

# Summary Graphs of NUTR630 Intake

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```
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 10:49:39 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?`),
```

```
  mutate(`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,
```

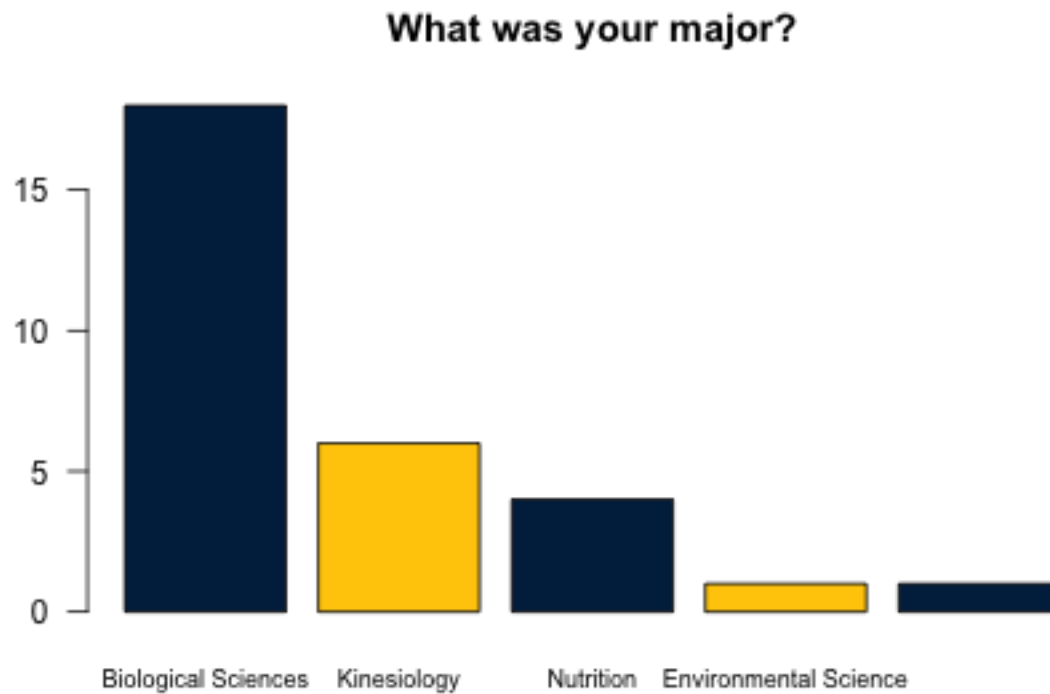
```
  las=1,
```

```
  cex.names=0.75,
```

```
  main="What was your major?",
```

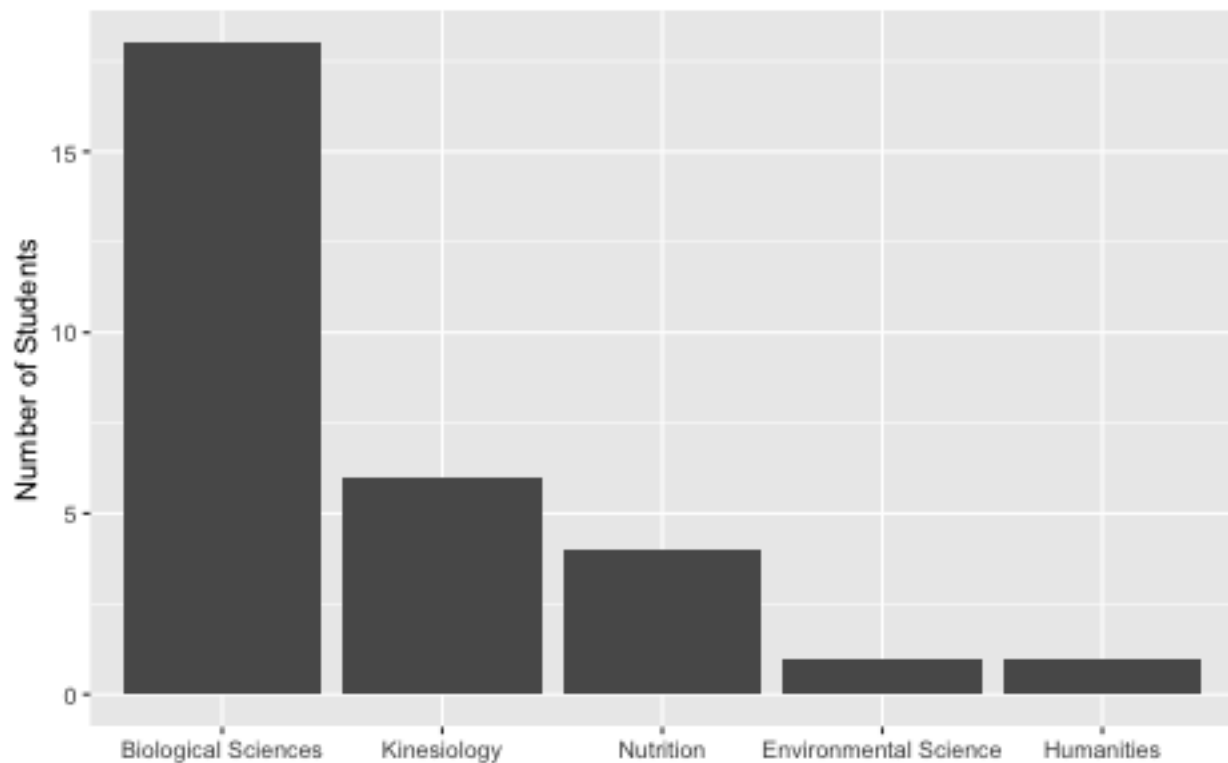
```
  col=color.scheme,
```

