

# Coronavirus in the Southeast

STAT 3480 Consulting Project

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## **Executive Summary**

# Introduction

## Project Description

- Restate the client's research problem (for clarification)
- Put the data and the research question in context.
- Why is the client's research relevant?
- Has this research question been studied previously?

## Data Summary & Discussion

- How was the data collected? – What is the sampling/ experimental design? – What are some potential biases?
- What variables are measured? What are the units?
- How large is the dataset?
- Some basic summary statistics and graphs of the data should be presented. (These basic distributions will be relevant for the methodology.)

## Methodology

- What variables are measured? What are the units?
- How large is the dataset?
- Some basic summary statistics and graphs of the data should be presented. (These basic distributions will be relevant for the methodology.)

## Results

- Test statistics
- P-values
- Confidence intervals
- Inference decisions (conclusions)

## Discussion

- Interpret and discuss the significance of the analysis results.
- Substantiate any conclusions with results.
- Tell the story of how you answered your client's research question(s).
- Discuss the limitations of the study (which can pertain to data, data collection, or methodology).
- Make sure to be delicate – the client doesn't want to hear what a bad job they've done.

## Conclusion

- The goal of this section is to address the client's bottom line: what does your progress mean for his/her research problem?

# Appendix

## Code

```
library(readr)
library(dplyr)
```

```
covid_data <- readr::read_csv("covid-data.csv") %>% as_tibble()
covid_data$Mask.Mandate <- dplyr::if_else(covid_data$Mask.Mandate.Start.Date == 'None',
                                          true=0, false=1) %>% as.factor()
covid_data %>% head()
```

```
## # A tibble: 6 x 8
##   State Total.Cases Total.Deaths Death.Rate.Pct Population.Esti~ Cases.Per.1000
##   <chr>      <dbl>      <dbl>      <dbl>      <dbl>      <dbl>
## 1 Alab~    186437      2892      1.55      4903185      38.0
## 2 Arka~    107679      1857      1.72      3017804      35.7
## 3 Flor~    776215     16505      2.13     21477737      36.1
## 4 Geor~    353372      7844      2.22     10617423      33.3
## 5 Kent~     99637      1428      1.43     4467673      22.3
## 6 Loui~    184724      5872      3.18     4648794      39.7
## # ... with 2 more variables: Mask.Mandate.Start.Date <chr>, Mask.Mandate <fct>
```

## Big Q1

```
mask.sample1 <- covid_data %>%
  filter(Mask.Mandate == 1) %>% pull(Cases.Per.1000)
mask.sample2 <- covid_data %>%
  filter(Mask.Mandate == 0) %>% pull(Cases.Per.1000)
```

```
wilcox.test(mask.sample1, mask.sample2, alternative="less")
```

```
##
##   Wilcoxon rank sum exact test
##
## data:  mask.sample1 and mask.sample2
## W = 14, p-value = 0.183
## alternative hypothesis: true location shift is less than 0
```

## Big Q2

```
case.rate <- covid_data$Cases.Per.1000
death.rate <- covid_data$Death.Rate.Pct
```

```

r.obs<-cor(rank(case.rate), rank(death.rate))

source("http://www4.stat.ncsu.edu/~lu/ST505/Rcode/functions-Ch5.R")
perm.r<-perm.approx.r(rank(case.rate),rank(death.rate),2000)

p.upper<-mean(perm.r >= r.obs)
p.lower<-mean(perm.r <= r.obs)
p.two.sided<-mean(abs(perm.r) >= abs(r.obs))

paste("Spearman's Correlation:", round(r.obs,4)) %>% print()

```

```
## [1] "Spearman's Correlation: 0.3022"
```

```
paste("p-value:", round(p.upper,3)) %>% print()
```

```
## [1] "p-value: 0.154"
```

```

tau.obs<-getTau(case.rate,death.rate)

perm.tau<-perm.approx.tau(case.rate,death.rate,2000)

p.upper.tau<-mean(perm.tau >= tau.obs)
p.lower.tau<-mean(perm.tau <= tau.obs)
p.two.sided.tau<-mean(abs(perm.tau) >= abs(tau.obs))

paste("Kendall's Tau:", round(tau.obs,4)) %>% print()

```

```
## [1] "Kendall's Tau: 0.2564"
```

```
paste("p-value:", round(p.upper.tau,3)) %>% print()
```

```
## [1] "p-value: 0.124"
```

## Figures

*Figure 1.* Distribution of Case Rates (per 1000), by State Mask Mandates

