2.0     snakecase_0.9.2
## [16] minqa_1.2.4        colorspace_1.3-2    sandwich_2.5-0
## [19] psych_1.8.4        htmltools_0.3.6     Matrix_1.2-14
## [22] survey_3.33-2      plyr_1.8.4         pkgconfig_2.0.2
## [25] broom_0.5.0        haven_1.1.2         purrr_0.2.5
## [28] xtable_1.8-2       mvtnorm_1.0-8       scales_1.0.0
## [31] stringdist_0.9.5.1 lme4_1.1-18-1       emmeans_1.2.3
## [34] tibble_1.4.2       effects_4.0-3       bayesplot_1.6.0
## [37] sjlabelled_1.0.13  TH.data_1.0-9       withr_2.1.2
## [40] TMB_1.7.14         nnet_7.3-12         lazyeval_0.2.1
## [43] mnormt_1.5-5       survival_2.42-6     magrittr_1.5
## [46] crayon_1.3.4       estimability_1.3     evaluate_0.11
## [49] nlme_3.1-137       MASS_7.3-50         foreign_0.8-71
## [52] tools_3.5.0        data.table_1.11.4   hms_0.4.2
## [55] multcomp_1.4-8     stringr_1.3.1       munsell_0.5.0
## [58] prediction_0.3.6   ggeffects_0.5.0     compiler_3.5.0
## [61] rlang_0.2.2        grid_3.5.0          nloptr_1.0.4
## [64] ggribes_0.5.0      labeling_0.3         rmarkdown_1.10
## [67] gtable_0.2.0       codetools_0.2-15    sjstats_0.17.0
## [70] curl_3.2           reshape2_1.4.3      sjmisc_2.7.4
## [73] R6_2.2.2           zoo_1.8-3           pwr_1.2-2
## [76] bindr_0.1.1        rprojroot_1.3-2     modeltools_0.2-22
## [79] stringi_1.2.4      parallel_3.5.0      Rcpp_0.12.18
## [82] tidyselect_0.2.4   coda_0.19-1
```