```
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') +
  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`,
```

```

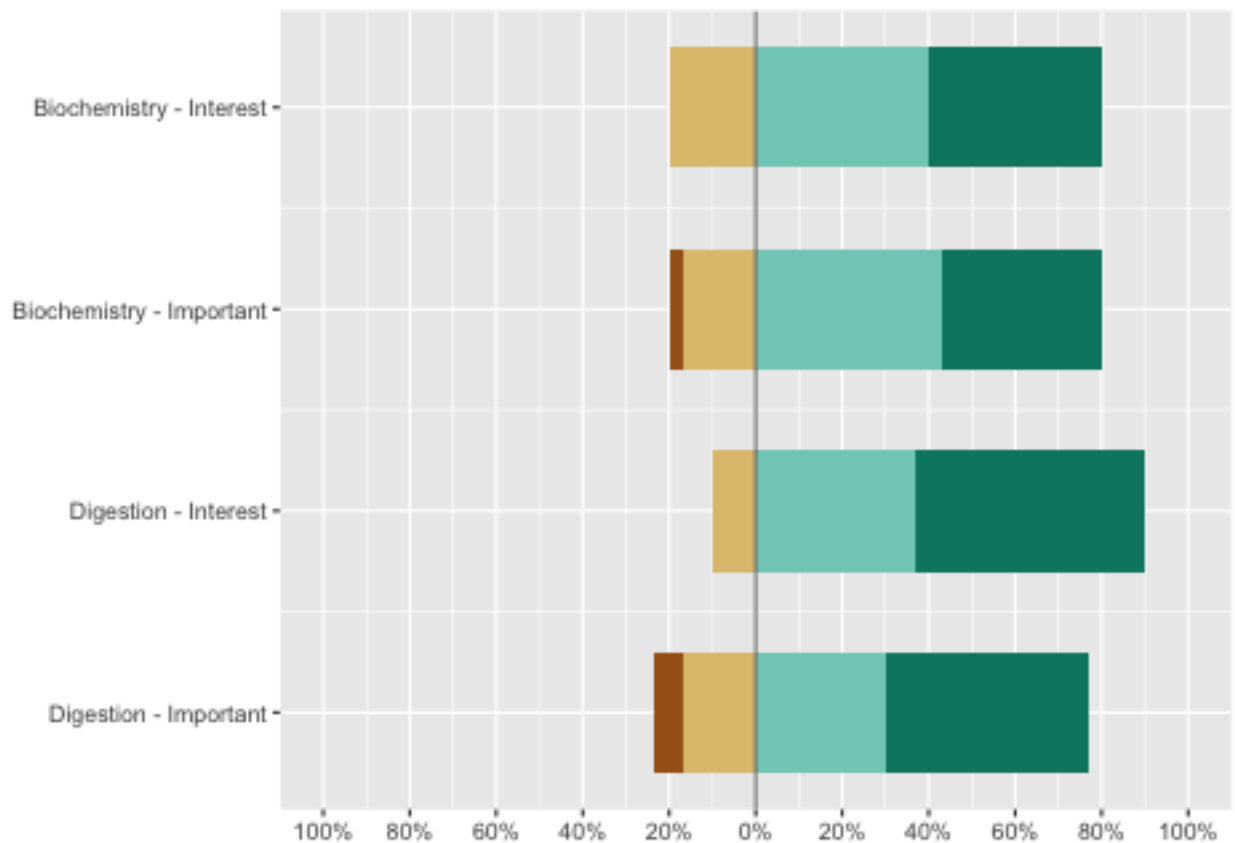
      '1'="Strongly Agree",
      '2'="Agree",
      '3'="Neutral",
      '4'="Disagree",
      '5'="Strongly Disagree")) %>%

