Title Here

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Abstract

Brief abstract here.

Introduction

Introduction for applied/clinical research study.

If you end up wanting to use an external reference system, one option is to create a .bib file (used often in LaTeX for references). You can export Google Scholar references as a BiBTeX entry to add to your .bib reference file. In the YAML header of this document you see:

bibliography: kaizer_simulation_sample1.bib
csl: alex_vancouver.csl

Change the bibliography file to your own file. The .csl file controls the style of the formatting (e.g., Vancouver, APA, MLA, etc.). You can use the alex_vancouver.csl file or download another file of your choosing to use. To reference the .bib file entries in the text, use square brackets with @ to add the reference in question: [@student1908probable; @wiki_Students_t-test] creates.^{1,2}

If you are not using a .bib file (e.g., manually entering your references by hand or just using footnotes), remove the bibliography and csl lines from the YAML header, as well as the chunk of code towards the end of the document that generates the references.

Hypothesis (or Research Question)

Brief description of the research question and/or hypothesis to be examined.

Materials and Methods

Describe how the data was collected. For example, what type of study was it (observational versus randomized; cohort versus cross-sectional versus case-control; etc.)? Where did the study take place? Were there certain sponsors (e.g., NIH, an industry group or company, etc.)?

Analysis Plan (or Statistical Methods)

This is sometimes included as a subsection of the "Materials and Methods" (or "Methods") section, but we can

also set it as its own section. We want to describe how we will be summarizing and analyzing the data. For example, do you report continuous variables as mean (standard deviation), median (1st quartile, 3rd quartile), median (interquartile range), median (minimum, maximum), etc.? Are categorical variables presented as N (%), % (N), etc.? What statistical methods were used to answer your research question(s)? How did you (briefly) evaluate any assumptions (e.g., graphical, a formal test, both)? What software and version did you use?

Results

Write your results in this section. The interpretation or implications of results will primarily appear in the following Discussion/Conclusion section.

For creating Table 1's, you may also use something like the tableone package:

Table 1: Descriptive Summary of Sample

	Budesonide	Nedocromil	Al
n	210	210	
Gender = Female (%)	84 (40.0)	70(33.3)	12
Race/Ethnicity (%)			
White	142 (67.6)	143 (68.1)	19
Black	27(12.9)	27(12.9)	34
Hispanic	20 (9.5)	23 (11.0)	25
Other	$21\ (10.0)$	17 (8.1)	21
Age (yrs) (mean (SD))	8.51(2.14)	8.30(2.17)	8.3
Hemoglobin (g/dl) (mean (SD))	$13.11 \ (1.27)$	$13.11 \ (1.29)$	13.

Here we see that our table is too wide and bleeds over. One option is to make the table font smaller (but check for readability):

Table 2: Descriptive Summary of Sample

	Budesonide	Nedocromil	Albuterol
n	210	210	274
Gender = Female (%)	84 (40.0)	70 (33.3)	128 (46.7)
Race/Ethnicity (%)			
White	142 (67.6)	143 (68.1)	194 (70.8)
Black	27 (12.9)	27 (12.9)	34 (12.4)
Hispanic	20 (9.5)	23 (11.0)	25 (9.1)
Other	21 (10.0)	17 (8.1)	21 (7.7)
Age (yrs) (mean (SD))	8.51 (2.14)	8.30 (2.17)	8.33 (2.17)
Hemoglobin (g/dl) (mean (SD))	13.11 (1.27)	13.11 (1.29)	13.15 (0.95)

Another option is to place tables and/or figures on their own page with a single column (e.g., make page 2 one column and revert back to two columns for page 3; make the 3rd page for your tables/figures that don't fit nicely in the text).

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Here we see the results for "Table 1," describing our sample, but formatted to only include one column:

Table 3: Descriptive Summary of Sample

	Budesonide	Nedocromil	Albuterol
n	210	210	274
Gender = Female (%)	84 (40.0)	70(33.3)	128 (46.7)
Race/Ethnicity (%)			
White	142 (67.6)	143 (68.1)	194 (70.8)
Black	27(12.9)	27(12.9)	34 (12.4)
Hispanic	20 (9.5)	$23\ (11.0)$	25 (9.1)
Other	$21\ (10.0)$	17 (8.1)	21 (7.7)
Age (yrs) (mean (SD))	8.51 (2.14)	8.30(2.17)	8.33(2.17)
Hemoglobin (g/dl) (mean (SD))	$13.11\ (1.27)$	$13.11 \ (1.29)$	$13.15 \ (0.95)$

An example of a figure is below. In the Rmd file, the chunk-name can be changed to whatever you want so that it can be referenced using \ref{tab:chunk-name} (where "tab" represents a table, "fig" is for a figure).

NOTE: the code chunks have echo=F to suppress the code from appearing in your limited 3 page report. It can still automatically appear at the end in the appendix with a nifty line of code that appears at the end!

