## P8130 Assignment 1

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Assignment 1 for Biostatistics P8130, using a dataset called Antibodies, practices data manipulation and descriptive statistics (including table, histogram, and boxplot generation). The dataset contains information on demographic variables, IgM antibodies, and self-reported smell loss for patients diagnosed with COVID-19 (via the PCR gold-standard).

Let's load the appropriate packages first.

```
library(arsenal)
library(dplyr)
library(ggplot2)
library(tidyverse)
library(knitr)
options(width = 100)
```

```
# Question 1
## Question 1, Part 1, Section a)
First, read the CSV and examine the basics.
```

```r

#Read the CSV data into a dataframe

antibodies\_df <- read.csv("/Users/emilhafeez/Google Drive/Columbia/Fall 2020/Classes/Biostatistics 1/As

I examine the basics of the data, to become familiar. Results are hidden for the sake of brevity.

```
names(antibodies_df)
nrow(antibodies_df)
ncol(antibodies_df)
head(antibodies_df)
tail(antibodies_df)
anyNA(antibodies_df)
str(antibodies_df)
```

Now, we can provide descriptive statistics for all variables of interest. We can see that some variable types need manipulation, too. I suppress the code output here.

```
#Make AgeCategory, Smell, and Gender to show N (%). Requires ensuring all unique values, too.
unique(antibodies_df$AgeCategory)
   antibodies_df <- antibodies_df %>%
        mutate(AgeCategory = factor(AgeCategory, labels = c("18-30", "31-50", "51+") ))
unique(antibodies_df$Smell)
   antibodies_df <- antibodies_df %>%
        mutate(Smell = factor(Smell, labels = c("Normal", "Altered", "Other")))
```

```
unique(antibodies_df$Gender)
   antibodies_df <- antibodies_df %>%
       mutate(Gender = factor(Gender, labels = c("Male", "Female")))
#To prepare a tidy table, let's change variable names/labels by creating a my_labels variable that will
my_labels <- list(AgeCategory = "Age Range (Years)", Antibody_IgM = "Antibody_Levels(IgM)", Smell = "Sm
#Clean the output by creating a my_controls variable that will modify the tableby() command
my_controls <- tableby.control(</pre>
             total = TRUE,
              test = FALSE,
              numeric.stats = c("meansd", "medianq1q3", "range", "Nmiss2"),
              cat.stats = c("countpct", "Nmiss2"),
              stats.labels = list(
              meansd = "Mean (SD)",
              medianq1q3 = "Median (Q1, Q3)",
              range = "Min - Max",
              Nmiss2 = "Missing",
              countpct = "N (%)"))
#Making a table
table_1 <- tableby( ~ AgeCategory + Antibody_IgM + Smell + Gender, data = antibodies_df, control = my_c
summary(table_1, title = "Descriptive Statistics: Antibodies & Smell Data", labelTranslations = my_labe
##
## Table: Descriptive Statistics: Antibodies & Smell Data
                             | Overall (N=1491)
## |:----:|
## |Age Range (Years)
                                 318 (21.3%)
## |- 18-30
                             ## I- 31-50
                              1
                                810 (54.3%)
## |- 51+
                             | 363 (24.3%)
## |- Missing
## |Antibody Levels(IgM)
                             ## |- Mean (SD)
                             0.124 (0.110)
                           | 0.091 (0.069, 0.129) |
## |- Median (Q1, Q3)
## |- Min - Max
                             0.048 - 1.048
## |- Missing
                                       1224
## |Smell Changes (Self Report) |
## |- Normal
                                  1047 (70.2%)
## |- Altered
                                  410 (27.5%)
                              1
## |- Other
                              34 (2.3%)
## |- Missing
  Ω
## |Gender (M/F)
                             ## |- Male
                                  981 (65.8%)
                             ## |- Female
                             510 (34.2%)
   1
## |- Missing
  0
   Ι
table_1
## tableby Object
##
## Function Call:
## tableby(formula = ~AgeCategory + Antibody_IgM + Smell + Gender,
```

```
## data = antibodies_df, control = my_controls)
##
## Variable(s):
## Overall ~ AgeCategory, Antibody_IgM, Smell, Gender
```

## Question 1, Part 1, Section b)

## Question 1, Part 2, Section a)

Let's display the descriptive statistics for all variables, this time stratified by Smell category

```
table_2 <- tableby( Smell ~ AgeCategory + Antibody_IgM + Smell + Gender, data = antibodies_df, control summary(table_2, title = "Descriptive Statistics: Antibodies & Smell Data", labelTranslations = my_labe
```

## Table: Descriptive Statistics: Antibodies & Smell Data ## ## | Normal (N=1047) Altered (N=410) Other (N=34) Tota ## |Age Range (Years) ## |- 18-30 245 (23.4%) 66 (16.1%) 7 (20.6%) 318 ## |- 31-50 23 (67.6%) 810 572 (54.6%) 215 (52.4%) ## |- 51+ 230 (22.0%) 129 (31.5%) 4 (11.8%) 363 ## |- Missing 0 0 0 ## |Antibody Levels(IgM) 0.110 (0.092) ## |- Mean (SD) 0.130 (0.119) 0.116 (0.068) 0.12 | 0.097 (0.072, 0.137) | 0.081 (0.065, 0.107) | 0.095 (0.083, 0.119) | 0.091 ( ## |- Median (Q1, Q3)