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`)))

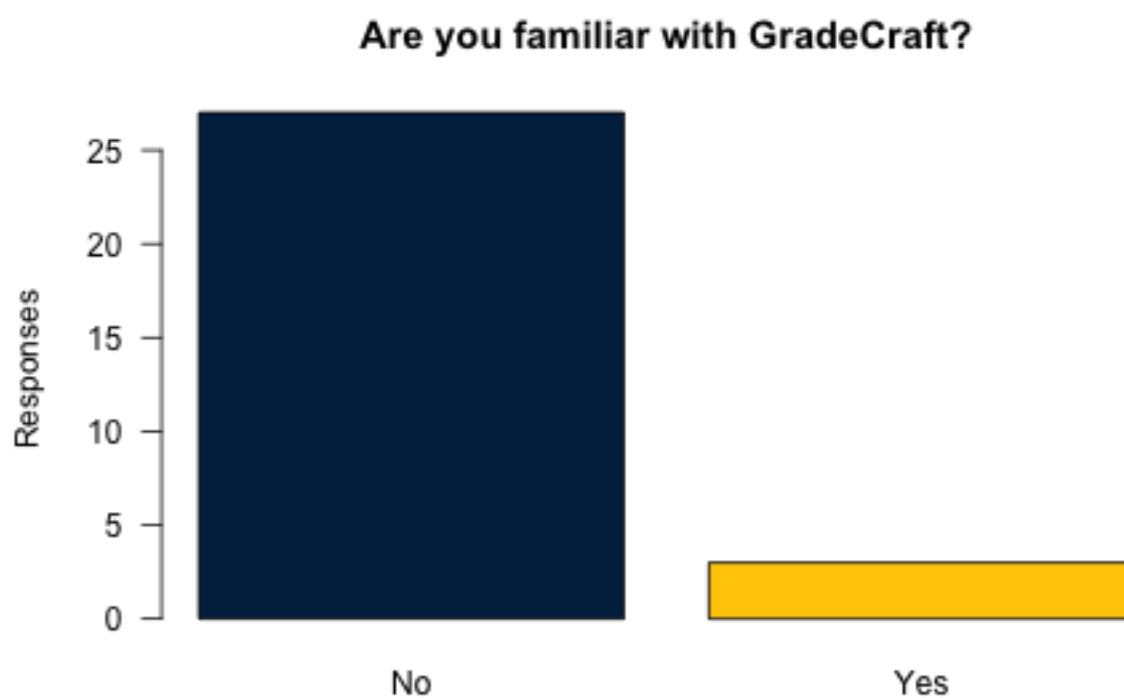
plot_likert(student.interest.data,
  sort.frq=NULL,
  values='hide',
  reverse.colors=TRUE,
  show.legend=FALSE,
  show.n=FALSE)

```



## 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          sjmisc_2.7.4       R6_2.2.2
## [73] zoo_1.8-3         pwr_1.2-2          bindr_0.1.1
## [76] rprojroot_1.3-2   modeltools_0.2-22  stringi_1.2.4
## [79] parallel_3.5.0    Rcpp_0.12.18       tidyselect_0.2.4
## [82] coda_0.19-1

```