Histogram of rnorm(100)

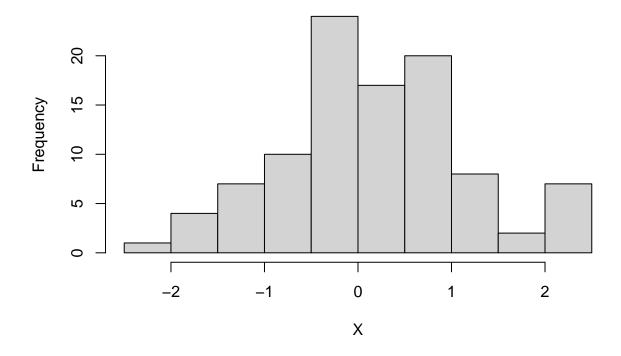


Figure 1: Caption for Figure

One example you can use to create a table in our PDF output example here is with the kableExtra package:

Table 4: Descriptive Summary of Sample

	Column 1 of Results	Column 2 of Results
Row 1	1	5
Row 2	2	6
Row 3	3	7
Row 4	4	8

Discussion (or Conclusion)

Write your conclusion here where you interpret the results for your given context, including any limitations.

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Eos ei justo doctus concludaturque. Per cu civibus mediocritatem, erant nullam populo eam et. Eum persius incorrupte ei, antiopam iudicabit instructior eum id. Qui ut zril eruditi disputando, nam ei molestie gloriatur, ex eos diceret recusabo necessitatibus. Ei vis idque delenit commune, malis aliquando philosophia sea ut.

There are some limitations with the given study. One is the discussion was written in Latin instead of English. Another is that data collection of potential confounders had high levels of missingness, which may lead to additional uncertainty for their effects. For the given project, certain models or methods may ultimately be more appropriate for the chosen research question but were not covered in the scope of BIOS 6611 (this would not be a reasonable limitation in a real paper, but for our class project it can very well be true!).

References

- 1. Student. The probable error of a mean. Biometrika 1908:1–25.
- 2. Wikipedia. Student's t-test Wikipedia, the free encyclopedia 2021.

Code Appendix

```
knitr::opts_chunk$set(echo = TRUE)
library(kableExtra) # load for tables
library(tableone)
library(labelled)
dat <- read.csv('camp_teach_project.csv')</pre>
# rename variables to have informative labels
dat$GENDERf <- factor(dat$GENDER,</pre>
                       levels=c('m','f'),
                       labels=c('Male','Female'))
dat$ETHNICf <- factor(dat$ETHNIC,</pre>
                       levels=c('w','b','h','o'),
                       labels=c('White','Black','Hispanic','Other'))
# create Table 1
variables <- c('GENDERf','ETHNICf','age_rz','hemog')</pre>
cat_vars <- c('GENDERf','ETHNICf')</pre>
strata <- 'TG'
# Modify labels
var_label(dat$GENDERf) <- 'Gender'</pre>
var_label(dat$ETHNICf) <- 'Race/Ethnicity'</pre>
var_label(dat$age_rz) <- 'Age (yrs)'</pre>
var_label(dat$hemog) <- 'Hemoglobin (g/dl)'</pre>
tab1 <- CreateTableOne(vars = variables,</pre>
                        factorVars = cat vars,
                        strata = strata,
                        test = FALSE,
                        data=dat)
tab1_forkbl <- print(tab1, varLabels=T, printToggle = F)</pre>
kbl(tab1_forkbl,
     caption = 'Descriptive Summary of Sample',
     booktabs=T, align='ccc',
     col.names = c('Budesonide','Nedocromil','Albuterol')) %>%
 add_indent(4:7) %>%
 kable_styling(latex_options = "HOLD_position")
kbl( tab1 forkbl,
     caption = 'Descriptive Summary of Sample',
     booktabs=T, align='ccc',
     col.names = c('Budesonide','Nedocromil','Albuterol')) %>%
  add indent(4:7) %>%
 kable_styling(latex_options = "HOLD_position", font_size = 4.5)
```

```
# ADDED font_size ARGUMENT AND MADE MUCH SMALLER
kbl( tab1_forkbl,
     caption = 'Descriptive Summary of Sample',
     booktabs=T, align='ccc',
     col.names = c('Budesonide','Nedocromil','Albuterol')) %>%
 add_indent(4:7) %>%
 kable styling(latex options = "HOLD position")
# Create figure to demonstrate something graphically
set.seed(515) # set seed to reproduce example figure
hist(rnorm(100), xlab='X')
# Extract results for null case and scenario with expected 80% power
tab_res <- matrix(1:8, nrow=4, ncol=2) # made up matrix with results
rownames(tab_res) <- c('Row 1','Row 2','Row 3','Row 4')</pre>
# Create table of results
kbl(tab_res,
    caption = 'Descriptive Summary of Sample',
   booktabs=T, align='cc',
   col.names = c('Column 1 of Results','Column 2 of Results')) %>%
   collapse_rows(columns=1, latex_hline='major', valign='middle') %>%
   kable_styling(latex_options = "HOLD_position")
```